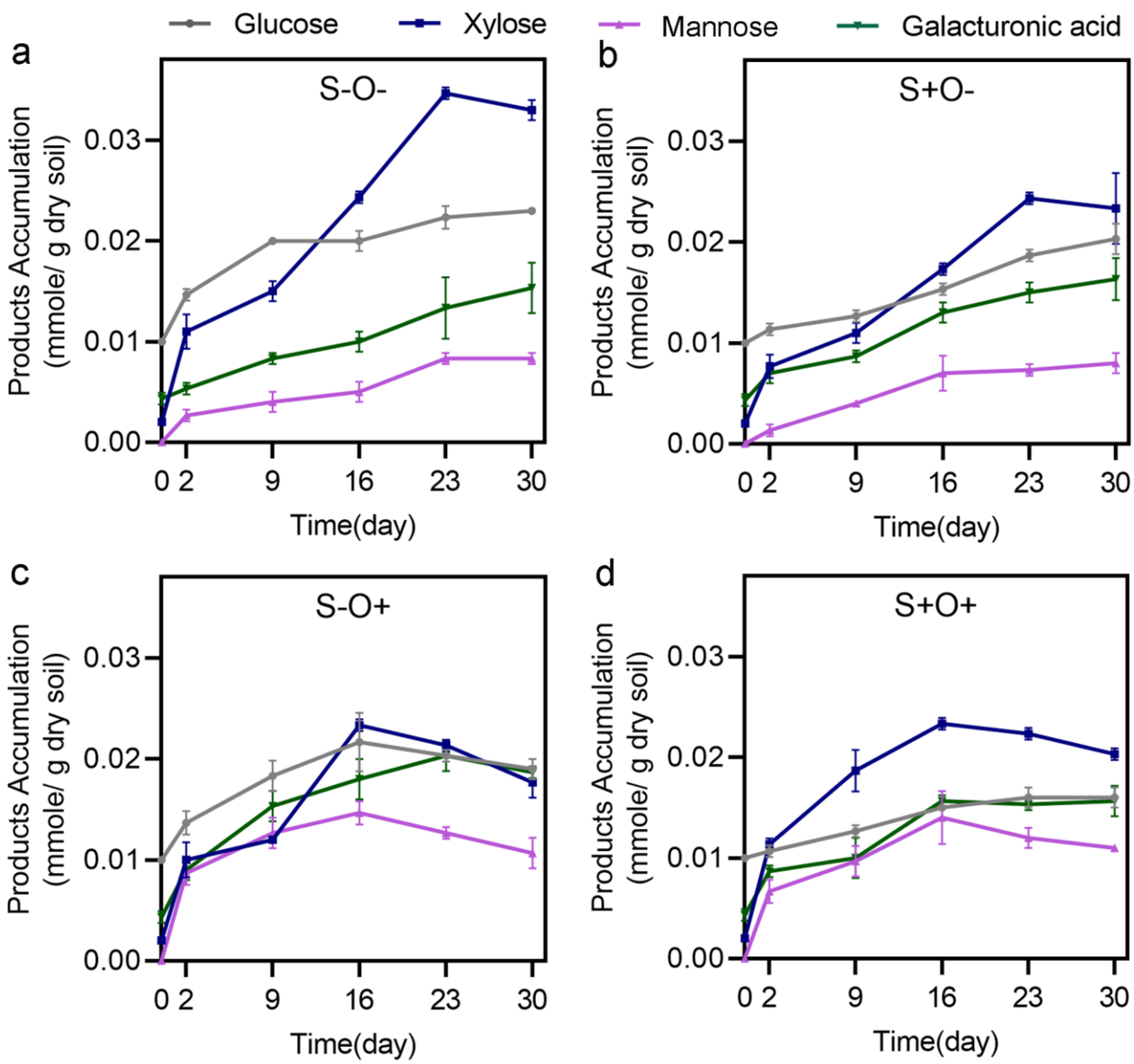
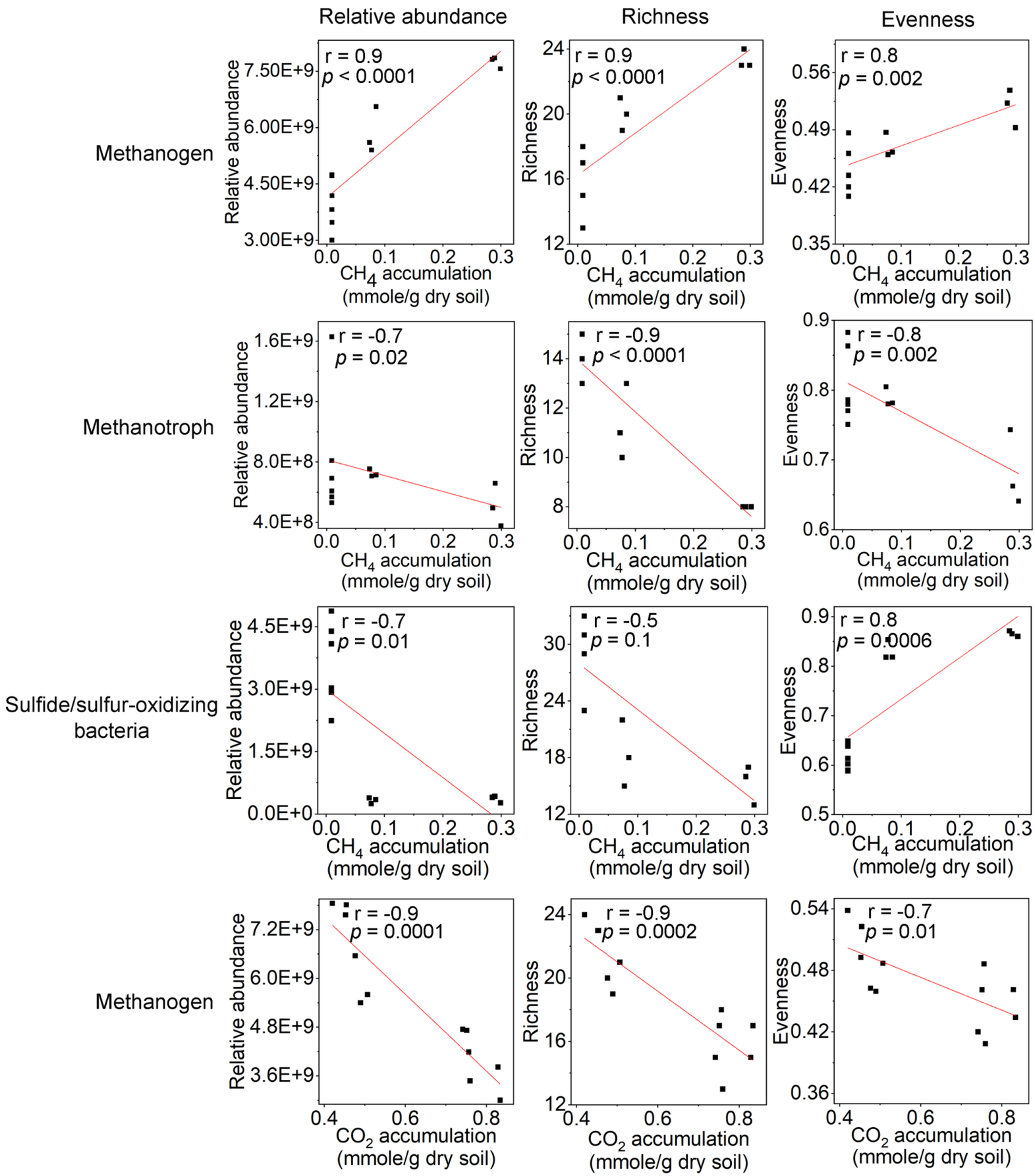


Supplementary Fig. 1: Accumulation of monosaccharides over a 30-day incubation under the four conditions. The error bars are defined as standard deviation.



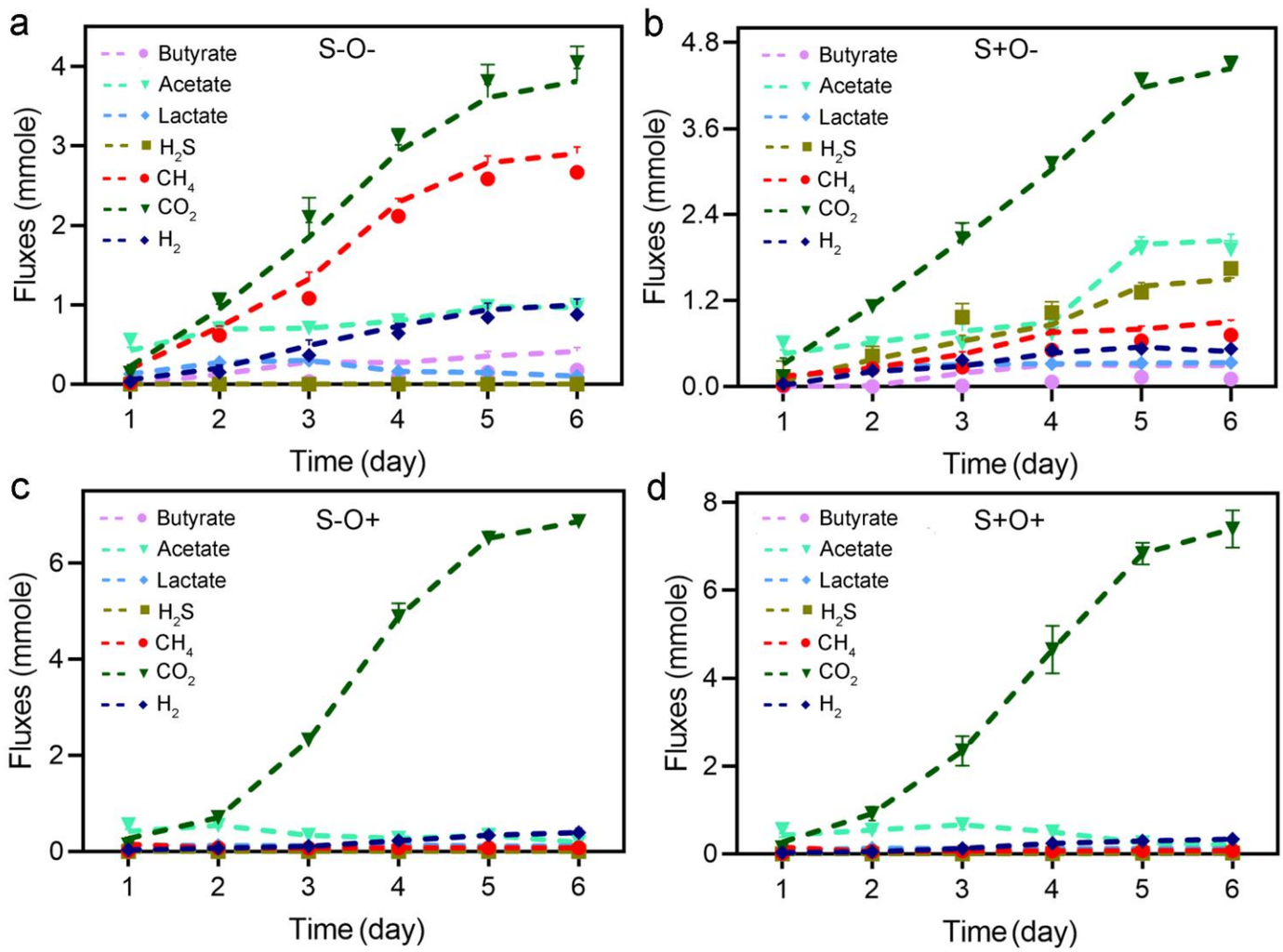
Supplementary Fig. 2: Correlation between the accumulations of CH_4 and CO_2 , and the proteome abundance, richness, and evenness of methanogen, methanotroph, and sulfide/sulfur-oxidizing bacterial communities. Each dot represents an experimental measurement (X-axis for geochemical measurements, Y-axis for metaproteomic measurements) from the four conditions with three replicates, and the red line displays best linear fit. r is the Pearson correlation coefficient, and *p* values were determined by t-test.

Reactions

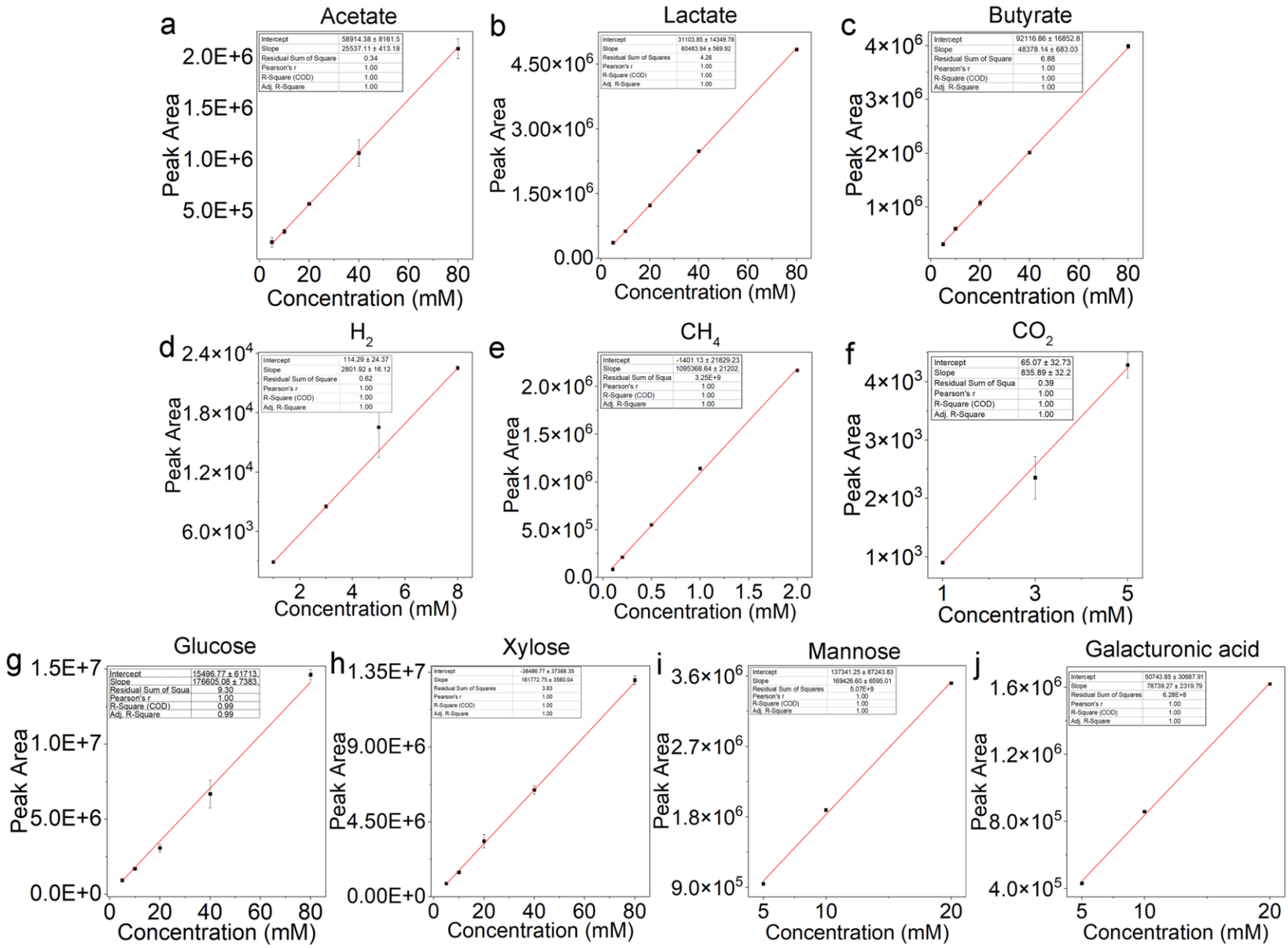
Glucose	Hydrogen	Carbon deoxide	Methane	Sulfide	Lactate	Acetate	Butyrate	
-1	0	6	0	0	0	0	0	Aerobic heterotroph
-1	0	0	0	0	2	0	0	Lactate fermentation
-1	4	2	0	0	0	2	0	Hydrogenic acetogenesis
0	0	1	0	0.5	-1	1	0	Sulfidogenic lactate oxidation
0	-2	0	0	0.5	0	0	0	Sulfidogenic hydrogen oxidation
0	-4	-1	1	0	0	0	0	Hydrogenic methanogenesis
0	0	1	1	0	0	-1	0	Acetoclastic methanogenesis
0	0	1	-1	0	0	0	0	Methane oxidation
-1	2	2	0	0	0	0	1	Butyrate production

Metabolites

Supplementary Fig. 3: The stoichiometric matrix in modeling analysis. Each matrix element is the stoichiometric coefficient of a metabolite in a reaction. Positive values correspond to the amounts of metabolites produced by the reaction. Negative values denote consumption. A value of zero indicates no involvement of metabolites in the reaction.



Supplementary Fig. 4: Model fitting and average fluxes under four conditions. (a-d) Modeling fitting in the S-O- (A), S+O- (B), S-O+ (C) and S+O+ (D) conditions. The resulting fits indicate the relative contribution of each reaction to the overall observed transformations. Deviations between the inferred metabolic transformations and the measured transformations indicate uncertainty in the understanding of metabolic transformations or limitations in analytical capacity.



Supplementary Fig. 5: Calibration curves of known standards.

Supplementary Table 1. Main functional guilts involved in methane metabolism and sulfate reduction.

Category	Species	Total proteome abundance											
		S-O-_1	S-O-_2	S-O-_3	S+O-_1	S+O-_2	S+O-_3	S-O+_1	S-O+_2	S-O+_3	S+O+_1	S+O+_2	S+O+_3
Methanogenesis	*Methanocella arvoryzae*	0.00	91120000.00	176782000.00	0.00	29252000.00	152051000.00	0.00	0.00	0.00	0.00	0.00	0.00
	Methanofollis fontis	11910000.00	46668400.00	0.00	15105000.00	27768800.00	20827600.59	24829200.00	21191400.00	24664500.00	11627000.00	14616800.00	13957500.00
	Methanofollis formosanus	84370000.00	9860000.00	4050717.44	43120500.00	37904000.00	37938709.50	32148000.00	21697700.00	23878800.00	19866000.00	17248000.00	20505000.00
	Methanomassiliicoccus luminyensis	358042738.00	331411600.00	345792201.60	267159000.00	224076500.00	285866559.30	71599054.32	65782400.00	45167682.51	22684200.00	31213600.00	8719049.25
	Methanoregula boonei	502717086.00	479540987.80	553420295.50	164136561.60	335738800.00	511337218.80	284195383.40	175885355.30	269216143.30	274182212.20	196811289.80	308598063.00
	Methanoregula formicica	1528983905.00	859756668.60	795420299.40	624551249.60	669905968.30	645203645.70	745692334.90	491797813.00	611151735.20	811158168.60	736824593.10	780961158.80
	Methanosarcina barkeri	0.00	277708.60	2616542.50	15409000.00	19668959.31	16232952.85	0.00	4300500.00	5653800.00	0.00	0.00	0.00
	Methanosarcina horonobensis	5210000.00	4753200.00	0.00	6146500.00	9918900.00	0.00	1645685.76	1573800.00	5337900.00	0.00	0.00	0.00
	Methanosarcina lacustris	0.00	0.00	0.00	6773500.00	9774700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Methanosarcina mazei	0.00	0.00	0.00	5424500.00	7210000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Methanosarcina spelaei	5640000.00	9934800.00	15520750.22	46879085.70	37257696.63	84866435.92	12790800.00	28026737.92	77138814.24	2895200.00	3062400.00	1740000.00
	Methanosarcina thermophila	0.00	0.00	0.00	3714500.00	3852200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Methanosarcina vacuolata	1002666.00	0.00	4738635.88	0.00	6756800.00	11487877.84	0.00	0.00	0.00	0.00	0.00	0.00
	Methanosphaerula palustris	293107853.00	60805600.00	236966700.00	643618678.70	111652000.00	396291486.00	153056400.00	121935957.30	312984000.00	152806500.00	27024800.00	38287500.00
	Methanospirillum lacunae	46830000.00	47893381.24	15631959.61	25194000.00	49666600.00	6832747.15	0.00	23676305.15	17172000.00	24891642.16	29103807.04	8249915.25
	Methanospirillum stamsii	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1836100.00	1660500.00	1424500.00	2103200.00	0.00
	Methanothrix harundinacea	62990000.00	40560034.80	35300100.00	34960000.00	12555700.00	38630902.82	7159200.00	2409500.00	5783400.00	2810500.00	22668800.00	6307500.00
	Methanothrix soehngenii	4523979093.00	5583763208.00	5220457833.00	4443857291.00	3826816195.00	2957875714.00	3370593032.00	3094589394.00	3218587908.00	2393909811.00	2365878057.00	1763694120.00
	Methanothrix thermoacetophila	391700000.00	287927037.50	160407612.30	214282000.00	185358800.00	239176326.20	45878132.64	135639600.00	106516178.60	102618076.30	34126218.72	54186612.00
Methanotroph	*Methylobacillus arboreus*	17109400.00	11545600.00	5167500.00	0.00	0.00	0.00	3008133.96	868658.91	527842.98	0.00	0.00	0.00
	Methylobacillus gramineus	0.00	0.00	0.00	3344000.00	0.00	393690.61	0.00	0.00	0.00	8720000.00	9016800.00	5621521.22
	Methylobacillus rhizosphaerae	17440500.00	28520800.00	47610000.00	0.00	0.00	0.00	2599200.00	4074800.00	10481400.00	0.00	0.00	0.00
	Methylobacter luteus	3680600.00	0.00	7072500.00	0.00	0.00	0.00	0.00	5984100.00	3888000.00	21080000.00	12702400.00	0.00
	Methylobacter psychrophilus	59197600.00	17177600.00	17107500.00	13985447.80	17777800.00	2013079.81	25057200.00	34251500.00	13856598.72	49430475.00	53378213.64	173798100.00
	Methylobacter tundripaludum	29905024.38	38182041.04	28837500.00	42417500.00	291777.37	52233508.35	36284193.60	17692716.94	32634900.00	49503075.00	71211026.64	87256560.63
	Methylobacterium gnaphalii	3984333.43	3940948.00	7116369.00	0.00	0.00	0.00	0.00	2635200.00	2106000.00	14550000.00	8812800.00	0.00
	Methyloceanibacter marginalis	0.00	0.00	0.00	3496000.00	7552992.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Methyloceanibacter methanicus	4712400.00	0.00	6427500.00	5155412.50	0.00	3065495.05	0.00	1903200.00	16969500.00	7940000.00	4127600.00	2516942.17
	Methyloceanibacter superfactus	189103309.80	378138387.40	73325940.00	180509500.00	33979700.00	57516581.88	198656400.00	68307800.00	247312282.90	41750000.00	32102800.00	158878600.00
	Methylocella silvestris	4650800.00	4963200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4700000.00	3536000.00	0.00
	Methylocystis parvus	52567900.00	45011521.28	34500000.00	89953704.50	122982000.00	40494000.00	49077727.32	56040700.00	37389600.00	58700000.00	77227600.00	66888425.45
	Methyloglobulus morosus	0.00	0.00	0.00	0.00	0.00	0.00	21477600.00	4648200.00	28422900.00	0.00	0.00	0.00
	Methylomagnum ishizawai	109386200.00	122390400.00	143707500.00	376285500.00	571722100.00	551830000.00	266912734.90	328966900.00	167985380.00	529840221.00	409133575.60	1125740277.00
	Methylomicrobium lacus	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1793400.00	1279800.00	0.00	0.00	0.00
	Methylotenera oryzisoli	0.00	1812800.00	1237500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Methylotenera versatilis	5028100.00	8395200.00	5542500.00	0.00	0.00	0.00	4947600.00	4825100.00	7047000.00	23510000.00	11968000.00	9345800.00
Sulfate-reducing bacteria	*Desulfacinum hydrothermale*	49596282.00	105434000.00	72480276.57	72036652.25	138807582.30	171901488.30	101403652.10	110905729.90	83940329.16	63217000.00	71531935.20	49786467.00
	Desulfacinum infernum	18431386.00	152421923.20	84246965.31	53104078.50	51448500.00	212216159.40	84818444.16	52719304.90	147063600.00	49380100.00	21183969.84	15361371.75
	Desulfamplus magnetovallimortis	3150000.00	4046000.00	0.00	0.00	0.00	0.00	0.00	5026400.00	3102300.00	3757600.00	2692800.00	0.00
	Desulfarculus baarsii	46546369.00	66299235.68	101171100.00	37935856.95	1122700.00	21180485.56	5310293.28	22019787.32	88334963.91	3426500.00	4312000.00	67129006.50
	Desulfatiglans anilini	110094313.00	349071871.20	122611181.60	289350996.20	309304616.30	356785731.00	157283070.80	146177189.00	224151255.00	195501911.20	269571288.80	237360882.00
	Desulfatirhabdium butyrativorans	46990000.00	75612090.00	106688500.00	132296449.00	96489187.69	181463519.20	119663957.80	65111067.55	84384747.81	85413511.26	37975220.80	13147500.00
	Desulfatitalea alkaliphila	24810000.00	82917948.12	217949303.20	14240779.30	338127591.50	47035051.40	17625004.20	180111258.40	223736127.20	11314969.05	29198400.00	130353467.30
	Desulfatitalea tepidiphila	13284275.00	44823343.76	41267900.00	20425000.00	83378500.00	35785456.93	68035200.00	61742634.74	130256100.00	48771800.00	115711200.00	16714495.50
	Desulfitibacter alkalitolerans	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5483900.00	523354.77	0.00	0.00	0.00
	Desulfobacca acetoxidans	893732402.00	992942834.00	702364347.20	1162852018.00	1578252132.00	1889985230.00	996889689.60	931353005.70	852188828.10	570621014.80	383356945.00	472086699.80
	Desulfobacter hydrogenophilus	0.00	0.00	0.00	12754825.40	10403000.00	0.00	10123200.00	0.00	18013197.15	0.00	0.00	0.00
	Desulfobacter postgatei	2250000.00	469943.92	0.00	0.00	1971428.24	1746919.10	0.00	568869.53	282956.49	3287900.00	0.00	3427500.00
	Desulfobulbus alkaliphilus	25920000.00	47321200.00	11274497.25	116251500.00	29633100.00	46480887.04	54829672.56	32403200.00	42444000.00	34371814.40	22764435.76	66691560.00
	Desulfobulbus elongatus	12670000.00	42432000.00	62493000.00	60011500.00	54445800.00	58548686.60	56680800.00	40327100.00	42346800.00	29421700.00	35173600.00	37605000.00
	Desulfobulbus oligotrophicus	2740000.00	0.00	4144637.10	0.00	5180900.00	9060453.10	0.00	0.00	0.00	4304300.00	4993134.96	2910000.00
	Desulfobulbus oralis	0.00	3372800.00	1657038.49	0.00	0.00	0.00	0.00	287476.53	307106.64	3183170.76	307067.20	400651.50
	Desulfobulbus propionicus	0.00	0.00	0.00	66338500.00	37399300.00	35491800.00	19357200.00	19703000.00	19739700.00	4150300.00	1707200.00	6045000.00
	Desulfobulbus rhabdoformis	9460000.00	12607200.00	0.00	28101000.00	16716900.00	10582225.56	4035600.00	10692202.00	9383406.93	2348500.00	0.00	1500000.00
	Desulfocapsa sulfexigens	4610000.00	2094400.00	0.00	0.00	4377500.00	19171395.99	2781600.00	2183800.00	4973400.00	0.00	1469600.00	1942500.00
	Desulfococcus multivorans	41980000.00	44789020.08	179872205.70	143440500.00	120540900.00	237463187.90	93320400.00	68002800.00	267094541.10	64385394.92	83747270.64	89170640.25
	Desulfocurvibacter africanus	1270000.00	5956800.00	2937829.71	10592500.00	11546300.00	1393700.26	6779135.40	5770600.00	4451879.88	5205200.00	2756157.36	7074987.75
	Desulfocurvus vexinensis	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8855000.00	0.00	15975000.00
	Desulfofalx alkaliphila	0.00	0.00	0.00	13309500.00	0.00	3084836.89	0.00	159210000.00	2980800.00	0.00	0.00	0.00
	Desulfoferrobacter suflitae	343454841.00	343200596.80	386479028.80	755193297.40	656756461.00	863539102.00	702434445.20	456933142.90	485661794.20	311571889.10	299061914.80	385897768.10
	Desulfofundulus thermobenzoicus	0.00	0.00	0.00	0.00	0.00	0.00	0.00	276820.44	20655000.00	0.00	0.00	0.00
	Desulfofustis glycolicus	1500000.00	7860800.00	1146819.74	21897500.00	21115000.00	4605200.00	5084400.00	1159000.00	2940300.00	10395000.00	20864800.00	0.00
	Desulfoglaeba alkanexedens	115230000.00	252497600.00	65063356.23	117763214.10	590352728.70	334857881.40	256687416.00	583130116.70	507555980.00	423271009.70	512670400.00	441607500.00
	Desulfogranum marinum	0.00	0.00	0.00	9690000.00	10609000.00	7900300.00	0.00	7795800.00	4074300.00	0.00	0.00	0.00
	Desulfogranum mediterraneum	5170000.00	6766000.00	5911500.00	4750475.00	28469200.00	3749597.51	2325600.00	2204252.08	51921000.00	0.00	19421600.00	3978023.25
	Desulfohalobium retbaense	3980000.00	1319200.00	0.00	0.00	3543200.00	331186.13	832154.40	0.00	464697.00	0.00	0.00	0.00
	Desulfohalovibrio alkalitolerans	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7176400.00	3977600.00	0.00
	Desulfolithobacter dissulfuricans	1030000.00	8092000.00	188717600.00	106400000.00	1369900.00	237643159.90	183084000.00	166694700.00	0.00	179410000.00	154000000.00	151237500.00
	Desulfoluna limicola	13010000.00	0.00	7882000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Desulfomarina profundi	0.00	0.00	0.00	0.00	0.00	0.00	3237600.00	2220400.00	25385400.00	0.00	0.00	0.00
	Desulfomonile tiedjei	81101467.00	124239390.50	226190761.80	249335075.30	207327367.20	165672733.00	205212338.50	168477210.90	121281546.20	65014659.71	150129153.70	50499714.75
	Desulfonatronum lacustre	0.00	0.00	0.00	0.00	0.00	0.00	18691339.68	1134600.00	1385100.00	2440900.00	0.00	1740000.00
	Desulfonatronum thioautotrophicum	0.00	0.00	0.00	0.00	0.00	0.00	5677200.00	1671400.00	2025000.00	0.00	0.00	0.00
	Desulfonatronum thiosulfatophilum	0.00	924800.00	6136700.00	1881000.00	0.00	8535500.00	6377910.12	1134600.00	0.00	0.00	4681600.00	567057.75
	Desulfonauticus submarinus	0.00	0.00	0.00	9937000.00	3203300.00	9598459.56	5973600.00	6421701.80	4625100.00	6457260.81	10919517.84	1567500.00
	Desulfonema ishimotonii	1358575.00	39168000.00	4042424.45	3992193.55	0.00	38945700.00	80028000.00	85687152.01	14890439.79	8570100.00	1091302.96	162517500.00

	Desulfonema limicola	79002548.00	76780863.12	131658875.90	137611449.20	133125887.00	136685757.70	127260849.40	89599119.83	64324219.77	90830740.00	89543803.36	98884860.15
	Desulfonema magnum	143957478.00	45621754.20	6991880.11	107699262.80	52711565.31	44447909.59	63589200.00	74335910.89	76282389.90	101521004.20	31249994.16	29626838.25
	Desulfonispora thiosulfatigenes	0.00	0.00	0.00	0.00	0.00	0.00	0.00	370562.19	186295.14	0.00	0.00	0.00
	Desulfopila aestuarii	19394874.00	28421187.52	14902925.28	12530500.00	2863400.00	7694947.78	5761751.52	10132100.00	8002800.00	35558600.00	38702400.00	23055000.00
	Desulfoprunum benzoelyticum	19197825.00	11938321.40	0.00	35836785.40	106429900.00	0.00	10237200.00	11260420.05	13936156.92	0.00	2490400.00	12735000.00
	Desulforapulum autotrophicum	2680000.00	1462000.00	1059718.01	0.00	0.00	0.00	25627200.00	5593700.00	1344600.00	1232000.00	12188000.00	0.00
	Desulforegula conservatrix	0.00	0.00	0.00	0.00	6205149.51	231848000.00	0.00	0.00	0.00	7338100.00	0.00	3165000.00
	Desulforhopalus singaporensis	3350000.00	0.00	18973100.00	14829500.00	27305300.00	39405648.32	6315600.00	11681500.00	9460800.00	4173400.00	0.00	4327500.00
	Desulfosalsimonas propionicica	27230000.00	8636000.00	17699655.93	29526000.00	11731700.00	14379984.33	13665462.72	38692300.00	148718038.00	9979200.00	4573044.08	6235604.25
	Desulfosarcina alkanivorans	55976960.00	41255500.04	32533372.18	77662500.00	43579300.00	58239900.00	114834646.40	79342700.00	37972800.00	52945200.00	42001941.52	41767500.00
	Desulfosarcina cetonica	10170000.00	12926976.12	8976939.29	31065000.00	47294869.47	22829516.76	13058560.92	43181900.00	25320600.00	23677500.00	14043839.66	14415000.00
	Desulfosarcina ovata	34020000	33830000	13259353.75	47547500	51446176.32	24627533.73	34154400	37252700	43772400	30723000	57780800	26107213.5
	Desulfosarcina widdelii	7362870	22249600	34734904.3	18069000	43946298.27	18269959.85	203250647.9	188616530.5	147260592.8	96237675.38	81760800	221752500
	Desulfoscipio geothermicus	0	0	0	0	0	0	0	0	0	1139600	861907.2	355342.5
	Desulfosediminicola flagellatus	6540000	2475200	0	3106500	1246300	0	0	1878800	3248100	0	0	0
	Desulfosediminicola ganghwensis	607108	664547	3541754.18	0	0	0	0	1471805.56	560163.6	0	0	0
	Desulfosoma caldarium	126939428	133488050.8	75889855.24	142720842.7	189460842	265489758.6	317296003.9	270196076.1	199131441.7	161809451.7	177790675	173036710.5
	Desulfospira joergensenii	43600000	66272800	349228900	42009000	18900500	21914400	280602908.3	97451152.07	46251000	14129500	177980000	244800000
	Desulfosudis oleivorans	9240000	21290800	22357079.06	31442925.2	33814900	31785912.19	13653048.12	29440968.02	46713462.21	188041700	110413600	41700000
	Desulfotomaculum copahuensis	31640000	5310800	31209415.19	137949500	35576200	23823573	6349786.32	68798864.03	7112592.18	5182100	4979336.56	1687500
	Desulfovermiculus halophilus	0	12899533.36	1068095.45	9690000	35514400	3978845.16	24810358.08	21087700	27256500	0	0	0
	Desulfovibrio aminophilus	0	0	0	0	0	0	22549200	0	12717000	0	0	0
	Desulfovibrio cuneatus	0	0	0	755834.25	644673.91	0	0	0	0	0	0	0
	Desulfovibrio inopinatus	3988584	1917600	0	0	0	0	0	0	0	0	0	0
	Desulfovibrio litoralis	0	0	0	7932500	8219400	0	0	0	0	13090000	11352000	0
	Desulfovibrio psychrotolerans	41280000	0	6305600	28376500	0	10599900	19174800	36500507.78	17455500	0	11744907.68	20992281.75
	Desulfovibrio sulfodismutans	1970000	0	13286800	3756083.4	13704139.7	94315960.93	5767195.25	2526473.6	6917818.77	9548000	21665600	3562500
	Desulfurella multipotens	0	5766400	22013300	0	0	0	0	0	0	0	0	0
	Desulfurispirillum indicum	393982	0	646430.97	0	0	0	0	0	0	0	0	0
	Desulfurivibrio alkaliphilus	0	433765.88	887749.66	0	769793.16	675169.96	0	0	0	877800	648177.2	665154
	Desulfuromonas acetexigens	0	0	0	1957000	0	736502.49	1552556.88	447973.02	0	0	976800	1350000
	Dethiosulfatarculus sandiegensis	16852251	5105819.44	4312822.09	22573768.9	33207230.9	3323441.83	7272087.36	8558300	5630623.47	4057900	13455200	6067500
	Dinghuibacter silviterrae	580459	550462.72	0	1016500	1174200	0	0	2275300	6235066.53	0	0	0
	Dissulfurimicrobium hydrothermale	32000000	29954000	53034600	42845000	118264600	51620671.76	116872800	37336745.19	93222900	46508000	31468800	30082500
	Dissulfurirhabdus thermomarina	0	0	0	7315000	638749.35	0	0	0	0	0	0	0
	Dissulfurispira thermophila	37428444	54764437.16	43878086.23	43871000	150915600	165207296.5	46135635.84	130381400	88632370.8	48433495.11	77849293.28	57457500
sulfide/sulfur-oxidizing bacteria	Lamprocystis purpurea	6330000	21783993.8	20476615.71	30798928.75	24932476.64	26293302.06	121709573.8	28523600	38641297.86	40002364.71	5212368.48	39067641.75
	Sulfuricaulis limicola	67870000	41276944.52	66965258.06	14516000	6082936.92	17082346.26	48361435.68	37332562.79	48698183.34	143367429.6	150842653.3	59893983.53
	Sulfuricella denitrificans	0	0	0	0	0	0	22138800	123470100	12004200	5854946.79	2728000	19833810.75
	Sulfuriferula multivorans	12325460	7548000	0	9329000	7745600	25685900	141865539.8	158095179.9	155576700	166859000	174053807.8	142252500
	Sulfuriferula nivalis	0	0	0	1729000	1761300	0	40584000	82833565.91	176282394.7	128528400	178314400	152542500
	Sulfuriferula plumbiphila	99691532	84799122.56	30057432.74	28215000	66064200	27899186.91	147394033.7	394587122.4	335390822.6	849440900	928391200	817200139.5
	Sulfuriferula thiophila	0	0	0	0	0	0	3078000	7039400	14474700	30661400	22906400	16867500
	Sulfuriflexus mobilis	0	0	0	0	0	0	0	4465200	3361500	4335100	4831200	6495000
	Sulfurifustis variabilis	0	0	0	0	0	0	0	2177700	3005100	2902900	5623200	8137500
	Sulfurimicrobium lacus	11160000	4358800	0	0	0	0	4833600	14963300	35996400	49665000	41333681.84	34652503.5
	Sulfurirhabdus autotrophica	21620000	41242000	36951531.01	13281000	9105200	34874453.09	46101600	113622016	86005800	121991100	198214139.2	173244867
	Sulfurisoma sediminicola	11143447	7485586.2	7151309.89	9623500	12699900	1305640.9	10337394.6	71735454.05	28879627.41	29138962.93	44121476.08	33483972.75
	Sulfuritalea hydrogenivorans	16385708	9752550.48	6787516.74	0	9352400	3090541.78	2964000	18130951.68	21495285.9	40740700	12096692.08	25259094.75
	Sulfuritortus calidifontis	17380000	9710400	2657528.9	0	36812200	2793911.32	104971200	133308789.4	100614212.4	177241526.8	186692000	129244215.8
	Sulfurivermis fontis	0	0	0	0	0	0	34678800	31469900	28609200	46169200	47819200	33480000
	sulfur-oxidizing symbionts	5800000	8296000	0	18278000	7230600	5041900	0	7722600	3215700	0	0	0
	Thioalkalivibrio sulfidiphilus	0	0	0	0	0	0	1145278.2	0	230806.26	218175.65	302638.16	11413101
	Thiobacillus denitrificans	44560000	65776726.4	33689509.01	111036000	81576000	40359055.73	588183426.4	976470579	880418728.1	1639208767	1908763183	1542461190
	Thiobacillus thioparus	41304533	34224400	37786786.55	40922961.9	46012198.11	32301642.98	814732376.7	679660838.6	861720150	635549734.8	695629565	637097069.3
	Thiocapsa imhoffii	8200000	4426800	8136808.17	0	4841000	15205100	8367600	0	2583900	8600900	5033600	8977500
	Thiocapsa rosea	0	0	0	3458000	4387800	4565500	1385790.84	2818200	5516100	4458300	0	8032500
	Thiocapsa roseopersicina	0	0	0	0	1534700	984691.01	0	11529000	1004400	15092000	9504000	6787500
	Thioclava electrotropha	0	0	0	4740500	6571400	0	42636000	34892000	7346700	89628000	89760000	81000000
	Thiocystis minor	0	0	0	4227500	23896000	0	15048000	4471300	11826000	8778000	27359200	10125000
	Thiocystis violacea	0	0	0	0	0	0	36229200	3737374.23	9995400	81991671.3	60183200	52350000
	Thioflavicoccus mobilis	13100000	4311200	12389969.15	17575000	2588333.35	0	0	0	0	0	7594400	7447890.75
	Thioflexithrix psekupsensis	0	0	0	17290000	17407000	0	0	23241000	4268700	21175000	0	379512
	Thiogranum longum	0	0	0	0	0	0	0	0	0	0	4637600	1935000
	Thiohalocapsa halophila	0	0	0	0	0	0	0	0	0	0	2147200	14925000
	Thiohalocapsa marina	0	30736000	9402100	14630000	9682000	13696500	6178800	32635000	4050000	0	0	0
	Thiohalomonas denitrificans	0	0	0	0	0	0	0	5575400	7087500	5867400	0	4777500
	Thiohalorhabdus denitrificans	0	0	0	5975500	7931000	0	0	0	0	0	0	0
	Thiomicrospira microaerophila	0	0	0	0	0	0	0	0	0	2733500	3220800	3229033.5
	Thiorhodococcus minor	2800000	11043200	0	2686033.8	332542.71	0	2453337	14341100	23611500	18172621.39	4191136.4	1065447
	Thiospirillum jenense	24000000	40256000	1972262.19	0	0	0	0	0	0	0	0	0
	Thiothrix eikelboomii	0	0	0	0	0	0	0	0	0	7059718.05	13024000	0
	Thiothrix fructosivorans	0	0	0	0	0	0	0	5996300	4941000	862400	2877600	2842500
	Thiothrix nivea	0	0	0	0	0	0	0	3574600	8425293.57	18195100	43225600	6765000

Supplementary Table 2. Summary of metaproteomic database searching results.

ID	Peak Height												KO Number	Description	Taxa
	S-O- 1	S-O- 2	S-O- 3	S+O- 1	S+O- 2	S+O- 3	S-O+ 1	S-O+ 2	S-O+ 3	S+O+ 1	S+O+ 2	S+O+ 3			
Ga0586324 0078845 1967 3262	6510000.00	0.00	0.00	0.00	0.00	0.00	1477296.36	0.00	0.00	0.00	0.00	0.00	KO:K00003	homoserine dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;Corallococcus;Corallococcus sp. H22C18031201;Corallococcus sp. H22C18031201
Ga0586324 0145763 870 2096	0.00	0.00	0.00	0.00	0.00	0.00	160742.51	0.00	0.00	0.00	0.00	0.00	KO:K00003	homoserine dehydrogenase	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter pauli;Solirubrobacter pauli DSM 14954
Ga0586324 0260785 1668 2189	207568.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00003	homoserine dehydrogenase	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas formicexedens;Dehalogenimonas formicexedens NSZ-14
Ga0586324 0502813 1 891	127031.00	0.00	0.00	0.00	0.00	0.00	0.00	1104100.00	0.00	1771000.00	0.00	0.00	KO:K00003	homoserine dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324 1832549 1 936	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	725802.00	0.00	0.00	KO:K00003	homoserine dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 1967702 1 909	438574.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00003	homoserine dehydrogenase	Archaea;Euryarchaeota;Methanococci;Methanococcales;Methanocaldococcaceae;Methanocaldococcus;Methanocaldococcus vulcanius;Methanocaldococcus vulcanius M7, DSM 12094
Ga0586324 2597129 2 715	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	433827.90	0.00	0.00	0.00	KO:K00003	homoserine dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter marginalis;Methyloceanibacter marginalis R-67177
Ga0586324 4195391 3 386	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1365000.00	KO:K00003	homoserine dehydrogenase	Bacteria;Firmicutes;Clostridia;Halanaerobiales;Halobacteroidaceae;Candidatus Frackibacter;Candidatus Frackibacter sp. WG12;Candidatus Frackibacter sp. WG12
Ga0586324 7253247 1 528	0.00	0.00	0.00	0.00	49852000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00003	homoserine dehydrogenase	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;unclassified Solirubrobacterales;unclassified Solirubrobacterales;Solirubrobacterales bacterium URHD0059;Solirubrobacterales bacterium URHD0059
Ga0586324 0025058 2814 3860	0.00	0.00	0.00	0.00	0.00	0.00	0.00	860100.00	0.00	0.00	0.00	0.00	KO:K00004	(R,R)-butanediol dehydrogenase/meso-butanediol dehydrogenase/diacetyl reductase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Lachnospiraceae;Anaerostipes;Anaerostipes rhamnosivorans;Anaerostipes rhamnosivorans 1y2
Ga0586324 0382308 3 1019	0.00	0.00	0.00	0.00	0.00	0.00	0.00	658800.00	0.00	0.00	0.00	1170000.00	KO:K00005	glycerol dehydrogenase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Thermoanaerosceptrum;Thermoanaerosceptrum fracticalcis;Thermoanaerosceptrum fracticalcis DRI-13
Ga0586324 1655994 2 979	6880000.00	768400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	741722.25	KO:K00010	myo-inositol 2-dehydrogenase/D-chiro-inositol 1-dehydrogenase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6179853 1 564	0.00	342329.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00010	myo-inositol 2-dehydrogenase/D-chiro-inositol 1-dehydrogenase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 0000005 55168 56490	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2849000.00	0.00	6165000.00	KO:K00012	UDPglucose 6-dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0017638 5301 6623	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2525600.00	0.00	KO:K00012	UDPglucose 6-dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0213322 395 1720	0.00	0.00	0.00	0.00	0.00	4367000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00012	UDPglucose 6-dehydrogenase	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Flavobacterium;Flavobacterium succinicans;Flavobacterium succinicans LMG 10402
Ga0586324 0290841 36 1349	0.00	0.00	0.00	0.00	0.00	0.00	467317.92	0.00	0.00	0.00	0.00	0.00	KO:K00012	UDPglucose 6-dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 1905144 1 711	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	793100.00	0.00	0.00	KO:K00012	UDPglucose 6-dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 7629892 1 519	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	272508.39	0.00	0.00	KO:K00012	UDPglucose 6-dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0262451 344 1663	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5702400.00	0.00	KO:K00013	histidinol dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Laribacter;Laribacter hongkongensis;Laribacter hongkongensis LHGZ1
Ga0586324 0336379 69 1367	0.00	0.00	0.00	0.00	0.00	0.00	2827200.00	0.00	0.00	0.00	0.00	0.00	KO:K00013	histidinol dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 1199669 163 1122	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5347500.00	KO:K00013	histidinol dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales A1
Ga0586324 0000007 28526 29476	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	472403.25	KO:K00018	glycerate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0071673 1 627	0.00	0.00	0.00	8578500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00023	acetoacetyl-CoA reductase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum;Herbaspirillum sp. K2R10-39;Herbaspirillum sp. K2R10-39
Ga0586324 2256833 409 858	0.00	0.00	3731974.99	0.00	0.00	6272600.00	4332000.00	2757200.00	2502900.00	3164700.00	0.00	0.00	KO:K00023	acetoacetyl-CoA reductase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 4860956 3 623	0.00	0.00	1144106.08	0.00	0.00	0.00	0.00	0.00	2008800.00	0.00	0.00	2775000.00	KO:K00023	acetoacetyl-CoA reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Alkalilimnicola;Alkalilimnicola ehrlichii;Alkalilimnicola ehrlichii MLHE-1
Ga0586324 0000238 38779 39711	0.00	0.00	0.00	0.00	0.00	2228146.62	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Achromatium;Achromatium sp. WMS3;Achromatium sp. WMS3
Ga0586324 0032997 1606 2535	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5947500.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0287020 1360 2097	0.00	0.00	0.00	0.00	0.00	846666.02	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;endosymbiont of Riftia pachyptila;endosymbiont of Riftia pachyptila (vent Mk28)
Ga0586324 0340850 875 1810	0.00	0.00	0.00	6840000.00	0.00	0.00	13862400.00	6222000.00	1263600.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0360500 1 540	1510000.00	0.00	0.00	4522000.00	7570500.00	2703879.66	0.00	3891800.00	2097900.00	0.00	0.00	1365000.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0428719 867 1754	0.00	0.00	13399400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 0554577 1 951	0.00	0.00	2831585.98	0.00	0.00	436866.74	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Woeseiaceae;Woeseia;Woeseia oceani;Woeseia oceani XK5
Ga0586324 0755426 539 1369	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4592700.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 1196366 706 1125	0.00	0.00	0.00	2118500.00	0.00	0.00	0.00	4532300.00	1701000.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324 1553294 680 1006	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22275000.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Seleniivibrio;Seleniivibrio woodruffii;Seleniivibrio woodruffii S4
Ga0586324 1845493 97 933	0.00	0.00	1084191.62	4978000.00	6787700.00	1584657.26	1316036.52	3434300.00	1846800.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1914176 3 653	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3995200.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 2063688 410 892	0.00	0.00	0.00	5339000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 3352322 3 683	0.00	0.00	0.00	0.00	0.00	0.00	0.00	811300.00	0.00	0.00	976800.00	1005000.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 3442363 1 720	0.00	0.00	0.00	0.00	0.00	13458300.00	0.00	0.00	1304100.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 5358720 1 600	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4148000.00	0.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio hydrogeniphilus;Thermodesulfovibrio hydrogeniphilus DSM 18151
Ga0586324 5849606 1 579	0.00	0.00	0.00	0.00	0.00	26162300.00	0.00	11956000.00	0.00	0.00	0.00	0.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Porphyrobacter;Porphyrobacter sp. AAP82;Porphyrobacter sp. AAP82
Ga0586324 6361370 1 558	0.00	0.00	0.00	0.00	0.00	0.00	7455600.00	5233800.00	5572800.00	0.00	0.00	2685000.00	KO:K00024	malate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0729134 3 1391	0.00	0.00	0.00	0.00	8888900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00029	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. PSR-1;Anaeromyxobacter sp. PSR-1
Ga0586324 0755447 2 1369	11300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00029	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 1007402 2 1210	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18656000.00	0.00	KO:K00029	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0000606 11127 12380	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	38984000.00	0.00	KO:K00031	isocitrate dehydrogenase	Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;Alicyclobacillus;Alicyclobacillus acidocaldarius;Alicyclobacillus acidocaldarius LAA1
Ga0586324 2002003 474 902	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3616800.00	0.00	KO:K00031	isocitrate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324 2734715 76 792	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	923400.00	0.00	0.00	0.00	KO:K00031	isocitrate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 2788721 3 695	0.00	0.00	0.00	0.00	0.00	21954100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00031	isocitrate dehydrogenase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0031695 3671 5137	0.00	0.00	0.00	0.00	0.00	0.00	1501405.08	0.00	0.00	0.00	0.00	0.00	KO:K00033	6-phosphogluconate dehydrogenase	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;unclassified Rhodothermaceae;Rhodothermaceae bacterium RA;Halothermobacillus malaysiensis RA
Ga0586324 1018913 1 1203	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4335000.00	KO:K00033	6-phosphogluconate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium lacus;Methylosarcina lacus LW14
Ga0586324 1893531 2 925	0.00	0.00	0.00	0.00	0.00	0.00	6726000.00	0.00	0.00	0.00	0.00	0.00	KO:K00033	6-phosphogluconate dehydrogenase	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Sunxiuqinia;Sunxiuqinia elliptica;Sunxiuqinia elliptica 114D
Ga0586324 2040485 2 799	0.00	0.00	0.00	0.00	0.00	0.00	2827200.00	0.00	0.00	0.00	0.00	0.00	KO:K00033	6-phosphogluconate dehydrogenase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 2088782 2 859	0.00	0.00	0.00	0.00	0.00	0.00	4810800.00	0.00	0.00	0.00	0.00	0.00	KO:K00033	6-phosphogluconate dehydrogenase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Lacunisphaera;Lacunisphaera limnophila;Opitutaceae bacterium IG16b
Ga0586324 2584116 3 779	0.00	4984400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00033	6-phosphogluconate dehydrogenase	Bacteria;Verrucomicrobia;Spartobacteria;Chthoniobacterales;Chthoniobacteraceae;Chthoniobacter;Chthoniobacter flavus;Chthoniobacter flavus Ellin428
Ga0586324 0251031 3 1406	0.00	911200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00036	glucose-6-phosphate 1-dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. PSR-1;Anaeromyxobacter sp. PSR-1
Ga0586324 0553196 3 527	696883.00	0.00	0.00	4902000.00	6499300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00042	2-hydroxy-3-oxopropionate reductase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Syntrophobotulus;Syntrophobotulus glycolicus;Syntrophobotulus glycolicus FlGlyR, DSM 8271
Ga0586324 0667409 273 1196	0.00	5589600.00	0.00	0.00	0.00	0.00	0.00	7015000.00	0.00	0.00	0.00	0.00	KO:K00042	2-hydroxy-3-oxopropionate reductase	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Moorella;Moorella thermoacetica;Moorella thermoacetica DSM 11768
Ga0586324 0080700 1374 2486	0.00	0.00	0.00	1805000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00052	3-isopropylmalate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 0108084 1932 2999	0.00	0.00	0.00	4949500.00	0.00	0.00	0.00	0.00	4187700.00	0.00	0.00	0.00	KO:K00052	3-isopropylmalate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0258097 637 1761	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	454591.50	KO:K00052	3-isopropylmalate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter marginalis;Methyloceanibacter marginalis R-67177
Ga0586324 1457159 3 1034	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	372270.36	0.00	0.00	KO:K00052	3-isopropylmalate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 0000037 18910 19926	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1403000.00	8181000.00	9471000.00	34760000.00	7080000.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0011512 4736 5797	0.00	0.00	0.00	1795500.00	0.00	0.00	0.00	0.00	1482300.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 0039922 1587 2603	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3117100.00	2438100.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0044729 388 1377	0.00	0.00	0.00	0.00	0.00	1594276.57	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0057865 1741 2739	0.00	0.00	0.00	0.00	1926100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Pseudanabaenaceae;Pseudanabaena;Pseudanabaena sp. 'Roaring Creek';Pseudanabaena sp. Roaring Creek
Ga0586324 0164613 547 1563	0.00	0.00	0.00	0.00	2925200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Acidihalobacter;Acidihalobacter ferrooxydans;Acidihalobacter ferrooxydans V8
Ga0586324 0219185 735 1751	0.00	0.00	0.00	0.00	0.00	0.00	0.00	524068.08	0.00	3711400.00	4144800.00	2497500.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0946541 3 728	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2421700.00	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 1501224 3 1004	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6344000.00	6795900.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324 1573152 612 1001	0.00	0.00	0.00	1881000.00	0.00	0.00	4833600.00	1958100.00	0.00	2733500.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloterricola;Methyloterricola oryzae;Methyloterricola oryzae 73a
Ga0586324 1871075 28 930	0.00	0.00	0.00	0.00	5510500.00	0.00	0.00	0.00	3183300.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2061862 1 705	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1441800.00	0.00	1390400.00	930000.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 2146832 73 876	0.00	0.00	0.00	817760.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324 2420743 3 734	0.00	2930800.00	0.00	0.00	5788600.00	0.00	0.00	1213900.00	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas sp. WBC-2;Dehalogenimonas sp. WBC-2
Ga0586324 2831769 3 779	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5985000.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 2910032 1 603	0.00	0.00	2168265.01	0.00	0.00	0.00	3260400.00	0.00	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3425754 3 281	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	644915.52	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Candidatus Methylopumilus;Candidatus Methylopumilus turicensis;Candidatus Methylopumilus turicensis MMS-10A-171
Ga0586324 3609987 362 706	0.00	0.00	0.00	0.00	0.00	0.00	12403200.00	0.00	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Candidatus Methylopumilus;Candidatus Methylopumilus turicensis;Candidatus Methylopumilus turicensis MMS-10A-171
Ga0586324 7181410 213 530	0.00	0.00	0.00	0.00	0.00	0.00	0.00	207667.79	0.00	0.00	0.00	0.00	KO:K00053	ketol-acid reductoisomerase	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas sp. WBC-2;Dehalogenimonas sp. WBC-2
Ga0586324 0001449 20691 22274	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1609300.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 0127315 1 1512	2770000.00	0.00	0.00	5415000.00	0.00	0.00	0.00	0.00	988200.00	0.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0441336 3 947	0.00	0.00	0.00	16340000.00	0.00	3799047.83	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2916780 2 772	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1514700.00	0.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4272258 3 659	0.00	0.00	0.00	4997000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5514232 1 591	0.00	0.00	0.00	4636000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 6126046 2 568	0.00	0.00	0.00	0.00	1596500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324 6244574 1 564	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	778265.82	0.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 6415862 2 556	0.00	0.00	0.00	2736000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00058	D-3-phosphoglycerate dehydrogenase	Bacteria;Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;Chloroflexi sp. G233
Ga0586324 0385632 643 1437	7210000.00	8024000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00059	3-oxoacyl-[acyl-carrier protein] reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324 2635495 410 805	0.00	0.00	0.00	0.00	2266000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00059	3-oxoacyl-[acyl-carrier protein] reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 2973754 2 544	0.00	0.00	0.00	0.00	0.00	0.00	0.00	549764.33	437533.65	0.00	0.00	0.00	KO:K00059	3-oxoacyl-[acyl-carrier protein] reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter marinus;Methylobacter marinus A45
Ga0586324 3659485 200 700	0.00	3474800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00059	3-oxoacyl-[acyl-carrier protein] reductase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324 0153596 2 757	1760000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00065	2-deoxy-D-gluconate 3-dehydrogenase	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324 0026778 2687 3535	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1976400.00	0.00	0.00	0.00	KO:K00074	3-hydroxybutyryl-CoA dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira;unclassified Azospira;Azospira sp. ZAP
Ga0586324 0174597 2249 2635	0.00	5263200.00	0.00	8274500.00	7343900.00	10004400.00	0.00	1165100.00	6058800.00	0.00	0.00	6645000.00	KO:K00074	3-hydroxybutyryl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfospira;Desulfospira joergensenii;Desulfospira joergensenii DSM 10085
Ga0586324 2091747 2 580	0.00	183370.16	1106120.47	0.00	638940.93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00074	3-hydroxybutyryl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324 0000018 73627 75090	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1098000.00	0.00	0.00	0.00	4322503.50	KO:K00088	IMP dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0000385 16260 17720	0.00	0.00	0.00	0.00	0.00	0.00	16735200.00	0.00	10611000.00	993300.00	4963200.00	0.00	KO:K00088	IMP dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324 0052310 3 791	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14344000.00	0.00	KO:K00088	IMP dehydrogenase	Bacteria;Acidobacteria;Blastocatellia;unclassified Blastocatellia;unclassified Blastocatellia;Chloracidobacterium;Chloracidobacterium thermophilum;Chloracidobacterium thermophilum OC1
Ga0586324 0102347 3 872	0.00	3950800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00088	IMP dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 0118577 1130 2659	0.00	0.00	0.00	3496000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00088	IMP dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter marginalis;Methyloceanibacter marginalis R-67177
Ga0586324 0452266 632 1714	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13552000.00	1293600.00	552920.25	KO:K00088	IMP dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 1922906 1 381	0.00	0.00	0.00	0.00	2739800.00	0.00	0.00	1762900.00	0.00	2048200.00	0.00	0.00	KO:K00088	IMP dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Aquincola;Aquincola tertiaricarbonis;Aquincola tertiaricarbonis MIMtkpLc11
Ga0586324 1781463 2 901	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2710400.00	2851200.00	0.00	KO:K00104	glycolate oxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0561832 69 1559	0.00	686800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00108	choline dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium lacus;Methylosarcina lacus LW14
Ga0586324 0000002 162709 164094	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5035800.00	17529600.00	0.00	KO:K00113	glycerol-3-phosphate dehydrogenase subunit C	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0002371 12216 13559	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	189283.23	0.00	0.00	0.00	KO:K00113	glycerol-3-phosphate dehydrogenase subunit C	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0007845 10314 11345	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2006900.00	3134700.00	0.00	0.00	0.00	KO:K00113	glycerol-3-phosphate dehydrogenase subunit C	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324 8163619 1 369	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1050000.00	KO:K00113	glycerol-3-phosphate dehydrogenase subunit C	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella massiliensis;Reyranella massiliensis 521, DSM 23428
Ga0586324 0007859 4741 6408	2810000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium canariense;Bradyrhizobium canariense GAS369
Ga0586324 0029023 1 2133	0.00	2801600.00	0.00	0.00	0.00	0.00	0.00	0.00	5362200.00	0.00	0.00	5520000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI 001;Burkholderiales sp. JOSHI 001
Ga0586324 0076382 1724 3529	12250000.00	2556800.00	528546.09	232558.10	338422.98	6279871.45	223118.06	383315.46	24369497.19	3177371.12	691326.24	1140000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Methyloversatilis;Methyloversatilis discipulorum;Methyloversatilis discipulorum FAM1
Ga0586324 0083097 1 1632	0.00	2312000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS478
Ga0586324 0145572 140 1879	0.00	0.00	0.00	0.00	0.00	3461482.70	0.00	0.00	0.00	0.00	3000800.00	1619916.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI 001;Burkholderiales sp. JOSHI 001
Ga0586324 0158644 796 2469	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2904000.00	1815000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia susongensis;Paraburkholderia susongensis LMG 29540
Ga0586324 0192193 568 2319	14205991.00	16708168.48	10214608.09	452620.85	6992300.23	386616.07	149187.92	484269.85	292687.02	9429314.51	403699.12	7005489.75	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Methyloversatilis;Methyloversatilis discipulorum;Methyloversatilis discipulorum FAM1
Ga0586324 0215684 143 1882	7710000.00	5290400.00	0.00	0.00	0.00	2254416.11	2508000.00	2604700.00	3377700.00	0.00	1460800.00	3285000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI 001;Burkholderiales sp. JOSHI 001
Ga0586324 0567520 157 1551	288700.00	1417181.88	1684518.52	423957.45	0.00	0.00	0.00	802933.85	0.00	2086700.00	0.00	1369850.25	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Methyloversatilis;Methyloversatilis universalis;Methyloversatilis universalis EHg5
Ga0586324 0952556 2 859	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2671800.00	0.00	5058900.00	0.00	0.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. STM 3843;Bradyrhizobium sp. STM 3843
Ga0586324 0953658 1 1167	0.00	6446400.00	15820300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5962500.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus sp. IDO;Cupriavidus sp. IDO
Ga0586324 1018899 2 679	0.00	24684000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8475000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI 001;Burkholderiales sp. JOSHI 001
Ga0586324 1052426 3 1004	0.00	0.00	27812200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 1392089 3 1052	0.00	2516000.00	7700196.04	1577000.00	269120.46	9686800.00	0.00	1488400.00	0.00	4958800.00	8069600.00	11445000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Methyloversatilis;Methyloversatilis discipulorum;Methyloversatilis discipulorum FAM1
Ga0586324 1460660 1 1032	5350000.00	5684800.00	0.00	0.00	4902800.00	17031300.00	1993727.76	3879600.00	3920400.00	4897200.00	2921600.00	3472500.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Methyloversatilis;Methyloversatilis discipulorum;Methyloversatilis discipulorum FAM1
Ga0586324 1461177 1 1032	0.00	2116454.44	0.00	0.00	0.00	0.00	0.00	128211.02	0.00	1131900.00	2340800.00	864315.75	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Methyloversatilis;Methyloversatilis universalis;Methyloversatilis universalis EHg5
Ga0586324 1808437 3 941	3910000.00	0.00	2841922.66	0.00	0.00	4764000.00	2371200.00	1409100.00	1911600.00	1940400.00	0.00	1522500.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI 001;Burkholderiales sp. JOSHI 001
Ga0586324 4028859 29 673	0.00	0.00	0.00	8170000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1890000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324 4800458 3 626	0.00	573420.20	0.00	0.00	0.00	0.00	0.00	1573800.00	0.00	434928.34	2076800.00	990000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii WSM2783
Ga0586324 5419857 3 596	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2873100.00	0.00	0.00	0.00	0.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI 001;Burkholderiales sp. JOSHI 001
Ga0586324 5724762 3 584	6130000.00	19856000.00	40704900.00	0.00	0.00	26162300.00	0.00	8784000.00	8343000.00	25949000.00	16632000.00	1965000.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 6493512 3 554	0.00	23936000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00114	alcohol dehydrogenase (cytochrome c)	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. Pch-M;Methylibium sp. Pch-M
Ga0586324 0001544 10986 12095	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1457900.00	1296000.00	0.00	0.00	0.00	KO:K00121	S-(hydroxymethyl)glutathione dehydrogenase/alcohol dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505

Ga0586324 4844825 1 420	0.00	0.00	0.00	1121000.00	5984300.00	0.00	0.00	0.00	0.00	0.00	0.00	2040000.00	KO:K00121	S-(hydroxymethyl)glutathione dehydrogenase/alcohol dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324 0068903 1 1809	0.00	5338000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00123	formate dehydrogenase major subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;unclassified Burkholderiaceae;Burkholderiaceae bacterium PBA;Burkholderiaceae bacterium PBA
Ga0586324 0417493 2 1774	0.00	0.00	0.00	0.00	2111500.00	25527100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00123	formate dehydrogenase major subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0490105 3 1511	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1451800.00	0.00	0.00	0.00	0.00	KO:K00123	formate dehydrogenase major subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 1645445 2 982	13100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00123	formate dehydrogenase major subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 1678795 110 973	0.00	0.00	0.00	4674000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00123	formate dehydrogenase major subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 2189294 3 869	0.00	0.00	5564196.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00123	formate dehydrogenase major subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Sinobacteraceae;Hydrocarboniphaga;Hydrocarboniphaga effusa;Hydrocarboniphaga effusa AP103
Ga0586324 3195700 2 742	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2880000.00	KO:K00123	formate dehydrogenase major subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter sp. Leaf400;Ramlibacter sp. Leaf400
Ga0586324 4389209 2 556	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1125900.00	536274.97	0.00	0.00	KO:K00123	formate dehydrogenase major subunit	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 2573282 552 812	0.00	0.00	0.00	0.00	0.00	0.00	1093442.40	0.00	0.00	0.00	0.00	0.00	KO:K00124	formate dehydrogenase iron-sulfur subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Leptothrix;Leptothrix cholodnii;Leptothrix cholodnii SP-6
Ga0586324 3257948 3 737	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1166400.00	0.00	0.00	0.00	KO:K00124	formate dehydrogenase iron-sulfur subunit	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Calderihabitans;Calderihabitans maritimus;Calderihabitans maritimus KKC1
Ga0586324 3862363 2 685	0.00	1611600.00	0.00	2764500.00	2132100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00124	formate dehydrogenase iron-sulfur subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Pseudodesulfovibrio;Pseudodesulfovibrio profundus;Pseudodesulfovibrio profundus 500-1
Ga0586324 6131834 265 567	0.00	0.00	0.00	1121000.00	0.00	0.00	0.00	258113.57	0.00	0.00	0.00	0.00	KO:K00124	formate dehydrogenase iron-sulfur subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0060940 152 1327	0.00	0.00	0.00	0.00	0.00	1174322.03	0.00	3397700.00	0.00	0.00	0.00	0.00	KO:K00125	formate dehydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0067805 2831 4081	1880000.00	17000000.00	16552200.00	18145000.00	0.00	0.00	12540000.00	0.00	13365000.00	0.00	0.00	10050000.00	KO:K00125	formate dehydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0335549 722 1873	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15400000.00	0.00	KO:K00125	formate dehydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0351754 95 1270	0.00	1897200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00125	formate dehydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus bourgensis;Methanoculleus bourgensis MS2
Ga0586324 0514119 1 843	0.00	0.00	0.00	1615000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00125	formate dehydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus sp. MH98A;Methanoculleus sp. MH98A
Ga0586324 0538212 2 1057	0.00	0.00	0.00	0.00	0.00	3055431.10	0.00	1836100.00	1660500.00	0.00	0.00	0.00	KO:K00125	formate dehydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus sp. MH98A;Methanoculleus sp. MH98A
Ga0586324 0811947 359 1327	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1146800.00	0.00	0.00	0.00	0.00	KO:K00125	formate dehydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0042298 2 1552	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2632500.00	0.00	0.00	1477500.00	KO:K00128	aldehyde dehydrogenase (NAD+)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS499
Ga0586324 0000003 78914 80026	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1174500.00	0.00	0.00	1875000.00	KO:K00133	aspartate-semialdehyde dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Thioalkalispiraceae;Sulfurivermis;Sulfurivermis fontis;Sulfurivermis fontis JG42
Ga0586324 0143030 976 2013	0.00	0.00	0.00	0.00	0.00	0.00	0.00	109246.12	0.00	0.00	0.00	0.00	KO:K00133	aspartate-semialdehyde dehydrogenase	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Calditerrivibrio;Calditerrivibrio nitroreducens;Calditerrivibrio nitroreducens Yu37-1, DSM 19672
Ga0586324 0789210 192 1214	0.00	0.00	0.00	0.00	0.00	1249311.36	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00133	aspartate-semialdehyde dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Deferrisoma;Deferrisoma camini;Deferrisoma camini S3R1
Ga0586324 8143512 2 505	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1072500.00	KO:K00133	aspartate-semialdehyde dehydrogenase	Bacteria;Coprothermobacterota;Coprothermobacteria;Coprothermobacterales;Coprothermobacteraceae;Coprothermobacter;Coprothermobacter platensis;Coprothermobacter platensis DSM 11748
Ga0586324 0000001 222665 223663	1060000.00	0.00	956649.60	1976000.00	1957000.00	2104298.50	9735600.00	11163000.00	11988000.00	0.00	13481600.00	12255000.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324 0002733 772 1785	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1814400.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 0002802 12818 13888	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	816200.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Firmicutes;unclassified Firmicutes;unclassified Firmicutes;unclassified Firmicutes;Hydrogenispora;Hydrogenispora ethanolica;Hydrogenispora ethanolica DSM 25471
Ga0586324 0003422 2950 3951	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13321000.00	0.00	13050000.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Novimethylophilus;Novimethylophilus kurashikiensis;Novimethylophilus kurashikiensis La2-4
Ga0586324 0013553 7091 8092	3180000.00	0.00	0.00	1387000.00	1359600.00	0.00	547366.44	719800.00	470181.51	6691300.00	8184000.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Codakia orbicularis gill symbiont;Codakia orbicularis gill symbiont
Ga0586324 0015731 2660 3673	0.00	2516000.00	0.00	0.00	0.00	0.00	4651200.00	30012000.00	7452000.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Pandoraea;Pandoraea thiooxydans;Pandoraea thiooxydans DSM 25325
Ga0586324 0018035 716 1726	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	365884.29	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Gemmatimonadetes;Longimicrobia;Longimicrobiales;Longimicrobiaceae;Longimicrobium;Longimicrobium terrae;Longimicrobium terrae CECT 8660
Ga0586324 0074606 1714 2739	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4096400.00	3537600.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Actinobacteria;Coriobacteriia;Eggerthellales;Eggerthellaceae;Slackia;Slackia piriformis;Slackia piriformis YIT 12062
Ga0586324 0082036 1334 2392	6090000.00	0.00	5855200.00	0.00	0.00	5835900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0082242 2840 3766	0.00	0.00	0.00	1729000.00	1761300.00	0.00	0.00	1701900.00	805374.09	5212900.00	4382400.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0085611 1568 2707	0.00	2522800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Calidithermus;Calidithermus chliarophilus;Meiothermus chliarophilus ALT-8, DSM 9957
Ga0586324 0092083 2587 3567	4500000.00	0.00	0.00	6659500.00	471816.22	0.00	0.00	4715300.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 0099870 131 1135	0.00	0.00	0.00	3790500.00	0.00	0.00	0.00	1165100.00	972000.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Carboxydothermus;Carboxydothermus islandicus;Carboxydothermus islandicus SET IS-9
Ga0586324 0100418 2488 3423	0.00	0.00	0.00	0.00	5057300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rubrivivax;Rubrivivax gelatinosus;Rubrivivax gelatinosus IL144
Ga0586324 0103761 946 1944	0.00	0.00	0.00	0.00	0.00	0.00	0.00	300231.02	365365.89	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 0160522 467 1507	0.00	0.00	0.00	0.00	0.00	10083800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Planctomycetes;Planctomycetia;Gemmatales;Gemmataceae;Zavarzinella;Zavarzinella formosa;Zavarzinella formosa DSM 19928
Ga0586324 0166635 856 1857	0.00	0.00	0.00	0.00	513980.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324 0216117 543 1544	3690000.00	2951200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiobaca;Thiobaca trueperi;Thiobaca trueperi DSM 13587
Ga0586324 0293051 705 1763	3160000.00	0.00	0.00	0.00	149746.55	3946211.76	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0452081 3 293	0.00	0.00	0.00	0.00	0.00	2456167.54	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 0557522 1 417	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1073600.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 0585333 3 989	0.00	0.00	0.00	0.00	2111500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324 0745820 1 624	0.00	775200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0787902 839 1345	887590.00	2917200.00	0.00	0.00	0.00	0.00	0.00	0.00	1271700.00	0.00	2622400.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Janthinobacterium;Janthinobacterium sp. B9-8;Janthinobacterium sp. B9-8
Ga0586324 0823836 1 987	16700000.00	0.00	7206400.00	19190000.00	0.00	4962500.00	6817200.00	10370000.00	10854000.00	0.00	10912000.00	8400000.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Firmicutes;unclassified Firmicutes;unclassified Firmicutes;unclassified Firmicutes;Hydrogenispora;Hydrogenispora ethanolica;Hydrogenispora ethanolica DSM 25471
Ga0586324 1161930 1 507	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1597500.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Firmicutes;unclassified Firmicutes;unclassified Firmicutes;unclassified Firmicutes;Hydrogenispora;Hydrogenispora ethanolica;Hydrogenispora ethanolica DSM 25471
Ga0586324 1213490 117 1118	0.00	0.00	0.00	0.00	0.00	0.00	0.00	370562.19	186295.14	95803.40	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Carboxydothermus;Carboxydothermus pertinax;Carboxydothermus pertinax Ug1
Ga0586324 1570723 1 393	0.00	0.00	0.00	0.00	0.00	0.00	0.00	346032.87	0.00	0.00	0.00	314784.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Ferriphaselus;Ferriphaselus amnicola;Ferriphaselus amnicola OYT1
Ga0586324 1805037 471 944	1630000.00	25024000.00	3070686.45	2289500.00	2873700.00	3101772.91	2325600.00	2415600.00	3231900.00	45507000.00	1786400.00	2107500.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas;Pseudoxanthomonas sp. OG2;Pseudoxanthomonas sp. OG2
Ga0586324 2084087 296 889	0.00	2074000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 2556392 7 813	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1927500.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 2725378 1 645	0.00	2992000.00	0.00	2403500.00	0.00	2014485.19	0.00	0.00	0.00	1978900.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio alcoholivorans;Desulfovibrio alcoholivorans DSM 5433
Ga0586324 2992414 271 762	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6968500.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter soli;Solirubrobacter soli DSM 22325
Ga0586324 3128612 1 666	4140000.00	4256800.00	0.00	0.00	0.00	4565500.00	509096.64	3050000.00	0.00	0.00	0.00	4042500.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Firmicutes;unclassified Firmicutes;unclassified Firmicutes;unclassified Firmicutes;Hydrogenispora;Hydrogenispora ethanolica;Hydrogenispora ethanolica DSM 25471
Ga0586324 3205221 316 741	0.00	0.00	0.00	0.00	0.00	6113800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Odoribacteraceae;Odoribacter;Odoribacter sp. AF15-53;Odoribacter sp. AF15-53
Ga0586324 3239904 3 566	0.00	3046400.00	0.00	2118500.00	0.00	0.00	0.00	2830400.00	1725300.00	3249400.00	4039200.00	1387500.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 3372229 5 724	0.00	0.00	0.00	0.00	0.00	8178200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 3889702 3 683	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1152800.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 4041407 138 674	0.00	0.00	0.00	0.00	6406600.00	0.00	0.00	0.00	6277500.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Acetivibrio;Acetivibrio thermocellus;Acetivibrio thermocellus ATCC 27405
Ga0586324 4234642 1 465	0.00	0.00	0.00	15580000.00	17201000.00	11473300.00	2781600.00	1903200.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 4758797 3 629	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2947500.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetobacterium;Candidatus Magnetobacterium casensis;Candidatus Magnetobacterium casensis MYR-1
Ga0586324 4856886 2 532	934007.00	5331200.00	0.00	1558000.00	1483200.00	0.00	1328674.56	1177300.00	1539000.00	0.00	0.00	5100000.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 611, DSM 198
Ga0586324 5818880 3 578	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4910400.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylobacillus;Methylobacillus rhizosphaerae;Methylobacillus rhizosphaerae Ca-68
Ga0586324 6081475 2 568	0.00	0.00	1417110.41	0.00	0.00	1741488.14	0.00	3348900.00	5427000.00	0.00	2736800.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium;Novosphingobium lentum;Novosphingobium lentum NBRC 107847
Ga0586324 6090820 3 383	0.00	0.00	0.00	12730000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 6151579 3 566	0.00	0.00	0.00	0.00	9012500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas sp. TF;Desulfuromonas sp. TF
Ga0586324 6309032 116 559	0.00	10608000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas sp. LW13;Methylomonas sp. LW13
Ga0586324 6704607 2 547	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1082400.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas sp. TF;Desulfuromonas sp. TF
Ga0586324 6820463 2 541	0.00	0.00	0.00	0.00	0.00	0.00	3306000.00	0.00	4714200.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Calidithermus;Calidithermus timidus;Meiothermus timidus DSM 17022
Ga0586324 6882224 23 541	0.00	0.00	1516097.07	7714000.00	0.00	0.00	0.00	3635600.00	3912300.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 7216091 3 530	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2502900.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 7414915 2 523	0.00	0.00	0.00	0.00	4120000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Pseudorhodoplanes;Pseudorhodoplanes sinuspersici;Pseudorhodoplanes sinuspersici RIPI110
Ga0586324 7572884 29 520	0.00	0.00	0.00	13775000.00	0.00	17190100.00	0.00	0.00	7508700.00	0.00	0.00	0.00	KO:K00134	glyceraldehyde 3-phosphate dehydrogenase	Bacteria;Firmicutes;unclassified Firmicutes;unclassified Firmicutes;unclassified Firmicutes;Hydrogenispora;Hydrogenispora ethanolica;Hydrogenispora ethanolica DSM 25471
Ga0586324 0000437 4149 5702	0.00	0.00	3683540.10	0.00	0.00	4922800.00	3237600.00	2397300.00	0.00	0.00	0.00	0.00	KO:K00138	aldehyde dehydrogenase	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas;Gemmatimonas aurantiaca;Gemmatimonas aurantiaca T-27T
Ga0586324 0945277 167 1243	0.00	0.00	0.00	0.00	0.00	0.00	4058400.00	0.00	0.00	0.00	0.00	0.00	KO:K00140	malonate-semialdehyde dehydrogenase (acetylating)/methylmalonate-semialdehyde dehydroger	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacterium;Desulfobacterium vacuolatum;Desulfobacterium vacuolatum DSM 3385
Ga0586324 0000423 30607 31635	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6836400.00	0.00	0.00	0.00	KO:K00145	N-acetyl-gamma-glutamyl-phosphate reductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0020730 1674 2732	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1262700.00	0.00	0.00	0.00	0.00	KO:K00145	N-acetyl-gamma-glutamyl-phosphate reductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0000011 100569 101825	0.00	0.00	0.00	0.00	0.00	0.00	1576802.40	0.00	1603800.00	5382300.00	5324000.00	5347500.00	KO:K00147	glutamate-5-semialdehyde dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0012925 8015 9088	0.00	0.00	0.00	0.00	0.00	0.00	0.00	111630000.00	0.00	1821877.75	0.00	0.00	KO:K00147	glutamate-5-semialdehyde dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324 3253916 1 735	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10530000.00	0.00	0.00	0.00	KO:K00147	glutamate-5-semialdehyde dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas aestuarii;Nitrosomonas aestuarii Nm69
Ga0586324 3565397 3 671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1957500.00	KO:K00147	glutamate-5-semialdehyde dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0716937 2 1030	0.00	0.00	1477002.35	0.00	0.00	0.00	3283200.00	0.00	0.00	0.00	0.00	0.00	KO:K00150	glyceraldehyde-3-phosphate dehydrogenase (NAD(P))	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0758393 858 1367	0.00	0.00	4936186.95	0.00	6035800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00150	glyceraldehyde-3-phosphate dehydrogenase (NAD(P))	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 7157457 3 533	0.00	0.00	0.00	0.00	0.00	2532748.84	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00150	glyceraldehyde-3-phosphate dehydrogenase (NAD(P))	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0000003 97280 98281	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6244700.00	2824800.00	6502500.00	KO:K00161	pyruvate dehydrogenase E1 component alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0067507 2687 4087	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1357500.00	KO:K00162	pyruvate dehydrogenase E1 component beta subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. URHD0069;Bradyrhizobium sp. URHD0069
Ga0586324 0010511 1327 4011	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1640900.00	0.00	0.00	0.00	0.00	KO:K00163	pyruvate dehydrogenase E1 component	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0299652 1 2058	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	160975.35	0.00	0.00	0.00	KO:K00163	pyruvate dehydrogenase E1 component	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus gilardii;Cupriavidus gilardii CR3
Ga0586324 1423867 2 1042	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5264300.00	0.00	0.00	0.00	0.00	KO:K00163	pyruvate dehydrogenase E1 component	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Pirellula;Pirellula staleyi;Pirellula staleyi DSM 6068
Ga0586324 2238652 3 860	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1512800.00	0.00	0.00	0.00	0.00	KO:K00163	pyruvate dehydrogenase E1 component	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas eutropha;Nitrosomonas eutropha Nm24
Ga0586324 0551009 546 1571	0.00	0.00	0.00	0.00	0.00	7423900.00	0.00	3190300.00	3831300.00	0.00	0.00	0.00	KO:K00169	pyruvate ferredoxin oxidoreductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3467679 1 405	0.00	1441600.00	0.00	1320500.00	1720100.00	422936.01	0.00	1354200.00	939600.00	0.00	0.00	0.00	KO:K00169	pyruvate ferredoxin oxidoreductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0551009 3 545	0.00	4168400.00	0.00	0.00	0.00	0.00	0.00	0.00	2454300.00	0.00	0.00	0.00	KO:K00170	pyruvate ferredoxin oxidoreductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 8095922 3 506	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1140000.00	KO:K00170	pyruvate ferredoxin oxidoreductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0928363 153 524	0.00	0.00	0.00	0.00	0.00	0.00	2690400.00	0.00	0.00	0.00	0.00	0.00	KO:K00171	pyruvate ferredoxin oxidoreductase delta subunit	Archaea;Crenarchaeota;Thermoprotei;Thermoproteales;Thermoproteaceae;Pyrobaculum;Pyrobaculum sp. WP30;Pyrobaculum sp. WP30
Ga0586324 0432004 115 651	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3562400.00	0.00	0.00	0.00	0.00	KO:K00172	pyruvate ferredoxin oxidoreductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0836466 862 1311	0.00	5399200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00172	pyruvate ferredoxin oxidoreductase gamma subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 1653619 117 752	0.00	0.00	0.00	10450000.00	0.00	2848482.94	0.00	0.00	33615000.00	0.00	0.00	0.00	KO:K00172	pyruvate ferredoxin oxidoreductase gamma subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 3749835 293 694	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7867200.00	0.00	KO:K00172	pyruvate ferredoxin oxidoreductase gamma subunit	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324 5389599 13 564	0.00	0.00	0.00	0.00	0.00	15244800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00172	pyruvate ferredoxin oxidoreductase gamma subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 8007698 194 508	0.00	0.00	0.00	0.00	0.00	0.00	0.00	23485000.00	0.00	0.00	0.00	0.00	KO:K00172	pyruvate ferredoxin oxidoreductase gamma subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfarculus;Desulfarculus baarsii;Desulfarculus baarsii 2st14, DSM 2075
Ga0586324 1042922 151 1191	13900000.00	0.00	0.00	8607000.00	13287000.00	0.00	0.00	0.00	0.00	0.00	0.00	1417500.00	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. OR-1;Geobacter sp. OR-1
Ga0586324 1102614 3 905	0.00	240985.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfofaba;Desulfofaba hansenii;Desulfofaba hansenii DSM 12642
Ga0586324 0020602 131 2548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4215100.00	0.00	0.00	0.00	0.00	KO:K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0092445 170 2680	13900000.00	20168800.00	0.00	22420000.00	0.00	25606500.00	11103600.00	0.00	24786000.00	1262800.00	0.00	2257500.00	KO:K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0096290 231 2696	3349790.00	18387200.00	8951700.00	5092000.00	71337800.00	9051600.00	32170800.00	18727000.00	5572800.00	16100700.00	0.00	10950000.00	KO:K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0108059 610 3075	240470.00	18033600.00	7882000.00	15485000.00	0.00	0.00	8344800.00	8784000.00	0.00	1610379.54	0.00	1471332.00	KO:K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0148932 1 2172	0.00	0.00	0.00	6184500.00	4816359.31	6592518.48	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri 3
Ga0586324 0698650 1 1416	6280000.00	12988000.00	0.00	4883000.00	4037600.00	0.00	1635959.28	10461500.00	5985900.00	5120500.00	9653600.00	6045000.00	KO:K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 1141555 1 1146	0.00	0.00	0.00	0.00	414144.46	0.00	0.00	519113.66	173831.67	0.00	0.00	0.00	KO:K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 2484576 2 823	0.00	19176000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0047107 1 1116	3850000.00	150892000.00	19029400.00	10830000.00	13493000.00	21676200.00	216372000.00	19739600.00	114566400.00	11242000.00	77352000.00	122700000.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0549039 273 1574	132110000.00	111044000.00	48793160.68	58140000.00	0.00	29060400.00	46758766.68	45329100.00	52594039.53	21714000.00	22862400.00	22822500.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0580456 113 1519	4770000.00	34068000.00	4919060.49	12654000.00	28840000.00	8337000.00	1731190.32	5111800.00	11907000.00	5698000.00	6820000.00	960000.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4003423 3 251	0.00	0.00	144691000.00	0.00	0.00	161182000.00	55176000.00	89060000.00	69660000.00	0.00	31416000.00	0.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4217445 3 662	0.00	34170000.00	0.00	0.00	14420000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4288142 1 657	0.00	0.00	2308817.96	0.00	0.00	0.00	0.00	246652.89	0.00	0.00	0.00	0.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanocellales;Methanocellaceae;Methanocella;Methanocella arvoryzae;Methanocella arvoryzae MRE50
Ga0586324 5210879 3 605	8650000.00	0.00	0.00	0.00	9074300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 6026791 1 570	0.00	0.00	0.00	4408000.00	5665000.00	0.00	0.00	3739300.00	4317300.00	0.00	0.00	0.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina mazei;Methanosarcina mazei YBB.H.M.1B.1
Ga0586324 7869255 1 345	0.00	9520000.00	0.00	0.00	0.00	0.00	0.00	0.00	5192100.00	0.00	0.00	0.00	KO:K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0047107 2388 3740	26800000.00	10132000.00	11541500.00	2679000.00	0.00	6550500.00	0.00	3531900.00	3507300.00	0.00	0.00	2565000.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0048671 1773 2717	3560000.00	3944000.00	9627300.00	7837500.00	6684700.00	15117823.52	11127277.80	12497375.00	11210400.00	10610600.00	11655337.76	5445000.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0059416 3142 4086	2430000.00	0.00	0.00	0.00	0.00	4724300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0125148 1885 2829	17580000.00	6242400.00	6814005.89	8474000.00	12988300.00	9968340.49	7546800.00	7027200.00	14855400.00	2470380.99	1660642.72	2853537.75	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0147716 298 1245	23400000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0154681 731 2269	2030000.00	1190000.00	1334304.37	1415500.00	2575000.00	0.00	1943346.60	4404200.00	13446000.00	1255100.00	1575200.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0190386 1512 2453	0.00	0.00	1896251.56	5928000.00	6097600.00	1499754.84	5084400.00	5959700.00	4212000.00	2171400.00	3018400.00	3180000.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0251909 1374 2225	5240000.00	4209200.00	0.00	13585000.00	17355500.00	0.00	10716000.00	1403000.00	8002800.00	5713400.00	0.00	6420000.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0277895 1208 2128	0.00	0.00	0.00	5149000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0420772 259 1203	1110000.00	1285200.00	1149302.57	1900000.00	1596500.00	1329398.17	2000408.16	2098400.00	1417500.00	1116500.00	1478400.00	1140000.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0624194 491 1489	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1152900.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0765685 140 1087	0.00	0.00	0.00	0.00	0.00	0.00	0.00	628300.00	793261.35	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1308214 3 593	0.00	0.00	0.00	198968.95	176959.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 2484922 1 573	0.00	0.00	0.00	0.00	27501000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109

Ga0586324 2668118 1 774	0.00	3712800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 2916911 2 772	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2379000.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina sp. BuS5;Desulfosarcina sp. BuS5
Ga0586324 3114661 123 749	0.00	0.00	0.00	15105000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3132122 3 749	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	396983.51	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 3773907 29 691	9150000.00	6800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 6069467 266 568	0.00	0.00	0.00	2137500.00	1751000.00	526219.53	0.00	695400.00	0.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 6267432 3 563	31230000.00	32408800.00	36707600.00	36033500.00	33093900.00	29298600.00	22389600.00	23338600.00	15985392.93	22645700.00	21498400.00	21420000.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 6478852 3 554	0.00	0.00	0.00	14563500.00	2914900.00	6947500.00	0.00	3775900.00	2057400.00	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 8084193 143 505	1680000.00	972400.00	4449248.25	7714000.00	12895600.00	7265100.00	0.00	0.00	4659414.03	0.00	0.00	0.00	KO:K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0413777 442 954	0.00	0.00	0.00	6270000.00	6180000.00	5716800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00195	acetyl-CoA decarbonylase/synthase complex subunit epsilon	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri 3
Ga0586324 1755254 356 868	0.00	0.00	0.00	3714500.00	3852200.00	0.00	0.00	0.00	2988900.00	0.00	0.00	0.00	KO:K00195	acetyl-CoA decarbonylase/synthase complex subunit epsilon	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina sp. DSM 11855;Methanosarcina sp. DSM 11855
Ga0586324 2280975 180 692	0.00	0.00	0.00	0.00	0.00	7423900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00195	acetyl-CoA decarbonylase/synthase complex subunit epsilon	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina horonobensis;Methanosarcina horonobensis HB-1
Ga0586324 0008881 6841 8193	3140000.00	2516000.00	0.00	5975500.00	1998200.00	0.00	0.00	0.00	0.00	1293600.00	3018400.00	1102500.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0013713 1337 2677	33500000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	29799000.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0016535 727 2067	0.00	0.00	0.00	0.00	0.00	0.00	3192000.00	5929200.00	7443900.00	0.00	0.00	2677500.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0053197 3504 4640	0.00	0.00	0.00	5586000.00	5901900.00	2307816.58	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0076486 2717 3895	0.00	0.00	0.00	0.00	0.00	845435.32	0.00	0.00	0.00	1901900.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0091922 3 350	0.00	0.00	0.00	5994500.00	2163000.00	0.00	4605600.00	1665300.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0209267 265 1608	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	847000.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0253929 903 2216	0.00	19992000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0412699 832 1785	0.00	0.00	0.00	0.00	0.00	0.00	2217774.24	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324 0483466 2 634	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6527000.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1473762 2 1027	0.00	0.00	0.00	8265000.00	12669000.00	26003500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 1503230 551 1018	0.00	0.00	0.00	0.00	395456.14	0.00	0.00	2061800.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 1583786 3 869	0.00	0.00	0.00	8407500.00	0.00	0.00	0.00	0.00	7063200.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina sp. BuS5;Desulfosarcina sp. BuS5
Ga0586324 2775484 1 786	0.00	0.00	0.00	0.00	1000615.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2910733 2 772	0.00	0.00	0.00	8882500.00	7436600.00	0.00	0.00	0.00	4592700.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 3638298 1 702	0.00	0.00	0.00	0.00	16274000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4011345 2 676	0.00	0.00	0.00	0.00	18746000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4724276 3 632	5330000.00	4508400.00	6643400.00	4227500.00	4305400.00	12068800.00	0.00	2928000.00	6301800.00	2402400.00	2939200.00	2842500.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4778256 2 628	0.00	0.00	0.00	0.00	0.00	59153000.00	0.00	0.00	38556000.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina sp. Kolksee;Methanosarcina sp. Kolksee
Ga0586324 5381534 2 598	1920000.00	12240000.00	0.00	13395000.00	14111000.00	8694300.00	12175200.00	11590000.00	9639000.00	0.00	0.00	8775000.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 5486413 3 593	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	670300.92	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 5716143 1 585	5850000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 6806504 3 542	393252.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 7948469 2 508	0.00	0.00	0.00	12730000.00	11639000.00	0.00	0.00	7381000.00	0.00	0.00	0.00	0.00	KO:K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0002429 11032 12942	0.00	0.00	0.00	0.00	0.00	0.00	2245252.80	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0009689 9758 10336	0.00	346733.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0017935 2919 4955	0.00	0.00	0.00	3610000.00	10186700.00	13061300.00	6315600.00	5856000.00	3280500.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324 0032078 209 2251	0.00	0.00	0.00	0.00	0.00	0.00	3693600.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324 0033443 450 2417	0.00	0.00	0.00	0.00	3306300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0059416 971 2995	0.00	0.00	0.00	0.00	0.00	13855300.00	0.00	0.00	0.00	0.00	0.00	745284.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0147716 1404 2849	0.00	0.00	0.00	0.00	0.00	2474993.28	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0172951 1984 2646	0.00	0.00	0.00	0.00	0.00	2793153.05	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0185286 357 2333	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	772743.24	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0222223 303 2330	0.00	0.00	0.00	3002000.00	2245400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324 0291747 2 1762	906787.00	0.00	0.00	0.00	0.00	0.00	0.00	2342400.00	0.00	0.00	0.00	1567500.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0325179 3 737	4290000.00	0.00	0.00	0.00	0.00	0.00	0.00	14030000.00	11664000.00	14399000.00	9152000.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0340151 2 958	0.00	53584000.00	0.00	0.00	170980000.00	0.00	0.00	90890000.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324 0342779 3 1787	0.00	7860800.00	0.00	13110000.00	9651100.00	0.00	0.00	0.00	4406400.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0357415 3 1568	0.00	0.00	7150100.00	4854500.00	0.00	0.00	33972000.00	0.00	0.00	21560000.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0360485 3 1784	14300000.00	0.00	9345800.00	0.00	12875000.00	0.00	15116400.00	7198000.00	8343000.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0406659 831 1796	6540000.00	3060000.00	0.00	10830000.00	0.00	0.00	0.00	0.00	0.00	8162000.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0874128 2 649	6540000.00	2475200.00	0.00	3106500.00	1246300.00	0.00	0.00	1878800.00	3248100.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0914745 1 1260	0.00	0.00	0.00	2593500.00	4346600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfopila;Desulfopila aestuarii;Desulfopila aestuarii DSM 18488
Ga0586324 0960244 3 1235	0.00	11621200.00	2936664.30	0.00	0.00	0.00	0.00	0.00	874800.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1069603 2 1141	1860000.00	5100000.00	0.00	0.00	0.00	0.00	5768400.00	4776300.00	5516100.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1165256 1 870	0.00	0.00	0.00	1054500.00	0.00	0.00	0.00	230228.64	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 1175033 38 1132	3330000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 1478217 1 1026	0.00	462922.24	0.00	0.00	0.00	8892800.00	0.00	0.00	9477000.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1640061 2 895	0.00	2454800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1891998 311 925	0.00	0.00	0.00	1159000.00	2369000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 1983577 2 778	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	578112.15	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 2135921 30 878	0.00	0.00	0.00	1045000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 2244057 1 861	4090000.00	0.00	0.00	0.00	0.00	0.00	0.00	628300.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2855795 182 778	3020000.00	3998400.00	7825700.00	16340000.00	10918000.00	57104519.70	24122400.00	7625000.00	10602900.00	4419800.00	11105600.00	15075000.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 3153100 220 747	0.00	0.00	0.00	0.00	0.00	727494.56	1246754.16	0.00	1134000.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3575595 3 707	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3043900.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 3789943 3 692	0.00	0.00	0.00	3439000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 4134727 104 667	0.00	0.00	0.00	216425.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 4510073 1 642	0.00	13260000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4788000 3 629	0.00	0.00	0.00	0.00	0.00	0.00	96444000.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 5091440 1 612	0.00	0.00	0.00	4104000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5265810 3 605	0.00	0.00	0.00	0.00	2121800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5577880 3 590	0.00	0.00	0.00	0.00	19158000.00	14847800.00	8253600.00	12200000.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5719635 1 582	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	473316.21	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 6602596 3 551	0.00	344543.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 7103589 1 534	0.00	0.00	0.00	0.00	0.00	0.00	0.00	157764.91	0.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 7382473 1 525	0.00	39236000.00	0.00	98800000.00	316807.40	0.00	0.00	52887000.00	43254000.00	0.00	0.00	0.00	KO:K00198	carbon-monoxide dehydrogenase catalytic subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 7570091 2 520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5892600.00	0.00	0.00	0.00	0.00	KO:K00200	formylmethanofuran dehydrogenase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0676120 424 1437	6490000.00	0.00	11823000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00201	formylmethanofuran dehydrogenase subunit B	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 1148343 1 1143	0.00	0.00	9120600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00205	4Fe-4S ferredoxin	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GKZPZ, DSM 4140
Ga0586324 0037004 4348 5121	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3721000.00	0.00	0.00	0.00	0.00	KO:K00208	enoyl-[acyl-carrier protein] reductase I	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira defluvii;Nitrospira defluvii
Ga0586324 0183631 1523 2305	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1355200.00	0.00	KO:K00208	enoyl-[acyl-carrier protein] reductase I	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas;Pseudomonas linyingensis;Pseudomonas linyingensis LMG 25967
Ga0586324 0528289 2 655	0.00	0.00	3052405.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00208	enoyl-[acyl-carrier protein] reductase I	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 7177985 3 530	0.00	0.00	0.00	0.00	1668600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00208	enoyl-[acyl-carrier protein] reductase I	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Balneatrichaceae;Pokkaliibacter;Pokkaliibacter plantistimulans;Pokkaliibacter plantistimulans L1E11
Ga0586324 7601373 2 517	0.00	0.00	2926761.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00208	enoyl-[acyl-carrier protein] reductase I	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter marinus;Methylobacter marinus A45
Ga0586324 0171168 616 1422	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4919200.00	0.00	KO:K00215	4-hydroxy-tetrahydrodipicolinate reductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 0438024 1 1434	425674.00	0.00	0.00	0.00	0.00	0.00	0.00	1439600.00	0.00	0.00	0.00	0.00	KO:K00219	2,4-dienoyl-CoA reductase (NADPH2)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324 4330780 3 653	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1064800.00	0.00	KO:K00228	coproporphyrinogen III oxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalkalivibrio;Thioalkalivibrio sulfidiphilus;Thioalkalivibrio sulfidophilus HL-EbGR7
Ga0586324 0057175 1788 3578	0.00	0.00	0.00	0.00	0.00	1010944.62	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Woeseiaceae;unclassified Woeseiaceae;unclassified Woeseiaceae;uncultured Woeseiaceae SAG 1868 B
Ga0586324 0058809 3010 4419	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	358526.96	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter superfactus;Methyloceanibacter superfactus R-67175
Ga0586324 0173151 2 619	0.00	0.00	0.00	7790000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Hymenobacteraceae;Pontibacter;Pontibacter oryzae;Pontibacter oryzae KIRAN
Ga0586324 0265555 191 2140	0.00	0.00	0.00	959500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus;Chloroflexus aggregans;Chloroflexus aggregans DSM 9485
Ga0586324 0532104 1 1434	0.00	0.00	0.00	57190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. OR-1;Geobacter sp. OR-1
Ga0586324 0565421 257 1552	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5661900.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0576188 1 1392	3120000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4301100.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 0666186 174 1448	0.00	0.00	0.00	0.00	0.00	0.00	0.00	817400.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324 0668243 314 1444	0.00	0.00	0.00	0.00	2183600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Hymenobacteraceae;Rufibacter;Rufibacter latericius;Rufibacter latericius bvd1
Ga0586324 0724072 1 972	14300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0948251 2 1243	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1075888.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324 1039564 3 1193	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	755011.53	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Roseimarinus;Roseimarinus sediminis;Roseimarinus sediminis DSM 28824
Ga0586324 1106617 1 1161	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8976000.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 1188999 1 1128	0.00	0.00	0.00	0.00	0.00	0.00	13406400.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 1400090 1 936	0.00	0.00	0.00	0.00	29355000.00	0.00	0.00	0.00	2867400.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324 1483764 1 630	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	138629.88	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 1497595 1 1020	0.00	0.00	0.00	3439000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Thermomonosporaceae;Thermomonospora;Thermomonospora curvata;Thermomonospora curvata DSM 43183
Ga0586324 1654603 3 608	0.00	0.00	0.00	0.00	2678000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas aromatica;Dechloromonas aromatica RCB
Ga0586324 1842949 1 936	0.00	0.00	0.00	0.00	701105.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus castenholzii;Roseiflexus castenholzii HLO8, DSM 13941
Ga0586324 1869805 2 514	0.00	0.00	0.00	5747500.00	0.00	6629900.00	0.00	0.00	3555900.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Sphingobacteriaceae;Mucilaginibacter;Mucilaginibacter sp. X4EP1;Mucilaginibacter sp. X4EP1
Ga0586324 1929326 1 918	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1474200.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 3809141 2 691	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6934400.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus sp. RS-1;Roseiflexus sp. RS-1
Ga0586324 5074373 3 614	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2156000.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1pr3, DSM 2032
Ga0586324 6566519 1 552	0.00	15436000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 1363083 2 475	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1640100.00	0.00	0.00	KO:K00240	succinate dehydrogenase / fumarate reductase iron-sulfur subunit	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;unclassified Zoogloeaceae;Zoogloeaceae bacteirum Par-f-2;Zoogloeaceae bacteirum Par-f-2
Ga0586324 0075554 2 1582	0.00	0.00	24884600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00244	fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0241395 106 2046	0.00	0.00	0.00	0.00	0.00	2995404.70	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00244	fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax carolinensis;Acidovorax carolinensis P4
Ga0586324 0985021 159 1223	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	670857.00	KO:K00244	fumarate reductase flavoprotein subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter thiogenes;Geobacter thiogenes ATCC BAA-34
Ga0586324 1029122 260 1198	0.00	0.00	18973100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00248	butyryl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1pr3, DSM 2032
Ga0586324 1218963 32 1114	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1984500.00	0.00	0.00	0.00	KO:K00248	butyryl-CoA dehydrogenase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Caldisalinibacter;Caldisalinibacter kiritimatiensis;Clostridiaceae bacterium L21-TH-D2
Ga0586324 1792850 3 311	0.00	1509600.00	0.00	6308000.00	6025500.00	5835900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00248	butyryl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324 0025665 4276 5418	0.00	1543600.00	3174436.09	1795500.00	2111500.00	0.00	0.00	1683600.00	0.00	0.00	0.00	0.00	KO:K00249	acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324 0032054 3246 4511	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1531200.00	0.00	KO:K00249	acyl-CoA dehydrogenase	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus sp. RS-1;Roseiflexus sp. RS-1
Ga0586324 0109383 1137 2423	0.00	0.00	0.00	11210000.00	0.00	0.00	0.00	199424.86	0.00	0.00	0.00	0.00	KO:K00249	acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;unclassified Spongiibacteraceae;marine gamma proteobacterium HTCC2143;Marine gamma proteobacterium sp. HTCC2143
Ga0586324 0120710 1722 2864	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3018400.00	0.00	0.00	KO:K00249	acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324 0294655 1 990	0.00	0.00	0.00	0.00	1040300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00249	acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 0551615 37 1287	2050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00249	acyl-CoA dehydrogenase	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus sp. RS-1;Roseiflexus sp. RS-1
Ga0586324 3899562 2 682	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	939600.00	0.00	0.00	0.00	KO:K00249	acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;unclassified Hyphomicrobiales;Rhizobiales bacterium YIM 77505;Rhizobiales bacterium YIM 77505
Ga0586324 0008898 9260 10444	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10736000.00	0.00	KO:K00253	isovaleryl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0147090 954 2144	0.00	16252000.00	26517300.00	0.00	0.00	23820000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00253	isovaleryl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 2656903 3 800	0.00	0.00	0.00	732181.15	0.00	549809.27	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00253	isovaleryl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 0093698 696 1982	0.00	0.00	0.00	3135000.00	2791300.00	0.00	3488400.00	0.00	0.00	0.00	0.00	0.00	KO:K00260	glutamate dehydrogenase	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324 0874120 3 860	0.00	0.00	0.00	0.00	2008500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00260	glutamate dehydrogenase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 1019905 1 570	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1366400.00	1652400.00	0.00	1320000.00	0.00	KO:K00260	glutamate dehydrogenase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0008686 4351 5697	0.00	0.00	0.00	31663500.00	0.00	24931600.00	0.00	5849900.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter thiogenes;Geobacter thiogenes ATCC BAA-34
Ga0586324 0011932 972 2309	0.00	0.00	0.00	0.00	1071200.00	0.00	0.00	0.00	0.00	10780000.00	0.00	13275000.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 0014023 3727 5064	0.00	0.00	0.00	0.00	0.00	3970000.00	0.00	969900.00	709378.56	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified Bacteroidales;unclassified Bacteroidales;Bacteroidales bacterium 6E;Bacteroidales bacterium 6E
Ga0586324 0028772 4653 5999	1390000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 0030454 3949 5310	0.00	0.00	0.00	0.00	927896.10	0.00	6178800.00	0.00	1028700.00	0.00	0.00	234629.25	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497

Ga0586324 0032905 3921 5417	0.00	2284800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0068126 1 1056	0.00	593742.68	34849700.00	0.00	0.00	0.00	747356.64	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0092990 1497 2831	0.00	8704000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 0111980 1845 3248	0.00	15096000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 0179203 1063 2400	0.00	972400.00	0.00	0.00	0.00	0.00	0.00	0.00	28593000.00	37653000.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PB90-1
Ga0586324 0186054 1089 2438	1790000.00	0.00	1524784.16	0.00	440862.66	0.00	0.00	590950.92	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina cetonica;Desulfosarcina cetonica JCM 12296
Ga0586324 0248429 542 1915	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	198219.96	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium MLMS-1;delta proteobacterium sp. MLMS-1
Ga0586324 0336544 3 1196	850950.00	0.00	0.00	0.00	1133000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 0352482 3 1364	65760000.00	2631600.00	2536906.15	0.00	0.00	0.00	7136400.00	1561600.00	2107815.21	2825900.00	2716736.88	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified Bacteroidales;unclassified Bacteroidales;Bacteroidales bacterium 6E;Bacteroidales bacterium 6E
Ga0586324 0465820 3 1052	0.00	26996000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Candidatus Hydrogenedentes;unclassified Candidatus Hydrogenedentes;unclassified Candidatus Hydrogenedentes;unclassified Candidatus Hydrogenedentes;unclassified Candidatus Hydrogenedentes;Hydrogenedentes bacterium JGI 0000077-D07;Hydrogenedentes bacterium JGI 0000077-D07 (contamination screened)
Ga0586324 0500303 3 377	0.00	0.00	0.00	60135000.00	30694000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 0555854 2 1294	845906.00	0.00	0.00	0.00	768591.15	0.00	1787241.84	0.00	2146500.00	0.00	1381600.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 0557853 3 1283	0.00	479123.24	0.00	978500.00	2058178.96	0.00	0.00	0.00	0.00	793100.00	770823.68	358455.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Dokdonia;Dokdonia sp. 4H-3-7-5;Dokdonia sp. 4H-3-7-5
Ga0586324 0682672 3 845	0.00	0.00	0.00	4085000.00	93627000.00	8138500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 0751368 171 1373	0.00	0.00	0.00	0.00	0.00	0.00	0.00	277658.58	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. OR-1;Geobacter sp. OR-1
Ga0586324 0906816 163 1266	0.00	0.00	0.00	0.00	0.00	0.00	12220800.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella massiliensis;Reyranella massiliensis 521, DSM 23428
Ga0586324 0929384 3 863	0.00	0.00	0.00	0.00	0.00	8972200.00	11331600.00	8174000.00	0.00	7530600.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified Bacteroidales;unclassified Bacteroidales;Bacteroidales bacterium 6E;Bacteroidales bacterium 6E
Ga0586324 0933455 3 1250	0.00	0.00	0.00	4702500.00	4356900.00	0.00	0.00	1579900.00	77193000.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 1044948 3 1190	573375.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	189302.08	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified Bacteroidales;unclassified Bacteroidales;Bacteroidales bacterium 6E;Bacteroidales bacterium 6E
Ga0586324 1075850 3 845	0.00	0.00	0.00	3040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 1369927 3 956	0.00	15300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 1584074 2 757	2670000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified Bacteroidales;unclassified Bacteroidales;Bacteroidales bacterium 6E;Bacteroidales bacterium 6E
Ga0586324 1588273 3 995	1140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Tenacibaculum;Tenacibaculum adriaticum;Tenacibaculum adriaticum DSM 18961
Ga0586324 1614471 1 990	0.00	0.00	0.00	0.00	2636800.00	2227368.50	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 1672889 1 975	0.00	15368000.00	0.00	0.00	0.00	0.00	0.00	0.00	3985200.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;Cloacimonetes bacterium SCGC AAA252-M08;Cloacimonetes bacterium SCGC AAA252-M08 (contamination screened)
Ga0586324 1711341 3 965	0.00	0.00	335788.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Confluentibacter;Confluentibacter citreus;Confluentibacter citreus XJNY
Ga0586324 2062633 1 891	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8550000.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324 2088401 1 888	0.00	0.00	0.00	0.00	4315700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324 2202616 3 866	74400000.00	850000.00	515893.23	950000.00	1256600.00	75033000.00	1652461.92	1982500.00	1004400.00	0.00	0.00	272833.50	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 2442559 1 831	0.00	0.00	0.00	2346500.00	0.00	0.00	0.00	7076000.00	0.00	7700000.00	10718400.00	105711.75	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Faecalibacterium;Faecalibacterium prausnitzii;Faecalibacterium prausnitzii 2789STDY5834930
Ga0586324 2699587 262 795	2090000.00	2094400.00	0.00	988000.00	0.00	333073.08	653404.68	1433500.00	947700.00	1155000.00	1214400.00	1042500.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 2895491 3 773	0.00	0.00	0.00	0.00	12257000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 3319486 1 729	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9516000.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324 3364032 3 725	0.00	0.00	0.00	6621500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified Bacteroidales;unclassified Bacteroidales;Bacteroidales bacterium 6E;Bacteroidales bacterium 6E
Ga0586324 3387266 1 723	0.00	0.00	0.00	0.00	0.00	19135400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 3634302 1 702	0.00	0.00	0.00	0.00	0.00	0.00	5335200.00	0.00	0.00	16170000.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfopila;Desulfopila aestuarii;Desulfopila aestuarii DSM 18488
Ga0586324 3646517 1 702	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5137500.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324 3767416 2 694	0.00	7276000.00	2842080.30	3306000.00	0.00	0.00	10579200.00	16280900.00	7808400.00	63240100.00	7972800.00	38400000.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 3823422 3 689	0.00	0.00	0.00	0.00	0.00	0.00	642358.08	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Maribacter;Maribacter cobaltidurans;Maribacter cobaltidurans B1
Ga0586324 4145543 176 667	0.00	0.00	0.00	6365000.00	5943100.00	59153000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 4172883 3 665	0.00	0.00	0.00	0.00	1421400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus sp. ER46;Opitutus sp. ER46
Ga0586324 4370703 86 652	0.00	0.00	0.00	0.00	49543000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 4712227 2 631	46500000.00	35428000.00	52640500.00	22705000.00	21733000.00	56374000.00	34200000.00	0.00	26082000.00	0.00	16808000.00	25650000.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 4728710 1 525	0.00	0.00	0.00	0.00	0.00	834962.46	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324 5345648 2 478	0.00	0.00	0.00	0.00	668354.64	0.00	0.00	719800.00	0.00	568025.92	58432000.00	421349.25	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Citrifermentans;Citrifermentans pelophilum;Geobacter pelophilus Dfr2
Ga0586324 5752561 3 581	0.00	0.00	0.00	825642.15	362506.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;unclassified Peptococcaceae;Peptococcaceae bacterium DCMF;Peptococcaceae bacterium DCMF
Ga0586324 5812287 2 568	498370.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324 5967626 2 574	0.00	2631600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 6118036 1 567	0.00	0.00	0.00	0.00	257134.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 6514359 3 554	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3180100.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;Cloacimonetes bacterium JGI 0000014-K11;Cloacimonetes bacterium JGI 0000014-K11 (contamination screened)
Ga0586324 6677739 1 546	0.00	70040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 6832207 160 543	1130000.00	539293.72	0.00	0.00	0.00	0.00	0.00	817400.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324 7233843 2 529	0.00	0.00	0.00	0.00	768163.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 7433660 1 522	0.00	0.00	2009938.15	0.00	0.00	0.00	0.00	0.00	0.00	1678600.00	0.00	0.00	KO:K00262	glutamate dehydrogenase (NADP+)	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Tenacibaculum;Tenacibaculum caenipelagi;Tenacibaculum caenipelagi CECT 8283
Ga0586324 0000001 156184 160662	0.00	0.00	0.00	0.00	0.00	0.00	1151393.16	2107368.83	0.00	14614600.00	7040000.00	17827500.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0020713 2689 7173	0.00	0.00	0.00	0.00	0.00	0.00	183150.58	1427400.00	6147900.00	1393700.00	0.00	437656.50	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0022846 2653 6981	0.00	0.00	0.00	0.00	0.00	0.00	211229.92	0.00	0.00	0.00	0.00	0.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Armatimonadetes;Chthonomonadetes;Chthonomonadales;Chthonomonadaceae;Chthonomonas;Chthonomonas calidirosea;Chthonomonas calidirosea T49, DSM 23976
Ga0586324 0067693 3 2561	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1350000.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum;Herbaspirillum sp. K1R23-30;Herbaspirillum sp. K1R23-30
Ga0586324 0093241 2 3223	0.00	0.00	5911500.00	0.00	4223000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter superfactus;Methyloceanibacter superfactus R-67175
Ga0586324 0673587 1 1440	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5569300.00	0.00	0.00	0.00	0.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium petroleiphilum;Methylibium petroleiphilum PM1
Ga0586324 1216031 1 1116	0.00	1244400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium UKL13-2;Betaproteobacteria bacterium UKL13-2
Ga0586324 1248798 2 1105	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	389169.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas agitata;Dechloromonas agitata is5
Ga0586324 1405554 2 1048	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1579500.00	0.00	0.00	0.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. SG708;Dechloromonas sp. SG708
Ga0586324 2252900 1 858	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4507900.00	0.00	0.00	0.00	0.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 7429040 1 522	4070000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00265	glutamate synthase (NADPH/NADH) large chain	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-DMM
Ga0586324 0167176 1775 2689	0.00	0.00	0.00	502386.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00266	glutamate synthase (NADPH/NADH) small chain	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324 0200422 141 1559	0.00	5827600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00266	glutamate synthase (NADPH/NADH) small chain	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0751029 214 1374	0.00	5093200.00	0.00	3904500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00266	glutamate synthase (NADPH/NADH) small chain	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Pirellula;Pirellula staleyi;Pirellula staleyi DSM 6068
Ga0586324 0756407 2 1090	0.00	0.00	0.00	5348500.00	6046100.00	6431400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00266	glutamate synthase (NADPH/NADH) small chain	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0848450 763 1302	0.00	0.00	0.00	22610000.00	0.00	0.00	0.00	13725000.00	0.00	0.00	0.00	0.00	KO:K00266	glutamate synthase (NADPH/NADH) small chain	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2184694 3 869	0.00	0.00	0.00	0.00	0.00	1199535.50	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00266	glutamate synthase (NADPH/NADH) small chain	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0000004 109487 110935	0.00	0.00	0.00	0.00	0.00	0.00	3670800.00	2976800.00	1409400.00	0.00	5438400.00	4642500.00	KO:K00283	glycine dehydrogenase subunit 2	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0023337 519 2012	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	994400.00	0.00	KO:K00283	glycine dehydrogenase subunit 2	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiales Family XVI. Incertae Sedis;Carboxydocella;Carboxydocella sporoproducens;Carboxydocella sporoproducens DSM 16521
Ga0586324 7044560 1 528	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6150000.00	KO:K00286	pyrroline-5-carboxylate reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum 31/32
Ga0586324 0010707 6837 8867	0.00	0.00	0.00	0.00	0.00	0.00	467751.12	0.00	0.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0021358 3 1469	11200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0054348 2 1690	7460000.00	0.00	3484046.68	0.00	0.00	174283000.00	152076000.00	0.00	3620700.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324 0072455 1 1383	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	111384.72	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0323763 272 1987	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4981900.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 1052693 1 981	0.00	378590.00	0.00	1273000.00	2049700.00	0.00	0.00	1830000.00	0.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1465804 1 1029	0.00	0.00	0.00	0.00	0.00	815469.76	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 1648706 231 980	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	216776.25	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 2298868 2 853	55000000.00	0.00	0.00	102600000.00	0.00	0.00	0.00	0.00	80352000.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 2936669 3 767	6300000.00	0.00	0.00	0.00	1421400.00	8178200.00	0.00	0.00	0.00	0.00	0.00	1380000.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 3752408 1 693	0.00	0.00	4241276.05	0.00	0.00	0.00	3420000.00	6893000.00	0.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4060651 1 672	0.00	0.00	0.00	0.00	10815000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 4285021 1 657	0.00	0.00	0.00	15010000.00	14626000.00	0.00	0.00	0.00	4114800.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 5898678 2 376	0.00	0.00	0.00	0.00	0.00	756995.63	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 6204116 93 563	0.00	0.00	0.00	0.00	0.00	1201615.78	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 8106829 3 506	0.00	27744000.00	52021200.00	0.00	2152700.00	136568000.00	22800000.00	0.00	50463000.00	0.00	7559200.00	0.00	KO:K00288	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase/f	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0246928 1238 2245	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1312200.00	0.00	0.00	0.00	KO:K00297	methylenetetrahydrofolate reductase (NADPH)	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0889749 359 1276	0.00	0.00	0.00	0.00	0.00	1173865.48	1907099.16	1268800.00	0.00	0.00	0.00	0.00	KO:K00297	methylenetetrahydrofolate reductase (NADPH)	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2295482 3 851	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	801488.52	0.00	0.00	0.00	KO:K00297	methylenetetrahydrofolate reductase (NADPH)	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324 2690226 1 798	0.00	0.00	0.00	1387000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00297	methylenetetrahydrofolate reductase (NADPH)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324 0007546 3786 4625	677922.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0010839 6085 6924	5930000.00	22780000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8008000.00	8245600.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0027622 464 1303	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15092000.00	0.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0031012 3875 4714	2380000.00	8098800.00	2440818.94	5985000.00	0.00	527636.82	9712800.00	4403650.39	3645000.00	0.00	9944000.00	2032500.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0101723 3297 3401	11400000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0219196 245 1087	0.00	5630400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanocorpusculaceae;Methanocorpusculum;Methanocorpusculum bavaricum;Methanocorpusculum bavaricum DSM 4179
Ga0586324 0223906 797 1639	16500000.00	631222.92	2559600.68	15874500.00	6365400.00	3730215.97	0.00	2013000.00	2081700.00	5982900.00	1223200.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GKZPZ, DSM 4140
Ga0586324 0317102 257 1096	6830000.00	4957200.00	3218834.27	0.00	3862500.00	3040984.27	0.00	3586800.00	1190700.00	870100.00	0.00	1605000.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0342133 1 525	30700000.00	0.00	33273300.00	25745000.00	21527000.00	0.00	0.00	0.00	0.00	0.00	0.00	24075000.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0408587 447 1289	6550000.00	0.00	11034800.00	10260000.00	11227000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis ethanolicus;Methanofollis ethanolicus JCM 15103
Ga0586324 0508055 486 1325	0.00	2543200.00	0.00	0.00	520163.39	0.00	0.00	1024800.00	0.00	0.00	0.00	3480000.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 1245046 2 787	0.00	70720000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19536000.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 2207042 3 626	3330000.00	0.00	0.00	0.00	0.00	0.00	1631385.60	1207800.00	2899800.00	1247400.00	0.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 2629042 1 714	0.00	2380000.00	0.00	0.00	0.00	0.00	0.00	15189000.00	0.00	0.00	0.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 3737181 6 695	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1901900.00	0.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 6682139 1 546	29000000.00	6310400.00	33909349.25	0.00	47895000.00	12584900.00	0.00	306188.89	0.00	0.00	19448000.00	0.00	KO:K00319	methylenetetrahydromethanopterin dehydrogenase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0000676 22706 23695	3650000.00	635547.04	10895705.22	42558914.15	42436000.00	630432.03	29643759.72	26535000.00	17690400.00	14553000.00	13552000.00	13725000.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324 0003276 653 1642	0.00	3114400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13829200.00	4672800.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0010839 8033 9022	0.00	45560000.00	202117000.00	116850000.00	57268000.00	66299000.00	54264000.00	33977000.00	47142000.00	34111000.00	19096000.00	33300000.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324 0029955 4003 4989	24295315.00	9316000.00	26775756.41	18581592.45	14028600.00	28158392.18	21477600.00	21197500.00	18281700.00	12104400.00	5473600.00	7305000.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0074860 1438 2463	0.00	0.00	0.00	1273000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0147711 1796 2782	9110000.00	0.00	16327000.00	16245000.00	15862000.00	12743700.00	10419600.00	0.00	11583000.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0211396 1 804	0.00	0.00	7825700.00	219450000.00	0.00	0.00	7045200.00	0.00	0.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0249475 1 861	1850000.00	0.00	3460057.25	0.00	2461700.00	737387.80	0.00	0.00	0.00	0.00	2508000.00	2362500.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0346381 1021 1929	166000000.00	0.00	0.00	203300000.00	0.00	299338000.00	62950800.00	60756000.00	226314000.00	110880000.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0351136 813 1802	9300000.00	8500000.00	10697000.00	20710000.00	19776000.00	14411100.00	9006000.00	16165000.00	12798000.00	5605600.00	5702400.00	4987500.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324 1053042 506 1186	0.00	91120000.00	176782000.00	0.00	0.00	152051000.00	0.00	0.00	99630000.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanocellales;Methanocellaceae;Methanocella;Methanocella arvoryzae;Methanocella arvoryzae MRE50
Ga0586324 3200496 2 742	0.00	0.00	0.00	8588000.00	18746000.00	0.00	9370800.00	10004000.00	0.00	0.00	2226400.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4031605 1 675	20300000.00	0.00	0.00	5833000.00	0.00	0.00	136662.29	0.00	0.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4081332 1 669	1120000.00	1047200.00	0.00	1358500.00	0.00	0.00	0.00	732000.00	688198.68	0.00	263289.84	335742.75	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4097756 3 668	75300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4186676 63 662	0.00	0.00	0.00	0.00	0.00	0.00	869368.56	0.00	0.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanobacteria;Methanobacteriales;Methanobacteriaceae;Methanobacterium;Methanobacterium sp. SMA-27;Methanobacterium sp. SMA-27
Ga0586324 4841177 3 626	0.00	1564000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4858464 3 611	0.00	0.00	0.00	0.00	0.00	0.00	137028000.00	0.00	0.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 5088018 3 611	20700000.00	0.00	0.00	8702000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 5431567 152 595	24700000.00	0.00	0.00	0.00	14852600.00	0.00	0.00	0.00	3159000.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324 5913206 2 574	0.00	0.00	0.00	0.00	0.00	3818222.93	0.00	1464000.00	980100.00	0.00	0.00	0.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 6216927 3 563	3250000.00	3631200.00	3649045.09	3306000.00	3594700.00	4287600.00	1766947.56	2250900.00	1944000.00	4173400.00	4540800.00	4012500.00	KO:K00320	5,10-methylenetetrahydromethanopterin reductase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0466237 226 1608	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10044000.00	0.00	0.00	6367500.00	KO:K00324	NAD(P) transhydrogenase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Noviherbaspirillum;Noviherbaspirillum sp. Root189;Noviherbaspirillum sp. Root189
Ga0586324 1269635 82 1095	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1531200.00	240813.75	KO:K00324	NAD(P) transhydrogenase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 8261528 3 239	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1020000.00	KO:K00324	NAD(P) transhydrogenase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP51;Betaproteobacteria bacterium AAP51
Ga0586324 3137418 3 569	0.00	2278000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00331	NADH-quinone oxidoreductase subunit B	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 8133884 2 505	0.00	0.00	0.00	0.00	0.00	4406700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00331	NADH-quinone oxidoreductase subunit B	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 0003069 5143 6264	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2818200.00	0.00	0.00	0.00	0.00	KO:K00333	NADH-quinone oxidoreductase subunit D	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0000030 29090 31450	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1848000.00	1988800.00	1117500.00	KO:K00336	NADH-quinone oxidoreductase subunit G	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255

Ga0586324 1168874 3 1136	0.00	0.00	0.00	1824000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00336	NADH-quinone oxidoreductase subunit G	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0022751 6184 6996	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2543200.00	0.00	KO:K00344	NADPH2:quinone reductase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS499
Ga0586324 0063496 1338 2729	0.00	7010800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4127200.00	0.00	0.00	KO:K00346	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 0087269 2902 3660	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1174500.00	0.00	0.00	0.00	KO:K00346	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacterales;Yersiniaceae;Chania;Chania multitudinisentens;Chania multitudinisentens RB-25
Ga0586324 0154193 1674 2792	0.00	0.00	8219800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00346	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 2187877 3 869	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2549800.00	0.00	0.00	0.00	0.00	KO:K00346	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324 2655027 1 801	0.00	6636800.00	0.00	0.00	0.00	0.00	0.00	872300.00	0.00	0.00	6872800.00	0.00	KO:K00346	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324 2802866 3 782	6930000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00346	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324 3244751 1 537	0.00	0.00	0.00	0.00	0.00	0.00	0.00	307716.94	0.00	2171400.00	0.00	0.00	KO:K00346	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 0226816 1 2334	7810000.00	0.00	0.00	0.00	598516.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00370	nitrate reductase alpha subunit	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira moscoviensis;Nitrospira moscoviensis NSP M-1
Ga0586324 0702168 1 1413	0.00	10404000.00	17678200.00	13015000.00	13287000.00	0.00	0.00	9150000.00	0.00	23100000.00	4276800.00	8925000.00	KO:K00370	nitrate reductase alpha subunit	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira lenta;Nitrospira lenta N. lenta BS10
Ga0586324 1546373 1 1008	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1368900.00	0.00	0.00	0.00	KO:K00370	nitrate reductase alpha subunit	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira japonica;Nitrospira japonica NJ11
Ga0586324 0017038 6378 7667	0.00	0.00	0.00	0.00	0.00	4764000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00371	nitrate reductase beta subunit	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira moscoviensis;Nitrospira moscoviensis NSP M-1
Ga0586324 1733195 3 959	0.00	0.00	0.00	8854000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00371	nitrate reductase beta subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 1781545 3 950	0.00	2189600.00	2972662.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00371	nitrate reductase beta subunit	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira japonica;Nitrospira japonica NJ11
Ga0586324 0006115 9453 11315	0.00	2964800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. PSR-1;Anaeromyxobacter sp. PSR-1
Ga0586324 0011253 2338 4311	0.00	741200.00	0.00	484169.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;unclassified Rhodothermaceae;Rhodothermaceae bacterium RA;Halothermobacillus malaysiensis RA
Ga0586324 0044754 194 2506	0.00	1217200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1609300.00	0.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa marina;Thiocapsa marina 5811, DSM 5653
Ga0586324 0192962 857 2515	0.00	2652000.00	2107202.03	0.00	0.00	0.00	0.00	0.00	2292300.00	0.00	0.00	5745000.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa roseopersicina;Thiocapsa roseopersicina DSM 217
Ga0586324 0663683 2 1141	0.00	5773200.00	0.00	0.00	3254800.00	0.00	0.00	4355400.00	4827600.00	685185.27	0.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa marina;Thiocapsa marina 5811, DSM 5653
Ga0586324 1001390 3 1214	5800000.00	8296000.00	0.00	6213000.00	7230600.00	5041900.00	0.00	6161000.00	3215700.00	0.00	0.00	2602500.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalbus;Thioalbus denitrificans;Thioalbus denitrificans DSM 26407
Ga0586324 1023610 3 1202	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1768800.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira;unclassified Azospira;Azospira sp. ZAP
Ga0586324 1111901 2 1105	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1213900.00	0.00	0.00	0.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324 2034537 3 896	0.00	0.00	0.00	0.00	0.00	0.00	7957200.00	21008400.00	15430500.00	0.00	0.00	4002632.25	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas agitata;Dechloromonas agitata is5
Ga0586324 2035543 2 895	0.00	3094000.00	0.00	0.00	0.00	0.00	0.00	0.00	3094200.00	0.00	0.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. SG708;Dechloromonas sp. SG708
Ga0586324 2639717 3 632	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	954800.00	6969600.00	4020000.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa marina;Thiocapsa marina 5811, DSM 5653
Ga0586324 3433664 84 719	0.00	0.00	0.00	0.00	2060000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Sedimenticola;Sedimenticola selenatireducens;Sedimenticola selenatireducens DSM 17993
Ga0586324 3522386 1 711	0.00	0.00	0.00	0.00	10918000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dechlorobacter;Dechlorobacter hydrogenophilus;Dechlorobacter hydrogenophilus LT-1
Ga0586324 6375887 3 557	0.00	0.00	0.00	0.00	0.00	0.00	8436000.00	9943000.00	1312200.00	0.00	9416000.00	0.00	KO:K00376	nitrous-oxide reductase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. HYN0024;Dechloromonas sp. HYN0024
Ga0586324 0000003 99423 102416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4623800.00	0.00	5305300.00	7418400.00	0.00	KO:K00382	dihydrolipoamide dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0089864 2539 3609	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4426400.00	0.00	KO:K00382	dihydrolipoamide dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rivibacter;Rivibacter subsaxonicus;Rivibacter subsaxonicus DSM 19570
Ga0586324 1405166 200 1045	0.00	0.00	0.00	0.00	0.00	5518300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00382	dihydrolipoamide dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter tataouinensis;Ramlibacter tataouinensis 5-10
Ga0586324 0000002 211845 213866	0.00	0.00	0.00	0.00	0.00	0.00	57684000.00	6551400.00	29848403.85	123816000.00	150656000.00	65400000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0005409 1 1071	0.00	0.00	2451977.60	2489000.00	1256600.00	5076272.26	177134499.60	160430000.00	140053041.90	72100148.89	60816800.00	205920000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0008738 6807 8732	210650000.00	16517200.00	245749500.00	55432500.00	57422500.00	77637462.92	172504800.00	81435000.00	23911200.00	35035000.00	207090400.00	16642500.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 0014308 7605 8675	0.00	0.00	2420759.25	0.00	1761300.00	0.00	0.00	0.00	0.00	4450600.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina sp. BuS5;Desulfosarcina sp. BuS5
Ga0586324 0032719 268 2280	0.00	4114000.00	0.00	0.00	0.00	0.00	10738800.00	6222000.00	6180300.00	14968800.00	8395200.00	5040000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Thioalkalispiraceae;Sulfurivermis;Sulfurivermis fontis;Sulfurivermis fontis JG42
Ga0586324 0037456 2363 4279	0.00	0.00	0.00	1605500.00	0.00	0.00	0.00	2177700.00	0.00	0.00	2596000.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 0041609 1769 3808	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17577000.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio yellowstonii;Thermodesulfovibrio yellowstonii DSM 11347
Ga0586324 0046593 893 2932	0.00	14708425.84	0.00	1567500.00	0.00	22390800.00	24624000.00	0.00	593073.90	11881100.00	44783200.00	17550000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio yellowstonii;Thermodesulfovibrio yellowstonii DSM 11347
Ga0586324 0057114 1 981	0.00	256181.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	916300.00	1029600.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324 0068875 1106 3082	28890000.00	31878400.00	13259353.75	47547500.00	51446176.32	23073004.80	26698800.00	36478000.00	40589100.00	22869000.00	47256000.00	25773726.75	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0072275 1 1707	0.00	6534800.00	0.00	0.00	326699.52	0.00	0.00	0.00	769468.41	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio yellowstonii;Thermodesulfovibrio yellowstonii DSM 11347
Ga0586324 0072572 2313 3995	0.00	30736000.00	0.00	0.00	9682000.00	0.00	0.00	32635000.00	0.00	30030000.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 611, DSM 198
Ga0586324 0083535 949 2982	0.00	0.00	0.00	43985000.00	71585000.00	31879100.00	0.00	33672000.00	0.00	0.00	0.00	35400000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324 0095010 3020 3514	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2864400.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324 0113654 2 1273	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	858600.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0124704 72 2075	1190000.00	3243600.00	1887412.46	1121000.00	0.00	0.00	815676.84	15170700.00	1611900.00	18552152.85	1029600.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio hydrogeniphilus;Thermodesulfovibrio hydrogeniphilus DSM 18151
Ga0586324 0128575 601 2604	0.00	7072000.00	22463700.00	612730.05	0.00	11513000.00	5631600.00	3483100.00	12069000.00	0.00	7198400.00	7132500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio hydrogeniphilus;Thermodesulfovibrio hydrogeniphilus DSM 18151
Ga0586324 0130014 3 1319	0.00	0.00	0.00	3410500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Thioglobus;Candidatus Thioglobus singularis;Candidatus Thioglobus singularis PS1
Ga0586324 0140711 2070 2915	0.00	0.00	0.00	0.00	0.00	0.00	2090951.52	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfopila;Desulfopila aestuarii;Desulfopila aestuarii DSM 18488
Ga0586324 0142556 2352 2897	0.00	3080400.00	2179457.45	8274500.00	19153930.47	35531500.00	8276400.00	1811700.00	7200900.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0145463 2 1045	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4754700.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324 0154655 217 2097	7030000.00	0.00	0.00	29640000.00	0.00	0.00	1010445.84	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0155179 2 1552	0.00	1448400.00	0.00	6213000.00	0.00	0.00	0.00	4465200.00	3361500.00	4335100.00	4831200.00	6495000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0180229 197 2161	0.00	1366800.00	0.00	3496000.00	92494000.00	0.00	0.00	2067900.00	0.00	28259000.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0194934 3 980	0.00	0.00	0.00	0.00	0.00	0.00	3374400.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfallas;Desulfallas alcoholivorax;Desulfotomaculum alcoholivorax DSM 16058
Ga0586324 0200605 1215 2471	0.00	0.00	0.00	0.00	0.00	0.00	3214800.00	701500.00	0.00	0.00	2173600.00	9975000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0271257 1614 2150	8160000.00	0.00	0.00	18525000.00	0.00	0.00	8048400.00	0.00	0.00	939400.00	2551959.52	421699.50	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 0282363 1478 2113	0.00	0.00	0.00	0.00	0.00	7622400.00	8208000.00	0.00	3985200.00	0.00	1663200.00	2355000.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 0306156 2 784	0.00	0.00	0.00	0.00	65920000.00	94883000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0310959 42 2006	6960000.00	3440800.00	81072000.00	10070000.00	11433000.00	193426359.85	1419265.80	4776300.00	5340048.12	0.00	0.00	31350000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0355347 696 1907	17500000.00	0.00	0.00	4208500.00	0.00	0.00	0.00	159210000.00	1417500.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 0393277 931 1821	15600000.00	2858152.88	3949946.07	0.00	0.00	3090541.78	0.00	36760.19	0.00	11349800.00	7048800.00	1777500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324 0414519 1 420	0.00	2223600.00	3557518.18	0.00	0.00	0.00	0.00	1878800.00	2041200.00	4412100.00	6230400.00	3472500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0469781 2 505	24000000.00	40256000.00	1972262.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	676091.68	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa roseopersicina;Thiocapsa roseopersicina DSM 217
Ga0586324 0483263 940 1662	0.00	0.00	0.00	0.00	0.00	0.00	1179396.12	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0501999 70 1635	0.00	2142000.00	0.00	0.00	0.00	0.00	0.00	0.00	2640600.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0506566 2 1369	8580000.00	12580000.00	0.00	1976000.00	0.00	943986.60	4468800.00	1525000.00	891000.00	3087700.00	1408000.00	3187500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324 0600243 3 527	0.00	0.00	0.00	10545000.00	10403000.00	6709300.00	141360000.00	47885000.00	8699400.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0603787 1 906	0.00	0.00	0.00	0.00	0.00	3232040.52	3283200.00	4007700.00	0.00	652526.49	1381600.00	1320000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324 0635473 191 1477	0.00	0.00	0.00	0.00	0.00	0.00	3146400.00	0.00	2259900.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324 0645393 2 1468	22760000.00	5902400.00	0.00	26077500.00	12679300.00	0.00	10807200.00	12187800.00	0.00	12212200.00	4963200.00	5467500.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 0659785 1 1452	1390000.00	1679600.00	0.00	675917.40	0.00	1808021.37	0.00	2232600.00	2470500.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0664042 109 1449	1140000.00	5310800.00	5098038.19	5643000.00	24565500.00	6781498.42	2063386.32	16189400.00	2843100.00	4381300.00	4400000.00	1687500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofundulus;Desulfofundulus thermosubterraneus;Desulfofundulus thermosubterraneus DSM 16057
Ga0586324 0749437 1182 1376	0.00	0.00	0.00	0.00	0.00	0.00	0.00	398197.63	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324 0751888 609 1373	23000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0758874 1 693	916369.00	0.00	0.00	0.00	0.00	285714.55	0.00	0.00	0.00	0.00	0.00	319006.50	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0908185 1 732	10660000.00	7140000.00	0.00	7343500.00	13287000.00	0.00	5244000.00	0.00	0.00	0.00	7312800.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 0913754 240 1262	0.00	0.00	0.00	6621500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 1049568 565 1188	925460.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 1071246 3 935	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5575400.00	7087500.00	5867400.00	0.00	4777500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 1119347 2 1156	9970000.00	1421200.00	0.00	206435000.00	99395000.00	359920200.00	50768383.80	81130000.00	46251000.00	1848000.00	2059200.00	2580000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 1145541 241 1146	0.00	239337.56	0.00	0.00	0.00	0.00	0.00	1599631.67	0.00	11899369.79	12279824.48	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 1178762 1 1131	10100000.00	9248000.00	9064300.00	13585000.00	8682900.00	22271700.00	14044800.00	10248000.00	9914400.00	0.00	0.00	2970000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 1281566 304 1092	0.00	447548.12	0.00	0.00	0.00	0.00	0.00	0.00	465178.95	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324 1307846 3 1034	103000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11259000.00	0.00	0.00	5887500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio islandicus;Thermodesulfovibrio islandicus DSM 12570
Ga0586324 1331044 636 1073	9730000.00	0.00	0.00	5244000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 1346276 1 615	0.00	8636000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1940400.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 1397345 7 1053	0.00	2400400.00	0.00	4436500.00	0.00	0.00	0.00	0.00	3466800.00	352951.06	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio hydrogeniphilus;Thermodesulfovibrio hydrogeniphilus DSM 18151
Ga0586324 1399658 3 1052	0.00	14531600.00	20042800.00	7571500.00	14265500.00	12783400.00	61491600.00	7564000.00	17309700.00	21556310.93	9603420.64	30277500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 1429045 261 1043	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	915300.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324 1433796 2 631	16200000.00	7412000.00	0.00	0.00	0.00	0.00	0.00	2171600.00	0.00	0.00	0.00	504890.25	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula multivorans;Sulfuriferula multivorans TTN
Ga0586324 1536243 1 1011	2390000.00	9458800.00	0.00	0.00	0.00	13220100.00	2394000.00	9394000.00	55080000.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 1555830 3 1004	785708.00	522797.60	0.00	0.00	0.00	0.00	2964000.00	2452200.00	2106000.00	1162700.00	1020800.00	4792500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 1638870 3 983	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	552157.76	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 611, DSM 198
Ga0586324 1651631 3 428	0.00	5059200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacula;Desulfobacula toluolica;Desulfobacula toluolica Tol2
Ga0586324 1657902 1 861	0.00	0.00	0.00	0.00	0.00	0.00	1053943.68	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofundulus;Desulfofundulus thermocisternus;Desulfofundulus thermocisternus DSM 10259
Ga0586324 1685144 395 970	6930000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 1716769 270 965	0.00	0.00	0.00	8160500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus mediterraneus;Desulfobulbus mediterraneus DSM 13871
Ga0586324 1764877 1 951	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	39424000.00	50248000.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 1847551 1 933	1030000.00	648122.96	0.00	461407.40	483546.89	444330.34	570218.88	350438.90	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324 1867848 1 930	0.00	0.00	0.00	2394000.00	1864300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 1959900 2 787	1120000.00	2067200.00	0.00	0.00	0.00	0.00	0.00	1854400.00	8748000.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 2040812 1 894	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1676700.00	1740200.00	1592800.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 2071586 468 890	0.00	0.00	0.00	6715600.00	0.00	0.00	0.00	30622000.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2219016 2 865	36000000.00	9125600.00	0.00	1472500.00	1143300.00	59947000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 2253579 2 859	0.00	5691600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2268807 1 855	0.00	0.00	0.00	0.00	0.00	0.00	0.00	222919.62	1425600.00	0.00	0.00	9150000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 2283428 3 671	54400000.00	31960000.00	16552200.00	4275000.00	325655100.00	224212678.05	12745200.00	0.00	13543200.00	0.00	4382400.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 2286594 1 681	0.00	0.00	0.00	0.00	1905500.00	0.00	0.00	2830400.00	2415723.75	7923300.00	6080800.00	2902500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thioploca;Thioploca ingrica;Thioploca ingrica Lake Okotanpe
Ga0586324 2348371 1 828	0.00	0.00	0.00	0.00	0.00	187018.76	2179755.24	939400.00	0.00	1170400.00	841886.32	772500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2432445 3 833	847825.00	2584000.00	0.00	8632866.60	8353300.00	0.00	6178800.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324 2441858 3 683	0.00	0.00	0.00	0.00	0.00	118128.54	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 2582724 3 812	28350000.00	25704000.00	30112612.93	45562000.00	41818000.00	49307400.00	97128000.00	40961500.00	30528900.00	24932600.00	5183200.00	20505000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 2639906 3 803	0.00	0.00	6981200.00	6716500.00	6252100.00	9091300.00	5152800.00	5014200.00	4649400.00	3403400.00	4954400.00	3510000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 2651662 50 802	0.00	0.00	0.00	0.00	0.00	355311.43	0.00	664900.00	0.00	1139600.00	861907.20	355342.50	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfallas;Desulfallas thermosapovorans;Desulfallas thermosapovorans DSM 6562
Ga0586324 2666361 3 383	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	50100000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2768881 64 786	1330000.00	284313.44	0.00	0.00	1122700.00	2376021.18	3442800.00	2116700.00	1085400.00	3426500.00	3132800.00	3052500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 3028006 1 759	0.00	0.00	0.00	0.00	0.00	0.00	2964000.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio islandicus;Thermodesulfovibrio islandicus DSM 12570
Ga0586324 3035968 3 674	1290000.00	0.00	0.00	1938000.00	0.00	13855300.00	36252000.00	5605900.00	4131000.00	1832600.00	985600.00	4170000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1pr3, DSM 2032
Ga0586324 3059403 1 756	0.00	0.00	0.00	0.00	0.00	36801900.00	0.00	0.00	299086.83	0.00	6758400.00	10200000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 3102018 1 750	30500000.00	0.00	20774700.00	125685000.00	11010700.00	17042074.58	4286400.00	52609464.03	3410892.18	800800.00	579336.56	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofundulus;Desulfofundulus australicus;Desulfofundulus australicus DSM 11792
Ga0586324 3102902 1 714	0.00	0.00	0.00	0.00	0.00	0.00	440961.12	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 3161249 1 744	0.00	0.00	0.00	0.00	0.00	9567700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3216323 385 741	0.00	2101200.00	0.00	0.00	46659000.00	0.00	0.00	6893000.00	6115500.00	2148300.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 3312272 1 732	3900000.00	0.00	5911500.00	21375000.00	0.00	22430500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 3351633 28 726	0.00	0.00	0.00	0.00	0.00	0.00	0.00	719800.00	0.00	486717.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 3404058 1 723	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	662831.91	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324 3543379 65 712	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	977900.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Beggiatoa;Beggiatoa sp. 'Orange Guaymas';Beggiatoa sp. Orange Guaymas
Ga0586324 3552065 2 709	1790000.00	1788400.00	0.00	2850000.00	3296000.00	4883100.00	1911659.16	1366400.00	1887300.00	770000.00	640607.44	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 3679387 3 701	16160000.00	15164000.00	7656800.00	32917500.00	29396200.00	26357365.95	19562400.00	17202000.00	15552000.00	7623000.00	8219200.00	5955000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 3758533 3 695	1280000.00	93792755.64	0.00	720062.95	1565600.00	854558.38	0.00	994300.00	1360800.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 3832797 2 544	19500000.00	26071200.00	27662684.09	31350000.00	28438300.00	44940400.00	12129600.00	36539000.00	27564300.00	8008000.00	8685600.00	21682500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 3972786 3 677	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	257287.80	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 4025496 2 673	0.00	0.00	0.00	2470000.00	3234200.00	3317125.56	4035600.00	3884602.00	2146500.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1pr3, DSM 2032
Ga0586324 4073583 3 392	18400000.00	0.00	0.00	3857000.00	0.00	3084836.89	0.00	0.00	1563300.00	1447600.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 4200489 3 632	30100000.00	0.00	0.00	0.00	0.00	451385.03	1737353.16	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4250192 1 468	10400000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109

Ga0586324 4371959 1 594	0.00	0.00	0.00	6469500.00	22248000.00	0.00	30780000.00	14579000.00	17415000.00	0.00	25256000.00	15525000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio thiophilus;Thermodesulfovibrio thiophilus DSM 17215
Ga0586324 4460902 3 647	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4666500.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324 4637138 3 635	10300000.00	0.00	0.00	0.00	27913000.00	0.00	2439600.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 4669016 114 635	22290000.00	2325600.00	15482500.00	18867000.00	11082800.00	9069687.32	5131801.20	2714500.00	2924100.00	4096400.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4669363 78 635	2360000.00	2060400.00	3092795.46	0.00	0.00	425921.45	0.00	652700.00	0.00	0.00	0.00	787500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Desulfovirgula;Desulfovirgula thermocuniculi;Desulfovirgula thermocuniculi DSM 16036
Ga0586324 4733930 2 487	3071313.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 4966543 3 617	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1963500.00	14784000.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 5110930 2 610	20200000.00	8636000.00	3816886.65	0.00	0.00	10163200.00	3488400.00	12566000.00	27099329.22	6583500.00	0.00	6652500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5134048 1 609	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2220400.00	5297400.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324 5197660 1 564	0.00	0.00	0.00	0.00	5098500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Desulfallaceae;Desulfoscipio;Desulfoscipio geothermicus;Desulfallas geothermicus DSM 3669
Ga0586324 5264039 45 605	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3037800.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324 5346895 2 601	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10370000.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 5476145 1 594	2900000.00	1339600.00	0.00	0.00	0.00	0.00	0.00	0.00	1182600.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Beggiatoa;Beggiatoa sp. 'Orange Guaymas';Beggiatoa sp. Orange Guaymas
Ga0586324 5639838 1 471	0.00	0.00	6587100.00	0.00	4933700.00	4724300.00	3009600.00	2135000.00	2389500.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5861616 1 579	0.00	7956000.00	0.00	5234500.00	5860700.00	10599900.00	0.00	5880400.00	6253200.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5881603 3 578	0.00	0.00	0.00	0.00	0.00	11155700.00	0.00	3696600.00	0.00	16786000.00	0.00	717534.75	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5962425 2 574	0.00	0.00	0.00	0.00	0.00	13021600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 6017615 2 571	8580000.00	8500000.00	0.00	12065000.00	0.00	12942200.00	0.00	0.00	7767900.00	10857000.00	0.00	8250000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfospira;Desulfospira joergensenii;Desulfospira joergensenii DSM 10085
Ga0586324 6534953 2 553	44400000.00	39236000.00	17396700.00	23750000.00	6684700.00	5359500.00	12836400.00	3385500.00	5759100.00	21252000.00	0.00	19275000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 6690651 1 546	0.00	0.00	0.00	0.00	0.00	200401.23	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio hydrogeniphilus;Thermodesulfovibrio hydrogeniphilus DSM 18151
Ga0586324 6866642 1 540	0.00	0.00	0.00	0.00	0.00	0.00	8276400.00	0.00	0.00	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 6920091 3 467	0.00	71400000.00	3822359.01	16055000.00	97438000.00	199651300.00	0.00	1653100.00	66460500.00	35112000.00	61195200.00	117750000.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 7352739 1 525	0.00	754800.00	0.00	0.00	4377500.00	19171395.99	2781600.00	2183800.00	1053000.00	0.00	1469600.00	1942500.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324 7688927 3 515	0.00	0.00	0.00	1767000.00	0.00	0.00	0.00	0.00	0.00	1917300.00	2543200.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 7838490 2 511	104000000.00	77520000.00	176782000.00	175750000.00	148320000.00	0.00	21956400.00	110410000.00	104490000.00	69762000.00	52096000.00	92250000.00	KO:K00394	adenylylsulfate reductase subunit A	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sulfaticallidus;Archaeoglobus sulfaticallidus PM70-1, DSM 19444
Ga0586324 7976711 3 509	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	196207.92	0.00	0.00	0.00	KO:K00394	adenylylsulfate reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0000002 211332 211817	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	252822.24	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0009502 1883 2362	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	840000.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324 0014308 7058 7543	1880000.00	0.00	0.00	0.00	0.00	2265416.98	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0032719 2335 2802	23400000.00	0.00	25335000.00	0.00	0.00	0.00	0.00	0.00	0.00	2340800.00	3097600.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Thioalkalispiraceae;Sulfurivermis;Sulfurivermis fontis;Sulfurivermis fontis JG42
Ga0586324 0046593 2947 3378	5420000.00	4025600.00	3904359.96	4740500.00	3872800.00	3954243.07	0.00	5740100.00	5848200.00	5936700.00	3960000.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetobacterium;Candidatus Magnetobacterium casensis;Candidatus Magnetobacterium casensis MYR-1
Ga0586324 0072572 1797 2264	0.00	2284800.00	12949000.00	2660000.00	0.00	4644900.00	0.00	2501000.00	1903500.00	800800.00	2824800.00	3285000.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 611, DSM 198
Ga0586324 0095010 2518 2991	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	32550000.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324 0154655 2116 2577	383584.00	1434800.00	3318175.62	2147000.00	0.00	2004659.44	686444.16	1018700.00	0.00	2410100.00	231169.84	1928871.75	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Dethiosulfatarculus;Dethiosulfatarculus sandiegensis;Dethiosulfatarculus sandiegensis SPR
Ga0586324 0200605 668 1135	0.00	0.00	0.00	0.00	0.00	0.00	23940000.00	15677000.00	14175000.00	23562000.00	23760000.00	25725000.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0246733 1369 1830	457802.00	0.00	0.00	494052.25	0.00	0.00	0.00	0.00	0.00	0.00	1707200.00	1425000.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Dethiosulfatarculus;Dethiosulfatarculus sandiegensis;Dethiosulfatarculus sandiegensis SPR
Ga0586324 0282363 1019 1465	1710000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Ammonifex;Ammonifex thiophilus;Ammonifex thiophilus SR
Ga0586324 0355574 1111 1572	1210000.00	519728.76	2338459.91	2308500.00	1854030.90	1537525.42	852617.40	762500.00	0.00	1663200.00	4408800.00	4117500.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324 0457934 1392 1703	0.00	1822400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2217600.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 0483263 460 921	1000000.00	30532000.00	13030989.69	41230000.00	32136000.00	40494000.00	2553600.00	25459813.39	28998000.00	26103000.00	10648000.00	1507500.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Dethiosulfatarculus;Dethiosulfatarculus sandiegensis;Dethiosulfatarculus sandiegensis SPR
Ga0586324 0560875 326 799	0.00	0.00	0.00	0.00	0.00	0.00	0.00	50203000.00	0.00	0.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 0731072 171 638	6600000.00	0.00	0.00	3296500.00	0.00	2506062.50	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 611, DSM 198
Ga0586324 1285972 2 349	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1742400.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 1651631 497 931	0.00	0.00	0.00	6336500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatibacillum;Desulfatibacillum alkenivorans;Desulfatibacillum alkenivorans DSM 16219
Ga0586324 1685144 3 383	0.00	25296000.00	0.00	0.00	0.00	50816000.00	0.00	0.00	20655000.00	0.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Ammonifex;Ammonifex thiophilus;Ammonifex thiophilus SR
Ga0586324 3256386 244 735	0.00	2794800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofundulus;Desulfofundulus salinum;Desulfofundulus salinum 435
Ga0586324 4242405 273 659	2100000.00	0.00	0.00	9880000.00	9177300.00	18460500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 5162953 157 609	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	757500.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 7463017 161 523	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	23793000.00	0.00	0.00	KO:K00395	adenylylsulfate reductase subunit B	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0000267 32259 33962	12600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GKZPZ, DSM 4140
Ga0586324 0005577 2364 4028	12950000.00	1795200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Candidatus Methanomassiliicoccus intestinalis;Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1
Ga0586324 0095431 2601 3506	2940000.00	3488400.00	0.00	0.00	2090900.00	0.00	0.00	3904000.00	3240000.00	1678600.00	0.00	2857500.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0159140 1464 2753	0.00	7684000.00	0.00	0.00	0.00	2168600.59	0.00	12383000.00	11178000.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis ethanolicus;Methanofollis ethanolicus JCM 15103
Ga0586324 0172585 1519 2649	0.00	0.00	0.00	0.00	4490800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324 0257221 978 2204	27860000.00	98804000.00	275025500.00	16435000.00	0.00	67410600.00	112563600.00	195749000.00	16807500.00	182028000.00	65322400.00	18030000.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0269169 3 1247	0.00	0.00	0.00	0.00	7694100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0316704 226 1920	0.00	0.00	139229900.00	0.00	28943000.00	24018500.00	0.00	0.00	0.00	16940000.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0432841 954 1745	0.00	0.00	0.00	4873500.00	5489900.00	3719635.92	0.00	2440000.00	512814.24	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina spelaei;Methanosarcina spelaei MC-15
Ga0586324 0460264 1 1161	0.00	2250800.00	0.00	0.00	0.00	2510695.49	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0623905 376 1488	2160000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Candidatus Methanomassiliicoccus intestinalis;Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1
Ga0586324 0630844 2 1480	6070000.00	8024000.00	0.00	0.00	0.00	0.00	17966400.00	1793400.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0719171 685 1398	0.00	16456000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanobacteria;Methanobacteriales;Methanobacteriaceae;Methanobacterium;Methanobacterium sp. SMA-27;Methanobacterium sp. SMA-27
Ga0586324 0761427 3 1364	0.00	4610400.00	9796200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0774128 1 915	13490000.00	11084000.00	7713100.00	4930500.00	0.00	0.00	0.00	3977200.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0800103 3 1292	156000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 1153740 3 848	962738.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324 1274864 1 1095	0.00	0.00	0.00	0.00	0.00	695615.46	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GKZPZ, DSM 4140
Ga0586324 1288639 84 1088	0.00	0.00	52753100.00	0.00	0.00	7701800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 2186377 2 595	977853.00	0.00	0.00	0.00	0.00	1940968.73	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324 2296551 2 772	69960000.00	61200000.00	27686797.38	30305000.00	20589700.00	25032874.70	32148000.00	40674800.00	69757200.00	8855000.00	6538400.00	13125000.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 3134344 2 748	913216.00	254367600.00	0.00	0.00	0.00	0.00	0.00	0.00	5151600.00	0.00	0.00	3075000.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 3280632 3 515	0.00	5433200.00	3969352.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 3576771 3 674	37800000.00	76976000.00	97455300.00	110798500.00	88312200.00	106435700.00	49498800.00	13700600.00	66760200.00	69531000.00	103144800.00	20497500.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 3682142 1 699	1530000.00	0.00	0.00	16055000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 3993454 2 676	5100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11259000.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina spelaei;Methanosarcina spelaei MC-15
Ga0586324 4220254 3 662	0.00	21148000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	21098000.00	17925600.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4302432 3 656	0.00	2862800.00	1289596.54	15105000.00	0.00	2258529.03	4582800.00	7076000.00	7857000.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;unclassified Methanosarcina;Methanosarcina sp. DH2
Ga0586324 5101883 2 598	0.00	0.00	0.00	0.00	0.00	21080700.00	13543200.00	12810000.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri 227
Ga0586324 5905733 3 575	0.00	3991600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis ethanolicus;Methanofollis ethanolicus JCM 15103
Ga0586324 6074327 3 569	0.00	28356000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00399	methyl-coenzyme M reductase alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 2323430 2 847	810498.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00400	methyl coenzyme M reductase system subunit A2	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0000267 29055 30368	92200000.00	84320000.00	56863000.00	40418698.10	53332332.92	52646701.98	32832000.00	67405000.00	27297000.00	50358000.00	22000000.00	34965000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0003112 7231 8535	7480000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4030400.00	4177500.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Candidatus Methanoperedenaceae;Candidatus Methanoperedens;Candidatus Methanoperedens nitroreducens;Candidatus Methanoperedens nitroreducens ANME-2d
Ga0586324 0005577 5233 6564	3360000.00	9452000.00	0.00	6773500.00	5974000.00	0.00	0.00	3690500.00	0.00	0.00	5288800.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324 0007977 3 848	0.00	0.00	0.00	0.00	0.00	0.00	167580000.00	0.00	183060000.00	274120000.00	362560000.00	148500000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0031912 3 1019	393870000.00	9241200.00	58664600.00	59755000.00	28737000.00	20445500.00	0.00	467522.91	17820000.00	14907200.00	8492000.00	10125000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0095431 3 1292	785340953.00	576878000.00	#############	715606500.00	769440900.00	346501600.00	561564000.00	389131200.00	473769000.00	378301000.00	365024000.00	375862500.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0134678 1663 2976	29100000.00	33986400.00	98468700.00	37563000.00	52385800.00	80114600.00	44916000.00	33159600.00	49839300.00	38985100.00	21982400.00	17137500.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0142898 1773 2894	0.00	24548000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0152511 1292 2602	602075.00	29539200.00	318798.75	0.00	0.00	0.00	0.00	382743.89	13861961.73	0.00	23548800.00	12166837.50	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0164625 1446 2708	50400000.00	3148400.00	6699700.00	17100000.00	110210000.00	71063000.00	79116000.00	0.00	47628000.00	42350000.00	0.00	1582500.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0191529 1821 2525	6530000.00	0.00	0.00	0.00	0.00	0.00	0.00	1342000.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324 0227838 3 692	0.00	8527200.00	0.00	0.00	8971300.00	0.00	0.00	0.00	3734100.00	0.00	3229600.00	1725000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0310286 3 932	0.00	0.00	0.00	1453500.00	1472900.00	0.00	887843.40	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina flavescens;Methanosarcina flavescens E03.2
Ga0586324 0506373 3 605	0.00	0.00	0.00	0.00	0.00	0.00	1738664.16	1323700.00	0.00	0.00	0.00	1665000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324 0669245 540 1445	60270000.00	0.00	91206000.00	42465000.00	0.00	3054240.10	0.00	4038200.00	31071600.00	0.00	0.00	37275000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0844541 224 1306	0.00	0.00	0.00	11305000.00	0.00	7820900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324 0854196 454 1299	407410.00	1870000.00	0.00	942854.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Candidatus Methanoperedenaceae;Candidatus Methanoperedens;Candidatus Methanoperedens nitroreducens;Candidatus Methanoperedens nitroreducens ANME-2d
Ga0586324 0889043 1 555	5210000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10575000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Candidatus Methanoperedenaceae;Candidatus Methanoperedens;Candidatus Methanoperedens nitroreducens;Candidatus Methanoperedens nitroreducens ANME-2d
Ga0586324 0943269 3 623	0.00	0.00	0.00	4883000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324 0946083 172 1242	12300000.00	237320000.00	20887300.00	0.00	0.00	16634300.00	0.00	0.00	200070000.00	0.00	0.00	5010000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 1065373 3 1181	749790000.00	#############	405198542.86	844312500.00	606278600.00	233447993.37	497925105.12	522172200.00	572491800.00	574011900.00	498740000.00	376222500.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 1069325 1 1179	196820000.00	146200000.00	191983000.00	0.00	0.00	271825900.00	134816400.00	42944000.00	49572000.00	85470000.00	35288000.00	123195000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 1395796 2 1051	25600000.00	7686737.00	0.00	11495000.00	11124000.00	8694300.00	6931200.00	4459100.00	5249016.27	0.00	0.00	3022500.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 1410674 3 572	4720000.00	7888000.00	0.00	3990000.00	3337200.00	0.00	0.00	1793400.00	0.00	0.00	0.00	3765000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 1427021 3 629	883652.00	5412800.00	627626.77	4365845.65	107830700.00	0.00	105868259.16	185019100.00	866700.00	192885000.00	171512000.00	3331557.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 1465892 3 1031	447148.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 1526255 3 692	0.00	3638000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10275000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 1591276 2 871	0.00	38941287.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 1673222 2 973	0.00	0.00	0.00	0.00	8868300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 2044502 1 894	34810000.00	352377964.52	168717959.58	373245500.00	181383000.00	161897012.88	209532000.00	199568871.85	278324100.00	211241800.00	123569600.00	21097500.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 2069110 1 591	2970000.00	4841600.00	15520750.22	36575000.00	9754100.00	21993800.00	0.00	17873000.00	16451100.00	2895200.00	3062400.00	1740000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina spelaei;Methanosarcina spelaei MC-15
Ga0586324 2831159 2 565	0.00	0.00	0.00	14155000.00	7189400.00	1880862.93	0.00	9394000.00	8262000.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina lacustris;Methanosarcina lacustris Z-7289
Ga0586324 3312776 1 732	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17700000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 3367902 644 727	0.00	67728000.00	0.00	30970000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 3893222 3 98	0.00	2713200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4042508 3 674	79300000.00	1734000.00	54273200.00	0.00	0.00	0.00	0.00	66490000.00	0.00	0.00	0.00	260118.75	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4450616 61 648	0.00	1557200.00	0.00	0.00	0.00	0.00	0.00	392605.15	0.00	0.00	0.00	442415.25	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4796160 3 626	229178.00	92480000.00	0.00	0.00	0.00	0.00	12859200.00	0.00	13284000.00	8162000.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 5084416 2 613	0.00	0.00	0.00	2907000.00	0.00	0.00	0.00	0.00	2543400.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina horonobensis;Methanosarcina horonobensis HB-1
Ga0586324 5234100 56 604	154800000.00	279317228.40	279698400.00	332120000.00	336604000.00	81107100.00	239400000.00	56608000.00	42240889.26	37499000.00	161216000.00	45225000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 5684930 3 584	76700000.00	0.00	6361900.00	0.00	0.00	0.00	6178800.00	26901000.00	0.00	0.00	0.00	20550000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 6009941 3 572	0.00	40664000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 6249662 2 553	0.00	112880000.00	94021000.00	822061.60	89919000.00	64314000.00	0.00	57462000.00	44550000.00	82390000.00	73480000.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 6761995 2 544	0.00	0.00	0.00	0.00	2667700.00	0.00	0.00	652700.00	0.00	0.00	1126400.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 6781589 1 543	33300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 7240576 3 374	0.00	0.00	27699600.00	14725000.00	11845000.00	16832800.00	0.00	0.00	17739000.00	8239000.00	0.00	6960000.00	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 7256471 1 528	3670000.00	1366800.00	1536387.59	0.00	7364500.00	6788700.00	2485200.00	4202900.00	5151600.00	1155000.00	0.00	322937.25	KO:K00401	methyl-coenzyme M reductase beta subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina lacustris;Methanosarcina lacustris Z-7289
Ga0586324 0000267 31489 32253	84370000.00	9860000.00	4050717.44	43120500.00	37904000.00	37938709.50	32148000.00	19721300.00	23878800.00	19866000.00	17248000.00	20505000.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus bourgensis;Methanoculleus bourgensis MS2
Ga0586324 0005577 4032 4811	1080000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;unclassified Methanomicrobiales;unclassified Methanomicrobiales;methanogenic archaeon mixed culture ISO4-G1;Unclassified archaeon ISO4-G1
Ga0586324 0095431 1815 2582	142800000.00	136292400.00	296701000.00	214700000.00	198378000.00	179047000.00	93708000.00	81313000.00	101331000.00	32648000.00	67496000.00	87000000.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0172585 741 1514	8220000.00	2109164.84	16383300.00	6802000.00	0.00	29576500.00	11696400.00	1677500.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324 0257221 196 963	251610000.00	202368000.00	163551500.00	65835000.00	33773700.00	59351500.00	39945600.00	8479000.00	7767900.00	6706700.00	5825600.00	33750000.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0417828 1 204	0.00	0.00	0.00	0.00	8466600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina horonobensis;Methanosarcina horonobensis HB-1
Ga0586324 0432841 197 943	1640000.00	3658400.00	0.00	0.00	4326000.00	19207800.89	0.00	4672600.00	3037500.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina lacustris;Methanosarcina lacustris Z-7289
Ga0586324 0458932 557 1324	0.00	5310800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0519656 259 1029	3960000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	795882.51	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324 0663604 1 648	20870000.00	16490000.00	36801475.75	16720000.00	25595500.00	30132300.00	16393200.00	12450100.00	9639000.00	8085000.00	8720800.00	7395000.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0774128 921 1355	8130000.00	34544000.00	1769447.07	16910000.00	16377000.00	0.00	0.00	18666000.00	0.00	0.00	0.00	13425000.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958

Ga0586324 1898585 2 673	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15631000.00	0.00	17700000.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 1914067 476 919	58730000.00	10907200.00	0.00	8227000.00	4387800.00	3970000.00	0.00	0.00	1952100.00	3488100.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 2168875 183 872	36500000.00	41480000.00	68686000.00	3125500.00	36771000.00	45774100.00	24624000.00	21777000.00	23660100.00	0.00	19976000.00	16687500.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324 2259985 441 857	0.00	9180000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 2666297 2 790	29770000.00	197077600.00	5028682.22	23227500.00	15450000.00	4009700.00	0.00	12810000.00	50916600.00	33572000.00	29559200.00	9825000.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 2763665 3 194	0.00	3808000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 3432428 127 720	47500000.00	33088800.00	0.00	24652500.00	43218800.00	4724300.00	64752000.00	0.00	20298600.00	759677.38	5315200.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 3458292 47 718	105220000.00	12002000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 3689976 3 575	0.00	5242800.00	0.00	0.00	58195000.00	0.00	0.00	0.00	0.00	0.00	1892000.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 3834023 3 689	2670000.00	5093200.00	0.00	1792085.70	18645596.63	0.00	12790800.00	6347337.92	19140300.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina spelaei;Methanosarcina spelaei MC-15
Ga0586324 4860244 302 625	9090000.00	0.00	0.00	1472500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4147500.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 4920357 161 622	0.00	0.00	0.00	59945000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 6706731 7 546	0.00	3338800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 7026917 96 536	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2403400.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 7443777 1 237	0.00	14824000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoplanus;Methanoplanus limicola;Methanoplanus limicola M3, DSM 2279
Ga0586324 7980584 1 507	0.00	3141600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00402	methyl-coenzyme M reductase gamma subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus bourgensis;Methanoculleus bourgensis MS2
Ga0586324 0000407 16454 17410	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19712000.00	20944000.00	20400000.00	KO:K00405	cytochrome c oxidase cbb3-type subunit 2	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0136816 1634 2581	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3519700.00	0.00	0.00	0.00	0.00	KO:K00405	cytochrome c oxidase cbb3-type subunit 2	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0169027 447 1403	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6768300.00	3943089.04	8760000.00	KO:K00405	cytochrome c oxidase cbb3-type subunit 2	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0222612 1409 2356	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	545163.85	851776.64	0.00	KO:K00405	cytochrome c oxidase cbb3-type subunit 2	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0629580 500 1456	0.00	0.00	0.00	0.00	0.00	0.00	12654000.00	0.00	1725300.00	7184100.00	10736000.00	7200000.00	KO:K00405	cytochrome c oxidase cbb3-type subunit 2	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0000002 10407 11393	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1320000.00	KO:K00406	cytochrome c oxidase cbb3-type subunit 3	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0006396 1783 2382	0.00	0.00	0.00	0.00	0.00	0.00	1205230.80	0.00	0.00	0.00	0.00	0.00	KO:K00411	ubiquinol-cytochrome c reductase iron-sulfur subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324 0015399 5457 6086	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	27489000.00	0.00	0.00	KO:K00411	ubiquinol-cytochrome c reductase iron-sulfur subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324 0816134 2 580	1380000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00411	ubiquinol-cytochrome c reductase iron-sulfur subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324 0169086 1 771	0.00	958800.00	0.00	1672000.00	1648000.00	0.00	1045313.88	0.00	1174500.00	0.00	0.00	0.00	KO:K00413	ubiquinol-cytochrome c reductase cytochrome c1 subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 0003931 9354 10520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3080000.00	1567500.00	KO:K00428	cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas acetexigens;Desulfuromonas acetexigens DSM 1397
Ga0586324 0009492 600 1604	8470000.00	0.00	0.00	0.00	0.00	10282300.00	0.00	0.00	0.00	0.00	0.00	4477500.00	KO:K00428	cytochrome c peroxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324 0078476 507 1595	1020000.00	0.00	1479794.83	0.00	0.00	0.00	0.00	793000.00	1287900.00	800800.00	771724.80	282831.00	KO:K00428	cytochrome c peroxidase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Candidatus Nitrospira nitrificans;Candidatus Nitrospira nitrificans COMA2
Ga0586324 0322406 3 620	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5825600.00	0.00	KO:K00428	cytochrome c peroxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter sp. BBA5.1;Methylobacter sp. BBA5.1
Ga0586324 0445644 358 1449	2550000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00428	cytochrome c peroxidase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Candidatus Nitrospira nitrificans;Candidatus Nitrospira nitrificans COMA2
Ga0586324 0864418 1 972	1703944.00	7684000.00	33498500.00	0.00	0.00	0.00	0.00	658800.00	7840800.00	9394000.00	0.00	6435000.00	KO:K00428	cytochrome c peroxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324 3178698 8 742	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15312000.00	0.00	KO:K00428	cytochrome c peroxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum 31/32
Ga0586324 4776736 3 356	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	583137.17	0.00	0.00	KO:K00428	cytochrome c peroxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylocaldum;Methylocaldum szegediense;Methylocaldum szegediense O-12
Ga0586324 5569871 3 590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2050400.00	0.00	KO:K00428	cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324 6671412 2 493	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6466000.00	0.00	0.00	0.00	0.00	KO:K00436	NAD-reducing hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0031028 121 1764	0.00	2998800.00	0.00	1634000.00	1895200.00	0.00	0.00	0.00	0.00	2102100.00	3722400.00	0.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0040009 820 2463	0.00	4420000.00	0.00	12996000.00	21939000.00	10996900.00	0.00	12932000.00	6212700.00	9394000.00	5676000.00	4680000.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 0089541 2 736	13400000.00	15300000.00	0.00	18430000.00	0.00	0.00	0.00	8845000.00	0.00	9163000.00	13728000.00	11475000.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 0363543 456 1883	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2211300.00	0.00	0.00	0.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0379005 1168 1851	0.00	0.00	0.00	7334000.00	0.00	0.00	0.00	23607000.00	0.00	0.00	20328000.00	0.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 0860535 133 1296	0.00	8772000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0884872 2 1279	0.00	671383.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 3053203 1 756	0.00	0.00	0.00	2394000.00	1987900.00	0.00	0.00	817400.00	0.00	0.00	0.00	0.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3529764 1 711	0.00	0.00	0.00	0.00	3460800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 3867077 1 642	0.00	31416000.00	0.00	54055000.00	66126000.00	10083800.00	44688000.00	33428000.00	0.00	19789000.00	0.00	0.00	KO:K00437	[NiFe] hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0005418 1075 2442	5080000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus thermophilus;Methanoculleus thermophilus DSM 2373
Ga0586324 0098772 2465 3448	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2032800.00	0.00	0.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324 0110913 1955 3262	0.00	5684800.00	0.00	5424500.00	7210000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus bourgensis;Methanoculleus bourgensis MBBA
Ga0586324 0198712 1 1140	5210000.00	4753200.00	0.00	3239500.00	2513200.00	0.00	1645685.76	1573800.00	1142100.00	1909600.00	0.00	0.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina acetivorans;Methanosarcina acetivorans C2A
Ga0586324 0713882 3 1181	0.00	0.00	44308100.00	0.00	0.00	0.00	0.00	0.00	27054000.00	0.00	0.00	0.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 1054547 1 1188	0.00	594642.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis ethanolicus;Methanofollis ethanolicus JCM 15103
Ga0586324 2626538 3 806	75200000.00	4338400.00	0.00	5310500.00	0.00	0.00	0.00	0.00	0.00	30261000.00	0.00	0.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4147740 3 665	0.00	12512000.00	0.00	9158000.00	0.00	0.00	0.00	5398500.00	0.00	0.00	0.00	6570000.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4216383 167 661	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	35325000.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 7086809 3 533	0.00	0.00	0.00	0.00	0.00	19532400.00	0.00	0.00	0.00	0.00	10912000.00	0.00	KO:K00440	coenzyme F420 hydrogenase subunit alpha	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0168802 1918 2676	0.00	0.00	0.00	7666500.00	12051000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00441	coenzyme F420 hydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0229114 786 1712	0.00	0.00	0.00	1719500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00441	coenzyme F420 hydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0274523 1327 2139	0.00	23460000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00441	coenzyme F420 hydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 1584353 264 998	58100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00441	coenzyme F420 hydrogenase subunit beta	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0030998 2041 2904	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2610300.00	0.00	0.00	KO:K00443	coenzyme F420 hydrogenase subunit gamma	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 1235981 199 1086	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1128500.00	0.00	0.00	0.00	1807500.00	KO:K00443	coenzyme F420 hydrogenase subunit gamma	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0776730 1 192	5090000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00518	nickel superoxide dismutase	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Psychroflexus;Psychroflexus torquis;Psychroflexus torquis ATCC 700755
Ga0586324 0057586 231 3143	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5490000.00	0.00	0.00	0.00	0.00	KO:K00525	ribonucleoside-diphosphate reductase alpha chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Ideonella;Ideonella sp. A 288;Ideonella sp. A 288
Ga0586324 0721191 3 752	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2891400.00	0.00	0.00	0.00	0.00	KO:K00528	ferredoxin--NADP+ reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0000004 1795 5466	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	696341.80	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0003216 8879 12556	0.00	0.00	0.00	0.00	0.00	0.00	354546.84	1836100.00	0.00	0.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 0023800 1943 5578	0.00	0.00	0.00	0.00	0.00	0.00	2275316.88	0.00	0.00	0.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Thermomonosporaceae;Actinomadura;Actinomadura sp. WAC 06369;Actinomadura sp. WAC 06369
Ga0586324 0056591 2337 4502	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	169118.18	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Sphingobacteriaceae;Solitalea;Solitalea canadensis;Solitalea canadensis USAM 9D, DSM 3403
Ga0586324 0108686 3 2138	0.00	0.00	0.00	0.00	0.00	0.00	642586.08	0.00	0.00	0.00	28336000.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So0149
Ga0586324 0190120 1 2535	0.00	0.00	0.00	0.00	0.00	0.00	251219.52	0.00	0.00	0.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0320323 316 951	0.00	0.00	0.00	2289500.00	4810100.00	4565500.00	0.00	0.00	2932200.00	0.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0328286 569 1975	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1701700.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. HYN0024;Dechloromonas sp. HYN0024
Ga0586324 0772135 515 1153	0.00	5385600.00	0.00	0.00	0.00	3285782.41	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Caldanaerobius;Caldanaerobius fijiensis;Caldanaerobius fijiensis DSM 17918
Ga0586324 3027710 476 760	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1372090.59	0.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacterales Family IV. Incertae Sedis;Mahella;Mahella australiensis;Mahella australiensis 50-1 BON, DSM 15567
Ga0586324 4389250 2 562	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	637730.01	0.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;unclassified Opitutaceae;Opitutaceae bacterium TSB47;Opitutaceae bacterium TSB47
Ga0586324 5723725 2 583	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1355200.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Deinococcus-Thermus;Deinococci;Trueperales;Trueperaceae;Truepera;Truepera radiovictrix;Truepera radiovictrix RQ-24, DSM 17093
Ga0586324 7559851 2 520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	770000.00	0.00	0.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 7894095 1 510	2310000.00	1292000.00	0.00	1567500.00	0.00	0.00	0.00	0.00	0.00	0.00	1830400.00	1327500.00	KO:K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Pleomorphomonadaceae;Pleomorphomonas;Pleomorphomonas koreensis;Pleomorphomonas koreensis DSM 23070
Ga0586324 3056202 2 757	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1804000.00	0.00	KO:K00567	methylated-DNA-[protein]-cysteine S-methyltransferase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina horonobensis;Methanosarcina horonobensis HB-1
Ga0586324 8236775 2 445	0.00	0.00	0.00	0.00	0.00	4406700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00567	methylated-DNA-[protein]-cysteine S-methyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae;Halomonas;Halomonas ilicicola;Halomonas ilicicola DSM 19980
Ga0586324 0345011 3 701	9270000.00	16728000.00	0.00	0.00	0.00	24256700.00	0.00	3324500.00	2713500.00	0.00	0.00	0.00	KO:K00577	tetrahydromethanopterin S-methyltransferase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0502518 420 1151	0.00	6752400.00	0.00	1881000.00	4562900.00	0.00	0.00	12200000.00	0.00	954800.00	0.00	0.00	KO:K00577	tetrahydromethanopterin S-methyltransferase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0604409 411 1133	0.00	1740800.00	0.00	0.00	0.00	0.00	9804000.00	0.00	0.00	0.00	0.00	0.00	KO:K00577	tetrahydromethanopterin S-methyltransferase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 2873307 88 774	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4479300.00	0.00	0.00	0.00	KO:K00577	tetrahydromethanopterin S-methyltransferase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 5430374 3 596	0.00	0.00	0.00	0.00	0.00	2675390.94	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00577	tetrahydromethanopterin S-methyltransferase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0502518 1153 1512	0.00	0.00	0.00	0.00	3471100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00578	tetrahydromethanopterin S-methyltransferase subunit B	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0000676 342 1379	0.00	4005200.00	0.00	0.00	5510500.00	0.00	3192000.00	3910100.00	4252500.00	0.00	4945600.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0029143 4841 5878	7270000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5297600.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 0133327 566 1603	0.00	0.00	4168271.84	4579000.00	0.00	0.00	0.00	3312300.00	0.00	0.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0172633 1714 2649	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	954800.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0200176 1696 2475	6200000.00	13328000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0235258 494 1531	4100000.00	4834800.00	0.00	5757000.00	5108800.00	0.00	6201600.00	4953200.00	7200900.00	7268800.00	4637600.00	2542500.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus marisnigri;Methanoculleus marisnigri JR1, DSM 1498
Ga0586324 0253111 561 1601	6180000.00	3689437.92	0.00	2992500.00	1977600.00	0.00	509324.64	1055300.00	972000.00	1255100.00	0.00	2475000.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0320598 1086 1994	10300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3900000.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0324697 826 1863	0.00	408703.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0331716 1246 1965	0.00	0.00	0.00	2954500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri Fusaro, DSM 804
Ga0586324 0481038 334 1374	0.00	606877.56	544403.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0785220 187 1098	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3839400.00	0.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanolobus;Methanolobus tindarius;Methanolobus tindarius DSM 2278
Ga0586324 1169601 1 945	8360000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 1756787 143 955	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2850000.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324 2293891 10 852	0.00	8568000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 2960723 109 765	14700000.00	0.00	18241200.00	0.00	0.00	1787496.47	1938209.76	1537200.00	0.00	687040.20	0.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 5482395 13 594	0.00	4039200.00	17621900.00	12730000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6480000.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 5958587 3 575	30100000.00	53108000.00	0.00	51300000.00	47689000.00	52801000.00	0.00	37332000.00	32643000.00	0.00	16192000.00	0.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 7713618 1 516	19800000.00	0.00	55230300.00	0.00	10506000.00	9607400.00	0.00	0.00	3815100.00	37422000.00	0.00	5122500.00	KO:K00584	tetrahydromethanopterin S-methyltransferase subunit H	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0000535 14767 16023	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7259000.00	0.00	0.00	0.00	0.00	KO:K00600	glycine hydroxymethyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0099684 3 485	11400000.00	0.00	18466400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	543215.25	KO:K00600	glycine hydroxymethyltransferase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0188092 1 1206	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	254373.75	KO:K00600	glycine hydroxymethyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324 0191219 567 1817	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8859422.11	0.00	0.00	KO:K00600	glycine hydroxymethyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0404757 255 1535	0.00	6426000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00600	glycine hydroxymethyltransferase	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 1528886 351 1013	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9592000.00	0.00	KO:K00600	glycine hydroxymethyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 1843878 2 934	0.00	0.00	0.00	0.00	0.00	5240400.00	0.00	0.00	0.00	4681600.00	0.00	0.00	KO:K00600	glycine hydroxymethyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0001379 559 2133	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4093100.00	0.00	0.00	2490400.00	0.00	KO:K00602	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0642177 1 1347	0.00	216692.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00602	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetobacterium;Candidatus Magnetobacterium casensis;Candidatus Magnetobacterium casensis MYR-1
Ga0586324 3298425 3 671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3037500.00	KO:K00602	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 5747152 2 556	0.00	0.00	0.00	0.00	0.00	2312838.63	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00602	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 6567321 2 550	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6544800.00	0.00	0.00	0.00	KO:K00602	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324 3629135 3 704	0.00	0.00	0.00	0.00	297415.59	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00605	aminomethyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So0008-312
Ga0586324 0320399 959 1825	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	595161.27	0.00	0.00	0.00	KO:K00606	3-methyl-2-oxobutanoate hydroxymethyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324 0000047 47834 48790	0.00	0.00	0.00	0.00	0.00	1019638.92	0.00	0.00	785835.27	0.00	0.00	318096.00	KO:K00609	aspartate carbamoyltransferase catalytic subunit	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0028981 2449 3444	0.00	1808800.00	2238898.99	0.00	1205100.00	2517365.09	0.00	0.00	939600.00	0.00	0.00	0.00	KO:K00609	aspartate carbamoyltransferase catalytic subunit	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0097906 1329 2282	0.00	0.00	16383300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00609	aspartate carbamoyltransferase catalytic subunit	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0857921 147 1127	12400000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00609	aspartate carbamoyltransferase catalytic subunit	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 2365091 2 610	0.00	0.00	2378686.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00609	aspartate carbamoyltransferase catalytic subunit	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 5734429 74 583	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2130000.00	KO:K00609	aspartate carbamoyltransferase catalytic subunit	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0000001 223778 225763	0.00	0.00	0.00	0.00	0.00	0.00	7273200.00	0.00	8505000.00	3203200.00	2208800.00	2017500.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0000401 4914 6935	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4083200.00	0.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0066885 2985 4157	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	594132.88	0.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324 0144642 1723 2877	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1837500.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula multivorans;Sulfuriferula multivorans TTN
Ga0586324 0413985 3 983	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11025000.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;unclassified Sulfuriferula;Sulfuriferula sp. AH1 re-analysis
Ga0586324 0516489 30 1616	0.00	46444000.00	353564000.00	0.00	0.00	0.00	0.00	44896000.00	0.00	0.00	0.00	0.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylococcus;Methylococcus capsulatus;Methylococcus capsulatus Texas, ATCC 19069
Ga0586324 0554142 1 903	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1878800.00	0.00	0.00	0.00	0.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 1107133 1 1161	13300000.00	25364000.00	0.00	0.00	0.00	0.00	23256000.00	17141000.00	0.00	11165000.00	2948000.00	31200000.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloglobulus;Methyloglobulus morosus;Methyloglobulus morosus KoM1
Ga0586324 1794392 3 947	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2982900.00	0.00	0.00	0.00	0.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 2295782 3 851	0.00	0.00	58552000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324 3276223 41 733	3620000.00	7548000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5651800.00	0.00	4597500.00	KO:K00615	transketolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloglobulus;Methyloglobulus morosus;Methyloglobulus morosus KoM1
Ga0586324 4539050 2 394	0.00	0.00	0.00	0.00	0.00	601724.96	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00615	transketolase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0006832 7913 8899	0.00	1944800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas sp. LW13;Methylomonas sp. LW13

Ga0586324 0087282 1815 2765	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11651000.00	0.00	1963500.00	0.00	22350000.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Candidatus Methylopumilus;Candidatus Methylopumilus planktonicus;Candidatus Methylopumilus planktonicus MMS-2-53
Ga0586324 0676559 198 1181	842621.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomarinum;Methylomarinum vadi;Methylomarinum vadi IT-4
Ga0586324 1667332 2 529	0.00	0.00	0.00	460913.40	0.00	0.00	895289.88	334369.06	0.00	0.00	0.00	0.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Acidocella;Acidocella aromatica;Acidocella aromatica DSM 27026
Ga0586324 3389030 161 724	0.00	6868000.00	0.00	0.00	0.00	0.00	14706000.00	8601000.00	8002800.00	5028100.00	7119200.00	4777500.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum miyakonense;Methylovulum miyakonense HT12
Ga0586324 5091533 111 611	0.00	2006000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloglobulus;Methyloglobulus morosus;Methyloglobulus morosus KoM1
Ga0586324 5505500 2 592	0.00	1972000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324 5881308 3 578	1993980.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum 31/32
Ga0586324 6666006 1 459	9200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00616	transaldolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloglobulus;Methyloglobulus morosus;Methyloglobulus morosus KoM1
Ga0586324 0000001 131005 132231	0.00	0.00	7262700.00	0.00	0.00	0.00	798369.36	496696.16	4082400.00	1570800.00	1548800.00	1012500.00	KO:K00620	glutamate N-acetyltransferase/amino-acid N-acetyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0014239 5372 6598	0.00	0.00	0.00	0.00	0.00	0.00	739458.72	580216.14	579751.02	893200.00	1144000.00	787500.00	KO:K00620	glutamate N-acetyltransferase/amino-acid N-acetyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324 0057163 1341 2297	2530000.00	0.00	0.00	1862000.00	1998200.00	0.00	0.00	0.00	0.00	1617000.00	2824800.00	0.00	KO:K00625	phosphate acetyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis parvus;Methylocystis parvus OBBP
Ga0586324 0121195 412 1362	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3472500.00	KO:K00625	phosphate acetyltransferase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 4021481 2 673	0.00	0.00	0.00	0.00	1452300.00	1633944.81	1028968.56	0.00	0.00	0.00	0.00	937500.00	KO:K00625	phosphate acetyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS242
Ga0586324 0031267 174 1358	0.00	467827.08	0.00	783222.75	797059.32	0.00	0.00	707600.00	458920.08	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. NZG;Methylibium sp. NZG
Ga0586324 0032785 4029 5219	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1091200.00	276912.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. PSR-1;Anaeromyxobacter sp. PSR-1
Ga0586324 0132964 2616 2996	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10575000.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0150139 1171 2616	0.00	0.00	512436.97	0.00	7961900.00	1113660.43	0.00	0.00	12958838.46	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324 0162834 1297 2724	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2433200.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324 0175962 128 1315	1450000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax ferrireducens;Rhodoferax ferrireducens T118
Ga0586324 0261347 1 1140	0.00	0.00	0.00	0.00	336076.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Indioceanicola;Indioceanicola profundi;Indioceanicola profundi SCSIO 08040
Ga0586324 0526880 335 1603	0.00	0.00	1276073.28	0.00	0.00	0.00	0.00	0.00	529790.22	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324 0778936 550 1353	0.00	0.00	0.00	22325000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0983266 3 896	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1104100.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dechlorobacter;Dechlorobacter hydrogenophilus;Dechlorobacter hydrogenophilus LT-1
Ga0586324 1285149 1 756	0.00	1740800.00	0.00	0.00	2770700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 1623132 105 986	0.00	3236800.00	0.00	0.00	6355100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324 1905346 1 666	0.00	0.00	707251.86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 1948913 77 913	11500000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodomicrobium;Rhodomicrobium udaipurense;Rhodomicrobium udaipurense JA643
Ga0586324 2435782 3 470	7340000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 3844000 3 686	0.00	1802000.00	0.00	0.00	1359600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 4607209 1 639	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	916300.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 5279422 2 604	0.00	0.00	891144.55	0.00	0.00	1012504.83	1336209.96	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS522
Ga0586324 5645522 1 588	0.00	1856400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Firmicutes;Bacilli;Bacillales;Thermoactinomycetaceae;Laceyella;Laceyella putida;Laceyella putida DSM 44608
Ga0586324 5826956 3 578	0.00	0.00	0.00	1282500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00626	acetyl-CoA C-acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Deferrisoma;Deferrisoma camini;Deferrisoma camini S3R1
Ga0586324 0381192 259 1536	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4470400.00	0.00	KO:K00627	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0211066 301 1500	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	602756.77	0.00	0.00	KO:K00632	acetyl-CoA acyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira multiformis;Nitrosospira multiformis Nl1
Ga0586324 3173758 1 744	0.00	0.00	0.00	0.00	0.00	1784348.26	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00639	glycine C-acetyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 7972110 2 508	3190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00639	glycine C-acetyltransferase	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Prolixibacter;Prolixibacter denitrificans;Prolixibacter denitrificans DSM 27267
Ga0586324 1297463 59 1087	0.00	0.00	0.00	6194000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00658	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas koreensis;Sphingomonas koreensis ABOJV
Ga0586324 1413418 1 876	2420000.00	6133600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1178100.00	0.00	0.00	KO:K00666	fatty-acyl-CoA synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 6528763 3 194	0.00	0.00	0.00	0.00	16068000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00666	fatty-acyl-CoA synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacterium;Desulfobacterium autotrophicum;Desulfobacterium autotrophicum HRM2, DSM 3382
Ga0586324 0008680 220 1104	0.00	0.00	1109194.45	4151500.00	5469300.00	1023366.75	1884650.28	4526200.00	5094900.00	0.00	0.00	1552500.00	KO:K00672	formylmethanofuran--tetrahydromethanopterin N-formyltransferase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0036510 2100 2918	3250000.00	0.00	0.00	0.00	0.00	0.00	0.00	3269600.00	0.00	0.00	2719200.00	1815000.00	KO:K00674	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium album;Methylomicrobium album BG8
Ga0586324 0113557 455 3007	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2311900.00	0.00	0.00	0.00	0.00	KO:K00688	starch phosphorylase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0450220 3 1319	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8239000.00	0.00	0.00	KO:K00688	starch phosphorylase	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sinica;Candidatus Brocadia sinica JPN1
Ga0586324 1252744 1 870	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2472800.00	0.00	KO:K00688	starch phosphorylase	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sinica;Candidatus Brocadia sinica JPN1
Ga0586324 2004684 2 901	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2055000.00	KO:K00688	starch phosphorylase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 2908841 1 771	0.00	3624400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00688	starch phosphorylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia sprentiae;Paraburkholderia sprentiae WSM5005
Ga0586324 6933597 3 539	0.00	0.00	0.00	0.00	0.00	0.00	8732400.00	0.00	0.00	0.00	0.00	0.00	KO:K00688	starch phosphorylase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324 0001390 14517 16952	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7725000.00	KO:K00700	1,4-alpha-glucan branching enzyme	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324 0076386 3 941	0.00	0.00	0.00	3173000.00	0.00	0.00	0.00	0.00	0.00	4504500.00	0.00	0.00	KO:K00756	pyrimidine-nucleoside phosphorylase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0000003 67559 69082	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2548700.00	0.00	0.00	KO:K00764	amidophosphoribosyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 2609340 3 806	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6367900.00	0.00	0.00	KO:K00764	amidophosphoribosyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylobacillus;Methylobacillus sp. MM3;Methylobacillus sp. MM2
Ga0586324 0000011 18843 20006	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3226300.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0000464 23162 24337	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9272000.00	12636000.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter marginalis;Methyloceanibacter marginalis R-67177
Ga0586324 0002541 16011 17150	0.00	288155.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	383348.35	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 0004912 2 421	0.00	0.00	0.00	0.00	0.00	1214010.12	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira japonica;Nitrospira japonica NJ11
Ga0586324 0035298 1435 2598	0.00	27336000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sapporoensis;Candidatus Brocadia sapporoensis 40
Ga0586324 0053628 42 1211	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	247837.50	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0078445 1223 2491	0.00	0.00	0.00	0.00	0.00	0.00	0.00	530357.18	0.00	185544.59	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0098631 1106 2287	0.00	0.00	0.00	6583500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Pseudohongiella;Pseudohongiella spirulinae;Pseudohongiella spirulinae KCTC 32221
Ga0586324 0293004 416 1612	0.00	0.00	0.00	0.00	0.00	294889.62	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. YIM ART13;Nocardioides sp. YIM ART13
Ga0586324 0306222 543 1763	0.00	0.00	0.00	0.00	893539.42	0.00	0.00	349834.39	0.00	1178100.00	0.00	12150000.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0368529 454 1722	2200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS138
Ga0586324 0604130 2 775	0.00	0.00	0.00	0.00	423347.51	0.00	0.00	341326.72	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified Myxococcales;Minicystis;Minicystis rosea;Minicystis rosea DSM 24000
Ga0586324 0646488 479 1465	0.00	0.00	0.00	2128000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324 1125837 646 1155	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4527600.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;Myxococcus;Myxococcus fulvus;Myxococcus fulvus DSM 16525
Ga0586324 1404974 3 614	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1320300.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium facile;Hyphomicrobium facile facile DSM 1565
Ga0586324 1432644 806 1042	0.00	0.00	0.00	1653000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatibacillum;Desulfatibacillum alkenivorans;Desulfatibacillum alkenivorans DSM 16219
Ga0586324 1677286 181 972	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1049200.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Acidobacteria;Blastocatellia;unclassified Blastocatellia;unclassified Blastocatellia;Chloracidobacterium;Chloracidobacterium thermophilum;Chloracidobacterium thermophilum B
Ga0586324 1703159 1 966	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	567437.40	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Actinobacteria;Actinomycetia;unclassified Actinomycetia;unclassified Actinomycetia;unclassified Actinomycetia;Actinobacteria bacterium IMCC26256;Actinobacteria bacterium IMCC26256
Ga0586324 1725743 2 883	0.00	0.00	0.00	0.00	0.00	0.00	0.00	564608.07	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 2373703 2 790	0.00	0.00	0.00	3097000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 2504088 3 821	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	159708.01	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sapporoensis;Candidatus Brocadia sapporoensis 40
Ga0586324 2577144 140 811	0.00	0.00	0.00	0.00	0.00	0.00	2781600.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 2669935 3 755	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1072500.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324 4393533 1 651	11500000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. XL1;Nocardioides sp. XL1
Ga0586324 4767419 1 621	0.00	0.00	0.00	0.00	0.00	19254500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 7943898 3 509	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	273408.75	KO:K00789	S-adenosylmethionine synthetase	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0162383 1952 2728	0.00	0.00	14581700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00791	tRNA dimethylallyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0017;Rhodospirillales bacterium URHD0017
Ga0586324 6787824 3 542	0.00	0.00	0.00	0.00	0.00	0.00	0.00	976000.00	0.00	0.00	0.00	0.00	KO:K00794	6,7-dimethyl-8-ribityllumazine synthase	Bacteria;Firmicutes;Clostridia;Thermosediminibacterales;Thermosediminibacteraceae;Thermosediminibacter;Thermosediminibacter oceani;Thermosediminibacter oceani JW/IW-1228P, DSM 16646
Ga0586324 0079055 269 1291	0.00	1366800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00809	deoxyhypusine synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-1
Ga0586324 0799327 3 1136	1640000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00809	deoxyhypusine synthase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 4801784 393 626	0.00	0.00	903147.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00812	aspartate aminotransferase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0000001 59872 61701	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5397700.00	0.00	4305000.00	KO:K00820	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0032971 3066 4925	0.00	0.00	0.00	0.00	0.00	258530.77	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00820	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 1736314 2 958	0.00	0.00	0.00	823137.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00820	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324 3537915 3 710	0.00	0.00	3972392.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00820	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0000003 17594 18766	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	528462.75	KO:K00821	acetylornithine/N-succinyldiaminopimelate aminotransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 3646771 83 703	0.00	0.00	729681.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00822	beta-alanine--pyruvate transaminase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Nitrospirillum;Nitrospirillum amazonense;Nitrospirillum amazonense BR 11140
Ga0586324 0360870 1 588	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	185147.27	0.00	0.00	KO:K00826	branched-chain amino acid aminotransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina cetonica;Desulfosarcina cetonica JCM 12296
Ga0586324 5977157 2 451	1290000.00	0.00	4393781.49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00830	alanine-glyoxylate transaminase/serine-glyoxylate transaminase/serine-pyruvate transaminase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324 0000005 67335 68417	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2835000.00	0.00	3256000.00	1912500.00	KO:K00831	phosphoserine aminotransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0261792 345 1907	2080000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00854	xylulokinase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Clostridium;Clostridium sp. KNHs216;Clostridium sp. KNHs216
Ga0586324 5982476 2 574	1790000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00854	xylulokinase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Clostridium;Clostridium sp. KNHs216;Clostridium sp. KNHs216
Ga0586324 0000013 94922 95812	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3574600.00	8425293.57	18195100.00	43225600.00	6765000.00	KO:K00855	phosphoribulokinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0007570 3 563	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3458700.00	0.00	0.00	4778400.00	0.00	KO:K00855	phosphoribulokinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324 0007597 4147 5034	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10065000.00	9558000.00	705822.81	8888000.00	10500000.00	KO:K00855	phosphoribulokinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324 0011325 1 336	0.00	0.00	7037500.00	5472000.00	6025500.00	3759863.93	15504000.00	0.00	0.00	11319000.00	0.00	0.00	KO:K00855	phosphoribulokinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0086170 915 1796	0.00	0.00	0.00	0.00	0.00	0.00	0.00	466332.19	0.00	0.00	301202.00	0.00	KO:K00855	phosphoribulokinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0435599 2 313	0.00	0.00	0.00	0.00	0.00	0.00	0.00	793000.00	0.00	0.00	0.00	0.00	KO:K00855	phosphoribulokinase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;unclassified Chromatiales;Thiohalobacter;Thiohalobacter thiocyanaticus;Thiohalobacter thiocyanaticus FOKN1
Ga0586324 0580733 489 1376	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3329100.00	0.00	0.00	0.00	KO:K00855	phosphoribulokinase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiogranum;Thiogranum longum;Thiogranum longum DSM 19610
Ga0586324 0768608 3 377	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2602500.00	KO:K00855	phosphoribulokinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0189746 3 830	1070000.00	1829200.00	1643526.49	0.00	0.00	841778.95	0.00	732000.00	1231200.00	1555400.00	0.00	0.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0235029 1492 2298	0.00	0.00	15388547.69	0.00	4645300.00	0.00	9484800.00	9949100.00	3742200.00	5305300.00	4452800.00	7499561.25	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0345198 1123 1929	0.00	0.00	0.00	0.00	0.00	0.00	4605600.00	0.00	0.00	0.00	0.00	0.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0495637 108 1604	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1401300.00	0.00	0.00	0.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0610455 3 1301	0.00	0.00	0.00	376563.85	2090900.00	1771453.70	960862.68	1354200.00	1134000.00	0.00	941600.00	741504.00	KO:K00864	glycerol kinase	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Nostocales;Hapalosiphonaceae;Fischerella;Fischerella thermalis;Fischerella thermalis CCMEE 5330
Ga0586324 1215220 3 641	0.00	26248000.00	7262700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9150000.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 1710511 389 964	0.00	0.00	40141900.00	38760000.00	42024000.00	50419000.00	54264000.00	31720000.00	33453000.00	42273000.00	46200000.00	34875000.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 1740299 3 959	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8624000.00	0.00	0.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 1856967 299 931	0.00	0.00	0.00	0.00	0.00	0.00	0.00	793000.00	0.00	0.00	0.00	0.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 2061252 1 729	0.00	0.00	0.00	0.00	2688300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 2527423 1 414	0.00	2441200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 4695881 2 514	30700000.00	2924000.00	15989200.00	0.00	0.00	0.00	0.00	963800.00	2673000.00	0.00	697616.48	0.00	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 5617154 3 587	0.00	0.00	1419508.79	1539000.00	2224800.00	422606.50	425591.64	283600.59	0.00	295865.57	482430.96	377618.25	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 7308322 1 528	0.00	0.00	648243.83	354258.80	0.00	0.00	411697.32	0.00	0.00	2025100.00	0.00	670894.50	KO:K00864	glycerol kinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0000001 219808 221244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1701900.00	0.00	2333100.00	2112000.00	0.00	KO:K00873	pyruvate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0658499 1 891	1190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00873	pyruvate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545889
Ga0586324 2022659 85 900	0.00	660086.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00873	pyruvate kinase	Bacteria;Verrucomicrobia;Spartobacteria;Chthoniobacterales;Chthoniobacteraceae;Chthoniobacter;Chthoniobacter flavus;Chthoniobacter flavus DSM 22515
Ga0586324 6148799 1 567	0.00	0.00	0.00	1216000.00	0.00	0.00	0.00	0.00	0.00	3865400.00	0.00	0.00	KO:K00873	pyruvate kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0445172 310 1443	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	427081.50	KO:K00874	2-dehydro-3-deoxygluconokinase	Bacteria;Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;Latescibacteria bacterium SCGC AAA252-B13;Latescibacteria bacterium SCGC AAA252-B13 (contamination screened)
Ga0586324 4827029 1 627	0.00	0.00	0.00	1092500.00	529531.24	2625126.77	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00895	pyrophosphate--fructose-6-phosphate 1-phosphotransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0048165 3 1106	0.00	0.00	0.00	0.00	7405700.00	0.00	0.00	0.00	1652400.00	0.00	0.00	0.00	KO:K00925	acetate kinase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina horonobensis;Methanosarcina horonobensis HB-1
Ga0586324 0000001 221333 222517	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9570900.00	0.00	7638400.00	0.00	0.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 0006147 2 1213	0.00	0.00	0.00	0.00	0.00	11870300.00	0.00	7259000.00	0.00	0.00	6045600.00	5812500.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 0013127 2192 3373	0.00	0.00	1417116.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0211041 507 1679	0.00	1407600.00	1213512.72	1510500.00	1586200.00	0.00	0.00	1848300.00	2284200.00	2656500.00	0.00	1035000.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324 0528637 3 785	0.00	1217200.00	0.00	198307.75	0.00	0.00	0.00	1073600.00	1806300.00	0.00	0.00	60398.03	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum miyakonense;Methylovulum miyakonense HT12
Ga0586324 0575363 1 918	0.00	0.00	4366988.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324 0710885 145 1407	0.00	0.00	0.00	9880000.00	11845000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Ectothiorhodospira;Ectothiorhodospira magna;Ectothiorhodospira magna B7-7
Ga0586324 0947291 3 1010	0.00	0.00	791752.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 2319952 289 849	0.00	0.00	0.00	2118500.00	5119100.00	0.00	0.00	2787700.00	0.00	0.00	0.00	0.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiorhodococcus;Thiorhodococcus drewsii;Thiorhodococcus drewsii AZ1
Ga0586324 2329215 2 664	0.00	1115200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00927	phosphoglycerate kinase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4235855 1 660	0.00	918000.00	0.00	0.00	3007600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00927	phosphoglycerate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Bordetella;Bordetella sp. N;Bordetella sp. N
Ga0586324 0018138 758 1645	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1311200.00	0.00	KO:K00930	acetylglutamate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira lacus;Nitrosospira lacus APG3
Ga0586324 0583270 117 1001	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2202200.00	0.00	0.00	KO:K00930	acetylglutamate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 0000070 48906 49562	0.00	0.00	0.00	0.00	0.00	0.00	18354000.00	15067000.00	16702200.00	3865400.00	5086400.00	8430000.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0001048 10750 11694	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1328400.00	1162700.00	0.00	1680000.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfurifustis;Sulfurifustis variabilis;Sulfurifustis variabilis skN76
Ga0586324 0020859 3521 4189	7390000.00	0.00	0.00	18430000.00	7755900.00	0.00	0.00	6832000.00	9315000.00	0.00	0.00	0.00	KO:K00939	adenylate kinase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6

Ga0586324 0033408 2929 3621	0.00	17340000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0034737 880 1524	9390000.00	21216000.00	19536100.00	22116000.00	0.00	9369200.00	0.00	0.00	3709800.00	0.00	0.00	2160000.00	KO:K00939	adenylate kinase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0057467 1360 2007	0.00	0.00	0.00	3401000.00	0.00	0.00	2325600.00	0.00	0.00	5374600.00	0.00	0.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0145170 2293 2874	0.00	0.00	0.00	0.00	19261000.00	0.00	0.00	23125100.00	12312000.00	0.00	0.00	0.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0186661 173 841	0.00	1183200.00	0.00	3030500.00	7354200.00	0.00	0.00	799100.00	217097.82	0.00	0.00	294338.25	KO:K00939	adenylate kinase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 0191452 1356 2003	0.00	16456943.84	34906000.00	50825000.00	45423000.00	48259911.53	27360000.00	32269000.00	20688572.88	25102000.00	29277600.00	15675000.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0701932 678 1325	0.00	0.00	0.00	0.00	3162100.00	6907800.00	4810800.00	0.00	0.00	0.00	5764000.00	3832500.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0887243 445 1092	0.00	385963.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6006000.00	0.00	0.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0960057 323 985	3310000.00	3155200.00	12723800.00	0.00	14317000.00	0.00	12836400.00	6405000.00	14904000.00	6814500.00	8800000.00	4177500.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Inmirania;Inmirania thermothiophila;Inmirania thermothiophila DSM 100275
Ga0586324 2952612 1 672	5190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00939	adenylate kinase	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Ilumatobacteraceae;Ilumatobacter;Ilumatobacter fluminis;Ilumatobacter fluminis DSM 18936
Ga0586324 3678679 3 626	22600000.00	24208000.00	0.00	25555000.00	0.00	0.00	0.00	27694000.00	51597000.00	27720000.00	0.00	0.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 6460918 1 555	3700000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00939	adenylate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 8114557 3 215	0.00	0.00	0.00	0.00	0.00	1800784.06	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00939	adenylate kinase	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324 0000184 28941 29372	0.00	0.00	5379374.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00940	nucleoside-diphosphate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324 0003751 7165 7590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1733400.00	0.00	0.00	0.00	KO:K00940	nucleoside-diphosphate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Noviherbaspirillum;Noviherbaspirillum massiliense;Noviherbaspirillum massiliense JC206
Ga0586324 0093725 1778 2203	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	750000.00	KO:K00940	nucleoside-diphosphate kinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 1426975 136 558	0.00	1332800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00940	nucleoside-diphosphate kinase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii WSM1741
Ga0586324 1858645 387 818	0.00	0.00	0.00	7628500.00	42642000.00	0.00	6406800.00	5063000.00	27378000.00	0.00	33528000.00	7875000.00	KO:K00940	nucleoside-diphosphate kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324 0000041 19268 20218	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1822500.00	KO:K00948	ribose-phosphate pyrophosphokinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 1399391 287 1051	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3003000.00	0.00	0.00	KO:K00948	ribose-phosphate pyrophosphokinase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0008738 9441 10673	0.00	20400000.00	0.00	109345000.00	69422000.00	0.00	0.00	0.00	666659.16	35112000.00	38720000.00	3660000.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0009502 2467 3675	0.00	0.00	14018700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0018169 1791 3047	0.00	0.00	0.00	0.00	0.00	0.00	1408866.72	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalkalivibrio;Thioalkalivibrio sulfidiphilus;Thioalkalivibrio sulfidophilus HL-EbGR7
Ga0586324 0046593 3503 4744	0.00	4148000.00	0.00	4750000.00	0.00	4287600.00	7546800.00	0.00	687195.09	0.00	0.00	1785000.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetoovum;Candidatus Magnetoovum chiemensis;Candidatus Magnetoovum chiemensis CS-04
Ga0586324 0057953 2783 4057	0.00	16592000.00	0.00	10165000.00	6664100.00	0.00	0.00	25986000.00	6747300.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0086383 1552 2793	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1069200.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetoovum;Candidatus Magnetoovum chiemensis;Candidatus Magnetoovum chiemensis CS-04
Ga0586324 0173887 1466 2641	14700000.00	0.00	36651300.00	0.00	0.00	0.00	675901.44	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 0200605 2 586	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7615300.00	7656000.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324 0299664 1108 2058	0.00	0.00	0.00	0.00	0.00	0.00	1602876.48	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0331734 614 1849	7170000.00	10200000.00	10386612.47	17765000.00	18540000.00	7662100.00	7296000.00	12242700.00	10611000.00	9471000.00	10190400.00	6855000.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0344379 1 978	0.00	0.00	0.00	2954500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0375356 391 1647	1600000.00	1924400.00	0.00	0.00	1503800.00	0.00	0.00	0.00	0.00	2764300.00	5394400.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0515793 3 926	0.00	10676000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0537992 3 1256	1710000.00	0.00	3089760.89	2308500.00	13390000.00	5716800.00	5358000.00	2641300.00	4446900.00	3264800.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0549740 537 1571	8070000.00	10404000.00	0.00	24320000.00	19776000.00	20286700.00	0.00	11651000.00	7605900.00	11242000.00	13376000.00	8100000.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetoovum;Candidatus Magnetoovum chiemensis;Candidatus Magnetoovum chiemensis CS-04
Ga0586324 0671325 119 721	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19703000.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfonema;Desulfonema limicola;Desulfonema limicola Jadebusen, DSM 2076
Ga0586324 0671325 699 1322	5700000.00	10744000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0700391 168 1397	17100000.00	19448000.00	41380500.00	0.00	43548400.00	27670900.00	0.00	29829000.00	47790000.00	6344800.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0780472 3 713	0.00	0.00	0.00	2014000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 0875961 1 843	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	508667.28	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0923162 3 959	0.00	29920000.00	0.00	0.00	0.00	0.00	0.00	38674000.00	35559000.00	0.00	25960000.00	21900000.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 1182430 676 1131	7930000.00	0.00	0.00	35910000.00	0.00	7622400.00	35568000.00	9211000.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 1539617 44 1009	30100000.00	377431.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 1602106 3 686	14000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1683363 256 972	0.00	0.00	0.00	0.00	0.00	0.00	5973600.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324 2391261 2 601	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6739200.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 2690852 2 796	0.00	2121600.00	0.00	15770000.00	0.00	0.00	0.00	0.00	6682500.00	5320700.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2858862 3 776	0.00	0.00	0.00	0.00	0.00	1027019.15	0.00	1842200.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 3104600 375 752	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12474000.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3520170 222 713	0.00	1278400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 3888883 3 668	0.00	0.00	0.00	0.00	0.00	8694300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5039500 2 616	18800000.00	22644000.00	0.00	7505000.00	12257000.00	4208200.00	4263600.00	19581000.00	6617700.00	14476000.00	10208000.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 5573539 2 589	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9234000.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 5667825 3 272	3760000.00	0.00	0.00	3353500.00	0.00	0.00	0.00	0.00	0.00	2902900.00	4021600.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetoovum;Candidatus Magnetoovum chiemensis;Candidatus Magnetoovum chiemensis CS-04
Ga0586324 7510884 2 520	215037.00	5038800.00	0.00	0.00	0.00	0.00	0.00	0.00	6706800.00	0.00	0.00	0.00	KO:K00958	sulfate adenylyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0001368 1948 4110	0.00	0.00	0.00	0.00	4830700.00	0.00	0.00	0.00	3288600.00	1386000.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0001370 13726 15861	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5837700.00	3564000.00	12273800.00	14044800.00	15022500.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0002100 12067 14229	0.00	0.00	0.00	0.00	0.00	0.00	12950400.00	0.00	0.00	1563100.00	34936000.00	4567500.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0002329 12843 14942	0.00	0.00	0.00	0.00	0.00	0.00	0.00	504851.25	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 0004094 2600 4711	0.00	0.00	0.00	0.00	1369900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazoonesis;Gemmatimonadetes bacterium KBS708
Ga0586324 0006042 3130 5280	0.00	0.00	0.00	0.00	0.00	0.00	0.00	707600.00	996300.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0009301 3 1310	0.00	3366000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta isovalerica;Spirochaeta isovalerica DSM 2461
Ga0586324 0010745 3311 5548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2737800.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0014811 6478 8535	0.00	0.00	0.00	0.00	0.00	0.00	3739200.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0017391 1 1248	0.00	0.00	0.00	0.00	0.00	0.00	606311.28	7838500.00	3896100.00	2533300.00	2930400.00	8325000.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0018681 4164 6476	0.00	0.00	0.00	0.00	0.00	0.00	2781600.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0029440 3 1472	0.00	0.00	0.00	0.00	114550.42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Actinobacteria;Actinomycetia;Glycomycetales;Glycomycetaceae;Glycomyces;Glycomyces arizonensis;Glycomyces arizonensis DSM 44726
Ga0586324 0038600 4142 5428	0.00	0.00	0.00	459599.55	0.00	0.00	0.00	1909300.00	260581.86	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0053148 2 1285	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3190300.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324 0073213 1547 3745	333422.00	1768000.00	0.00	1624500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324 0104103 3 1781	0.00	1856400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	703169.39	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0121032 2052 3131	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8703200.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0122637 1 1206	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5703500.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira;unclassified Azospira;Azospira sp. ZAP
Ga0586324 0175914 3 1895	3560000.00	0.00	0.00	2945000.00	0.00	1302727.71	1413438.12	2202100.00	2519100.00	0.00	0.00	495704.25	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0177209 3 620	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2208200.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis parvus;Methylocystis parvus OBBP
Ga0586324 0184497 185 2359	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1146800.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0221149 2 1105	2710000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0228457 1 1938	3160000.00	6936000.00	2305676.42	0.00	0.00	0.00	4879200.00	4148000.00	9882000.00	8547000.00	13552000.00	3270000.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0266664 1290 2168	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	328119.66	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas agitata;Dechloromonas agitata is5
Ga0586324 0299496 1079 2056	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7832000.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Verrucomicrobia;Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;Spartobacteria bacterium LR76;Spartobacteria bacterium LR76
Ga0586324 0312556 2 1459	0.00	1428000.00	0.00	770002.55	0.00	1324630.20	971843.16	982100.00	1004400.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0319417 980 1999	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1239300.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 0326625 3 1721	0.00	707200.00	0.00	0.00	0.00	0.00	0.00	464332.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 0329812 2 1969	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2476600.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira moscoviensis;Nitrospira moscoviensis NSP M-1
Ga0586324 0443178 3 1151	2050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0462311 137 1696	877296.00	0.00	0.00	0.00	0.00	845915.69	587907.12	596430.55	0.00	3934700.00	6107200.00	832500.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0519142 1 1611	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1838700.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0587382 1 1527	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1159000.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 0598543 1 1515	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	547621.50	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0702725 844 1413	0.00	625166.16	0.00	0.00	0.00	1932020.35	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324 0768569 1 1359	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	519551.82	4820200.00	7136800.00	4905000.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324 1046793 2 1033	0.00	0.00	0.00	367191.15	0.00	927602.41	0.00	738100.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1599991 3 992	0.00	0.00	0.00	0.00	3110600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 1600664 1 993	0.00	0.00	0.00	0.00	0.00	0.00	19448400.00	0.00	0.00	0.00	0.00	10725000.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum 31/32
Ga0586324 2096603 2 886	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	219087.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Roseimicrobium;Roseimicrobium gellanilyticum;Roseimicrobium gellanilyticum DSM 25532
Ga0586324 2242229 2 862	0.00	0.00	0.00	0.00	0.00	0.00	134702.40	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Thermomonosporaceae;Thermomonospora;Thermomonospora cellulosilytica;Thermomonospora cellulosilytica DSM 45823
Ga0586324 2382067 2 838	0.00	0.00	3264302.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324 2876056 2 526	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	710862.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP65;Rubrivivax sp. AAP65
Ga0586324 2876665 3 776	0.00	0.00	0.00	0.00	1112400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Faecalibacterium;Faecalibacterium prausnitzii;Faecalibacterium prausnitzii 2789STDY5834930
Ga0586324 2952665 1 768	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	994400.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 3407941 3 722	0.00	0.00	0.00	2356000.00	307652.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 3655171 3 701	507689.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Verrucomicrobia;Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;Spartobacteria bacterium LR76;Spartobacteria bacterium LR76
Ga0586324 4028824 1 675	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	378465.75	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 5008984 1 615	10100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfurivibrio;Desulfurivibrio alkaliphilus;Desulfurivibrio alkaliphilus AHT2
Ga0586324 5304746 3 602	0.00	0.00	0.00	0.00	0.00	0.00	2530800.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosovibrio;Nitrosovibrio sp. Nv4;Nitrosovibrio sp. Nv4
Ga0586324 5319008 158 601	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	871933.92	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Kuenenia;Candidatus Kuenenia stuttgartiensis;Candidatus Kuenenia stuttgartiensis MBR1
Ga0586324 6372709 2 559	0.00	0.00	0.00	0.00	0.00	3016167.80	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Salinivirgaceae;Salinivirga;Salinivirga cyanobacteriivorans;Salinivirga cyanobacteriivorans L21-Spi-D4
Ga0586324 6437556 3 557	0.00	6147200.00	4402918.98	6526500.00	0.00	0.00	3534000.00	3525800.00	4592700.00	0.00	0.00	12750000.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 7074902 1 534	0.00	0.00	0.00	0.00	0.00	0.00	0.00	281802.31	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 7620469 1 519	0.00	1176400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 8043305 3 506	0.00	0.00	0.00	0.00	0.00	0.00	1552379.04	0.00	0.00	0.00	0.00	0.00	KO:K00962	polyribonucleotide nucleotidyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0000002 32082 32951	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1403000.00	0.00	3826900.00	0.00	8400000.00	KO:K00963	UTP--glucose-1-phosphate uridylyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0178351 2 136	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5597900.00	0.00	0.00	KO:K00963	UTP--glucose-1-phosphate uridylyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. URHA0013;Bradyrhizobium sp. URHA0013
Ga0586324 0287651 963 1841	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	451273.13	0.00	0.00	KO:K00963	UTP--glucose-1-phosphate uridylyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. NpAV;Nitrosospira sp. NpAV
Ga0586324 1053206 3 245	0.00	0.00	0.00	0.00	0.00	0.00	0.00	138928.72	0.00	0.00	0.00	0.00	KO:K00963	UTP--glucose-1-phosphate uridylyltransferase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum;Herbaspirillum rubrisubalbicans;Herbaspirillum seropedicae Os45
Ga0586324 0066025 562 2190	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1134000.00	0.00	0.00	0.00	KO:K00970	poly(A) polymerase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Caenimonas;Caenimonas koreensis;Caenimonas koreensis DSM 17982
Ga0586324 0676191 1 1077	0.00	0.00	0.00	0.00	2719200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00975	glucose-1-phosphate adenylyltransferase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 7445173 2 523	0.00	1509600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K00989	ribonuclease PH	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Stappiaceae;Stappia;Stappia sp. ARW1T;Stappia sp. ARW1T
Ga0586324 0002895 13062 15833	0.00	0.00	0.00	3686000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 0012712 1320 4142	0.00	0.00	0.00	0.00	6025500.00	0.00	0.00	0.00	0.00	9086000.00	0.00	3270000.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0026074 2270 5020	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9720000.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0039278 1 1764	0.00	0.00	2951144.66	0.00	0.00	1268946.98	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0053355 3382 4632	0.00	0.00	0.00	0.00	1452300.00	0.00	0.00	0.00	0.00	0.00	0.00	4665000.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 0055648 2419 4539	8190000.00	10404000.00	0.00	4892500.00	0.00	3819068.54	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Deferribacter;Deferribacter desulfuricans;Deferribacter desulfuricans SSM1
Ga0586324 0067701 1 2373	0.00	0.00	0.00	0.00	1823100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 0070688 563 3391	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1757700.00	1809500.00	2173600.00	2865000.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfurifustis;Sulfurifustis variabilis;Sulfurifustis variabilis skN76
Ga0586324 0072270 1322 4003	0.00	0.00	0.00	16305834.20	7694100.00	0.00	0.00	0.00	18468000.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thioflavicoccus;Thioflavicoccus mobilis;Thioflavicoccus mobilis 8321
Ga0586324 0074994 1525 3933	4550000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio hydrogeniphilus;Thermodesulfovibrio hydrogeniphilus DSM 18151
Ga0586324 0106064 1549 3336	1730000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Calditerrivibrio;Calditerrivibrio nitroreducens;Calditerrivibrio nitroreducens Yu37-1, DSM 19672
Ga0586324 0107803 1102 3309	0.00	0.00	0.00	1586500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324 0124958 1 1827	0.00	0.00	1045890.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;Marinimicrobia bacterium JGI 0000039-D08;Marinimicrobia bacterium JGI 0000039-D08 (contamination screened)
Ga0586324 0263241 1 1446	0.00	0.00	0.00	1263500.00	0.00	0.00	0.00	0.00	939600.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0263331 270 2180	0.00	0.00	0.00	0.00	0.00	165549000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 0307839 2 2032	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	145723.05	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thioploca;Thioploca ingrica;Thioploca ingrica Lake Okotanpe
Ga0586324 0366005 3 1655	0.00	5841200.00	0.00	0.00	0.00	3463828.97	0.00	0.00	0.00	0.00	0.00	2167500.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 0373156 2 1864	8280000.00	1516400.00	0.00	6346000.00	1091800.00	0.00	0.00	7088200.00	826200.00	2340800.00	2710400.00	2715000.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 0407685 1 1794	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2415000.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0490081 236 1654	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1842200.00	1530900.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 0529416 2 1402	949465.00	6745600.00	0.00	1586500.00	4511400.00	0.00	0.00	6161000.00	4617000.00	4697000.00	5438400.00	2092500.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloglobulus;Methyloglobulus morosus;Methyloglobulus morosus KoM1

Ga0586324 0573186 2 1543	0.00	0.00	0.00	0.00	0.00	0.00	4468800.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Prosthecobacter;Prosthecobacter vanneervenii;Prosthecobacter vanneervenii DSM 12252
Ga0586324 0588571 127 1527	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1894200.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 0645498 3 857	0.00	0.00	0.00	2498500.00	0.00	0.00	0.00	0.00	4001400.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Prosthecobacter;Prosthecobacter vanneervenii;Prosthecobacter vanneervenii DSM 12252
Ga0586324 0681531 664 1431	0.00	8908000.00	0.00	0.00	288256.83	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 0708751 2 463	0.00	1482400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 0815359 2 1327	0.00	1720400.00	2750632.21	0.00	0.00	0.00	0.00	732000.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 0842789 2 1306	0.00	0.00	0.00	0.00	0.00	2228067.22	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 0857313 2 1297	2430000.00	0.00	0.00	4598000.00	6355100.00	0.00	0.00	3605100.00	3539700.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0899167 1 1272	0.00	2284800.00	0.00	4845000.00	0.00	6232900.00	5791200.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1006885 2 922	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1355200.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324 1024913 148 1200	0.00	0.00	0.00	0.00	3440200.00	1530327.81	0.00	2098400.00	0.00	0.00	4109600.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;unclassified Opitutaceae;Opitutaceae bacterium;Opitutaceae bacterium TAV3
Ga0586324 1417947 3 1046	0.00	0.00	0.00	0.00	0.00	0.00	0.00	454523.81	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 1489919 1 1023	0.00	0.00	0.00	0.00	0.00	2439231.52	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 1753045 1 954	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	431321.76	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 1757151 2 955	0.00	0.00	0.00	0.00	0.00	0.00	0.00	817400.00	0.00	0.00	0.00	324107.25	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 2128486 1 852	0.00	0.00	436782.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Thermoclostridium;Thermoclostridium caenicola;Thermoclostridium caenicola DSM 19027
Ga0586324 3099012 1 750	0.00	0.00	0.00	2346500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobotulus;Desulfobotulus sapovorans;Desulfobotulus sapovorans DSM 2055
Ga0586324 3112058 3 749	0.00	1373600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324 3971727 2 679	0.00	0.00	0.00	386348.85	0.00	4843400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 3988390 3 677	8840000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 4192866 15 662	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3977200.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324 4200438 15 662	0.00	0.00	0.00	0.00	3594700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;unclassified Opitutaceae;Opitutaceae bacterium EW11;Opitutaceae bacterium EW11
Ga0586324 4371104 1 522	0.00	0.00	0.00	0.00	0.00	0.00	1854734.40	0.00	1579500.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5236640 3 605	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2257000.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoguttaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 6170799 2 565	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	580466.48	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 6341735 2 559	0.00	0.00	0.00	1121000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324 6344377 1 558	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	330219.99	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus sp. ER46;Opitutus sp. ER46
Ga0586324 6430069 2 556	0.00	215389.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Draconibacterium;Draconibacterium orientale;Draconibacterium orientale FH5
Ga0586324 6527845 3 551	0.00	0.00	0.00	0.00	1740700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324 6647208 1 549	0.00	9363600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 7040427 2 535	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1640900.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 7639387 1 516	0.00	0.00	0.00	2945000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01006	pyruvate,orthophosphate dikinase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;Bacteroides acidifaciens;Bacteroides acidifaciens 1e8A
Ga0586324 0062816 2755 4281	3650000.00	3250400.00	4672601.61	4294000.00	4253900.00	0.00	8048400.00	4050400.00	3717900.00	3842300.00	3792800.00	3165000.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0135424 92 1774	0.00	0.00	0.00	4854500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0234527 1038 2300	0.00	0.00	0.00	3809500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0455699 654 1706	0.00	0.00	0.00	0.00	0.00	2377692.55	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Inmirania;Inmirania thermothiophila;Inmirania thermothiophila DSM 100275
Ga0586324 0456925 157 1704	0.00	2148800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0638308 2 1048	5360000.00	7881200.00	4575326.47	0.00	7642600.00	0.00	2121259.56	1537200.00	3604500.00	13767600.00	16456000.00	8025000.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0828998 229 1317	683854.00	1319200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0946464 2 1243	6580000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3207600.00	0.00	0.00	0.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 1109716 150 1160	0.00	0.00	0.00	0.00	0.00	0.00	5335200.00	0.00	0.00	4134900.00	0.00	0.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 6068272 3 569	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2580000.00	KO:K01007	pyruvate,water dikinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0003104 696 1733	0.00	7344000.00	0.00	0.00	0.00	12942200.00	0.00	0.00	0.00	8778000.00	9240000.00	0.00	KO:K01039	glutaconate CoA-transferase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0056515 3902 4504	4640000.00	7140000.00	0.00	8987000.00	0.00	0.00	0.00	0.00	0.00	3056900.00	3836800.00	0.00	KO:K01039	glutaconate CoA-transferase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacula;Desulfobacula toluolica;Desulfobacula toluolica Tol2
Ga0586324 2580066 3 812	5410000.00	5868400.00	0.00	5196500.00	6870100.00	1482124.07	0.00	4331000.00	1887300.00	0.00	0.00	0.00	KO:K01039	glutaconate CoA-transferase subunit A	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Quasibacillus;Quasibacillus thermotolerans;Quasibacillus thermotolerans SGZ-8
Ga0586324 3454815 31 717	0.00	0.00	0.00	1453500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01039	glutaconate CoA-transferase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 7613355 20 517	0.00	7276000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01039	glutaconate CoA-transferase subunit A	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Quasibacillus;Quasibacillus thermotolerans;Quasibacillus thermotolerans SGZ-8
Ga0586324 0003104 1736 2503	15570000.00	19108000.00	0.00	0.00	0.00	901809.32	5084400.00	0.00	4414500.00	3726800.00	2666400.00	5017500.00	KO:K01040	glutaconate CoA-transferase subunit B	Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;Effusibacillus;Effusibacillus lacus;Effusibacillus lacus DSM 27172
Ga0586324 0079188 690 1589	0.00	2686000.00	2875105.88	0.00	0.00	2771603.89	0.00	0.00	1409400.00	0.00	0.00	0.00	KO:K01040	glutaconate CoA-transferase subunit B	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofarcimen;Desulfofarcimen acetoxidans;Desulfofarcimen acetoxidans DSM 771
Ga0586324 0468029 1326 1688	2570000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01040	glutaconate CoA-transferase subunit B	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofarcimen;Desulfofarcimen acetoxidans;Desulfofarcimen acetoxidans DSM 771
Ga0586324 1911111 79 846	5400000.00	7344000.00	1856115.29	5985000.00	1555300.00	1594328.18	3643672.56	4373700.00	1020600.00	877800.00	808435.76	3609060.00	KO:K01040	glutaconate CoA-transferase subunit B	Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;Effusibacillus;Effusibacillus lacus;Effusibacillus lacus DSM 27172
Ga0586324 3524985 1 552	277392.00	0.00	0.00	0.00	5644400.00	0.00	29001600.00	0.00	0.00	2610300.00	0.00	0.00	KO:K01040	glutaconate CoA-transferase subunit B	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfosporosinus;Desulfosporosinus orientis;Desulfosporosinus orientis Singapore I, DSM 765
Ga0586324 7610785 2 334	0.00	0.00	0.00	0.00	3399000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01040	glutaconate CoA-transferase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 1483937 255 1025	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2684000.00	0.00	KO:K01046	triacylglycerol lipase	Bacteria;Actinobacteria;Actinomycetia;Streptomycetales;Streptomycetaceae;Streptomyces;Streptomyces sp. Mg1;Streptomyces sp. Mg1
Ga0586324 0006638 3229 4302	0.00	0.00	0.00	6555000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01053	gluconolactonase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI 001;Burkholderiales sp. JOSHI 001
Ga0586324 0018497 421 1656	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	885000.00	KO:K01053	gluconolactonase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Boseaceae;Bosea;Bosea sp. LC85;Bosea sp. LC85
Ga0586324 0057890 2038 3096	7690000.00	7140000.00	5967800.00	7391000.00	8559300.00	4327300.00	0.00	0.00	4479300.00	4858700.00	0.00	7320000.00	KO:K01053	gluconolactonase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus sp. ASC-9842;Cupriavidus tamaulipasensis ASC-9842
Ga0586324 0365164 1340 1882	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	400068.00	KO:K01053	gluconolactonase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;unclassified Hyphomicrobiales;Rhizobiales bacterium YIM 77505;Rhizobiales bacterium YIM 77505
Ga0586324 0669765 544 1443	0.00	2652000.00	4073518.94	2593500.00	3687400.00	3016862.55	1483032.84	0.00	5556600.00	4727800.00	2666400.00	4838445.00	KO:K01053	gluconolactonase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 5747177 3 563	0.00	0.00	11597800.00	0.00	0.00	0.00	0.00	0.00	0.00	5428500.00	0.00	0.00	KO:K01053	gluconolactonase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 4568759 1 519	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	683942.25	KO:K01061	carboxymethylenebutenolidase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella sp. OAS946;Reyranella sp. OAS946
Ga0586324 2160468 188 874	3290000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01077	alkaline phosphatase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Desulfallaceae;Desulfoscipio;Desulfoscipio gibsoniae;Desulfallas gibsoniae Groll, DSM 7213
Ga0586324 1113056 3 1160	4240000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01081	5'-nucleotidase	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. Root122;Nocardioides sp. Root122
Ga0586324 4185838 2 664	1320000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01081	5'-nucleotidase	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides soli;Nocardioides soli DSM 105498
Ga0586324 0003161 11133 15230	0.00	0.00	260243.94	0.00	0.00	1418250.74	970582.32	0.00	1085400.00	1500923.27	463838.32	832500.00	KO:K01119	2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Beutenbergiaceae;Salana;Salana multivorans;Salana multivorans DSM 13521
Ga0586324 2050843 2 895	0.00	3706000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01178	glucoamylase	Bacteria;Chloroflexi;Ktedonobacteria;Ktedonobacterales;Ktedonobacteraceae;Ktedonobacter;Ktedonobacter racemifer;Ktedonobacter racemifer SOSP1-21, DSM 44963
Ga0586324 0484346 49 1662	0.00	0.00	0.00	0.00	1328700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01179	endoglucanase	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Niastella;Niastella koreensis;Niastella koreensis GR20-10, DSM 17620
Ga0586324 1257648 1 1101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2586400.00	0.00	0.00	0.00	0.00	KO:K01190	beta-galactosidase	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium URHE0068;Acidobacteriaceae bacterium URHE0068
Ga0586324 0823852 3 1319	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1200000.00	KO:K01214	isoamylase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Pelobacter;Pelobacter propionicus;Pelobacter propionicus DSM 2379
Ga0586324 0000011 20366 21802	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12012000.00	0.00	9750000.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0002917 1643 2935	0.00	3746800.00	0.00	0.00	0.00	0.00	21477600.00	0.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324 0053628 1508 2764	0.00	0.00	0.00	0.00	2997300.00	0.00	0.00	4202900.00	5589000.00	0.00	3212000.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0161725 2 1048	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10125000.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0170397 390 1646	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2980800.00	13090000.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324 0176469 1815 2624	0.00	0.00	0.00	0.00	15759000.00	0.00	0.00	0.00	0.00	0.00	7471200.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 0512168 3 1040	0.00	4454000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Aquabacterium;Aquabacterium tepidiphilum;Aquabacterium tepidiphilum YIM 730274
Ga0586324 0616485 554 1495	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13176000.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;unclassified Burkholderiaceae;Burkholderiaceae bacterium PBA;Burkholderiaceae bacterium PBA
Ga0586324 1759418 181 954	0.00	0.00	0.00	0.00	0.00	0.00	3237600.00	0.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfocapsa;Desulfocapsa sulfexigens;Desulfocapsa sulfexigens DSM 10523
Ga0586324 2723529 27 794	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4851900.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 3224310 1 738	0.00	0.00	0.00	0.00	3007600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324 3281469 1 735	0.00	0.00	5425749.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfonema;Desulfonema limicola;Desulfonema limicola Jadebusen, DSM 2076
Ga0586324 4150652 1 666	17800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Xanthobacter;Xanthobacter autotrophicus;Xanthobacter autotrophicus Py2
Ga0586324 4537571 3 641	0.00	0.00	0.00	4940000.00	0.00	0.00	6703200.00	0.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium ailaaui;Acidobacterium ailaaui PMMR2
Ga0586324 5897568 2 577	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7136100.00	11550000.00	570970.40	10875000.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Archangiaceae;Archangium;Archangium sp. Cb G35;Archangium sp. Cb G35
Ga0586324 6556621 2 550	0.00	0.00	0.00	4294000.00	0.00	0.00	0.00	0.00	0.00	839300.00	0.00	5400000.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Ahniella;Ahniella affigens;Ahniella affigens D13
Ga0586324 6741891 3 545	4030000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01251	adenosylhomocysteinase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324 0000037 26947 28452	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4535300.00	4250400.00	0.00	KO:K01255	leucyl aminopeptidase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0102001 433 1935	0.00	0.00	0.00	0.00	0.00	0.00	1230757.68	0.00	0.00	0.00	0.00	0.00	KO:K01255	leucyl aminopeptidase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0147937 844 2331	0.00	0.00	0.00	0.00	0.00	0.00	629665.32	0.00	0.00	0.00	0.00	0.00	KO:K01255	leucyl aminopeptidase	Bacteria;Fibrobacteres;Fibrobacteria;unclassified Fibrobacteria;unclassified Fibrobacteria;Fibrobacteria bacterium AD312;Fibrobacteria bacterium AD312 AD 312
Ga0586324 0851941 3 1091	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	787500.00	KO:K01255	leucyl aminopeptidase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 4538733 1 642	0.00	0.00	0.00	0.00	0.00	0.00	2177685.00	0.00	0.00	0.00	0.00	0.00	KO:K01255	leucyl aminopeptidase	Bacteria;Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;Verrucomicrobia bacterium LW23;Verrucomicrobia bacterium LW23
Ga0586324 1923500 1 804	0.00	0.00	0.00	5168000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01270	dipeptidase D	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinifilaceae;Ancylomarina;Ancylomarina subtilis;Ancylomarina subtilis DSM 28825
Ga0586324 0000137 32897 35299	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3357200.00	32648000.00	4657500.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0010606 3967 6381	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5266800.00	0.00	4725000.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0014466 5954 8443	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7700000.00	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0022685 3046 5049	0.00	1285200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;Candidatus Desulfofervidaceae;Candidatus Desulfofervidus;Candidatus Desulfofervidus auxilii;delta proteobacterium HotSeep1
Ga0586324 0033750 4643 5794	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3968800.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira briensis;Nitrosospira briensis C-128
Ga0586324 0110198 1013 3271	0.00	0.00	0.00	3790500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 0128720 1 1245	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17479000.00	15752000.00	3945000.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324 0136108 3 2129	0.00	0.00	3153143.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 0157983 209 2650	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	461977.67	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0201531 3 1262	0.00	0.00	0.00	927759.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 0390849 2 1828	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	478444.50	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 0675852 3 1439	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1425000.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324 0681878 272 1432	0.00	1475600.00	0.00	2327500.00	2997300.00	0.00	0.00	0.00	0.00	0.00	0.00	2025000.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324 0990913 3 1220	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	247740.57	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylotenera;Methylotenera versatilis;Methylotenera versatilis 79
Ga0586324 2829375 3 641	0.00	0.00	12836400.00	5586000.00	0.00	1821594.80	0.00	0.00	2867400.00	0.00	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324 4128190 3 668	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	439994.94	0.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5119985 2 610	0.00	5514800.00	0.00	0.00	0.00	0.00	0.00	0.00	6536700.00	0.00	4100800.00	4515000.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 5488961 3 593	0.00	727600.00	0.00	0.00	0.00	0.00	0.00	628300.00	305336.79	2025100.00	2622400.00	0.00	KO:K01338	ATP-dependent Lon protease	Bacteria;Candidatus Fervidibacteria;unclassified Candidatus Fervidibacteria;unclassified Candidatus Fervidibacteria;unclassified Candidatus Fervidibacteria;Fervidibacteria bacterium JGI 0000001-B9;Fervidibacteria bacterium JGI 0000001-B9 (contamination screened)
Ga0586324 0115112 702 2552	0.00	276321.40	0.00	2726500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01342	subtilisin	Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Vibrio;Vibrio sp. EJY3;Vibrio sp. EJY3
Ga0586324 0392996 143 772	0.00	0.00	0.00	0.00	0.00	0.00	563777.88	0.00	0.00	0.00	0.00	0.00	KO:K01358	ATP-dependent Clp protease protease subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 8280633 1 501	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1655500.00	0.00	0.00	KO:K01358	ATP-dependent Clp protease protease subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0000169 21223 22101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4769600.00	6495000.00	KO:K01423	predicted Zn-dependent protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0001043 10586 11659	0.00	0.00	1627317.72	1463000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	862500.00	KO:K01424	L-asparaginase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Achromobacter;Achromobacter xylosoxidans;Achromobacter xylosoxidans IYER ADAF13
Ga0586324 0042502 3286 4374	67392.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01424	L-asparaginase	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Halioglobus;Halioglobus lutimaris;Halioglobus lutimaris HF004
Ga0586324 0099996 1316 2383	0.00	294108.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01424	L-asparaginase	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Flavobacterium;Flavobacterium sp. URHB0058;Flavobacterium sp. URHB0058
Ga0586324 0385181 401 1465	0.00	368766.72	0.00	0.00	0.00	1048806.51	0.00	640500.00	0.00	119502.46	0.00	0.00	KO:K01424	L-asparaginase	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Flavobacterium;Flavobacterium saccharophilum;Flavobacterium saccharophilum DSM 1811
Ga0586324 6269408 240 563	0.00	0.00	0.00	0.00	0.00	0.00	4126800.00	0.00	1255500.00	0.00	1795200.00	3727500.00	KO:K01424	L-asparaginase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PB90-1
Ga0586324 0001043 7467 8687	0.00	0.00	2852107.33	2128000.00	0.00	0.00	0.00	0.00	0.00	954800.00	0.00	668823.75	KO:K01425	glutaminase	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;Oceanicoccus;Oceanicoccus sagamiensis;Oceanicoccus sagamiensis NBRC 107125
Ga0586324 0027881 5418 6350	0.00	0.00	0.00	0.00	5273600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01425	glutaminase	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 0077702 1242 2270	0.00	1183200.00	1699015.77	0.00	667065.08	682466.82	0.00	1104100.00	834300.00	0.00	819329.28	990000.00	KO:K01425	glutaminase	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Flavisolibacter;Flavisolibacter tropicus;Flavisolibacter tropicus LCS9
Ga0586324 0088508 252 1295	0.00	0.00	0.00	0.00	966008.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01425	glutaminase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0134455 57 1124	0.00	0.00	0.00	0.00	0.00	2427873.35	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01425	glutaminase	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Halioglobus;Halioglobus sediminis;Halioglobus sediminis U0301 U0301
Ga0586324 0270362 519 1559	0.00	4576400.00	0.00	0.00	0.00	29116976.47	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01425	glutaminase	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;unclassified Alteromonadaceae;Alteromonadaceae bacterium 1081L.S.0a.03;Alteromonadaceae bacterium 1081L.S.0a.03
Ga0586324 0942500 321 1244	0.00	0.00	12836400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01425	glutaminase	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;unclassified Alteromonadaceae;Alteromonadaceae bacterium 1081L.S.0a.03;Alteromonadaceae bacterium 1081L.S.0a.03
Ga0586324 2083398 2 889	0.00	0.00	0.00	5434000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01425	glutaminase	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;unclassified Alteromonadaceae;Alteromonadaceae bacterium 1081L.S.0a.03;Alteromonadaceae bacterium 1081L.S.0a.03
Ga0586324 7489879 1 522	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1108800.00	0.00	KO:K01448	N-acetylmuramoyl-L-alanine amidase	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 1984603 3 905	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3402000.00	0.00	0.00	0.00	KO:K01464	dihydropyrimidinase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324 0000007 110868 112097	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4981900.00	2024000.00	0.00	KO:K01478	arginine deiminase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Rhizobium;Rhizobium sp. YR295;Rhizobium sp. YR295
Ga0586324 0098969 984 2249	0.00	0.00	0.00	0.00	2410200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01478	arginine deiminase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324 0000241 25343 26230	0.00	0.00	0.00	0.00	2430800.00	0.00	0.00	0.00	4811400.00	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324 0017644 5900 6820	0.00	5555600.00	15088400.00	5105871.90	3172400.00	9840701.02	21158400.00	1409100.00	2106000.00	3803800.00	5693600.00	5947500.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0069787 2794 3684	0.00	6752400.00	0.00	16055000.00	40788000.00	2903499.20	0.00	10736000.00	18063000.00	3896200.00	0.00	3922500.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 0234267 1 495	0.00	0.00	0.00	0.00	0.00	0.00	5084400.00	0.00	0.00	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0439497 65 964	0.00	0.00	0.00	0.00	0.00	0.00	10693200.00	0.00	0.00	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0466468 1205 1690	0.00	4630800.00	0.00	14535000.00	18643000.00	7463600.00	0.00	2659600.00	8910000.00	0.00	0.00	4942500.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0842840 2 538	0.00	0.00	0.00	0.00	0.00	10560200.00	0.00	9333000.00	8910000.00	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0955091 78 986	0.00	0.00	0.00	0.00	1359600.00	0.00	0.00	1067500.00	0.00	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660

Ga0586324 1124653 1 807	0.00	727600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324 2730062 2 535	0.00	0.00	0.00	0.00	0.00	1847173.51	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 3305410 140 730	0.00	0.00	0.00	0.00	1606800.00	0.00	0.00	1409100.00	0.00	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324 3668690 1 702	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	441556.92	0.00	0.00	0.00	KO:K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324 0689083 7 693	0.00	0.00	0.00	0.00	0.00	0.00	1761329.64	0.00	0.00	0.00	0.00	0.00	KO:K01507	inorganic pyrophosphatase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio inopinatus;Desulfovibrio inopinatus DSM 10711
Ga0586324 0004139 1672 3147	0.00	0.00	0.00	2546000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01524	exopolyphosphatase/guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 0072301 2224 3717	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1262800.00	0.00	0.00	KO:K01524	exopolyphosphatase/guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa roseopersicina;Thiocapsa roseopersicina DSM 217
Ga0586324 2223888 3 863	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11529000.00	0.00	15092000.00	9504000.00	6787500.00	KO:K01524	exopolyphosphatase/guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa roseopersicina;Thiocapsa roseopersicina DSM 217
Ga0586324 3140380 2 748	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1386000.00	0.00	0.00	KO:K01531	Mg2+-importing ATPase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. PSR-1;Anaeromyxobacter sp. PSR-1
Ga0586324 3680882 3 701	0.00	0.00	0.00	0.00	0.00	17507700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01537	Ca2+-transporting ATPase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina mazei;Methanosarcina mazei 3.H.A.2.4
Ga0586324 0140086 1186 2121	1630000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01551	arsenite-transporting ATPase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0187333 1068 2054	1260000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01551	arsenite-transporting ATPase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 1839571 2 808	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	349374.06	0.00	0.00	0.00	KO:K01551	arsenite-transporting ATPase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 4168625 1 321	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2490000.00	KO:K01551	arsenite-transporting ATPase	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324 5925554 3 575	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2787700.00	0.00	0.00	0.00	0.00	KO:K01551	arsenite-transporting ATPase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0088131 587 2197	0.00	0.00	0.00	14630000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01576	benzoylformate decarboxylase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0088;Rhodospirillales bacterium URHD0088
Ga0586324 0030710 4622 6064	0.00	0.00	0.00	2527000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01577	oxalyl-CoA decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. EUR3 1.2.1;Polaromonas sp. EUR3 1.2.1
Ga0586324 0280958 1 1716	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2827500.00	KO:K01577	oxalyl-CoA decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. EUR3 1.2.1;Polaromonas sp. EUR3 1.2.1
Ga0586324 7585586 3 518	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1976400.00	0.00	0.00	0.00	0.00	KO:K01577	oxalyl-CoA decarboxylase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia birgiae;Afipia birgiae 34632
Ga0586324 0008831 9359 10780	0.00	0.00	0.00	0.00	0.00	0.00	0.00	156165.49	0.00	0.00	0.00	0.00	KO:K01580	glutamate decarboxylase	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Shewanellaceae;Shewanella;Shewanella sp. cp20;Shewanella sp. cp20
Ga0586324 5873646 69 578	0.00	0.00	7262700.00	0.00	0.00	6868100.00	0.00	738100.00	0.00	0.00	0.00	0.00	KO:K01580	glutamate decarboxylase	Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Vibrio;Vibrio breoganii;Vibrio breoganii ZF-55
Ga0586324 0000007 104139 106559	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4109600.00	6720000.00	KO:K01581	ornithine decarboxylase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium sophorae;Mesorhizobium sophorae ICMP 19535
Ga0586324 0007318 6848 9091	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1170400.00	1760000.00	1185000.00	KO:K01584	arginine decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0025661 1467 4226	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3067500.00	KO:K01584	arginine decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia fungorum;Paraburkholderia fungorum GAS106B
Ga0586324 0094753 3 1739	0.00	897600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1672000.00	1515000.00	KO:K01584	arginine decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia;Ralstonia sp. 25mfcol4.1;Ralstonia sp. 25MFCol4.1
Ga0586324 0135668 1 2175	0.00	7344000.00	0.00	0.00	0.00	0.00	1580929.20	1317600.00	0.00	0.00	0.00	16350000.00	KO:K01584	arginine decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus plantarum;Cupriavidus plantarum ASC-64
Ga0586324 1089376 1 897	0.00	231897.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	764123.36	0.00	0.00	KO:K01584	arginine decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus plantarum;Cupriavidus plantarum ASC-64
Ga0586324 1102099 1 1164	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2085600.00	0.00	KO:K01584	arginine decarboxylase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia broomeae;Afipia broomeae GAS525
Ga0586324 1690420 1 969	0.00	0.00	0.00	0.00	0.00	1533341.04	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01584	arginine decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus plantarum;Cupriavidus plantarum MA1-2za
Ga0586324 0023837 6022 6528	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2140600.00	0.00	0.00	KO:K01588	5-(carboxyamino)imidazole ribonucleotide mutase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0000002 19492 22308	0.00	0.00	0.00	0.00	0.00	0.00	198004.32	0.00	0.00	0.00	0.00	0.00	KO:K01595	phosphoenolpyruvate carboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0202422 275 2119	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3052500.00	KO:K01596	phosphoenolpyruvate carboxykinase (GTP)	Bacteria;Planctomycetes;Planctomycetia;Gemmatales;Gemmataceae;Gemmata;Gemmata obscuriglobus;Gemmata obscuriglobus DSM 5831
Ga0586324 0927541 183 1253	10800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01596	phosphoenolpyruvate carboxykinase (GTP)	Bacteria;Actinobacteria;Actinomycetia;Frankiales;Frankiaceae;Frankia;Frankia inefficax;Frankia inefficax EuI1c
Ga0586324 1548495 406 1008	0.00	1638800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01596	phosphoenolpyruvate carboxykinase (GTP)	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run_A_D11
Ga0586324 6415023 1 555	0.00	0.00	0.00	0.00	0.00	2249802.97	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01599	uroporphyrinogen decarboxylase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;unclassified Opitutaceae;Opitutaceae bacterium;Opitutaceae bacterium TAV3
Ga0586324 0000011 64953 66374	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15092000.00	2921600.00	16725000.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 0000656 9055 10434	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6767200.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 0037134 4148 5527	0.00	1339600.00	0.00	0.00	0.00	0.00	0.00	0.00	11664000.00	0.00	0.00	5445000.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax antarcticus;Rhodoferax antarcticus DSM 24876
Ga0586324 0069998 2528 3964	52570000.00	21222800.00	102785902.23	93271000.00	100394100.00	65761827.24	0.00	33964800.00	24957433.26	18403000.00	12346400.00	5685000.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Eukaryota;Streptophyta;Magnoliopsida;Malpighiales;Salicaceae;Populus;Populus trichocarpa;Populus balsamifera trichocarpa
Ga0586324 0469282 982 1686	0.00	0.00	0.00	0.00	0.00	0.00	49248000.00	0.00	0.00	0.00	41536000.00	46725000.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Acidithiobacillia;Acidithiobacillales;Acidithiobacillaceae;Acidithiobacillus;Acidithiobacillus ferrooxidans;Acidithiobacillus ferrooxidans ATCC 53993
Ga0586324 0731259 3 1049	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5499900.00	0.00	0.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0890895 3 1253	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11590000.00	0.00	0.00	0.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfurifustis;Sulfurifustis variabilis;Sulfurifustis variabilis skN76
Ga0586324 1095597 1 1050	0.00	3413600.00	0.00	0.00	0.00	3349346.08	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Eukaryota;Streptophyta;Magnoliopsida;Malpighiales;Salicaceae;Populus;Populus trichocarpa;Populus balsamifera trichocarpa
Ga0586324 1176306 1 945	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2502900.00	2240700.00	0.00	1762500.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Eukaryota;Bacillariophyta;Coscinodiscophyceae;Thalassiosirales;Thalassiosiraceae;Thalassiosira;Thalassiosira pseudonana;Thalassiosira pseudonana CCMP 1335
Ga0586324 1293263 448 1086	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3110400.00	0.00	0.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula thiophila;Sulfuriferula thiophila mst6
Ga0586324 1870281 1 891	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2316600.00	0.00	0.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Limnohabitans;Limnohabitans sp. 63ED37-2;Limnohabitans sp. 63ED37-2
Ga0586324 2387207 1 837	0.00	2176000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Allochromatium;Allochromatium warmingii;Allochromatium warmingii DSM 173
Ga0586324 3945909 3 680	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3796100.00	0.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324 6832111 2 541	0.00	0.00	0.00	0.00	8167900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula thiophila;Sulfuriferula thiophila mst6
Ga0586324 8050146 2 505	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1927800.00	0.00	5676000.00	0.00	KO:K01601	ribulose-bisphosphate carboxylase large chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Sphaerotilus;Sphaerotilus montanus;Sphaerotilus montanus DSM 21226
Ga0586324 0432435 64 1620	0.00	2679200.00	56300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01604	acetyl-CoA carboxylase carboxyltransferase component	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinifilaceae;Ancylomarina;Ancylomarina subtilis;Ancylomarina subtilis DSM 28825
Ga0586324 1080705 3 1175	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	647326.08	0.00	0.00	0.00	KO:K01604	acetyl-CoA carboxylase carboxyltransferase component	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2288425 2 502	0.00	0.00	0.00	0.00	0.00	0.00	0.00	31415000.00	0.00	0.00	0.00	0.00	KO:K01604	acetyl-CoA carboxylase carboxyltransferase component	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Sediminitomix;Sediminitomix flava;Sediminitomix flava DSM 28229
Ga0586324 2679214 48 797	0.00	0.00	0.00	0.00	0.00	8972200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01604	acetyl-CoA carboxylase carboxyltransferase component	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 3724333 3 695	0.00	0.00	0.00	2061500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01604	acetyl-CoA carboxylase carboxyltransferase component	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 4998944 165 617	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1117600.00	0.00	KO:K01604	acetyl-CoA carboxylase carboxyltransferase component	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Salinivirgaceae;Salinivirga;Salinivirga cyanobacteriivorans;Salinivirga cyanobacteriivorans L21-Spi-D4
Ga0586324 3081647 2 370	0.00	2801600.00	0.00	0.00	0.00	0.00	0.00	368418.04	0.00	0.00	0.00	862500.00	KO:K01607	4-carboxymuconolactone decarboxylase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0051560 2 1189	0.00	0.00	0.00	0.00	0.00	0.00	475886.16	0.00	0.00	0.00	0.00	0.00	KO:K01610	phosphoenolpyruvate carboxykinase (ATP)	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324 0047080 2 1321	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1976400.00	0.00	0.00	0.00	0.00	KO:K01615	glutaconyl-CoA decarboxylase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter lithotrophicus;Ramlibacter lithotrophicus RBP-1
Ga0586324 0121115 1 1479	0.00	0.00	0.00	0.00	1720100.00	1541070.63	0.00	0.00	3491100.00	0.00	0.00	0.00	KO:K01615	glutaconyl-CoA decarboxylase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 1353430 3 1067	0.00	0.00	0.00	0.00	1833400.00	733910.08	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01615	glutaconyl-CoA decarboxylase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 1426755 1 1041	0.00	0.00	0.00	866133.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01615	glutaconyl-CoA decarboxylase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324 1791803 2 946	0.00	0.00	0.00	0.00	0.00	0.00	0.00	550489.62	2527200.00	0.00	0.00	0.00	KO:K01615	glutaconyl-CoA decarboxylase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 3507117 3 713	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1360300.00	0.00	0.00	0.00	0.00	KO:K01615	glutaconyl-CoA decarboxylase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0002350 3357 4397	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1655500.00	0.00	3727500.00	KO:K01619	deoxyribose-phosphate aldolase	Bacteria;Chloroflexi;Chloroflexia;Kallotenuales;Kallotenuaceae;Kallotenue;Kallotenue papyrolyticum;Kallotenue papyrolyticum JKG1
Ga0586324 0357590 1 1899	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	20713000.00	19360000.00	0.00	KO:K01621	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira multiformis;Nitrosospira multiformis NI1
Ga0586324 0820728 2 1150	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	476397.46	0.00	0.00	KO:K01621	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium URHE0068;Acidobacteriaceae bacterium URHE0068
Ga0586324 2022343 1 900	0.00	0.00	0.00	0.00	0.00	1733115.41	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01621	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 89;Acidobacteriaceae bacterium KBS 89, DSM 24296
Ga0586324 3479160 160 717	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3157500.00	KO:K01623	fructose-bisphosphate aldolase class I	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 0000001 218717 219784	0.00	0.00	0.00	0.00	0.00	0.00	0.00	37197800.00	0.00	2648800.00	2147200.00	654325.50	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324 0000401 3 875	0.00	0.00	0.00	0.00	0.00	0.00	10396800.00	0.00	0.00	24871000.00	26400000.00	17025000.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfurifustis;Sulfurifustis variabilis;Sulfurifustis variabilis skN76
Ga0586324 0001255 3421 4488	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1207800.00	0.00	0.00	436299.60	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0006832 6731 7810	595749.00	518258.60	13005300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	310264.50	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 0008824 3 329	0.00	0.00	0.00	0.00	5438400.00	0.00	5061600.00	0.00	0.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. NZG;Methylibium sp. NZG
Ga0586324 0013553 2980 4044	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1579500.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;unclassified Alteromonadaceae;Alteromonadaceae bacterium 2719K.STB50.0a.01;Alteromonadaceae bacterium 2719K.STB50.0a.01
Ga0586324 0083446 1858 2937	0.00	1142400.00	0.00	0.00	0.00	0.00	0.00	1305400.00	0.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter marinus;Methylobacter marinus A45
Ga0586324 0116333 1365 2429	0.00	0.00	3661566.21	0.00	0.00	0.00	14637600.00	0.00	0.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira;unclassified Azospira;Azospira sp. ZAP
Ga0586324 0137442 120 1184	0.00	0.00	13343100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 0205310 1650 2444	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	823900.00	1540000.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Rhodocyclus;Rhodocyclus tenuis;Rhodocyclus tenuis DSM 109
Ga0586324 0237412 556 1635	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4171500.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 0345032 1014 1931	12700000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Halioglobus;Halioglobus sediminis;Halioglobus sediminis U0301 U0301
Ga0586324 1195375 367 1125	0.00	5154400.00	0.00	0.00	0.00	0.00	0.00	7320000.00	10530000.00	10934000.00	12672000.00	9900000.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;unclassified Chromatiales;Thiohalobacter;Thiohalobacter thiocyanaticus;Thiohalobacter thiocyanaticus FOKN1
Ga0586324 2923935 492 770	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2387000.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324 4118822 3 509	823075.00	181369.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324 6019010 1 570	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6937500.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiobaca;Thiobaca trueperi;Thiobaca trueperi DSM 13587
Ga0586324 7017408 142 537	6070000.00	5304000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter whittenburyi;Methylobacter whittenburyi ACM 3310
Ga0586324 7674346 1 489	0.00	0.00	0.00	0.00	0.00	3075165.97	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01624	fructose-bisphosphate aldolase class II	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 0024967 4697 5542	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2257500.00	KO:K01627	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase)	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0027087 1669 2988	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	440930.25	KO:K01637	isocitrate lyase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP99;Methylibium sp. AAP99
Ga0586324 0572149 3 1004	0.00	15232000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01637	isocitrate lyase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run_A_D11
Ga0586324 0375934 538 1434	0.00	0.00	6136700.00	0.00	0.00	5994700.00	0.00	0.00	0.00	0.00	2921600.00	595407.75	KO:K01644	citrate lyase subunit beta/citryl-CoA lyase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfofustis;Desulfofustis glycolicus;Desulfofustis glycolicus DSM 9705
Ga0586324 0624373 78 974	1500000.00	5535200.00	1146819.74	2992500.00	0.00	4605200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01644	citrate lyase subunit beta/citryl-CoA lyase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfofustis;Desulfofustis glycolicus;Desulfofustis glycolicus DSM 9705
Ga0586324 1306750 422 1081	3620000.00	4658000.00	0.00	0.00	0.00	0.00	4446000.00	0.00	1782000.00	0.00	0.00	315144.00	KO:K01644	citrate lyase subunit beta/citryl-CoA lyase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfofustis;Desulfofustis glycolicus;Desulfofustis glycolicus DSM 9705
Ga0586324 3864232 17 685	0.00	140766.12	0.00	0.00	0.00	0.00	0.00	186946.09	0.00	0.00	0.00	0.00	KO:K01644	citrate lyase subunit beta/citryl-CoA lyase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfofustis;Desulfofustis glycolicus;Desulfofustis glycolicus DSM 9705
Ga0586324 4861346 2 187	0.00	0.00	0.00	235814.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01644	citrate lyase subunit beta/citryl-CoA lyase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;unclassified Peptococcaceae;Peptococcaceae bacterium CEB3;Peptococcaceae bacterium CEB3
Ga0586324 0001131 4083 5378	0.00	0.00	0.00	0.00	0.00	0.00	1289456.28	228266.27	1101600.00	0.00	0.00	1500000.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0010533 8008 9339	0.00	0.00	0.00	6897000.00	13287000.00	5518300.00	7501200.00	0.00	6463800.00	5189800.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324 0016290 3605 4900	0.00	0.00	0.00	0.00	0.00	0.00	4195200.00	0.00	0.00	0.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Archangiaceae;Stigmatella;Stigmatella aurantiaca;Stigmatella aurantiaca DSM 17044
Ga0586324 0038359 3 923	0.00	0.00	0.00	0.00	9640800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324 0078366 2 766	0.00	3202800.00	0.00	0.00	0.00	0.00	16780800.00	4068700.00	11583000.00	6876100.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Ideonella;Ideonella sp. A 288;Ideonella sp. A 288
Ga0586324 0150270 1061 2341	0.00	0.00	0.00	0.00	0.00	0.00	1931369.76	0.00	0.00	0.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324 0910436 58 1263	0.00	0.00	0.00	0.00	0.00	0.00	5586000.00	0.00	0.00	0.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324 1166305 341 1135	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3150400.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Derxia;Derxia gummosa;Derxia gummosa DSM 723
Ga0586324 2700769 1 417	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3564000.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Malonomonas;Malonomonas rubra;Malonomonas rubra DSM 5091
Ga0586324 2813544 63 782	0.00	0.00	0.00	0.00	0.00	0.00	1521209.16	0.00	0.00	0.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geothermobacter;Geothermobacter ehrlichii;Geothermobacter ehrlichii DSM 15274
Ga0586324 3270106 78 734	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7747000.00	0.00	0.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324 3661136 3 542	14700000.00	0.00	0.00	0.00	0.00	0.00	1433757.48	0.00	0.00	0.00	0.00	2235000.00	KO:K01647	citrate synthase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 6192135 2 565	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	27216000.00	0.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geoalkalibacter;Geoalkalibacter ferrihydriticus;Geoalkalibacter ferrihydriticus DSM 17813
Ga0586324 7265254 2 301	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5349700.00	0.00	0.00	0.00	0.00	KO:K01647	citrate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Azohydromonas;Azohydromonas australica;Azohydromonas australica DSM 1124
Ga0586324 0002719 3080 4630	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	270383.52	0.00	KO:K01649	2-isopropylmalate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Tepidimonas;Tepidimonas taiwanensis;Tepidimonas taiwanensis VT154-175
Ga0586324 0035173 4010 5557	0.00	0.00	0.00	0.00	0.00	0.00	1458645.96	0.00	0.00	660854.04	0.00	2242500.00	KO:K01649	2-isopropylmalate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324 0047902 1119 2666	0.00	0.00	0.00	0.00	0.00	0.00	0.00	811300.00	0.00	0.00	0.00	0.00	KO:K01649	2-isopropylmalate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324 0372236 517 1866	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	732468.42	0.00	524899.76	0.00	KO:K01649	2-isopropylmalate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylobacillus;Methylobacillus sp. MM3;Methylobacillus sp. MM2
Ga0586324 0862753 2 1294	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1687500.00	KO:K01649	2-isopropylmalate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324 6514484 3 554	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	396637.50	KO:K01649	2-isopropylmalate synthase	Bacteria;Chloroflexi;Dehalococcoidia;Dehalococcoidales;Dehalococcoidaceae;Dehalococcoides;Dehalococcoides mccartyi;Dehalococcoides mccartyi GY50
Ga0586324 0000003 91033 92700	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	184881.84	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324 0000037 20444 22156	0.00	0.00	0.00	0.00	0.00	0.00	239128.68	2677900.00	252072.81	5320700.00	2332000.00	7080000.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0000431 12081 13790	0.00	1700000.00	0.00	11590000.00	0.00	0.00	0.00	5075200.00	0.00	6552700.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 0014235 1101 2777	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	839300.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0015292 3519 5309	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	133126.74	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 0016207 1152 2822	0.00	0.00	0.00	3724000.00	0.00	9845600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0038292 3096 4820	0.00	0.00	0.00	648755.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Chloroflexi;Dehalococcoidia;Dehalococcoidales;Dehalococcoidaceae;Dehalococcoides;Dehalococcoides mccartyi;Dehalococcoides mccartyi VS
Ga0586324 0039922 3122 4834	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1190700.00	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324 0190220 395 2113	0.00	0.00	0.00	4018500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Chloroflexi;Dehalococcoidia;Dehalococcoidales;Dehalococcoidaceae;Dehalococcoides;Dehalococcoides mccartyi;Dehalococcoides mccartyi VS
Ga0586324 0467894 2 1432	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2115000.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Oscillatoriales;Microcoleaceae;Microcoleus;Microcoleus sp. PCC 7113;Microcoleus sp. PCC 7113
Ga0586324 2583062 1 810	3970000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;Thermobaculum;Thermobaculum terrenum;Thermobaculum terrenum YNP1, ATCC BAA-798
Ga0586324 2595013 2 577	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4471200.00	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 3727638 1 696	0.00	0.00	0.00	0.00	0.00	5756500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 6721905 171 545	0.00	0.00	0.00	0.00	0.00	0.00	16438800.00	1433500.00	0.00	0.00	0.00	0.00	KO:K01652	acetolactate synthase-1/2/3 large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. 770b2;Variovorax sp. 770b2
Ga0586324 0108934 1296 1781	0.00	1298800.00	0.00	0.00	0.00	0.00	0.00	0.00	10854000.00	0.00	0.00	0.00	KO:K01653	acetolactate synthase-1/3 small subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324 2929277 2 403	0.00	1441600.00	0.00	0.00	0.00	0.00	0.00	0.00	2251800.00	0.00	0.00	0.00	KO:K01653	acetolactate synthase-1/3 small subunit	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 4252587 1 660	0.00	0.00	0.00	2926000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01667	tryptophanase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Salinivirgaceae;Salinivirga;Salinivirga cyanobacteriivorans;Salinivirga cyanobacteriivorans L21-Spi-D4
Ga0586324 3235915 2 739	3220000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01668	tyrosine phenol-lyase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 4544117 3 641	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2305800.00	0.00	0.00	0.00	0.00	KO:K01668	tyrosine phenol-lyase	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 0006505 4456 5031	5040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01673	carbonic anhydrase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter marinus;Methylobacter marinus A45
Ga0586324 0009019 4665 5249	9110000.00	10268000.00	21337700.00	0.00	11742000.00	15165400.00	0.00	11285000.00	12879000.00	0.00	18744000.00	8625000.00	KO:K01673	carbonic anhydrase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium agile;Methylomicrobium agile ATCC 35068
Ga0586324 0025501 2250 2831	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1134600.00	0.00	0.00	0.00	0.00	KO:K01673	carbonic anhydrase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium lacus;Methylosarcina lacus LW14
Ga0586324 1143222 317 904	0.00	0.00	0.00	0.00	0.00	0.00	69084000.00	0.00	0.00	0.00	0.00	67425000.00	KO:K01673	carbonic anhydrase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis parvus;Methylocystis parvus OBBP
Ga0586324 3086010 3 275	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5617500.00	KO:K01673	carbonic anhydrase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloprofundus;Methyloprofundus sedimenti;Methyloprofundus sedimenti WF1

Ga0586324_7134363_3_533	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	626386.77	0.00	424179.36	0.00	KO:K01673	carbonic anhydrase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_7608941_1_420	0.00	6772800.00	1997343.84	1178000.00	8930100.00	0.00	1567107.84	5282600.00	4738500.00	7161000.00	7312800.00	5572500.00	KO:K01673	carbonic anhydrase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_0444947_2_1555	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2535300.00	0.00	0.00	0.00	KO:K01676	fumarate hydratase class I	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1394746_1_1053	0.00	1931200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01679	fumarate hydratase class II	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiales Family XVII. Incertae Sedis;Thermaerobacter;Thermaerobacter subterraneus;Thermaerobacter subterraneus C21, DSM 13965
Ga0586324_0000793_19927_22575	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2299700.00	0.00	0.00	0.00	0.00	KO:K01681	aconitate hydratase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiooarus;Thiobacillus thiooarus DSM 505
Ga0586324_0006682_8298_11117	0.00	0.00	0.00	0.00	8507800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01681	aconitate hydratase	Bacteria;Firmicutes;Bacilli;Bacillales;Alicyclobacillaceae;Alicyclobacillus;Alicyclobacillus macrosporangiidus;Alicyclobacillus macrosporangiidus DSM 17980
Ga0586324_0019988_972_3620	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3572800.00	0.00	KO:K01681	aconitate hydratase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiooarus;Thiobacillus thiooarus DSM 505
Ga0586324_1080172_1_1173	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1216600.00	0.00	0.00	KO:K01681	aconitate hydratase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324_1138273_3_1049	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1769000.00	0.00	0.00	0.00	0.00	KO:K01681	aconitate hydratase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiooarus;Thiobacillus thiooarus DSM 505
Ga0586324_1438703_1_1040	0.00	0.00	0.00	0.00	1792200.00	0.00	0.00	1213900.00	0.00	0.00	0.00	0.00	KO:K01681	aconitate hydratase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodoazofra;Rhodoazofra globiformis;Rhodoazofra globiformis DSM 161
Ga0586324_3282799_3_734	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1698400.00	0.00	KO:K01681	aconitate hydratase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium petroleiphilum;Methylibium petroleiphilum PM1
Ga0586324_4660419_3_635	0.00	1740800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01681	aconitate hydratase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus sp. GAS368;Opitutus sp. GAS368
Ga0586324_0010177_7747_10116	0.00	1020000.00	0.00	2137500.00	0.00	0.00	0.00	1198800.00	0.00	0.00	0.00	0.00	KO:K01682	aconitate hydratase 2/2-methylisocitrate dehydratase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;[Polyangium] brachysporum;Polyangium brachysporum DSM 7029
Ga0586324_0259536_2_2092	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1231200.00	0.00	0.00	0.00	0.00	KO:K01682	aconitate hydratase 2/2-methylisocitrate dehydratase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP51;Betaproteobacteria bacterium AAP51
Ga0586324_7913473_2_511	3940000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01682	aconitate hydratase 2/2-methylisocitrate dehydratase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Azonexus;Azonexus hydrophilus;Azonexus hydrophilus DSM 23864
Ga0586324_0023853_4338_6833	0.00	0.00	0.00	0.00	0.00	0.00	1726300.00	1684800.00	0.00	0.00	900000.00	KO:K01687	dihydroxy-acid dehydratase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiooarus;Thiobacillus thiooarus DSM 505
Ga0586324_4089078_3_671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	384945.44	0.00	0.00	KO:K01687	dihydroxy-acid dehydratase	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PR90-1
Ga0586324_0000002_36711_37994	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	23100000.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0002948_13928_15211	0.00	0.00	701008.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0000645_5510_6805	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	515145.00	KO:K01689	enolase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_0012096_3217_4653	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1918400.00	0.00	KO:K01689	enolase	Bacteria;Tenericutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;Acholeplasma;Acholeplasma brassicae;Acholeplasma brassicae 0502
Ga0586324_0012602_3470_4750	0.00	0.00	0.00	1458250.00	1957000.00	0.00	0.00	2287500.00	2211300.00	2564100.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0012988_1971_3260	0.00	381137.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0014827_2667_3956	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3336700.00	0.00	0.00	4735500.00	279102.56	3690000.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_0049291_2333_3610	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2955000.00	KO:K01689	enolase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes;Alistipes indistinctus;Alistipes indistinctus YIT 12060
Ga0586324_0068805_1422_2717	0.00	507819.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324_0073340_816_2120	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Caldithrichaeota;Caldithrichae;Caldithrichales;Caldithrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324_0081131_305_1588	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	215006.00	214029.75	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0084561_2264_3544	0.00	0.00	0.00	0.00	0.00	0.00	2751100.00	2778300.00	3388000.00	3687200.00	2790000.00	KO:K01689	enolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum 31/32
Ga0586324_0124146_1_1098	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	932800.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0125913_1_633	0.00	0.00	0.00	0.00	0.00	0.00	0.00	980100.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Ferriphaselus;Ferriphaselus amnicola;Ferriphaselus amnicola OYT1
Ga0586324_0129165_745_2022	0.00	7344000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1162700.00	0.00	KO:K01689	enolase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes;Alistipes sp. An31A;Alistipes sp. An31A
Ga0586324_0133132_231_1511	0.00	0.00	0.00	11210000.00	0.00	0.00	0.00	0.00	0.00	0.00	8547000.00	7656000.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfocaperonia;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_0155704_3_1313	0.00	0.00	1651126.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1590000.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. NpAV;Nitrosospira sp. NpAV
Ga0586324_0218062_518_1801	4060000.00	0.00	0.00	0.00	0.00	0.00	4654300.00	0.00	0.00	7345800.00	0.00	4260000.00	KO:K01689	enolase	Archaea;Euryarchaeota;unclassified Euryarchaeota;unclassified Euryarchaeota;unclassified Euryarchaeota;Euryarchaeota archaeon SCGC AAA252-I15 (contamination screened)
Ga0586324_0355736_1_1242	1880000.00	884000.00	0.00	0.00	4253900.00	2039980.53	3260400.00	0.00	1239300.00	1370600.00	0.00	1470000.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI_001;Burkholderiales sp. JOSHI_001
Ga0586324_0566292_221_1516	0.00	0.00	0.00	12350000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0573970_1302_1544	0.00	0.00	0.00	0.00	957484.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium;Comamonadaceae sp. OA5E58
Ga0586324_0632361_2_1132	0.00	0.00	0.00	0.00	0.00	2508000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes;Alistipes sp. An31A;Alistipes sp. An31A
Ga0586324_0967476_1_945	0.00	0.00	0.00	12445000.00	0.00	0.00	2159400.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324_0988249_239_1219	1050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfuriroma;Sulfuriroma sedimnicola;Sulfuriroma sedimnicola DSM 26916
Ga0586324_1063918_85_777	0.00	657540.96	0.00	894610.25	1153600.00	0.00	1146800.00	798829.64	885500.00	719947.36	615881.25	KO:K01689	enolase	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter modestus;Edaphobacter modestus DSM 18101
Ga0586324_1286941_107_1090	3150000.00	4046000.00	0.00	0.00	4532000.00	0.00	3928400.00	3102300.00	3757600.00	2692800.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324_1462201_153_1031	0.00	300583.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Beggiatoa;Beggiatoa alba;Beggiatoa alba B18LD
Ga0586324_1556903_983_1003	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2779700.00	2437600.00	3802500.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira multiformis;Nitrosospira multiformis NI1
Ga0586324_1627883_3_986	0.00	0.00	0.00	17641500.00	15645700.00	7816793.83	0.00	625149.00	2618000.00	2807200.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1670959_3_887	0.00	3114400.00	0.00	0.00	4326000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum 31/32
Ga0586324_1907544_2_922	0.00	0.00	0.00	1102000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_2115540_3_881	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2505000.00	KO:K01689	enolase	Bacteria;Acidobacteria;Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2286772_1_687	0.00	0.00	0.00	3572000.00	0.00	308021.58	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoplaeba;Desulfoplaeba alkanexedens;Desulfoplaeba alkanexedens ALDC
Ga0586324_2380084_1_837	0.00	0.00	0.00	0.00	2935500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_2946523_1_816	2730000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_2739620_2_790	0.00	0.00	0.00	0.00	5150000.00	0.00	2787700.00	0.00	4242700.00	0.00	5190000.00	KO:K01689	enolase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run_A_D11
Ga0586324_3093656_2_751	0.00	466857.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Xenophilus;Xenophilus sp. E41;Xenophilus sp. E41
Ga0586324_3771142_1_693	3570000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Akkermansiaceae;Akkermansia;Akkermansia sp. KLE1798;Akkermansia sp. KLE1798
Ga0586324_3797872_1_690	0.00	0.00	0.00	0.00	5747400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run_A_D11
Ga0586324_3913961_1_681	0.00	0.00	0.00	0.00	0.00	0.00	3294000.00	3645000.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_3991981_124_678	1170000.00	952000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_4301279_379_657	0.00	0.00	0.00	0.00	0.00	0.00	5239900.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas thiophila;Desulfuromonas thiophila DSM 8987
Ga0586324_4428305_3_647	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8210400.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Granulosicoccaceae;Sulfuriflexus;Sulfuriflexus mobilis;Sulfuriflexus mobilis aks1
Ga0586324_4701635_3_632	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1342500.00	KO:K01689	enolase	Bacteria;Caldithrichaeota;Caldithrichae;Caldithrichales;Caldithrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324_4928770_1_420	1970000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01689	enolase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Sutterellaceae;Sutterella;Sutterella parvirubra;Sutterella parvirubra YIT 11816
Ga0586324_5767279_2_580	5050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1640100.00	0.00	1875000.00	KO:K01689	enolase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_6108104_2_568	1200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01693	imidazoleglycerol-phosphate dehydratase	Bacteria;Spirochaetes;Spirochaetia;Spirochetales;Spirochetaceae;Spirochaeta;Spirochaeta africana;Spirochaeta africana Z-7692, DSM 8902
Ga0586324_6133384_1_567	1950000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01693	imidazoleglycerol-phosphate dehydratase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sulfurreducens ATCC BAA-1139
Ga0586324_0031138_4230_4817	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1031800.00	1284800.00	0.00	KO:K01693	imidazoleglycerol-phosphate dehydratase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Methyloversatilis;Methyloversatilis universalis;Methyloversatilis universalis FAM5
Ga0586324_0269262_1040_1711	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1665000.00	KO:K01693	imidazoleglycerol-phosphate dehydratase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP51;Betaproteobacteria bacterium AAP51
Ga0586324_0524449_712_1349	0.00	2930800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01693	imidazoleglycerol-phosphate dehydratase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Thiocapsa;Thiocapsa marina;Thiocapsa marina 5811, DSM 5653
Ga0586324_0981295_735_1223	0.00	0.00	0.00	0.00	0.00	0.00	19459000.00	18873000.00	0.00	0.00	0.00	0.00	KO:K01693	imidazoleglycerol-phosphate dehydratase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Parvibium;Parvibium lacunae;Parvibium lacunae KM89
Ga0586324_3554928_205_711	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1470000.00	KO:K01695	triose/phosphate isomerase	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0114909_1486_2712	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10241000.00	4356000.00	0.00	0.00	KO:K01696	tryptophan synthase beta chain	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Pigmentiphaga;Pigmentiphaga sp. NML030171;Pigmentiphaga sp. NML030171
Ga0586324_0710170_415_1407	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3927000.00	0.00	0.00	0.00	KO:K01696	tryptophan synthase beta chain	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_1630123_3_761	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1724800.00	0.00	KO:K01696	tryptophan synthase beta chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Pandoraea;Pandoraea pulmonicola;Pandoraea pulmonicola NCTC 13159
Ga0586324_3246913_2_736	0.00	0.00	0.00	0.00	0.00	0.00	1640900.00	0.00	0.00	0.00	0.00	0.00	KO:K01696	tryptophan synthase beta chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herminiimonas;Herminiimonas sp. CN;Herminiimonas sp. CN
Ga0586324_6767694_2_544	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2292300.00	0.00	0.00	0.00	0.00	KO:K01696	tryptophan synthase beta chain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified Oxalobacteraceae;Oxalobacteraceae bacterium IMCC9480;beta proteobacterium sp. IMCC9480
Ga0586324_0077970_3014_3862	0.00	0.00	0.00	0.00	0.00	0.00	1695800.00	0.00	0.00	0.00	0.00	0.00	KO:K01698	porphobilinogen synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0123432_344_1279	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10472000.00	KO:K01710	dTDP-glucose 4,6-dehydratase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_0460038_32_1048	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2475000.00	KO:K01711	GDP-mannose 4,6-dehydratase	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324_3412142_1_723	54300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01711	GDP-mannose 4,6-dehydratase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodospirillales;Rhodospirillaceae;Magnetospirillum;Magnetospirillum sp. WD;Magnetospirillum sp. WD
Ga0586324_0022106_6140_7096	0.00	0.00	0.00	1463000.00	4356900.00	0.00	268196.40	1360300.00	0.00	0.00	0.00	0.00	KO:K01714	4-hydroxy-tetrahydrodipicolinate synthase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0046543_1913_2848	8630000.00	0.00	13512000.00	1577000.00	1998200.00	0.00	2302800.00	1423100.00	0.00	4019400.00	0.00	0.00	KO:K01714	4-hydroxy-tetrahydrodipicolinate synthase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0067970_3308_4123	0.00	0.00	0.00	0.00	1168500.00	2121800.00	0.00	1671400.00	0.00	0.00	0.00	0.00	KO:K01714	4-hydroxy-tetrahydrodipicolinate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0370288_303_1178

Ga0586324_0774052_1_1251	0.00	0.00	0.00	0.00	0.00	944649.59	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01848	methylmalonyl-CoA mutase N-terminal domain/subunit
Ga0586324_1720164_354_962	0.00	2903600.00	2760833.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01848	methylmalonyl-CoA mutase N-terminal domain/subunit
Ga0586324_1724375_3_962	0.00	6392000.00	9233200.00	0.00	0.00	0.00	3967200.00	0.00	0.00	0.00	0.00	0.00	KO:K01848	methylmalonyl-CoA mutase N-terminal domain/subunit
Ga0586324_2377158_3_839	0.00	224221.84	0.00	0.00	0.00	0.00	0.00	0.00	438722.73	0.00	0.00	0.00	KO:K01848	methylmalonyl-CoA mutase N-terminal domain/subunit
Ga0586324_0507793_410_1627	0.00	0.00	4600785.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01858	mvo-inositol-1-ohosphate synthase
Ga0586324_2995723_3_761	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1271700.00	0.00	0.00	0.00	1215000.00	KO:K01858	mvo-inositol-1-phosphate synthase
Ga0586324_3725454_3_695	0.00	0.00	0.00	0.00	0.00	0.00	0.00	915300.00	0.00	0.00	0.00	0.00	KO:K01858	mvo-inositol-1-phosphate synthase
Ga0586324_0000423_34769_35959	0.00	0.00	0.00	0.00	0.00	1113837.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01866	tyrosyl-tRNA synthetase
Ga0586324_0000586_13358_14560	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1478400.00	0.00	0.00	0.00	KO:K01867	tryptophanyl-tRNA synthetase
Ga0586324_0024769_895_2802	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	802500.00	0.00	KO:K01868	threonyl-tRNA synthetase
Ga0586324_1331682_1_1005	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1385100.00	0.00	0.00	0.00	0.00	KO:K01868	threonyl-tRNA synthetase
Ga0586324_1893074_2_844	0.00	240503.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01868	threonyl-tRNA synthetase
Ga0586324_0303982_3_929	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1644300.00	0.00	0.00	0.00	0.00	KO:K01869	leucyl-tRNA synthetase
Ga0586324_0009510_149_2830	0.00	0.00	0.00	0.00	0.00	490795.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01872	alanyl-tRNA synthetase
Ga0586324_0087944_611_3349	0.00	2135200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01872	alanyl-tRNA synthetase
Ga0586324_0171329_1_1340	0.00	0.00	0.00	0.00	0.00	0.00	3693600.00	0.00	0.00	0.00	0.00	0.00	KO:K01872	alanyl-tRNA synthetase
Ga0586324_0257727_2_766	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1347500.00	0.00	0.00	0.00	KO:K01872	alanyl-tRNA synthetase
Ga0586324_0463865_1_1677	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1108800.00	0.00	0.00	KO:K01872	alanyl-tRNA synthetase
Ga0586324_0719407_3_1400	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6172500.00	0.00	KO:K01872	alanyl-tRNA synthetase
Ga0586324_4397453_3_605	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1638680.00	0.00	0.00	0.00	KO:K01873	valyl-tRNA synthetase
Ga0586324_8195938_1_501	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15092000.00	0.00	0.00	0.00	KO:K01873	valyl-tRNA synthetase
Ga0586324_0098615_2_1627	0.00	0.00	0.00	0.00	0.00	0.00	1415200.00	0.00	0.00	0.00	0.00	0.00	KO:K01874	methionyl-tRNA synthetase
Ga0586324_0000014_13008_14789	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11500000.00	0.00	3388000.00	9847500.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_0000100_43706_45502	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4030400.00	0.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_0005072_2752_4554	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	223333.88	0.00	552129.75	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_0022446_2838_4679	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1900800.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_0161140_3_1163	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7461300.00	0.00	0.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_0300550_1_1110	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2002500.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_3180476_1_744	0.00	0.00	0.00	0.00	0.00	0.00	0.00	557953.92	0.00	0.00	0.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_3331213_1_714	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6853000.00	5359200.00	2010000.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_3731106_1_696	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3574600.00	0.00	0.00	0.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_6519505_2_553	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1279800.00	0.00	0.00	0.00	KO:K01876	aspartyl-tRNA synthetase
Ga0586324_0302496_3_1010	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5727900.00	0.00	0.00	0.00	0.00	KO:K01879	glycyl-tRNA synthetase/beta-chain
Ga0586324_5070130_1_612	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1498500.00	0.00	0.00	0.00	KO:K01880	glycyl-tRNA synthetase
Ga0586324_1402820_24_1049	22100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01881	prolyl-tRNA synthetase
Ga0586324_0239529_3_815	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2544300.00	2535000.00	0.00	KO:K01892	histidyl-tRNA synthetase
Ga0586324_4190210_2_664	0.00	0.00	0.00	0.00	0.00	1884116.76	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01892	histidyl-tRNA synthetase
Ga0586324_0125442_1085_2473	0.00	0.00	0.00	1216000.00	0.00	0.00	7940000.00	80028000.00	82594000.00	14256000.00	1247400.00	808168.24	KO:K01893	asparaginyl-tRNA synthetase
Ga0586324_0000123_46446_48416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2958500.00	0.00	0.00	8415774.44	KO:K01895	acetyl-CoA synthetase
Ga0586324_0011980_414_2393	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2772000.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0020828_1_1560	3960000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0026882_1_1752	11100000.00	55216000.00	0.00	14449500.00	0.00	0.00	0.00	38198200.00	48276000.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0026882_2085_4106	3890000.00	6120000.00	0.00	0.00	13390000.00	8485795.60	0.00	11907200.00	11809800.00	0.00	0.00	3225000.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0026882_4561_6459	0.00	0.00	1106272.48	4617000.00	5191200.00	2844370.02	0.00	7259000.00	7184700.00	5443900.00	6450400.00	6682500.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0048598_1389_3383	0.00	0.00	0.00	0.00	0.00	17745900.00	0.00	10858000.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0063721_2538_4268	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	68040000.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0071218_2742_4034	451788.00	39168000.00	0.00	0.00	0.00	7940000.00	80028000.00	82594000.00	14256000.00	1247400.00	808168.24	36450000.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0099152_1104_3086	0.00	0.00	5073938.09	0.00	16377000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0123298_2_1615	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1563300.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0156934_1_1689	0.00	1387200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1617000.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0184767_2_1783	80900000.00	232412723.56	329355000.00	23674000.00	111549000.00	226369400.00	147766800.00	141825000.00	154467000.00	89782000.00	128568000.00	118650000.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0273610_1251_2144	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2572500.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0281551_156_2114	0.00	0.00	0.00	1444000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0338197_1414_1947	0.00	0.00	0.00	0.00	0.00	0.00	35112000.00	20374000.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0432787_1_354	0.00	0.00	0.00	0.00	0.00	0.00	8800800.00	7747000.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0469707_1_1686	3102597.00	101360800.00	0.00	0.00	0.00	0.00	732512.64	0.00	823500.00	569059.02	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0499595_1_1638	0.00	2386800.00	13343100.00	10260000.00	0.00	10044100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0618063_3_1496	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1104100.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0680543_443_1432	0.00	0.00	0.00	0.00	0.00	0.00	0.00	738100.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0734981_3_1385	1670000.00	0.00	2084180.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0827138_2_1318	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16275000.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0852764_2_1300	37800000.00	0.00	0.00	0.00	0.00	1318400.00	0.00	2758800.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0896192_84_1274	0.00	1686400.00	0.00	25460000.00	3872800.00	0.00	0.00	15006000.00	26082000.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0927146_1_720	0.00	6351200.00	0.00	0.00	0.00	0.00	0.00	1586000.00	748737.27	104720000.00	1918400.00	142597500.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0928951_1_1254	9470000.00	18218156.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1570800.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_0991946_539_1219	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6407100.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1124373_1_1035	84000000.00	21630800.00	0.00	2422500.00	0.00	0.00	0.00	0.00	649178.55	0.00	0.00	741612.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1203537_342_1151	13000000.00	0.00	0.00	17385000.00	8291500.00	0.00	0.00	3074400.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1433018_2_1039	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3900000.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1555587_3_1004	1390000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1634321_416_985	0.00	0.00	0.00	0.00	0.00	0.00	1053300.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1742430_252_959	0.00	0.00	0.00	0.00	0.00	0.00	384086.50	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1838812_1_936	2080000.00	2169200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1851312_3_929	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1270500.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_1933884_2_796	0.00	0.00	2646150.67	0.00	0.00	2918400.00	0.00	0.00	1717200.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_2062576_1_450	0.00	0.00	2671660.20	1434500.00	1483200.00	0.00	0.00	3623400.00	4600800.00	1755600.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_2281009_1_855	1950000.00	836400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_2329313_3_587	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6520500.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_2689522_2_796	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1439600.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_3003435_1_759	0.00	0.00	0.00	9975000.00	14214000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_3306518_202_756	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22725000.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_3269833_3_734	0.00	634864.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_3296253_3_584	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1950000.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_3357151_1_726	0.00	2244000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_3388155_2_724	0.00	0.00	0.00	0.00	0.00	8198800.00	0.00	0.00	0.00	2394700.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_3468872_3_716	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1098000.00	589111.38	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_3718950_3_698	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1781200.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_4092525_2_670	0.00	0.00	0.00	19198300.00	0.00	5695900.00	0.00	0.00	4422600.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_4195005_3_662	7720000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_4582791_2_640	0.00	1591200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_5025484_50_616	45200000.00	38964000.00	0.00	19190000.00	27192000.00	18579600.00	14272800.00	9821000.00	20655000.00	22360800.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_5264864_3_605	0.00	0.00	0.00	0.00	0.00	980784.53	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_5321395_3_365	13740000.00	0.00	0.00	1871500.00	0.00	5402002.82	2576400.00	2409500.00	2073600.00	1239700.00	1900800.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_5367519_164_598	0.00	5936400.00	0.00	7324500.00	9064000.00	0.00	0.00	5313100.00	7468200.00	1863400.00	3924800.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_5546180_3_572	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6067600.00	0.00	49725000.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_5642605_1_588	0.00	1502800.00	0.00	0.00	0.00	0.00	0.00	0.00	2187000.00	1439900.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_5713005_34_585	69900000.00	56576000.00	49487700.00	23655000.00	13184000.00	37437100.00	15982800.00	23045800.00	19553400.00	5197500.00	11528000.00	15135000.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_5820712_3_578	1910000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_6882291_125_541	0.00	0.00	0.00	0.00	0.00	0.00	2297558.10	0.00	0.00	0.00	0.00	0.00	KO:K01895	acetyl-CoA synthetase
Ga0586324_7509090_112_522	0.00	0.00	0.00	4389000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01896	medium-chain acyl-CoA synthetase
Ga0586324_4041257_40_672	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2156000.00	0.00	0.00	KO:K01896	medium-chain acyl-CoA synthetase
Ga0586324_0262442_258_1961	0.00	0.00	0.00	1358500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01897	long-chain acyl-CoA synthetase
Ga0586324_0312153_2_374	0.00	0.00	0.00	443887.60	0.00	0.00	0.00	478801.20	426867.57	0.00	0.00	0.00	KO:K01897	long-chain acyl-CoA synthetase
Ga0586324_5535383_3_590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2818800.00	0.00	0.00	0.00	0.00	KO:K01897	long-chain acyl-CoA synthetase
Ga0586324_0843547_575_1306	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2077500.00	KO:K01902	succinyl-CoA synthetase alpha subunit
Ga0586324_1939910_141_1019	0.00	0.00	0.00	1444000.00	6901000.00	5280100.00	0.00	0.00	0.00	0.00	0.00	KO:K01902	succinyl-CoA synthetase alpha subunit
Ga0586324_5257265_290_604	0.00	0.00	0.00	3382000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01902	succinyl-CoA synthetase alpha subunit
Ga0586324_7497443_133_522	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1352700.00	0.00	0.00	KO:K01902	succinyl-CoA synthetase alpha subunit
Ga0586324_0104753_2390_3355	0.00	8432000.00	0.00	1615000.00	5829800.00	0.00	0.00	1836100.00	3547800.00	1355200.00	6538400.00	8250000.00	KO:K01903	succinyl-CoA synthetase beta subunit
Ga0586324_0178732_463_1626	0.00	0.00	7262700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01903	succinyl-CoA synthetase beta subunit
Ga0586324_0867594_2_412	11400000.00	8160000.00	16270700.00	0.00	14626000.00	0.00	8983200.00	8357000.00	8748000.00	13244000.00	0.00	7447500.00	KO:K01903	succinyl-CoA synthetase beta subunit
Ga0586324_0985329_2_934	0.00	9968800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1247400.00	0.00	0.00	KO:K01903	succinyl-CoA synthetase beta subunit
Ga0586324_8285042_2_499	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5953500.00	0.00	0.00	0.00	KO:K01903	succinyl-CoA synthetase beta subunit
Ga0586324_0050041_1992_3878	0.00	0.00	1423556.76	0.00	0.00	0.00	0.00	0.00	1571400.00	3649800.00	0.00	458315.25	KO:K01908	propionyl-CoA synthetase
Ga0586324_0071218_677_2581	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14717700.00	0.00	0.00	0.00	KO:K01908	propionyl-CoA synthetase
Ga0586324_0269832_94_2013	0.00	0.00	0.00	0.00	4181800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01908	propionyl-CoA synthetase
Ga0586324_1111371_3_1160	0.00	7643200.00	0.00	0.00	3677100.00	0.00	5175600.00	4196800.00	7168500.00	8631700.00	4945600.00	5212500.00	KO:K01908	propionyl-CoA synthetase
Ga0586324_1974689_80_907	0.00	3162000.00	6756000.00	6726000.00	4624700.00	4327300.00	19585200.00	1421300.00	3709800.00	0.00	748454.96	6517500.00	KO:K01908	propionyl-CoA synthetase
Ga0586324_4472634_1_645	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1738500.00	0.00	0.00	0.00	0.00	KO:K01908	propionyl-CoA synthetase
Ga0586324_6684701_225_548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1006500.00	0.00	0.00	0.00	0.00	KO:K01908	propionyl-CoA synthetase
Ga0586324_7874620_262_510	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	315879.75	0.00	0.00	0.00	KO:K01912	phenylacetate-CoA ligase
Ga0586324_0000035_2669_4078	1010000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1305000.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0004232_3423_4757	1080000.00	2536400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0008932_581_1990	11600000.00	0.00	8107200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0034848_2_520	0.00	4515200.00	6474500.00	4075500.00	0.00	4525800.00	0.00	2318000.00	1863000.00	0.00	1716000.00	3322500.00	KO:K01915	glutamine synthetase
Ga0586324_0044888_3_782	0.00	0.00	0.00	0.00	0.00	1446596.54	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0053397_1540_2952	1970000.00	985086.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	469450.52	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0078508_378_1793	0.00	567791.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0114939_1844_3211	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	21945000.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0142475_1_1947	5680000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0143141_854_2263	0.00	5304000.00	0.00	0.00	0.00	623508.35	7182000.00	0.00	17439300.00	80850000.00	9829600.00	1702500.00	KO:K01915	glutamine synthetase
Ga0586324_0158561_1134_2546	0.00	0.00	0.00	0.00	0.00	1098010.69	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0189793_351_1763	0.00	0.00	0.00	3590757.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0203462_2_520	442906.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0252535_1488_2222	13800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0392178_369_1823	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1150200.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase
Ga0586324_0674082_1_723	0.00	669545.00	0

Ga0586324_0954393_3_1127	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4447500.00	KO:K01915	glutamine synthetase	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazooensis;Gemmatimonadetes bacterium KB5708
Ga0586324_0963047_1_741	0.00	0.00	0.00	0.00	2987000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_1047107_203_1189	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1093400.00	0.00	795000.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylotuvimicrobium;Methylotuvimicrobium buryatense;Methylotuvimicrobium buryatense 5G
Ga0586324_1268046_2_721	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5236000.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_1296513_258_1085	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4200000.00	KO:K01915	glutamine synthetase	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira lenta;Nitrospira lenta N; lenta BS10
Ga0586324_1302157_1_285	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2560800.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfurifustis;Sulfurifustis variabilis;Sulfurifustis variabilis skN76
Ga0586324_1964561_1_909	0.00	0.00	0.00	6469500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2247358_3_461	0.00	0.00	0.00	0.00	2873700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus sp. RS-1;Roseiflexus sp. RS-1
Ga0586324_2731795_31_792	0.00	1863200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324_2964906_2_766	0.00	30464000.00	0.00	40755000.00	0.00	46846000.00	70452000.00	74420000.00	0.00	106260000.00	476319.36	99750000.00	KO:K01915	glutamine synthetase
Ga0586324_3211795_2_739	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	64395000.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter tataouinensis;Ramlibacter tataouinensis S-10
Ga0586324_3381102_2_724	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	372427.50	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas gracilis;Methylomonas gracilis Niagara R
Ga0586324_3775338_1_693	0.00	0.00	0.00	0.00	0.00	0.00	4934900.00	0.00	0.00	0.00	6723200.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Ectothiorhodospira;Ectothiorhodospira sp. BSL-9;Ectothiorhodospira sp. BSL-9
Ga0586324_4573284_3_482	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1108800.00	KO:K01915	glutamine synthetase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_4657805_158_634	0.00	91486.52	47235700.00	0.00	0.00	0.00	0.00	0.00	0.00	31801000.00	34050000.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324_5098573_3_611	0.00	0.00	0.00	0.00	0.00	0.00	10328400.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_5187566_1_606	626176.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Fibrobacteres;Fibrobacteria;unclassified Fibrobacteria;unclassified Fibrobacteria;unclassified Fibrobacteria;Fibrobacteria bacterium AD312;Fibrobacteria bacterium AD312 AD_312
Ga0586324_5947572_3_575	0.00	1373600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01915	glutamine synthetase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. URHD0069;Bradyrhizobium sp. URHD0069
Ga0586324_0164779_1704_2591	0.00	0.00	0.00	0.00	0.00	0.00	198967.36	13932000.00	0.00	1452000.00	772500.00	KO:K01923	phosphoribosylaminoimidazole-succinocarboxamide synthase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomagnum;Methylomagnum ishizawai;Methylomagnum ishizawai 175
Ga0586324_0000002_38919_40568	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1355200.00	0.00	KO:K01937	CTP synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324_0016274_6464_8092	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	404463.75	KO:K01937	CTP synthase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 4255
Ga0586324_0004695_10245_11984	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	277078.50	KO:K01938	CTP synthase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodopilum;Rhodopilum sp. 22-YC6860;Rhodopilum sp. 22-YC6860
Ga0586324_0032718_2118_3794	0.00	0.00	0.00	0.00	0.00	1415200.00	0.00	0.00	0.00	0.00	0.00	KO:K01938	formate--tetrahydrofolate ligase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methylocaniabacter;Methylocaniabacter superfactus;Methylocaniabacter superfactus R-67175
Ga0586324_0244934_378_2141	0.00	0.00	0.00	0.00	7543000.00	0.00	581903.40	0.00	0.00	0.00	0.00	KO:K01938	formate--tetrahydrofolate ligase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium EN84
Ga0586324_0376185_606_1859	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2205000.00	KO:K01938	formate--tetrahydrofolate ligase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodopilum;Rhodopilum sp. 22-YC6860;Rhodopilum sp. 22-YC6860
Ga0586324_0610033_1130_2900000.00	0.00	3963942.25	2118500.00	13287000.00	0.00	4719600.00	0.00	0.00	0.00	0.00	0.00	KO:K01938	formate--tetrahydrofolate ligase	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_1217988_1_1089	0.00	0.00	0.00	0.00	0.00	0.00	945500.00	0.00	0.00	0.00	0.00	KO:K01938	formate--tetrahydrofolate ligase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhodopilaceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324_0000002_96468_97760	0.00	0.00	0.00	0.00	0.00	0.00	4477400.00	6543047.97	0.00	0.00	413851.50	KO:K01939	adenylosuccinate synthase	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Prolixibacter;Prolixibacter denitrificans;Prolixibacter denitrificans DSM 27267
Ga0586324_0140213_2_1096	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	994400.00	0.00	KO:K01939	adenylosuccinate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0269212_2_793	0.00	0.00	0.00	0.00	0.00	0.00	1150200.00	0.00	0.00	0.00	0.00	KO:K01939	adenylosuccinate synthase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-B84
Ga0586324_0434229_456_1745	0.00	0.00	0.00	0.00	0.00	4678700.00	5896800.00	5405400.00	0.00	0.00	0.00	KO:K01939	adenylosuccinate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Sulfuritalea;Sulfuritalea hydrogenivorans;Sulfuritalea hydrogenivorans sk43H
Ga0586324_1188691_527_1126	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7573500.00	0.00	0.00	0.00	KO:K01939	adenylosuccinate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_3575377_3_707	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	446810.32	0.00	0.00	KO:K01939	adenylosuccinate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosospira;Nitrosospira briensis;Nitrosospira briensis Nsp8
Ga0586324_5845274_1_579	12800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01939	adenylosuccinate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_0000003_15190_16422	0.00	0.00	0.00	0.00	0.00	5929200.00	0.00	2340800.00	1364000.00	5902500.00	KO:K01940	arginino succinate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0284102_152_1306	0.00	0.00	0.00	0.00	0.00	0.00	0.00	342422.08	0.00	0.00	0.00	KO:K01940	arginino succinate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_5761231_2_583	0.00	0.00	0.00	0.00	0.00	1689700.00	0.00	0.00	0.00	0.00	0.00	KO:K01940	arginino succinate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp13;Nitrosospira sp. Nsp13
Ga0586324_0000018_72011_73573	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3045000.00	KO:K01951	GMP synthase [glutamine-hydrolysing]	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0200613_2_1324	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	410499.76	0.00	KO:K01951	GMP synthase [glutamine-hydrolysing]	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_2132602_1_879	0.00	0.00	0.00	0.00	710739.84	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01951	GMP synthase [glutamine-hydrolysing]	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula multivorans;Sulfuriferula multivorans TTN
Ga0586324_0000030_8858_12061	0.00	0.00	0.00	0.00	5038800.00	799100.00	3572100.00	3434200.00	2728000.00	19620000.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0001926_5182_8409	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	478732.50	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324_0003837_6141_9359	0.00	0.00	0.00	0.00	0.00	0.00	915300.00	0.00	0.00	0.00	0.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_1187023_2_1129	0.00	0.00	0.00	0.00	136564.61	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP51;Betaproteobacteria bacterium AAP51
Ga0586324_1261158_2_1099	0.00	0.00	0.00	3619500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324_2336718_1_846	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	311728.56	0.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_2402826_1_837	0.00	0.00	0.00	0.00	0.00	0.00	229173.95	0.00	0.00	0.00	0.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Acidihalobacter;Acidihalobacter prosperus;Acidihalobacter prosperus F5
Ga0586324_2433908_1_831	0.00	0.00	0.00	0.00	0.00	0.00	145771.70	0.00	0.00	0.00	0.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Rhodocyclales bacterium P3M
Ga0586324_4148247_1_666	0.00	0.00	0.00	0.00	3544029.56	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_8033815_1_507	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3515400.00	0.00	0.00	0.00	KO:K01955	carbamoyl-phosphate synthase large subunit	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofarcimen;Desulfofarcimen intricatum;Desulfofarcimen intricatum NBRC 109411
Ga0586324_0484716_578_1660	0.00	0.00	0.00	0.00	0.00	0.00	1238300.00	1571400.00	0.00	0.00	0.00	KO:K01956	carbamoyl-phosphate synthase small subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324_0157150_3_1064	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2112000.00	0.00	0.00	KO:K01959	pyruvate carboxylase subunit A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa rosea;Thiocapsa rosea DSM 235
Ga0586324_6492234_3_554	0.00	0.00	0.00	0.00	0.00	1671400.00	0.00	0.00	0.00	0.00	0.00	KO:K01959	pyruvate carboxylase subunit A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324_0037097_2_571	0.00	0.00	3711098.95	0.00	8559300.00	8495800.00	0.00	5008100.00	7411500.00	4519900.00	4628800.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfogalaeba;Desulfogalaeba alkanexedens;Desulfogalaeba alkanexedens ALDC
Ga0586324_0223331_1191_2351	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1485000.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0242358_1077_2264	0.00	0.00	0.00	0.00	349170.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0253491_3_1652	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1539000.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324_0704890_255_1412	3090000.00	13872000.00	0.00	23085000.00	25132000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0738637_2_1384	0.00	0.00	0.00	0.00	0.00	14649300.00	0.00	0.00	0.00	0.00	4136000.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_1307662_1_1008	0.00	0.00	0.00	0.00	4830700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324_2223330_3_578	0.00	0.00	0.00	8521500.00	12669000.00	4605200.00	0.00	0.00	9153000.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324_2303162_3_851	0.00	0.00	0.00	14725000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobulbus;Desulfobulbus propinicus;Desulfobulbus propinicus 1pr3, DSM 2032
Ga0586324_3009546_3_554	0.00	0.00	0.00	0.00	15721200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobulbus;Desulfobulbus propinicus;Desulfobulbus propinicus 1pr3, DSM 2032
Ga0586324_3376139_1_726	0.00	2332400.00	0.00	0.00	3419600.00	0.00	0.00	11468000.00	0.00	8932000.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_4649803_1_635	0.00	307368.84	0.00	2916500.00	962671.99	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_5196215_94_606	0.00	0.00	0.00	4978000.00	257174.52	0.00	3488400.00	0.00	0.00	0.00	0.00	KO:K01960	pyruvate carboxylase subunit B	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_5659920_1_585	22990000.00	24153600.00	21337700.00	37525000.00	33372000.00	26321100.00	40287600.00	38674000.00	36774000.00	22099000.00	19184000.00	900000.00	KO:K01960	pyruvate carboxylase subunit B
Ga0586324_1000001_71417_72283	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1782000.00	0.00	0.00	KO:K01963	acetyl-CoA carboxylase carboxyl transferase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0385529_134_1669	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3465000.00	0.00	KO:K01966	propionyl-CoA carboxylase beta chain	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis parvus;Methylocystis parvus OBBP
Ga0586324_2153160_1_876	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3996300.00	3889600.00	KO:K01966	propionyl-CoA carboxylase beta chain	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run_A_D11
Ga0586324_3724665_1_696	0.00	0.00	0.00	0.00	1087800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01966	propionyl-CoA carboxylase beta chain	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324_6071201_139_570	0.00	0.00	0.00	0.00	1153600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01966	propionyl-CoA carboxylase beta chain	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Pseudorhodoplanes;Pseudorhodoplanes sinuspersici;Pseudorhodoplanes sinuspersici RIPI110
Ga0586324_6695013_2_547	0.00	0.00	0.00	0.00	0.00	291855.34	0.00	0.00	0.00	0.00	0.00	KO:K01966	propionyl-CoA carboxylase beta chain	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithrichaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_3568232_1_708	0.00	0.00	2539130.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01968	3-methylcrotonyl-CoA carboxylase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Bordetella;Bordetella hinzii;Bordetella hinzii ATCC 51730
Ga0586324_0171315_733_2403	0.00	17952000.00	18330379.20	13395000.00	13390000.00	14530200.00	12654000.00	10187000.00	5054400.00	0.00	0.00	KO:K01969	3-methylcrotonyl-CoA carboxylase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_0814648_196_1326	0.00	0.00	50117669.70	0.00	0.00	3970000.00	6657600.00	8601000.00	8505000.00	0.00	0.00	KO:K01969	3-methylcrotonyl-CoA carboxylase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_0434807_893_1744	0.00	0.00	0.00	0.00	0.00	0.00	1098230.40	0.00	0.00	0.00	0.00	KO:K01989	putative ABC transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax antarcticus;Rhodoferax antarcticus DSM 24876
Ga0586324_2755831_1_789	1350000.00	1652400.00	0.00	2346500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01989	putative ABC transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax antarcticus;Rhodoferax antarcticus DSM 24876
Ga0586324_7978686_83_508	0.00	0.00	0.00	0.00	1462600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01990	ABC-2 type transport system ATP-binding protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Marinilabilia;Marinilabilia rubra;Marinilabilia rubra WET16
Ga0586324_4647728_2_634	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	20240000.00	0.00	KO:K01996	branched-chain amino acid transport system ATP-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfotomaculum;Desulfotomaculum nigrificans;Desulfotomaculum carboxydivorans CO-1-SRB, DSM 14880
Ga0586324_0004047_61496_62782	10400000.00	6181200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3352500.00	KO:K01997	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chlorobi;Chlorobia;Chlorobiales;Chlorobiaceae;Ancalochlorothrix;Kallotenue papyrolyticum;Kallotenue papyrolyticum MGS1
Ga0586324_0001442_3241_4533	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	413034.75	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia alkanii;

Ga0586324 0111580 1393 2577	9791532.00	17955122.56	2852968.72	0.00	13287000.00	6232900.00	9348000.00	17735222.35	15262622.64	66389400.00	76806400.00	36568084.50	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0120267 770 2026	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	24543000.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0129944 341 1474	0.00	3318400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0130101 1312 2493	3190000.00	4807600.00	4193342.23	0.00	3399000.00	0.00	0.00	4416400.00	7889400.00	0.00	12144000.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Dankookia;Dankookia rubra;Dankookia rubra JCM30602
Ga0586324 0138051 1 1374	0.00	0.00	0.00	0.00	3079700.00	0.00	3214800.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS165
Ga0586324 0139990 412 1587	0.00	0.00	0.00	0.00	0.00	0.00	0.00	744200.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. Root411;Variovorax sp. Root411
Ga0586324 0140221 1760 2902	9070000.00	12321600.00	7431600.00	1558000.00	7004000.00	0.00	8664000.00	13603000.00	2300400.00	27720000.00	26804800.00	14287500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas jejuensis;Polaromonas jejuensis NBRC 106434
Ga0586324 0141244 1671 2885	0.00	0.00	0.00	0.00	0.00	2742745.96	0.00	3531900.00	3790800.00	15939000.00	5860800.00	4776012.75	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Pandoraea;Pandoraea thiooxydans;Pandoraea thiooxydans DSM 25325
Ga0586324 0150506 1077 2279	0.00	0.00	0.00	0.00	0.00	0.00	0.00	902800.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324 0150727 2 700	0.00	0.00	0.00	207233.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0151613 1771 2814	961978.00	128921.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4514400.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0157471 278 1531	0.00	0.00	0.00	11780000.00	10403000.00	6510800.00	5494800.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0159712 850 1992	0.00	2420800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Desulfovirgula;Desulfovirgula thermocuniculi;Desulfovirgula thermocuniculi DSM 16036
Ga0586324 0169318 214 1461	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2263100.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. KBS0725;Bradyrhizobium sp. KBS0725
Ga0586324 0173027 1639 2646	0.00	0.00	0.00	4265500.00	0.00	0.00	0.00	0.00	3515400.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0088;Rhodospirillales bacterium URHD0088
Ga0586324 0173127 747 1961	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3993300.00	0.00	0.00	5827500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga;Hydrogenophaga sp. PML113;Hydrogenophaga sp. PML113
Ga0586324 0174010 1104 2495	0.00	0.00	0.00	0.00	2327800.00	0.00	0.00	2446100.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0185860 1326 2561	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	972000.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia terricola;Paraburkholderia terricola LMG 20594
Ga0586324 0190376 1476 2531	0.00	0.00	0.00	2802500.00	0.00	0.00	2758800.00	0.00	2770200.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0191621 640 1956	0.00	2264400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Deferrisoma;Deferrisoma camini;Deferrisoma camini S3R1
Ga0586324 0194603 1037 2284	0.00	605510.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio ferrophilus;Desulfovibrio ferrophilus IS5
Ga0586324 0209445 3 1157	0.00	0.00	0.00	2555500.00	0.00	0.00	0.00	0.00	1134000.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0219033 286 1416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1346400.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0221128 1123 2364	0.00	4182000.00	0.00	0.00	0.00	0.00	0.00	0.00	2486700.00	2263800.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;unclassified Solirubrobacterales;unclassified Solirubrobacterales;Solirubrobacterales bacterium URHD0059;Solirubrobacterales bacterium URHD0059
Ga0586324 0225573 3 1112	0.00	0.00	0.00	1149500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	421020.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324 0225640 3 506	0.00	0.00	0.00	0.00	5974000.00	0.00	0.00	0.00	3029400.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 0233062 1541 2305	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5205200.00	11202400.00	3607500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 0234962 334 1509	0.00	2774400.00	0.00	3182500.00	0.00	2361336.15	2986800.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 0238988 1050 2279	0.00	4114000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324 0243009 222 1388	5910000.00	3991600.00	2636759.83	3857000.00	4027300.00	1758801.31	1367468.76	1964200.00	1514700.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0255222 373 1551	0.00	0.00	0.00	1406000.00	4078800.00	0.00	0.00	576601.28	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0265577 1683 2171	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	72688000.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0273414 851 2107	0.00	4080000.00	8276100.00	0.00	3728600.00	5875600.00	4856400.00	4123600.00	4098600.00	9471000.00	9152000.00	9075000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Glaciimonas;Glaciimonas immobilis;Glaciimonas immobilis DSM 23240
Ga0586324 0275499 345 1619	0.00	0.00	0.00	0.00	1524400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0276570 107 1336	0.00	0.00	0.00	0.00	0.00	0.00	0.00	957700.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatibacillum;Desulfatibacillum aliphaticivorans;Desulfatibacillum aliphaticivorans AK-01
Ga0586324 0280953 3 1271	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2263800.00	2376000.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Archaea;Euryarchaeota;Halobacteria;Haloferacales;Haloferacaceae;Halobellus;Halobellus limi;Halobellus limi CGMCC 1.10331
Ga0586324 0282627 407 1669	0.00	0.00	0.00	0.00	0.00	9131000.00	2371200.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0315081 1237 2010	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1995000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324 0321895 2 1198	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2286900.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azovibrio;Azovibrio restrictus;Azovibrio restrictus DSM 23866
Ga0586324 0326187 745 1980	11100000.00	7140000.00	0.00	0.00	3172400.00	0.00	0.00	2507100.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0326441 958 1980	0.00	0.00	0.00	0.00	0.00	3839950.74	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. Root404;Rhizobacter sp. Root404
Ga0586324 0326822 349 1650	0.00	0.00	2365084.18	297490.60	0.00	0.00	4491600.00	0.00	0.00	0.00	2261600.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. OAE829;Bradyrhizobium sp. OAE829 (Illumina draft)
Ga0586324 0355022 666 1907	4250000.00	0.00	8219800.00	0.00	8827100.00	12584900.00	22412400.00	0.00	6447600.00	3834600.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0370354 306 1586	0.00	0.00	7600500.00	0.00	0.00	5597700.00	4582800.00	2690100.00	2486700.00	0.00	2613600.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Acuticoccaceae;Amorphus;Amorphus coralli;Amorphus coralli DSM 19760
Ga0586324 0374484 368 1537	8030000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0381317 474 1718	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3326400.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 0381918 2 1081	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	471377.07	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0385410 624 1838	118724.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324 0387607 559 1833	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5878400.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0389883 780 1829	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2367200.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0391594 100 1218	5900000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. KBS0725;Bradyrhizobium sp. KBS0725
Ga0586324 0391949 92 1336	2810000.00	0.00	0.00	0.00	0.00	1506055.23	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified Oxalobacteraceae;Oxalobacteraceae bacterium IMCC9480;beta proteobacterium sp. IMCC9480
Ga0586324 0395314 477 1736	821204.00	2522800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0397175 1 951	0.00	1013200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0430382 122 1390	34950000.00	12920000.00	0.00	10206678.40	1503800.00	0.00	0.00	0.00	0.00	11781000.00	8333600.00	3367500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0434930 2 844	8110000.00	8228000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3380300.00	2666400.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0441081 388 1539	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	831600.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0475817 115 1449	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1919700.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Thiomonas;Thiomonas arsenitoxydans;Thiomonas arsenitoxydans 3As
Ga0586324 0486535 1 981	0.00	0.00	0.00	3201500.00	0.00	0.00	0.00	2281400.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0491881 72 1358	0.00	0.00	0.00	0.00	0.00	0.00	6885600.00	564686.15	427910.85	719973.10	786690.96	125596.50	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324 0500137 815 1639	0.00	2359600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;unclassified Solirubrobacterales;unclassified Solirubrobacterales;Solirubrobacterales bacterium URHD0059;Solirubrobacterales bacterium URHD0059
Ga0586324 0510468 66 1322	6190000.00	9588000.00	3729987.60	0.00	0.00	1757340.35	1928205.12	4026000.00	10773000.00	4242700.00	5878400.00	4650000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. PDC80;Variovorax sp. PDC80
Ga0586324 0519395 336 1577	3630000.00	7072000.00	5855200.00	0.00	0.00	0.00	0.00	0.00	3960900.00	4673900.00	5491200.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0529584 890 1597	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	996300.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 0552256 548 1570	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	780000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0555484 746 1564	0.00	0.00	0.00	6631000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 0617698 192 1496	7550000.00	6670800.00	7206400.00	11400000.00	11742000.00	7622400.00	11172000.00	9760000.00	9072000.00	0.00	7224800.00	6090000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Thermomicrobia;Thermomicrobiales;Thermomicrobiaceae;Thermomicrobium;Thermomicrobium roseum;Thermomicrobium roseum DSM 5159
Ga0586324 0622428 575 1489	0.00	8751600.00	0.00	0.00	1771600.00	0.00	0.00	0.00	0.00	5243700.00	4382400.00	2040000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0634350 998 1477	0.00	768400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. OAE819;Bradyrhizobium sp. OAE819
Ga0586324 0637657 214 1473	2160000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;Phreatobacter;Phreatobacter stygius;Phreatobacter stygius KCTC 52518
Ga0586324 0660989 1 327	0.00	1013200.00	0.00	0.00	1297800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0687283 586 1428	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1109700.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0695736 174 1391	20200000.00	20332000.00	0.00	17765000.00	22454000.00	13617100.00	0.00	1140700.00	23328000.00	970200.00	0.00	17925000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Thermomicrobia;Thermomicrobiales;Thermomicrobiaceae;Thermomicrobium;Thermomicrobium roseum;Thermomicrobium roseum DSM 5159
Ga0586324 0701796 3 914	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2587500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia sp. URHE0060;Dongia sp. URHE0060
Ga0586324 0715666 313 1401	951359.00	2516000.00	0.00	0.00	0.00	0.00	11149200.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0717404 3 746	0.00	0.00	0.00	0.00	1050600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga;Hydrogenophaga borbori;Hydrogenophaga borbori LA-38
Ga0586324 0744731 1 999	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1597500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0761397 3 1175	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5544000.00	3487500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia sp. URHE0060;Dongia sp. URHE0060
Ga0586324 0767327 93 1262	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5266800.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. C04;Polaromonas sp. C04
Ga0586324 0769873 464 1360	4620000.00	4909600.00	0.00	5491000.00	4346600.00	3562590.66	3944400.00	0.00	3828250.35	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0774711 3 656	967277.00	2196400.00	3356825.57	2783500.00	0.00	2894824.75	6224400.00	1390800.00	4446900.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0791490 106 1344	0.00	0.00	0.00	0.00	0.00	31363000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0798405 198 1337	1180000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2786400.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324 0798484 714 1337	3850000.00	1230800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0803995 258 1334	0.00	0.00	0.00	0.00	0.00	871129.16	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Stellaceae;Stella;Stella humosa;Stella humosa DSM 5900
Ga0586324 0810320 149 1330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	945500.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS242
Ga0586324 0833728 209 1312	2130000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pelomonas;Pelomonas puraquae;Pelomonas puraquae CCUG 52769
Ga0586324 0835679 137 1303	0.00	0.00	0.00	0.00	0.00	1873180.98	0.00	0.00	0.00	0.00	0.00	4297500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0837668 402 1310	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	839300.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia sp. URHE0060;Dongia sp. URHE0060
Ga0586324 0838107 755 1309	639041.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0850265 395 1303	0.00	28356000.00	62493000.00	42655000.00	40479000.00	45655000.00	41952000.00	34953000.00	35640000.00	26334000.00	32560000.00	31500000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324 0943069 386 1246	0.00	0.00	0.00	0.00	0.00	2128551.23	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP51;Betaproteobacteria bacterium AAP51
Ga0586324 0976788 2 637	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	585476.43	578982.80	559779.75	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas jejuensis;Polaromonas jejuensis NBRC 106434
Ga0586324 0999571 180 1214	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1223100.00	0.00	1830400.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Kallotenuales;Kallotenuaceae;Kallotenue;Kallotenue papyrolyticum;Kallotenue papyrolyticum JKG1
Ga0586324 1000411 2 1030	0.00	5208800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Thermomicrobia;Thermomicrobiales;Thermomicrobiaceae;Thermomicrobium;Thermomicrobium roseum;Thermomicrobium roseum DSM 5159
Ga0586324 1005979 172 1212	0.00	0.00	0.00	0.00	0.00	0.00	901313.64	0.00	0.00	2094400.00	3704800.00	2700000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia sp. 1NLS2;Afipia sp. 1NLS2
Ga0586324 1019476 3 1067	0.00	0.00	4042424.45	452105.95	0.00	0.00	0.00	0.00	0.00	2240700.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 1065950 307 1182	3430000.00	3209600.00	5855200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 1077015 533 1177	0.00	782000.00	4497576.17	0.00	9548100.00	0.00	0.00	0.00	0.00	0.00	1927200.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 1195691 82 1125	0.00	0.00	0.00	0.00	0.00	0.00	0.00	387983.18	694434.87	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 1232760 361 1110	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	693372.96	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfopila;Desulfopila sp. IMCC35005;Desulfopila sp. IMCC35005
Ga0586324 1257558 428 1099	4860000.00	4182000.00	0.00	0.00	0.00	3538191.04	1937069.76	2177700.00	2016900.00	0.00	0.00	4102500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Paracoccus;Paracoccus pantotrophus;Paracoccus pantotrophus DSM 2944
Ga0586324 1272706 3 731	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2939200.00	2025000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica BiS0
Ga0586324 1290433 3 974	13200000.00	38624000.00	6080400.00	3344000.00	0.00	0.00	7546800.00	7442000.00	5200200.00	28182000.00	10736000.00	9225000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Thermomicrobia;Thermomicrobiales;Thermomicrobiaceae;Thermomicrobium;Thermomicrobium roseum;Thermomicrobium roseum DSM 5159
Ga0586324 1302609 406 1083	0.00	0.00	5451467.07	0.00	0.00	0.00	0.00	677100.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax koreense;Rhodoferax koreense DCY110
Ga0586324 1341950 338 1069	0.00	1462000.00	1059718.01	0.00	0.00	0.00	4993200.00	988200.00	0.00	1232000.00	2508000.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324 1361201 2 973	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2226500.00	1344600.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacterium;Desulfobacterium autotrophicum;Desulfobacterium autotrophicum HRM2, DSM 3382
Ga0586324 1363727 83 1063	0.00	0.00	0.00	0.00	3563800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;unclassified Eubacteriales;unclassified Eubacteriales;Clostridiales bacterium PH28 bin88;Clostridiales bacterium PH28 bin88
Ga0586324 1392794 866 1054	0.00	3617600.00	0.00	0.00	0.00	4525800.00	0.00	3477000.00	3920400.00	2279200.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Pseudaminobacter;Pseudaminobacter manganicus;Pseudaminobacter manganicus JH-7
Ga0586324 1483572 225 1025	778904.00	394489.08	0.00	0.00	0.00	7423900.00	16712400.00	0.00	6828300.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 1599366 1 993	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2571800.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Noviherbaspirillum;Noviherbaspirillum denitrificans;Noviherbaspirillum denitrificans TSA40
Ga0586324 1600509 107 994	0.00	6766000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus mediterraneus;Desulfobulbus mediterraneus DSM 13871
Ga0586324 1600840 3 992	639171.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	435950.91	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 1653280 1 978	0.00	0.00	2394410.85	0.00	0.00	2112444.94	1939559.52	1427400.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 1720874 3 962	0.00	0.00	0.00	0.00	0.00	0.00	0.00	677100.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Thermomicrobia;Thermomicrobiales;Thermomicrobiaceae;Thermomicrobium;Thermomicrobium roseum;Thermomicrobium roseum DSM 5159
Ga0586324 1721926 2 361	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4048000.00	7410000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia massiliensis;Afipia massiliensis LC387
Ga0586324 1729228 195 962	0.00	843200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2499200.00	1387500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. Root16D2;Rhizobacter sp. Root16D2
Ga0586324 1808877 122 943	0.00	1747600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfonema;Desulfonema limicola;Desulfonema limicola Jadebusen, DSM 2076
Ga0586324 1814175 1 942	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	997500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 1839227 1 936	0.00	0.00	0.00	7201000.00	737798.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 1891133 1 924	0.00	3270800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 1911993 1 921	0.00	0.00	0.00	8027500.00	1431700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 1916237 100 921	0.00	0.00	0.00	0.00	0.00	0.00	0.00	515840.40	0.00	763972.44	0.00	5986373.25	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. OV700;Variovorax sp. OV700
Ga0586324 1935117 3 554	0.00	3794400.00	0.00	0.00	3697700.00	0.00	0.00	0.00	0.00	0.00	8113600.00	2017500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 1939908 124 915	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4752000.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. HYN0024;Dechloromonas sp. HYN0024
Ga0586324 1945572 2 448	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1178100.00	1452000.00	1110000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas jejuensis;Polaromonas jejuensis NBRC 106434
Ga0586324 1979620 3 908	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19197000.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 2059459 1 891	0.00	0.00	0.00	0.00	0.00	0.00	0.00	515041.30	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Actinomycetia;Frankiales;Frankiaceae;Frankia;Frankia elaeagni;Frankia elaeagni BMG5.12
Ga0586324 2126576 36 881	0.00	0.00	0.00	0.00	0.00	4327300.00	0.00	988200.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 2218808 146 865	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	32400000.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia sp. URHE0060;Dongia sp. URHE0060
Ga0586324 2254755 1 858	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1634800.00	0.00	2664200.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Kallotenuales;Kallotenuaceae;Kallotenue;Kallotenue papyrolyticum;Kallotenue papyrolyticum JKG1
Ga0586324 2265438 2 721	3920000.00	7677200.00	9521014.05	411958.95	0.00	1352368.59	3260400.00	1177300.00	1287900.00	0.00	0.00	3037500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 2327196 1 846	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1549400.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia mobilis;Dongia mobilis CGMCC 1.7660
Ga0586324 2333501 2 820	0.00	0.00	0.00	0.00	3594700.00	0.00	0.00	3489200.00	5354100.00	8778000.00	6996000.00	4567500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;unclassified Solirubrobacterales;unclassified Solirubrobacterales;Solirubrobacterales bacterium URHD0059;Solirubrobacterales bacterium URHD0059
Ga0586324 2420736 2 832	0.00	3277600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2865000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Merismopediaceae;Merismopedia;Merismopedia glauca;Merismopedia glauca CCAP 1448/3
Ga0586324 2497281 3 821	6940000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia terricola;Paraburkholderia terricola LMG 20594
Ga0586324 2539154 1 816	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9240000.00	10120000.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 2886093 106 774	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4127200.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 3122252 149 748	0.00	0.00	0.00	0.00	0.00	0.00	2827200.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS478

Ga0586324 3127526 3 455	0.00	0.00	0.00	0.00	0.00	0.00	1421575.44	0.00	0.00	2171400.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Kallotenuales;Kallotenuaceae;Kallotenue;Kallotenue papyrolyticum;Kallotenue papyrolyticum JKG1
Ga0586324 3193123 120 743	9920000.00	0.00	0.00	0.00	7302700.00	8813400.00	0.00	6771000.00	6682500.00	0.00	0.00	11550000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 3194836 1 684	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6147900.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum;Herbaspirillum robiniae;Herbaspirillum robiniae HZ10
Ga0586324 3297303 1 732	8290000.00	6453200.00	0.00	0.00	1318400.00	0.00	0.00	0.00	0.00	0.00	5922400.00	5610000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 3347053 3 728	1130000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema primitia;Treponema primitia ZAS-2
Ga0586324 3446255 2 718	0.00	2108000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	440502.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3660172 42 701	0.00	2067200.00	0.00	0.00	1133000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Ideonella;Ideonella sp. A 288;Ideonella sp. A 288
Ga0586324 3696861 3 404	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1854900.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 3721274 3 695	0.00	0.00	0.00	0.00	0.00	5637400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3805167 2 691	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	495897.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Actinomycetia;Streptomycetales;Streptomycetaceae;Streptomyces;Streptomyces sp. QL37;Streptomyces sp. QL37
Ga0586324 3822931 3 689	0.00	379045.60	1874643.62	0.00	0.00	0.00	2302800.00	1952000.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324 3842650 1 687	0.00	6228800.00	0.00	9880000.00	9228800.00	0.00	3944400.00	0.00	6245100.00	0.00	7321600.00	7072500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Roseiarcaceae;Roseiarcus;Roseiarcus fermentans;Roseiarcus fermentans DSM 24875
Ga0586324 3889230 3 683	5500000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 3970555 1 678	14100000.00	14293600.00	0.00	8702000.00	0.00	5955000.00	1608715.56	6161000.00	6182341.20	3472700.00	1953600.00	2760000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 3996975 2 676	2880000.00	3440800.00	0.00	4987500.00	0.00	0.00	0.00	5331400.00	4212000.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 4106299 3 653	0.00	1795200.00	0.00	0.00	0.00	0.00	1889296.92	7930000.00	1344600.00	10703000.00	16896000.00	2895000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylobacteriaceae;Methylobacterium;Methylobacterium crusticola;Methylobacterium crusticola MIMD6
Ga0586324 4132245 1 666	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1992600.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Pseudorhodoplanes;Pseudorhodoplanes sinuspersici;Pseudorhodoplanes sinuspersici RIPI110
Ga0586324 4142061 2 667	0.00	0.00	0.00	0.00	2482300.00	0.00	12859200.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 4157606 1 666	0.00	0.00	0.00	0.00	11742000.00	0.00	0.00	0.00	0.00	0.00	6890400.00	8475000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS242
Ga0586324 4269433 2 658	0.00	6555200.00	0.00	3287000.00	0.00	0.00	2394000.00	0.00	4608900.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 4535180 33 641	0.00	0.00	0.00	0.00	0.00	0.00	3853200.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium jicamae;Bradyrhizobium jicamae PAC68
Ga0586324 4537252 1 642	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1365000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula multivorans;Sulfuriferula multivorans TTN
Ga0586324 4647427 1 636	0.00	0.00	0.00	2669500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 4724334 2 631	0.00	1414400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 4764405 3 629	0.00	775200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 4798595 2 370	0.00	0.00	12554900.00	0.00	0.00	0.00	0.00	8723000.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 4911705 2 622	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	854700.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia sp. URHE0060;Dongia sp. URHE0060
Ga0586324 5421083 1 597	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3936600.00	0.00	0.00	7200000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Nostocales;Calotrichaceae;Calothrix;Calothrix desertica;Calothrix desertica PCC 7102
Ga0586324 5531583 3 590	0.00	0.00	2249607.25	3534000.00	0.00	5002200.00	0.00	3678300.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 5598731 1 339	0.00	0.00	0.00	0.00	0.00	0.00	1279415.16	1891000.00	2211300.00	1232000.00	0.00	3165000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Candidimonas;Candidimonas bauzanensis;Candidimonas bauzanensis CGMCC 1.10190
Ga0586324 5627504 2 586	250476.00	1122000.00	0.00	900312.15	0.00	0.00	1036433.28	526968.63	13608000.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 5634709 3 587	0.00	1380400.00	0.00	0.00	0.00	0.00	0.00	1329800.00	1628100.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324 5748569 3 581	0.00	0.00	0.00	0.00	0.00	0.00	6156000.00	0.00	0.00	0.00	0.00	2212500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5934463 1 576	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4001400.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 6011290 1 573	0.00	0.00	12160800.00	12065000.00	0.00	0.00	14774400.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Roseiarcaceae;Roseiarcus;Roseiarcus fermentans;Roseiarcus fermentans DSM 24875
Ga0586324 6019969 3 572	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	295590.24	2655000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 6113169 1 567	0.00	3624400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Oscillatoriales;Microcoleaceae;Microcoleus;Microcoleus sp. PCC 7113;Microcoleus sp. PCC 7113
Ga0586324 6366183 1 558	0.00	2570400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1918400.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Kallotenuales;Kallotenuaceae;Kallotenue;Kallotenue papyrolyticum;Kallotenue papyrolyticum JKG1
Ga0586324 6572246 1 552	0.00	553772.96	0.00	0.00	0.00	0.00	0.00	628300.00	0.00	0.00	0.00	440794.50	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324 6590820 3 551	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6036800.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 6619265 1 549	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2446100.00	0.00	10626000.00	0.00	11775000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 6834269 1 348	0.00	0.00	5686300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 6926063 3 539	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1087500.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;unclassified Solirubrobacterales;unclassified Solirubrobacterales;Solirubrobacterales bacterium URHD0059;Solirubrobacterales bacterium URHD0059
Ga0586324 6934991 1 540	4410000.00	0.00	0.00	0.00	30282000.00	0.00	0.00	0.00	14661000.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 7270410 2 529	0.00	0.00	0.00	0.00	0.00	3890290.34	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 7410547 2 523	0.00	0.00	13286800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324 7658989 1 516	2940000.00	284199.88	0.00	492873.30	30282000.00	17388600.00	831224.16	847900.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 7847692 1 399	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1586000.00	0.00	0.00	0.00	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Geminicoccaceae;Geminicoccus;Geminicoccus roseus;Geminicoccus roseus DSM 18922
Ga0586324 8036773 59 505	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	870100.00	857258.16	0.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia violacea;Massilia violacea CECT 8897
Ga0586324 8233062 2 502	0.00	4474400.00	0.00	0.00	0.00	0.00	0.00	0.00	2462400.00	0.00	0.00	2475000.00	KO:K01999	branched-chain amino acid transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324 0517839 89 1072	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12320000.00	0.00	0.00	KO:K02002	glycine betaine/proline transport system substrate-binding protein	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 0013583 2452 3204	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	30975000.00	KO:K02003	putative ABC transport system ATP-binding protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Silvibacterium;Silvibacterium bohemicum;Acidobacteriaceae bacterium S15
Ga0586324 0059739 226 963	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	747181.26	0.00	0.00	0.00	KO:K02003	putative ABC transport system ATP-binding protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324 0719113 17 718	7300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02003	putative ABC transport system ATP-binding protein	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Gramella;Gramella fulva;Gramella fulva SH35
Ga0586324 0034208 171 2795	0.00	0.00	0.00	0.00	0.00	1390623.51	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02004	putative ABC transport system permease protein	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazoonesis;Gemmatimonadetes bacterium KBS708
Ga0586324 1518127 3 860	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	679045.50	KO:K02005	HlyD family secretion protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Draconibacterium;Draconibacterium orientale;Draconibacterium orientale FH5
Ga0586324 7594958 2 520	0.00	0.00	0.00	0.00	0.00	6590200.00	0.00	0.00	0.00	2841300.00	2569600.00	0.00	KO:K02005	HlyD family secretion protein	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Schleiferiaceae;Owenweeksia;Owenweeksia hongkongensis;Owenweeksia hongkongensis DSM 17368
Ga0586324 1756950 30 953	0.00	8160000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02010	iron(III) transport system ATP-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0027290 173 1189	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1117800.00	0.00	0.00	0.00	KO:K02012	iron(III) transport system substrate-binding protein	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Salirhabdus;Salirhabdus euzebyi;Salirhabdus euzebyi DSM 19612
Ga0586324 0440390 150 1160	0.00	0.00	0.00	0.00	2317500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02012	iron(III) transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobotulus;Desulfobotulus alkaliphilus;Desulfobotulus alkaliphilus ASO4-4
Ga0586324 0002704 3 2534	0.00	0.00	0.00	0.00	0.00	474677.02	0.00	0.00	0.00	1054900.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythrobacter;Erythrobacter sp. SG61-1L;Erythrobacter sp. SG61-1L
Ga0586324 0002891 137 3106	5360000.00	1448400.00	0.00	0.00	1946700.00	5637400.00	0.00	2104500.00	0.00	3967823.86	5317324.32	3150000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;unclassified Sphingomonadaceae;unclassified Sphingomonadaceae;Sphingomonadaceae bacterium R-39594
Ga0586324 0003622 10750 13386	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6327200.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium;Sphingobium sp. SYK-6;Sphingobium sp. SYK-6
Ga0586324 0005583 2386 5343	20080645.00	12573200.00	38903300.00	14535000.00	15522100.00	11314500.00	6589200.00	15451300.00	17139600.00	12009807.04	20688800.00	15135000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;unclassified Sphingomonadaceae;unclassified Sphingomonadaceae;Sphingomonadaceae bacterium R-39594
Ga0586324 0007783 5976 9671	1840000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium;Sphingobium sp. SYK-6;Sphingobium sp. SYK-6
Ga0586324 0012541 7850 9220	0.00	0.00	0.00	0.00	20497000.00	33506800.00	0.00	19825000.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium;Phenylobacterium sp. Root700;Phenylobacterium sp. Root700
Ga0586324 0024366 3179 5590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	671686.40	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 0024695 1234 3771	16450000.00	3032800.00	8557600.00	8455000.00	18952000.00	9964700.00	0.00	12742900.00	2988900.00	7931000.00	17644000.00	9315000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium;Novosphingobium sp. B 225;Novosphingobium sp. B 225 B 225
Ga0586324 0026501 255 3314	0.00	150162.36	0.00	3002000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;alpha proteobacterium Q-1;Alpha proteobacterium Q-1
Ga0586324 0029416 144 3044	5058848.00	7650000.00	2303711.55	10554500.00	14058549.31	10877800.00	16297918.80	13853100.00	8910000.00	14414400.00	10956000.00	9643459.50	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium URHA0028;Comamonadaceae bacterium URHA0028
Ga0586324 0029718 3429 6158	0.00	904400.00	1917983.36	2888000.00	1720100.00	2557037.30	2207500.56	6222000.00	5022000.00	0.00	4435200.00	2175000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;unclassified Cellvibrionaceae;Cellvibrionaceae bacterium 1162T.S.0a.05;Cellvibrionaceae bacterium 1162T.S.0a.05
Ga0586324 0035918 189 3239	477548.00	0.00	0.00	0.00	2430800.00	0.00	0.00	0.00	802137.33	267296.26	660277.20	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomonadales;Hyphomonadaceae;Henriciella;Henriciella barbarensis;Henriciella barbarensis CCUG 66934
Ga0586324 0035918 3309 5624	0.00	0.00	0.00	0.00	0.00	1266088.58	0.00	0.00	0.00	1547700.00	0.00	1252500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas sp. Root710;Sphingomonas sp. Root710
Ga0586324 0042146 2262 5048	0.00	342159.00	0.00	0.00	2811900.00	0.00	0.00	7356600.00	1231200.00	1455300.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Collimonas;Collimonas sp. OK412;Collimonas sp. OK412
Ga0586324 0043243 2132 5134	4780000.00	0.00	0.00	2204000.00	4490800.00	0.00	0.00	3995500.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis;Sphingopyxis flava;Sphingopyxis flava R11H
Ga0586324 0049329 1372 4410	1623861.00	1026800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4185000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia namucuonensis;Massilia namucuonensis CGMCC 1.11014
Ga0586324 0052059 849 3599	55154884.00	95737200.00	30675021.22	70566000.00	106076209.33	25737498.09	35796000.00	121146000.00	154280700.00	240694300.00	227400800.00	105615000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. Root16D2;Rhizobacter sp. Root16D2
Ga0586324 0055574 2 2032	0.00	0.00	0.00	51775000.00	0.00	107984000.00	0.00	0.00	0.00	90860000.00	880000.00	97500000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas;Pseudoxanthomonas suwonensis;Pseudoxanthomonas suwonensis J42
Ga0586324 0075194 710 3673	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1763300.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Altererythrobacter;Altererythrobacter sp. Root672;Altererythrobacter sp. Root672
Ga0586324 0090931 2709 3590	0.00	0.00	0.00	0.00	919157.58	0.00	0.00	0.00	0.00	0.00	1645600.00	1297500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;unclassified Spongiibacteraceae;marine gamma proteobacterium HTCC2143;Marine gamma proteobacterium sp. HTCC2143
Ga0586324 0098872 689 3448	0.00	0.00	0.00	6621500.00	4779200.00	5677100.00	0.00	0.00	6484615.38	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. OV335;Rhizobacter sp. OV335
Ga0586324 0113532 1326 3227	0.00	2951200.00	0.00	12948500.00	9947851.24	5875600.00	28500000.00	9894200.00	6326100.00	1439900.00	0.00	1282500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Iodobacter;Iodobacter sp. H11R3;Iodobacter sp. H11R3
Ga0586324 0136992 984 2954	0.00	0.00	46391200.00	10260000.00	0.00	16038800.00	0.00	0.00	0.00	0.00	140503.44	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Duganella;Duganella sp. CF458;Duganella sp. CF458
Ga0586324 0141669 3 1694	0.00	0.00	0.00	0.00	0.00	0.00	0.00	223751.66	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0152736 1802 2806	6330000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	558973.71	247569.63	1249600.00	855000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Undibacterium;Undibacterium pigrum;Undibacterium pigrum DSM 19792
Ga0586324 0168909 1 2676	1924951.00	1924400.00	0.00	7182000.00	13472400.00	0.00	0.00	4758000.00	3879900.00	3873100.00	3132800.00	1290000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Tibeticola;Tibeticola sediminis;Tibeticola sediminis DSM 101684
Ga0586324 0199535 1 2478	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2384800.00	1162500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Halioglobus;Halioglobus sp. HI00S01;Halioglobus sp. HI00S01
Ga0586324 0209486 1 1797	5420000.00	0.00	0.00	0.00	0.00	0.00	5152800.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas;Pseudoxanthomonas suwonensis;Pseudoxanthomonas suwonensis J42
Ga0586324 0209895 279 2420	0.00	0.00	0.00	0.00	831274.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium;Novosphingobium sp. B 225;Novosphingobium sp. B 225 B 225
Ga0586324 0242681 1089 2264	0.00	0.00	0.00	1710000.00	0.00	0.00	7729200.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Janthinobacterium;Janthinobacterium sp. CG3;Janthinobacterium sp. CG3
Ga0586324 0264597 65 2176	528064.00	1523200.00	0.00	0.00	0.00	6113800.00	0.00	3531900.00	2430000.00	0.00	4153600.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium;Comamonadaceae sp. OAS658
Ga0586324 0288755 2 2092	0.00	0.00	0.00	5443500.00	0.00	8614900.00	6543600.00	0.00	5589000.00	7522900.00	0.00	10875000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia namucuonensis;Massilia namucuonensis CGMCC 1.11014
Ga0586324 0306867 1 1893	9680000.00	5276800.00	0.00	3819000.00	1256600.00	6907800.00	1787980.56	6594100.00	9801000.00	0.00	0.00	1747500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium URHA0028;Comamonadaceae bacterium URHA0028
Ga0586324 0316530 1420 2007	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	882900.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Janthinobacterium;unclassified Janthinobacterium;Janthinobacterium sp. HH101
Ga0586324 0319519 1 1506	0.00	0.00	0.00	1187500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Collimonas;Collimonas sp. OK412;Collimonas sp. OK412
Ga0586324 0338689 1 1014	7120000.00	5467200.00	0.00	5890000.00	3079700.00	4843400.00	0.00	5483900.00	5159700.00	8547000.00	7673600.00	5715000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter tataouinensis;Ramlibacter tataouinensis 5-10
Ga0586324 0493314 3 1649	6390000.00	9180000.00	806869.08	0.00	931959.45	1333304.65	0.00	1024800.00	842400.00	1686300.00	1531200.00	2242500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Altererythrobacter;Altererythrobacter atlanticus;Altererythrobacter atlanticus 26DY36
Ga0586324 0536881 3 1589	566561.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 0563977 3 1556	0.00	2244000.00	0.00	0.00	1215400.00	0.00	0.00	0.00	419076.99	962500.00	0.00	922500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;unclassified Sphingomonadaceae;unclassified Sphingomonadaceae;Sphingomonadaceae bacterium R-39594
Ga0586324 0572483 366 1544	0.00	6113200.00	11654100.00	0.00	0.00	0.00	0.00	0.00	4325400.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas sp. SRS2;Sphingomonas sp. SRS2
Ga0586324 0653422 1 588	0.00	4746400.00	0.00	0.00	0.00	0.00	2895600.00	0.00	1790100.00	4242700.00	5112800.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium URHA0028;Comamonadaceae bacterium URHA0028
Ga0586324 0654255 320 1459	2240000.00	0.00	2974846.96	1596000.00	2626500.00	0.00	2462400.00	0.00	0.00	2002000.00	2692800.00	2122500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Collimonas;Collimonas sp. OK412;Collimonas sp. OK412
Ga0586324 0669081 1 849	1770000.00	1380400.00	5437921.29	12084000.00	8847700.00	5438900.00	0.00	8039800.00	2446200.00	20266400.00	14484800.00	1912500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Niveibacterium;Niveibacterium umoris;Niveibacterium umoris DSM 106739
Ga0586324 0686484 1 1428	2260000.00	14484000.00	0.00	0.00	0.00	36682800.00	0.00	0.00	0.00	17941000.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;alpha proteobacterium Q-1;Alpha proteobacterium Q-1
Ga0586324 0783023 1 1350	3590000.00	4816887.44	5289351.22	10355000.00	16366700.00	4922800.00	4104000.00	10028400.00	5540400.00	4019400.00	2648800.00	3247500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0811372 589 1329	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5328400.00	2816000.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia flava;Massilia flava CGMCC 1.10685
Ga0586324 0896310 322 1272	2880000.00	0.00	0.00	2251500.00	0.00	0.00	0.00	0.00	1992600.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rivibacter;Rivibacter subsaxonicus;Rivibacter subsaxonicus DSM 19570
Ga0586324 0908515 1 993	0.00	472976.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Maricaulales;Maricaulaceae;Maricaulis;Maricaulis salignorans;Maricaulis salignorans DSM 16077
Ga0586324 0956193 1 1239	8220000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1555200.00	0.00	0.00	1290000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia niastensis;Massilia niastensis DSM 21313
Ga0586324 1004783 2 1213	0.00	0.00	0.00	2574500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. CF059;Methylibium sp. CF059
Ga0586324 1082175 409 1173	0.00	627921.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas leidyi;Sphingomonas leidyi DSM 4733
Ga0586324 1273692 573 1094	0.00	0.00	0.00	3809500.00	0.00	1175123.97	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium URHA0028;Comamonadaceae bacterium URHA0028
Ga0586324 1274503 545 1093	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7198000.00	5418900.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Paucibacter;Paucibacter sp. KCTC 42545;Paucibacter sp. KCTC 42545
Ga0586324 1348275 1 1068	1140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium;Sphingobium sp. SYK-6;Sphingobium sp. SYK-6
Ga0586324 1435057 1 1041	0.00	1496000.00	0.00	0.00	1833400.00	0.00	0.00	2464400.00	1782000.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Aquincola;Aquincola tertiaricarbonis;Aquincola tertiaricarbonis MIMtkpLc11
Ga0586324 1534195 2 1012	7181625.00	3814800.00	2951944.12	0.00	0.00	0.00	0.00	1103994.47	0.00	0.00	1786400.00	2475000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Parahaliea;Parahaliea mediterranea;Parahaliea mediterranea DSM 21924
Ga0586324 1559587 1 840	0.00	0.00	0.00	0.00	3728600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 1746616 3 956	0.00	0.00	0.00	0.00	0.00	0.00	3420000.00	0.00	0.00	0.00	1003200.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas desiccabilis;Sphingomonas desiccabilis DSM 16792
Ga0586324 1786598 2 817	0.00	0.00	0.00	0.00	3635900.00	0.00	0.00	0.00	0.00	5751900.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PB90-1
Ga0586324 1849201 3 935	8140000.00	0.00	0.00	3325000.00	0.00	0.00	0.00	0.00	0.00	4004000.00	776548.08	133110.75	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas carotinifaciens;Sphingomonas carotinifaciens L9-754
Ga0586324 1914154 3 920	0.00	0.00	0.00	0.00	7828000.00	0.00	0.00	0.00	0.00	0.00	1496000.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium URHA0028;Comamonadaceae bacterium URHA0028
Ga0586324 2197932 3 869	0.00	0.00	0.00	0.00	0.00	0.00	0.00	829600.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythrobacter;Erythrobacter sp. SG61-1L;Erythrobacter sp. SG61-1L
Ga0586324 2369356 1 840	0.00	1938000.00	0.00	4341500.00	0.00	1025093.70	0.00	2366800.00	0.00	0.00	3220800.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium;Comamonadaceae sp. OAS658
Ga0586324 2468168 1 825	2500000.00	2788000.00	3186810.83	835600.05	1236000.00	0.00	1349889.96	805200.00	4916700.00	18865000.00	24843873.12	781905.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Collimonas;Collimonas sp. OK412;Collimonas sp. OK412
Ga0586324 2570696 3 812	0.00	0.00	0.00	3135000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus sp. ER46;Opitutus sp. ER46
Ga0586324 2679148 1 495	433152.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	210641.20	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium;Comamonadaceae sp. OAS658
Ga0586324 2717030 2 793	0.00	0.00	0.00	0.00	900517.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Halioglobus;Halioglobus pacificus;Halioglobus pacificus RR3-57
Ga0586324 2844060 3 779	0.00	0.00	0.00	3011500.00	3357800.00	0.00	0.00	3074400.00	3037500.00	3603600.00	0.00	3337500.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas leidyi;Sphingomonas leidyi DSM 4733
Ga0586324 2941761 1 768	1120000.00	0.00	0.00	0.00	0.00	2183456.33	0.00	0.00	0.00	0.00	0.00	1005000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Lysobacter;Lysobacter antibioticus;Lysobacter antibioticus 13-6
Ga0586324 3178487 2 574	0.00	863600.00	0.00	0.00	2914900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Paraglaciecola;Paraglaciecola sp. MB-3u-78;Paraglaciecola sp. MB-3u-78
Ga0586324 3186393 3 743	1510000.00	3039600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium;Comamonadaceae sp. OAS658
Ga0586324 3329483 2 730	0.00	0.00	0.00	0.00	0.00	6034400.00	0.00	0.00	2308500.00	0.00	0.00	3690000.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium;Sphingobium sp. B12D2A;Sphingobium sp. B12D2A
Ga0586324 3538615 3 710	3770000.00	2978400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Altererythrobacter;Altererythrobacter atlanticus;Altererythrobacter atlanticus 26DY36
Ga0586324 3669325 3 701	6190000.00	614557.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Pelomonas;Pelomonas saccharophila;Pelomonas saccharophila DSM 654
Ga0586324 3700876 1 699	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	425893.14	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia namucuonensis;Massilia namucuonensis CGMCC 1.11014
Ga0586324 3954688 3 632	0.00	0.00	0.00	1406000.00	2070300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis;Sphingopyxis sp. MG;Sphingopyxis sp. MG
Ga0586324 4118922 2 667	3310000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Frateuria;Frateuria sp. Soil773;Frateuria sp. Soil773
Ga0586324 4184351 3 665	0.00	1312400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythrobacter;Erythrobacter sp. SG61-1L;Erythrobacter sp. SG61-1L
Ga0586324 4248628 150 659	0.00	0.00	0.00	0.00	0.00	2179375.17	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium URHA0028;Comamonadaceae bacterium URHA0028

Ga0586324_4435807_2_649	0.00	0.00	0.00	0.00	0.00	0.00	10242600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_4548026_1_642	0.00	0.00	0.00	0.00	0.00	0.00	1972505.52	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_5300730_3_602	0.00	0.00	0.00	0.00	0.00	0.00	121474.46	0.00	218193.95	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_5797868_1_579	0.00	646722.16	0.00	0.00	0.00	8147300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_5819553_1_578	368788.00	734400.00	0.00	0.00	363343.83	0.00	7957200.00	756400.00	8910000.00	413613.20	0.00	6720000.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_6143111_2_565	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5418900.00	7137900.00	1865600.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_6200431_2_565	5750000.00	4882400.00	0.00	9690000.00	0.00	0.00	0.00	0.00	0.00	5775000.00	3352800.00	4897500.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_6447792_1_555	840122.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_6518970_1_552	0.00	0.00	0.00	0.00	0.00	0.00	0.00	921100.00	572241.51	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_7163010_3_530	0.00	429721.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_7344699_3_527	1860000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_7611086_2_517	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	261524.56	1072500.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_7718698_1_516	0.00	3175600.00	0.00	0.00	0.00	0.00	0.00	0.00	3612600.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_7848633_2_511	0.00	0.00	0.00	0.00	1390500.00	0.00	0.00	0.00	692982.54	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_7981204_1_507	0.00	0.00	0.00	1757500.00	2832500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02014	iron complex outermembrane receptor protein
Ga0586324_1482272_2_1027	81100000.00	100404800.00	96836000.00	77520000.00	61903000.00	120529200.00	94916400.00	73242700.00	64962000.00	84700000.00	89680800.00	88147500.00	KO:K02024	maltoporin
Ga0586324_4505996_2_643	0.00	0.00	0.00	2337000.00	0.00	0.00	0.00	2080000.00	1660500.00	0.00	0.00	0.00	KO:K02024	maltoporin
Ga0586324_8113544_234_503	5490000.00	6432800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1909600.00	0.00	787500.00	KO:K02024	maltoporin
Ga0586324_0133145_1787_2674	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1620000.00	0.00	0.00	0.00	KO:K02026	multiple sugar transport system permease protein
Ga0586324_0002768_3057_4370	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1563300.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0004543_5116_6426	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	497165.04	0.00	0.00	418787.25	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0005220_3428_4849	995083.00	1122000.00	0.00	2413000.00	2534884.59	0.00	3142147.80	2940200.00	1709100.00	0.00	1821600.00	1515000.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0006105_10114_11586	6870000.00	5848000.00	1202601.78	3619500.00	3502000.00	4565500.00	518674.92	2641300.00	1790100.00	0.00	620312.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0008566_6256_7587	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1733600.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0010779_7276_8706	4440000.00	8540800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3195500.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0010825_130_1665	0.00	924800.00	0.00	0.00	0.00	0.00	0.00	216137.64	0.00	0.00	1320000.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0012760_6679_7980	0.00	2883200.00	0.00	1966500.00	1792200.00	0.00	0.00	1744600.00	0.00	6421800.00	5350400.00	2700000.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0017818_2876_4204	6840000.00	8976000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3075000.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0019574_3138_4418	0.00	0.00	6868600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0026292_781_2310	0.00	2219472.40	3888854.94	0.00	0.00	0.00	2241788.48	3013400.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0040747_2397_3839	1360000.00	4413200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0041937_315_1670	0.00	0.00	3780387.36	0.00	4974900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0056785_2829_4241	0.00	0.00	14975800.00	3524500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0072185_186_1727	2520000.00	1462000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0112384_926_2365	0.00	8432000.00	0.00	0.00	0.00	0.00	0.00	5062500.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0197573_3_1253	0.00	0.00	8163500.00	0.00	6159400.00	6868100.00	0.00	3745400.00	3823200.00	3311000.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0211741_331_1635	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3249400.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0284540_915_2105	3160000.00	9588000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0367272_2_1039	2320000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0380406_1_1380	0.00	822800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0454741_250_1710	0.00	563885.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0490053_1_1088	3780000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3796100.00	0.00	2175000.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0511879_2_988	0.00	897600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0687487_1_939	0.00	0.00	0.00	10925000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0757472_3_1187	1530000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0864730_3_1004	0.00	0.00	5219505.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0906963_1_1265	6040000.00	7255600.00	4746754.34	7163000.00	4676200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_1054469_3_917	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1215000.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_1099724_196_1164	5730000.00	5827600.00	6966077.82	8436000.00	7227171.13	0.00	3670800.00	0.00	3476900.00	4874100.00	3344000.00	6817500.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_1270454_90_1094	0.00	0.00	0.00	0.00	609826.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_1385347_1_1056	0.00	2516000.00	0.00	0.00	0.00	0.00	3214800.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_1549075_2_1006	0.00	0.00	0.00	2622000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_2983970_1_612	0.00	0.00	736708.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_2990319_1_762	0.00	727600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_3116081_1_750	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	617875.29	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_3710006_3_347	12000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_4828929_3_626	1080000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_5502893_1_593	0.00	4513588.40	0.00	4683500.00	0.00	0.00	0.00	0.00	0.00	2048200.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_6447106_1_555	17200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_6851984_1_542	1020000.00	0.00	34286700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_7854389_2_511	0.00	1006400.00	0.00	0.00	0.00	1606063.50	0.00	0.00	858600.00	0.00	0.00	0.00	KO:K02027	multiple sugar transport system substrate-binding protein
Ga0586324_0028656_2_907	0.00	0.00	7713100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_0033343_2107_2922	0.00	1229918.04	0.00	2812000.00	0.00	0.00	7159200.00	0.00	0.00	6414100.00	3106400.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_0057444_1319_2146	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4589200.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_0063684_888_1713	0.00	5317600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_0141148_997_1818	0.00	0.00	0.00	4873500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_0148029_2054_2848	0.00	0.00	0.00	0.00	0.00	9647100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_0226309_463_1212	0.00	1727200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_0549274_975_1574	0.00	0.00	0.00	0.00	0.00	921850.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_1998008_3_350	0.00	415484.08	0.00	1976000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_2084228_2_484	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3927700.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_3365737_248_727	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1344600.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_5226036_2_604	0.00	178674.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02030	polar amino acid transport system substrate-binding protein
Ga0586324_0341563_932_1939	0.00	3019200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02032	peptide/nickel transport system ATP-binding protein
Ga0586324_0000019_21816_24407	19000000.00	0.00	10008845.10	3619500.00	2564700.00	2438985.38	7041643.20	7557900.00	2583900.00	6360200.00	4796000.00	3945000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0000272_26498_28426	0.00	3536000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0000907_6169_7908	0.00	1360000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2140600.00	1293600.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0001936_7157_9292	0.00	2393600.00	0.00	0.00	3780100.00	0.00	1851663.24	5209400.00	1871100.00	0.00	1311200.00	429330.75	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0001998_17754_19544	0.00	4186730.76	0.00	0.00	0.00	0.00	0.00	1250500.00	3564000.00	0.00	5016000.00	4575000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0003145_4680_6461	0.00	856800.00	0.00	0.00	1174200.00	0.00	0.00	0.00	0.00	4951100.00	1812800.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0003635_1485_3230	7690000.00	3189200.00	0.00	0.00	0.00	0.00	0.00	5526600.00	5192100.00	0.00	0.00	1080000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0007399_5215_6909	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3757500.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0012773_5921_7636	0.00	12920000.00	0.00	0.00	0.00	0.00	0.00	4684800.00	0.00	0.00	7224800.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0014535_2924_4981	32040000.00	22504595.92	0.00	10070000.00	0.00	2195410.00	13793146.37	11248400.00	10449000.00	14925117.78	23654400.00	64620000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0023171_3339_5420	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3129300.00	1368900.00	4533300.00	2428800.00	750000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0028684_3831_5830	18600000.00	2781200.00	11316300.00	0.00	0.00	0.00	0.00	2147200.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0029403_1_1217	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5977800.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0036883_1489_3414	0.00	1523200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3041500.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0043667_3073_5124	0.00	0.00	0.00	0.00	0.00	0.00	2121679.08	0.00	0.00	0.00	6573600.00	5310000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0048661_2145_4196	12280000.00	9744400.00	0.00	4233200.00	2794850.00	4527914.19	4655494.00	1506000.00	8010900.00	6583500.00	21172800.00	4819600.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0059223_2805_4403	0.00	4576400.00	8107200.00	4408000.00	5376600.00	0.00	7957200.00	5593700.00	6480000.00	0.00	906400.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0062208_77_2233	0.00	3672000.00	0.00	0.00	0.00	0.00	0.00	3483100.00	3474900.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0062557_710_2329	0.00	9588000.00	8670200.00	0.00	0.00	0.00	0.00	0.00	0.00	11858000.00	11616000.00	1530000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0068177_509_2257	3830000.00	0.00	0.00	793604.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0074399_2054_3949	0.00	6650400.00	0.00	0.00	1472900.00	2618389.68	0.00	2799900.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0088374_3277_3638	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1701900.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0101802_3_1826	0.00	0.00	0.00	541947.45	0.00	2950015.69	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0123166_757_3105	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5768400.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0162930_1095_2723	0.00	5168000.00	0.00	5871000.00	1627400.00	0.00	0.00	0.00	3053700.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0174072_1311_2639	0.00	3019200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0178360_2_2335	3800000.00	3325200.00	0.00	0.00	0.00	0.00	4012800.00	5441200.00	2867400.00	8316000.00	7814400.00	6930000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0201315_950_2467	1230000.00	0.00	0.00	0.00	6374500.00	8476900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0202829_1_1605	0.00	931600.00	0.00	0.00	1444000.00	0.00	0.00	0.00	0.00	1539000.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0206541_2_1750	0.00	0.00	0.00	2489000.00	0.00	0.00	2713200.00	0.00	1360800.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0214231_1113_2399	0.00	1672800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0230572_2_2029	2130000.00	3950800.00	0.00	1377500.00	1163900.00	0.00	0.00	0.00	1142100.00	0.00	1856800.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0256811_672_2207	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1128500.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0263496_2_1726	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	152123.02	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0278365_57_2126	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2564100.00	2050400.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0305797_3_1166	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	562399.20	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0320949_1_1548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	444002.53	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0321242_808_1992	1730000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0365080_2_1882	13673704.00	20323905.96	28656700.00	5263000.00	3584400.00	2590492.49	3579600.00	8576600.00	10918800.00	11111100.00	7893600.00	3907500.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0426076_399_1757	0.00	8364000.00	17790800.00	0.00	0.00	0.00	0.00	0.00	1150200.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0474303_3_1626	2360000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1522500.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0498076_634_1641	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	587576.43	0.00	0.00	1057500.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0512241_1_1203	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1077300.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0520359_816_1610	0.00	0.00	0.00	2916500.00	0.00	0.00	1372053.84	0.00	826200.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0532211_1_1596	0.00	0.00	0.00	0.00	2338100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0571536_1_1545	13710000.00	0.00	0.00	0.00	0.00	0.00	5796200.00	11012400.00	0.00	0.00	0.00	2481600.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0588782_2_1525	3540000.00	0.00	952674.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1532300.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0616346_3_881	0.00	2597600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0848622_3_1304	0.00	0.00	0.00	0.00	0.00	6153500.00	6612000.00	0.00	0.00	3523500.00	3880800.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0897867_268_1272	0.00	0.00	0.00	0.00	0.00	0.00	3100800.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0904805_1_1008	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5528600.00	5086400.00	4687500.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0933310_3_1250	0.00	2645200.00	3479621.50	0.00	4037600.00	0.00	3169200.00	3220800.00	3256200.00	4858700.00	5139200.00	3592500.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0941009_159_1247	0.00	0.00	0.00	0.00	0.00	0.00	2964000.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_0958491_3_1235	608745.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_1005395_2_1210	0.00	0.00	0.00	0.00	0.00	0.00	2918400.00	2854800.00	1903500.00	0.00	0.00	3317600.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_1045598_3_1190	0.00	0.00	3271975.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Ga0586324_1802373_1_777	0.00	172854.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_1985302_1_905	0.00	0.00	890643.48	0.00	1102100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_1998411_3_902	0.00	504577.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2461992_1_828	0.00	0.00	0.00	0.00	1833400.00	0.00	0.00	3043900.47	0.00	1848000.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2631910_3_803	6360000.00	0.00	11091100.00	0.00	7333600.00	0.00	0.00	0.00	0.00	0.00	8025000.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2706644_2_796	2010000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2726113_3_794	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2818800.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2778502_329_787	0.00	3175600.00	0.00	0.00	3726714.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2819041_2_781	0.00	0.00	0.00	0.00	0.00	0.00	1695800.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2820145_3_782	0.00	0.00	0.00	0.00	0.00	1080818.04	1323700.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2837286_13_780	0.00	0.00	0.00	1596000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_3161446_3_746	0.00	858800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_3369313_2_727	0.00	6738800.00	6024100.00	7799500.00	7642600.00	4327300.00	4560000.00	0.00	9234000.00	8778000.00	10472000.00	7575000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_3562698_3_710	0.00	0.00	0.00	0.00	0.00	0.00	1202460.60	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_3770465_2_694	0.00	0.00	0.00	0.00	0.00	0.00	0.00	72981.01	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_3890864_2_685	0.00	3427200.00	4490155.83	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_4206806_2_661	3210000.00	1006000.00	0.00	3078000.00	0.00	0.00	0.00	2726700.00	1919700.00	6237000.00	0.00	8325000.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_5014743_3_617	0.00	4780400.00	0.00	7020500.00	0.00	0.00	0.00	1878800.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_5871918_1_576	0.00	0.00	0.00	0.00	578826.00	1749687.96	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_5965983_3_572	0.00	3529200.00	0.00	2641000.00	0.00	0.00	0.00	4733600.00	6708600.00	6398700.00	5112800.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_6271209_2_562	0.00	0.00	0.00	0.00	0.00	0.00	6543600.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_6516357_269_553	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	217121.25	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_7190220_3_530	0.00	0.00	0.00	4740500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_7273037_1_528	5630000.00	4902800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1372500.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_7325205_1_525	26100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_7913060_3_509	0.00	2284800.00	39260651.61	0.00	0.00	3389454.99	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02035	peptide/nickel transport system substrate-binding protein
Ga0586324_2537977_306_818	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2692500.00	KO:K02036	phosphate transport system ATP-binding protein
Ga0586324_0244160_2_331	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1368900.00	0.00	0.00	0.00	0.00	KO:K02039	phosphate transport system protein
Ga0586324_3575851_3_545	0.00	0.00	0.00	1920049.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02039	phosphate transport system protein
Ga0586324_0000330_18723_19742	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4065600.00	6967500.00	0.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0002092_12647_13666	0.00	0.00	0.00	0.00	0.00	0.00	4593300.00	0.00	0.00	0.00	0.00	0.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0011195_2807_3823	0.00	0.00	0.00	0.00	0.00	7113600.00	1756800.00	1773900.00	2764300.00	2552000.00	7455000.00	0.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0013473_3562_4611	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7854000.00	12584000.00	0.00	0.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0016031_3366_4211	0.00	2475200.00	3699613.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0018253_3079_4116	0.00	0.00	0.00	0.00	0.00	0.00	2006900.00	0.00	0.00	17224900.00	5156800.00	0.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0025081_5299_6348	0.00	0.00	0.00	6072928.75	4871900.00	0.00	1043100.00	3191400.00	924000.00	0.00	0.00	1252000.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0028264_5420_6307	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1620000.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0871830_195_1007	0.00	0.00	15482500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0874367_448_1287	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3697500.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_1457350_1_939	1720000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02040	phosphate transport system substrate-binding protein
Ga0586324_0000004_8057_82490	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5706465.00	KO:K02051	NitT/TauT family transport system substrate-binding protein
Ga0586324_0000582_18939_20570	0.00	1054000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02051	NitT/TauT family transport system substrate-binding protein
Ga0586324_2859778_2_778	0.00	0.00	0.00	0.00	0.00	0.00	1348100.00	1684800.00	0.00	0.00	0.00	0.00	KO:K02051	NitT/TauT family transport system substrate-binding protein
Ga0586324_0270177_1_939	0.00	0.00	0.00	5842500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02052	putative spermidine/putrescine transport system ATP-binding protein
Ga0586324_3560828_124_708	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3391600.00	0.00	0.00	0.00	0.00	KO:K02052	putative spermidine/putrescine transport system ATP-binding protein
Ga0586324_0008056_7618_8946	0.00	0.00	0.00	0.00	0.00	0.00	0.00	622200.00	0.00	0.00	0.00	0.00	KO:K02055	putative spermidine/putrescine transport system substrate-binding protein
Ga0586324_0043327_3_1010	0.00	0.00	12667500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02055	putative spermidine/putrescine transport system substrate-binding protein
Ga0586324_0475222_751_1677	0.00	2298400.00	0.00	0.00	0.00	0.00	1091900.00	0.00	0.00	0.00	0.00	0.00	KO:K02055	putative spermidine/putrescine transport system substrate-binding protein
Ga0586324_4387707_1_651	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1963500.00	0.00	0.00	0.00	KO:K02055	putative spermidine/putrescine transport system substrate-binding protein
Ga0586324_0041529_4274_5236	0.00	4630800.00	5345195.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_0141170_1697_2692	3060000.00	1693200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2295000.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_0167201_1688_2794	0.00	0.00	0.00	0.00	3450500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_0538390_570_1553	1500000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_0903093_110_1198	1210000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_1003139_80_1162	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2253800.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_1633117_320_985	0.00	0.00	0.00	0.00	2197375.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_2067519_144_890	0.00	0.00	18267090.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_2607227_1_492	0.00	2611200.00	0.00	0.00	0.00	0.00	0.00	1726300.00	1368800.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_3060140_3_755	0.00	4243200.00	0.00	0.00	0.00	0.00	0.00	0.00	915300.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_3380632_3_725	0.00	5827600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6667500.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_6810456_48_542	0.00	6936000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1742400.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_7534709_1_519	0.00	0.00	0.00	2071000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02058	simple sugar transport system substrate-binding protein
Ga0586324_2151783_42_875	0.00	319780.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02067	phospholipid/cholesterol/gamma-HCH transport system substrate-binding protein
Ga0586324_0899492_737_1063	0.00	0.00	0.00	0.00	1205100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02107	V/A-type H+-transporting ATPase subunit G/H
Ga0586324_0000001_71963_72433	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4319700.00	5456000.00	4875000.00	KO:K02109	F-type H+-transporting ATPase subunit a
Ga0586324_0000102_12104_12685	0.00	0.00	0.00	0.00	0.00	0.00	480698.91	0.00	0.00	0.00	0.00	0.00	KO:K02109	F-type H+-transporting ATPase subunit b
Ga0586324_0000524_24570_25040	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5768400.00	0.00	0.00	0.00	3682500.00	KO:K02109	F-type H+-transporting ATPase subunit b
Ga0586324_0219056_1922_2530	0.00	0.00	3401000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02109	F-type H+-transporting ATPase subunit b
Ga0586324_1371552_379_987	0.00	0.00	0.00	0.00	0.00	3293111.03	1851763.56	0.00	2559600.00	475628.23	0.00	0.00	KO:K02109	F-type H+-transporting ATPase subunit b
Ga0586324_3017929_1_521	0.00	0.00	0.00	0.00	0.00	3411143.10	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02109	F-type H+-transporting ATPase subunit b
Ga0586324_5941300_170_574	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5937300.00	0.00	0.00	0.00	0.00	KO:K02109	F-type H+-transporting ATPase subunit b
Ga0586324_7437370_43_522	0.00	0.00	0.00	978500.00	1256600.00	302864.55	0.00	750300.00	614310.48	0.00	0.00	0.00	KO:K02109	F-type H+-transporting ATPase subunit b
Ga0586324_6925671_3_191	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8357000.00	0.00	0.00	0.00	0.00	KO:K02110	F-type H+-transporting ATPase subunit c
Ga0586324_0000001_69794_71341	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5669340.00	2121300.00	8061900.00	42240000.00	95242500.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0000524_25626_27167	0.00	0.00	0.00	0.00	0.00	47652000.00	40522300.00	30456000.00	25487000.00	46024000.00	29700000.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0000808_25068_26609	0.00	0.00	0.00	1045000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0002013_6939_8480	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3134674.47	0.00	28336000.00	32128800.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0002419_11842_13407	0.00	0.00	15595100.00	19380000.00	16480000.00	18936900.00	0.00	6710000.00	7095600.00	7499800.00	6274400.00	6930000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0003391_13966_15507	0.00	0.00	0.00	0.00	0.00	0.00	2255996.16	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0005566_7808_9325	0.00	7004000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3037500.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0008747_6339_7856	42900000.00	0.00	71501000.00	969000.00	39243000.00	118306000.00	93252000.00	0.00	739229.47	0.00	25256000.00	63000000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0026187_5371_6537	0.00	0.00	20831000.00	0.00	10004400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0041167_2442_3983	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2112000.00	2167500.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0041233_4042_5202	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2402400.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0056416_2_1249	0.00	0.00	0.00	3549754.41	5358000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0060913_76_1599	34340000.00	91392000.00	34737100.00	10469000.00	142984600.00	68006100.00	47880000.00	33489000.00	24405300.00	83437200.00	31926400.00	32250000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0063998_2590_4098	0.00	3787600.00	0.00	7058500.00	0.00	0.00	0.00	14023900.00	13527000.00	623556.78	6478800.00	4665000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0064613_3127_4224	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11097000.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0074767_1538_3058	23900000.00	0.00	0.00	0.00	51294000.00	29139800.00	0.00	22997000.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0081172_1202_2725	0.00	0.00	0.00	611508.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0081762_877_2418	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13475000.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0084842_1_1235	0.00	0.00	0.00	0.00	4398100.00	0.00	0.00	1342000.00	3871800.00	4296600.00	8976000.00	1350000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0085483_1439_2980	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7476700.00	8016800.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0114086_1734_3221	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3975000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0127188_1140_2669	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7063200.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0150677_2290_2823	0.00	0.00	0.00	7334000.00	36565000.00	15205100.00	12790800.00	3977200.00	3734100.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0158659_1_1236	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3397500.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0169296_2_1165	0.00	0.00	0.00	0.00	0.00	0.00	10966800.00	0.00	4438800.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0172003_1424_2653	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1393200.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0172380_496_2043	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2827500.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0195810_1049_2500	0.00	39916000.00	86139000.00	29830000.00	0.00	51610000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0227902_2_1495	0.00	0.00	0.00	0.00	594093.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0302532_1_1065	8290000.00	0.00	14300200.00	5168000.00	4779200.00	16912200.00	9644400.00	5447300.00	7419600.00	8791200.00	13950000.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0304569_217_1752	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2837967.05	5945400.00	0.00	0.00	795000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0310401_550_2025	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1650000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0330161_823_1968	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10368000.00	23408000.00	2948000.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0330685_1757_1966	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2580300.00	0.00	2063600.00	2349600.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0390798_937_1827	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2147200.00	2430000.00	3372600.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0393358_1386_1823	0.00	0.00	0.00	0.00	0.00	0.00	0.00	36234000.00	33372000.00	26411000.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0480409_3_944	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9856000.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0536721_365_1588	8410000.00	33252000.00	0.00	41135000.00	96408000.00	122276000.00	13530709.68	0.00	9169200.00	4196500.00	1795200.00	8737500.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0543783_386_1579	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	23485000.00	28160000.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0573113_1_1251	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18954000.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0700345_3_1415	0.00	618855.08	0.00	0.00	0.00	831810.49	0.00	7660800.00	0.00	0.00	12551000.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0723293_2_1396	12600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0723161_629_1396	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	969900.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0726423_39_1394	0.00	20060000.00	0.00	0.00	26828000.00	3831600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0750617_639_1373	0.00	31348000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0779771_332_1339	1010000.00	2080800.00	5524527.58	0.00	5994600.00	0.00	4970400.00	2860900.00	8100000.00	2671900.00	2288000.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0813683_44_1327	3050000.00	21624000.00	0.00	3961500.00	0.00	0.00	0.00	1166149.32	3946700.00	0.00	19825726.69	8694400.00	7800000.00	KO:K02111
Ga0586324_0854583_1_1298	0.00	1462000.00	0.00	0.00	0.00	0.00	0.00	2616900.00	0.00	1309000.00	0.00	3414229.50	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0875723_783_1286	0.00	0.00	0.00	0.00	0.00	4247900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0896203_1_1071	0.00	0.00	0.00	0.00	0.00	659198.65	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0925125_1_1254	0.00	0.00	0.00	6460000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0926215_392_1255	0.00	0.00	0.00	11618500.00	72821000.00	77172798.24	0.00	3907437.96	1304100.00	6976200.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0935114_86_1249	7140000.00	0.00	7037500.00	5491000.00	7374800.00	3842531.24	79822800.00	2610800.00	2794500.00	3449600.00	2420000.00	2835000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0972030_911_1228	0.00	0.00	0.00	11875000.00	6334500.00	11870300.00	6999600.00	8540000.00	6123600.00	4643100.00	5139200.00	2617500.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0988878_1_1076	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4725600.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_1056312_1_1185	1200000.00	16333600.00	0.00	0.00	0.00	12875000.00	0.00	0.00	21716000.00	23004000.00	26950000.00	27896000.00	840000.00	KO:K02111
Ga0586324_1304267_2_1084	0.00	0.00	1906120.95	3135000.00	3059100.00	0.00	0.00	2244800.00	1466100.00	0.00	0.00	5630616.75	KO:K02111	F-type H+-trans

Ga0586324_1926553_1_882	0.00	0.00	0.00	0.00	4346600.00	6364271.27	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1940453_243_914	0.00	0.00	0.00	0.00	919790.00	0.00	0.00	0.00	2733500.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_1981772_1_906	0.00	0.00	1516311.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum miyakonense;Methylovulum miyakonense HT12
Ga0586324_2099567_3_884	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15246000.00	10208000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_2163977_3_875	2440000.00	14416000.00	559093.34	0.00	658873.49	0.00	0.00	14518000.00	17010000.00	0.00	9150000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Marinobacterium;Marinobacterium lutimaris;Marinobacterium lutimaris DSM 22012
Ga0586324_2188619_3_608	0.00	611032.36	0.00	0.00	4132500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_2602352_1_723	0.00	0.00	0.00	0.00	2356000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus mediterraneus;Desulfobulbus mediterraneus DSM 13871
Ga0586324_2752996_3_788	0.00	0.00	0.00	0.00	7436600.00	0.00	8572800.00	5471700.00	3960900.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2828084_3_527	0.00	1353200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2866790_1_777	0.00	5113600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2892485_1_762	0.00	0.00	0.00	897628.40	22557000.00	1737971.04	0.00	1053000.00	0.00	2560800.00	1012500.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324_3497667_1_714	0.00	0.00	0.00	0.00	605091.01	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_3682930_362_700	0.00	1298800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. WSM2254;Bradyrhizobium sp. WSM2254
Ga0586324_4190606_3_662	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2409500.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Verrucomicrobia;Spartobacteria;Chthoniobacterales;Chthoniobacteraceae;Chthoniobacter;Chthoniobacter flavus;Chthoniobacter flavus Ellin428
Ga0586324_4388021_1_651	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2684000.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarculaceae;Desulfoarculales;Desulfoarculales alkanexedens;Desulfoarculales alkanexedens ALDC
Ga0586324_4402512_2_649	9060000.00	0.00	357231.35	0.00	0.00	0.00	0.00	4111400.00	4965300.00	0.00	11616000.00	7020000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4483113_1_645	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3653100.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4496120_2_643	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6265600.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4503758_62_643	4090000.00	0.00	0.00	8417000.00	10609000.00	11949700.00	7774800.00	1146800.00	0.00	0.00	1205600.00	1230000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4546583_391_642	0.00	0.00	0.00	3771500.00	0.00	2489590.97	0.00	1970300.00	2276100.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4614294_1_537	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1441800.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4739257_3_512	0.00	0.00	0.00	0.00	0.00	4922800.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4833078_8_625	0.00	0.00	0.00	921500.83	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4896602_3_623	0.00	0.00	0.00	5329500.00	1369900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_4972470_158_619	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	53055000.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_5166791_3_407	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4912600.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_5437166_1_441	0.00	904400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_5649367_3_587	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	534474.75	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_5809929_30_581	0.00	0.00	0.00	0.00	14133200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_5961788_3_572	3310000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	757500.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_6142220_3_566	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4666200.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_6443197_1_555	0.00	0.00	0.00	0.00	0.00	0.00	1582972.28	860100.00	0.00	847000.00	1328800.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_6879627_3_539	0.00	3699200.00	0.00	0.00	8796200.00	0.00	0.00	3611200.00	3604500.00	2171400.00	2156000.00	2047500.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_6890196_186_539	0.00	0.00	0.00	0.00	0.00	2715480.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_7134917_1_531	14000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_7372957_3_524	0.00	0.00	5686300.00	0.00	0.00	0.00	0.00	3568500.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_7653908_1_516	0.00	3005600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_8178600_2_502	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5465600.00	0.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_8204170_1_384	0.00	0.00	0.00	21945000.00	23690000.00	0.00	0.00	0.00	0.00	12551000.00	15310000.00	2730000.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_8305578_1_360	0.00	0.00	0.00	0.00	0.00	1550003.13	0.00	1000400.00	1417500.00	0.00	0.00	KO:K02111	F-type H+-transporting ATPase subunit alpha
Ga0586324_0000001_67484_68863	0.00	5650800.00	0.00	0.00	0.00	0.00	12615290.16	11104742.33	20650912.74	14652894.92	134237466.88	9517500.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0000290_24862_26298	0.00	0.00	0.00	0.00	17201000.00	0.00	0.00	4312700.00	4560300.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0000524_28100_29479	0.00	0.00	0.00	0.00	0.00	0.00	29184000.00	13583620.30	16694100.00	11688600.00	11052800.00	10200000.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0001726_9325_10746	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1881343.30	0.00	0.00	0.00	26699.55	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0003019_15038_16471	0.00	0.00	0.00	0.00	204466.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0005566_10342_11766	1694760.00	3216400.00	0.00	243763.15	4223000.00	855118.15	1482412.48	2293600.00	1798200.00	2471700.00	0.00	640310.75	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0005643_10111_11634	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1769000.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0006195_1_1065	0.00	0.00	0.00	0.00	2863400.00	0.00	0.00	0.00	0.00	12012000.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0008047_3960_5378	1688689.00	1380400.00	1655529.65	4398500.00	1627400.00	2820033.92	2221150.92	1652177.07	2089800.00	0.00	0.00	11512500.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0014086_8338_8733	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1155000.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0015259_2_1414	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	30537000.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0015993_3462_4883	0.00	670694.20	0.00	0.00	0.00	1767622.65	0.00	0.00	1587600.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0022066_5788_7101	6860000.00	0.00	0.00	0.00	0.00	0.00	0.00	8662000.00	0.00	0.00	5288800.00	7725000.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0023875_5019_6434	0.00	0.00	0.00	1719500.00	0.00	3145808.15	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0025745_6478_2857	0.00	0.00	0.00	2470000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0025999_3300_4721	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	72415.43	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0029967_5011_6132	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16409000.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0031467_4794_5993	0.00	0.00	0.00	1824000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0031564_1264_2676	0.00	809200.00	0.00	0.00	0.00	0.00	0.00	5563200.00	0.00	1177300.00	1198800.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0033563_4368_5813	0.00	0.00	0.00	0.00	0.00	1122700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0035361_3255_4673	2250000.00	8059877.48	0.00	3838000.00	15250465.31	19351102.01	0.00	9371110.36	0.00	14352800.00	3682562.24	441024.75	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0036132_1_1470	0.00	1455200.00	0.00	3391500.00	0.00	5756500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0036372_2904_4313	1488821.00	2278000.00	1711148.42	0.00	1184500.00	5163159.68	839644.72	3141500.00	29670300.00	0.00	0.00	997500.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0038418_4132_5442	6640000.00	1298800.00	901785.25	0.00	0.00	54368.53	14500800.00	2379000.00	0.00	0.00	0.00	8400000.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0042799_2430_3830	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	941600.00	0.00	0.00	KO:K02112
Ga0586324_0045726_3090_4598	1130000.00	2482000.00	0.00	0.00	0.00	0.00	0.00	0.00	16409000.00	0.00	0.00	1950000.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0045889_4034_4984	49300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0048863_1889_3307	4470000.00	8908000.00	0.00	0.00	0.00	0.00	0.00	5563200.00	0.00	5694300.00	0.00	5324000.00	8475000.00	KO:K02112
Ga0586324_0069998_223_1719	17310000.00	28220000.00	5279780.22	18382500.00	40180300.00	7895246.19	20018400.00	5599800.00	8464500.00	29290800.00	9618400.00	15108974.25	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0071678_1320_2741	0.00	1210400.00	0.00	0.00	0.00	0.00	0.00	0.00	6561000.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0079096_913_2289	0.00	999600.00	0.00	5272500.00	0.00	0.00	0.00	0.00	663875.19	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0095662_1422_2834	22200000.00	3128000.00	0.00	7229500.00	0.00	0.00	0.00	4324900.00	4657500.00	0.00	3669600.00	5437500.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0099773_1269_2687	5720000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0103312_2656_3375	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4774000.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0107286_2_931	19600000.00	0.00	0.00	0.00	969986.13	37164000.00	3117100.00	28026000.00	0.00	0.00	0.00	4342500.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0132779_1462_2856	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13603000.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0135477_1_1110	300000.00	0.00	2252382.84	3429500.00	4202400.00	2470804.18	0.00	2305800.00	0.00	0.00	1751200.00	13218225.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0139246_1_675	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	347278.50	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0169296_2314_2673	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	832500.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0170721_1854_2664	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1971200.00	0.00	0.00	KO:K02112
Ga0586324_0174945_957_2381	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3836900.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0183678_502_2040	0.00	0.00	0.00	0.00	1025517.44	0.00	0.00	6832000.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0193593_3_920	0.00	0.00	0.00	0.00	3635900.00	2729827.58	269083.32	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0199258_559_1962	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	119710.67	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0211149_120_1529	1440000.00	0.00	0.00	0.00	1823100.00	0.00	2530800.00	994300.00	996300.00	0.00	404868.64	1282500.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0256224_574_1950	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1030900.00	3345300.00	649074.58	3671721.04	2662500.00	KO:K02112	F-type H+-transporting ATPase subunit beta
Ga0586324_0288794_689_2092	28950000.00	81600000.00	2691400.00	18857500.00	57165000.00	61932000.00	29412000.00	50813000.00	22275000.00	62370000.00	52712000.00	59940000.00	0.00	KO:K02112
Ga0586324_0318311_394_1872	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3484800.00	0.00	KO:K02112
Ga0586324_0330685_1_729	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	121612.04	0.00	2733500.00	3220800.00	3229033.50	KO:K02112
Ga0586324_0331576_605_1532	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	194936.48	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0348588_2_268	0.00	0.00	0.00	829237.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0353783_1_1226	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1560999.72	1830000.00	6342300.00	1532300.00	1504800.00	8295000.00	KO:K02112
Ga0586324_0359566_3_926	0.00	77390800.00	16965135.65	581429.34	32473750.41	1786837.00	5586606.20	12798000.00	21684769.48	3996300.00	14414400.00	128343467.20	48900000.00	KO:K02112
Ga0586324_0371952_38_1453	0.00	0.00	0.00	0.00	8654500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0423419_398_1762	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4446400.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0428488_505_1755	0.00	0.00	0.00	0.00	15862000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0462827_2_400	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7747000.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0500042_829_1638	922541.00	3110490.68	1974362.18	3091034.00	0.00	1785916.41	2429469.96	3336700.00	6169834.48	2394700.00	2613600.00	1102500.00	KO:K02112
Ga0586324_0524059_501_1604	0.00	0.00	329435.51	4854500.00	0.00	0.00	0.00	0.00	5941400.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0554419_340_1575	3656594.00	2091242.08	2297040.00	2647432.45	32362600.00	4072648.32	5745600.00	2506486.34	3815100.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0570762_907_1548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	527805.52	0.00	0.00	KO:K02112
Ga0586324_0651745_573_1460	4790000.00	0.00	0.00	0.00	0.00	71460000.00	0.00	0.00	3574600.00	2899800.00	0.00	1056000.00	0.00	KO:K02112
Ga0586324_0688876_2_1249	0.00	0.00	0.00	0.00	14420000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0691757_611_1423	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8239000.00	6635200.00	0.00	KO:K02112
Ga0586324_0730066_1_594	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1000400.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0792510_12_1343	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1079700.00	0.00	13360000.00	507563.21	0.00	0.00	KO:K02112
Ga0586324_0803547_590_1333	9242548.00	7571841.48	4359050.02	44935000.00	39886682.02	22704871.46	14658015.12	13834465.11	22009819.77	8393000.00	3379200.00	14186616.75	KO:K02112
Ga0586324_0819837_2_1294	0.00	0.00	0.00	0.00	0.00	0.00	1215759.84	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0826206_2_1117	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	430502.16	0.00	0.00	KO:K02112
Ga0586324_0830203_2_1294	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1832600.00	1645600.00	174588.75	KO:K02112
Ga0586324_0892885_3_1019	0.00	459749.36	0.00	0.00	790861.70	243725.81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_0990869_1_996	0.00	0.00	0.00	0.00	0.00	4208200.00	210883.99	0.00	1773900.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_1138994_398_1147	3568407.00	924800.00	0.00	1024100.00	8178200.00	0.00	5234861.76	5055623.27	1036800.00	5220600.00	6784800.00	3862500.00	KO:K02112
Ga0586324_1144032_363_1145	0.00	0.00	0.00	0.00	0.00	0.00	0.00	46284000.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_1154491_3_1139	0.00	1536800.00	0.00	0.00	31827000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_1173504_2_655	0.00	0.00	0.00	673344.10	27398000.00	0.00	0.00	0.00	191252.08	51921000.00	0.00	8404000.00	0.00	KO:K02112
Ga0586324_1297400_3_536	0.00	0.00	0.00	0.00	0.00	0.00	304323.13	0.00	0.00	0.00	0.00	7911200.00	0.00	KO:K02112
Ga0586324_1321835_1_1077	8360000.00	24956000.00	6835252.96	12872500.00	8095800.00	14331700.00	9416400.00	40504000.00	9711900.00	28259000.00	4743200.00	4282500.00	0.00	KO:K02112
Ga0586324_1352244_13_1071	4280000.00	0.00	0.00	0.00	6308000.00	12751400.00	4987534.82	0.00	0.00	2114100.00	0.00	0.00	0.00	KO:K02112
Ga0586324_1362985_3_623	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	972000.00	0.00	0.00	0.00	KO:K02112
Ga0586324_1395531_1_1053	8940000.00	11573600.00	6643400.00	2593500.00	17520300.00	49188300.00	32193600.00	16610300.00	9234000.00	0.00	2235200.00	1215900.00	0.00	KO:K02112
Ga0586324_1408783_2_481	0.00	382779.48	0.00	0.00	0.00	0.00	0.00	1476200.00	1352700.00	1370600.00	0.00	1327500.00	0.00	KO:K02112
Ga0586324_1421456_1_930	0.00	8296000.00	0.00	0.00	0.00	0.00	0.00	0.00	13728.85	0.00	0.00	0.00	0.00	KO:K02112
Ga0586324_1444813_3_1037	2720000.00	1679600.00	22294800.00	3315500.00	3254800.00	4128800.00	2394000.00	1427400.00	0.00	1694000.00	2279200

Ga0586324_1945358_3_914	0.00	0.00	0.00	0.00	0.00	1690048.85	0.00	0.00	1377000.00	18634000.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Deferrisoma;Deferrisoma camini;Deferrisoma camini S3R1
Ga0586324_1968621_3_908	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8019000.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium sp. ORS 3324;Mesorhizobium sp. ORS 3324
Ga0586324_2004515_2_901	0.00	0.00	0.00	0.00	916896.73	1246214.76	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324_2095376_1_882	0.00	0.00	0.00	0.00	0.00	14292000.00	12562800.00	0.00	7946100.00	8624000.00	0.00	17040000.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324_2122718_2_880	0.00	0.00	0.00	662150.95	2698600.00	0.00	0.00	0.00	1255500.00	4096400.00	0.00	423564.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Thermonemataceae;Thermonema;Thermonema laosum;Thermonema laosum DSM 5718
Ga0586324_2122784_31_882	2677392.00	0.00	0.00	2755000.00	47606600.00	0.00	0.00	0.00	2567700.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_2184869_58_870	4910000.00	4120800.00	0.00	1548500.00	2008500.00	12346700.00	0.00	9699000.00	14661000.00	0.00	0.00	4777500.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2193072_1_447	938584.00	1917600.00	0.00	3629000.00	0.00	0.00	0.00	3013400.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_2295258_314_853	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1920000.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Blastopirellula;Blastopirellula marina;Blastopirellula marina DSM 3645
Ga0586324_2301720_1_852	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	234618.75	KO:K02112	F-type H+-transporting ATPase subunit beta	Eukaryota;Streptophyta;Bryopsida;Funariales;Funariaceae;Physcomitrium;Physcomitrium patens;Physcomitrella patens patens
Ga0586324_2353130_72_842	0.00	0.00	564672.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324_2474440_3_827	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1044900.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Cruella;Cruella takakiae;Cruella takakiae DSM 26897
Ga0586324_2482331_3_824	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	258976.41	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter modestus;Edaphobacter modestus DSM 18101
Ga0586324_2531558_3_545	0.00	0.00	0.00	0.00	0.00	0.00	0.00	392836.95	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Cystobacterineae;Haliangiaceae;Geobacter;Geobacter sp.|Geobacter sp. OR-0501
Ga0586324_2560614_1_813	0.00	0.00	0.00	0.00	0.00	3693600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylotenera;Methylotenera mobilis;Methylotenera mobilis JI3
Ga0586324_2704697_1_578	21460000.00	17326400.00	0.00	38000000.00	41292700.00	41934931.35	28411080.00	20252000.00	16327994.58	21413700.00	14784000.00	3645000.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2769912_1_693	0.00	1842800.00	1931123.78	9386000.00	0.00	0.00	0.00	0.00	0.00	1540000.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_2865457_544_777	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1101100.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Candidatus Nitrospira inopinata;Candidatus Nitrospira inopinata ENR4
Ga0586324_3241292_1_738	0.00	0.00	0.00	0.00	0.00	0.00	3885700.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Alcanivoracaceae;Alcanivorax;Alcanivorax borkumensis;Alcanivorax borkumensis SK2
Ga0586324_3363165_381_725	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	28513000.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiosaurus;Thiobacillus thiosaurus DSM 505
Ga0586324_3383490_1_723	150700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomagnum;Methylomagnum ishizawai;Methylomagnum ishizawai 175
Ga0586324_3729624_3_392	3140000.00	0.00	0.00	0.00	0.00	0.00	0.00	19337000.00	0.00	0.00	0.00	1410000.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_3831818_1_687	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1047200.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Fungi;Ascomycota;Pancytomycetia;Pirellulales;Pirellulaceae;Rhodopirellula;Rhodopirellula europaea;Rhodopirellula europaea 6C
Ga0586324_3851641_2_688	0.00	1298800.00	2045542.27	0.00	11639000.00	2396974.84	0.00	0.00	3985200.00	1509200.00	1258400.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum miyakonense;Methylovulum miyakonense HT12
Ga0586324_3872611_1_684	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4932900.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Immirania;Immirania thermothiophila;Immirania thermothiophila DSM 100275
Ga0586324_3958217_84_680	607108.00	664547.08	0.00	1520000.00	0.00	0.00	0.00	0.00	1471805.56	560163.60	0.00	710144.25	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_3980352_3_677	0.00	0.00	0.00	997500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324_4038283_1_672	0.00	498168.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324_4087231_249_671	6100000.00	8364000.00	0.00	4600850.00	41097000.00	37397400.00	10852800.00	16531000.00	16200000.00	4458300.00	9592000.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_4124227_2_667	0.00	5725600.00	0.00	0.00	0.00	0.00	0.00	1933700.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Sphingobacteriaceae;Pedobacter;unclassified Pedobacter;Pedobacter alexeii DJ4
Ga0586324_4124370_1_669	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1994300.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;unclassified Chitinophagaceae;Chitinophagaceae bacterium IBVUCB2;Chitinophagaceae bacterium IBVUCB2
Ga0586324_4171769_2_664	479436.00	380230.16	0.00	1700500.00	0.00	0.00	0.00	780800.00	236179.80	383269.04	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324_4209262_98_661	0.00	0.00	636190000.00	0.00	0.00	0.00	0.00	1933700.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_4332108_2_655	0.00	0.00	0.00	0.00	0.00	0.00	803939.40	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Calderihabitans;Calderihabitans maritimus;Calderihabitans maritimus KKC1
Ga0586324_4590874_2_640	251661.00	0.00	0.00	0.00	0.00	749402.25	0.00	0.00	1189500.00	0.00	0.00	817945.04	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96; DSM 24297
Ga0586324_4791598_2_628	0.00	0.00	0.00	0.00	0.00	0.00	0.00	475382.15	1854900.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_4938910_1_621	32000000.00	29954000.00	53034600.00	42845000.00	42230000.00	49571210.87	32604000.00	25216045.19	29970000.00	36498000.00	24200000.00	19800000.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_5451485_1_594	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	473910.83	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Thermanaerothrix;Thermanaerothrix daeninsis;Thermanaerothrix daeninsis GNS-1
Ga0586324_5507693_3_473	0.00	0.00	0.00	0.00	3306300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobulbales;Desulfobulbaceae;Desulfopyrunum;Desulfopyrunum benzoelyticum;Desulfopyrunum benzoelyticum DSM 28570
Ga0586324_5749551_2_583	0.00	0.00	0.00	21517500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Micrococcaceae;Paenarthrobacter;Paenarthrobacter nicotinovorans;Paenarthrobacter nicotinovorans Hce-1
Ga0586324_5831344_2_580	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13376000.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Reichenbachiellaceae;Marinoscillum;Marinoscillum furvescens;Marinoscillum furvescens DSM 4134
Ga0586324_5844883_1_579	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2238700.00	0.00	1566400.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum psychrotolerans;Methylovulum psychrotolerans HV10 M2
Ga0586324_5979342_180_572	0.00	4930000.00	0.00	15010000.00	0.00	0.00	0.00	0.00	0.00	4335100.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_5989301_3_572	0.00	0.00	0.00	0.00	749402.25	0.00	0.00	1189500.00	0.00	0.00	817945.04	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium denitrificans;Hyphomicrobium denitrificans ATCC 51888
Ga0586324_6011243_101_571	0.00	1944800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3375000.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Thermanaerothrix;Thermanaerothrix daeninsis;Thermanaerothrix daeninsis GNS-1
Ga0586324_6108708_274_570	0.00	0.00	0.00	6697500.00	0.00	0.00	0.00	0.00	0.00	3634400.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium;Bradyrhizobium japonicum JS
Ga0586324_6415463_2_544	0.00	0.00	0.00	755834.25	644673.91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_6418987_1_399	0.00	3338800.00	0.00	7400500.00	10500000.00	0.00	3055200.00	4495700.00	4317300.00	4034800.00	4716800.00	2392500.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Marichromatium;Marichromatium gracile;Marichromatium gracile YL28
Ga0586324_6488391_2_496	0.00	0.00	0.00	0.00	0.00	0.00	5175600.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Rayanella;Rayanella massiliensis;Rayanella massiliensis 521, DSM 23428
Ga0586324_6644129_3_548	0.00	2706400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Acidobacteria;Acidobacteria;Bivobacteriales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_7123841_1_534	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2107500.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Ideonella;Ideonella sp. A288;Ideonella sp. A 288
Ga0586324_7138225_118_531	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	758315.52	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Bradyrhizobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium canariense;Bradyrhizobium canariense GAS369
Ga0586324_7290063_2_529	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6075000.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Allochromatium;Allochromatium warmingii;Allochromatium warmingii DSM 173
Ga0586324_7454891_3_524	1710000.00	0.00	0.00	0.00	0.00	0.00	0.00	2737800.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobulbales;Desulfobulbaceae;Desulfopyrunum;Desulfopyrunum benzoelyticum;Desulfopyrunum benzoelyticum DSM 28570
Ga0586324_7468820_205_522	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4699200.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_8061864_1_507	0.00	221550.80	383377.10	1045000.00	1060900.00	305698.34	489899.04	664900.00	371339.64	0.00	0.00	490147.50	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_8243576_2_502	3850000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Endozoicomonadaceae;Parendozoicomonas;Parendozoicomonas haliclonae;Parendozoicomonas haliclonae ERS1628946
Ga0586324_8257854_1_501	0.00	0.00	0.00	490577.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Pharaobacter;Pharaobacter diazotrophicus;Pharaobacter diazotrophicus DSM 102969
Ga0586324_8293552_97_501	0.00	0.00	0.00	969000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02112	F-type H+-transporting ATPase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run_B_J11
Ga0586324_0000001_71430_71960	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2677500.00	KO:K02113	F-type H+-transporting ATPase subunit delta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0592615_3_392	0.00	0.00	0.00	16720000.00	176130000.00	5875600.00	0.00	0.00	1206900.00	0.00	0.00	0.00	KO:K02113	F-type H+-transporting ATPase subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1310703_553_1080	3360000.00	0.00	0.00	3144500.00	2945800.00	0.00	0.00	2031300.00	2187000.00	2148300.00	0.00	0.00	KO:K02113	F-type H+-transporting ATPase subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_2023252_112_663	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1346400.00	0.00	KO:K02113	F-type H+-transporting ATPase subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_4858125_50_625	0.00	0.00	0.00	1577000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02113	F-type H+-transporting ATPase subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_5359186_45_590	0.00	0.00	0.00	1235000.00	11742000.00	0.00	0.00	1201700.00	0.00	0.00	0.00	0.00	KO:K02113	F-type H+-transporting ATPase subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_6333523_285_560	0.00	0.00	0.00	1016500.00	0.00	0.00	0.00	0.00	431714.61	0.00	0.00	0.00	KO:K02113	F-type H+-transporting ATPase subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_6660940_248_547	0.00	0.00	0.00	10640000.00	11474200.00	4168500.00	0.00	0.00	694132.74	0.00	0.00	0.00	KO:K02113	F-type H+-transporting ATPase subunit delta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_7047004_1495_1902	0.00	0.00	0.00	0.00	0.00	1282350.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02114	F-type H+-transporting ATPase subunit epsilon	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0000001_68894_69766	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1909300.00	915300.00	0.00	0.00	0.00	KO:K02115	F-type H+-transporting ATPase subunit gamma	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_1050284_1_699	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3775900.00	0.00	0.00	0.00	KO:K02115	F-type H+-transporting ATPase subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1531791_1_826	0.00	0.00	0.00	0.00	0.00	0.00	1351776.96	0.00	0.00	0.00	0.00	0.00	KO:K02115	F-type H+-transporting ATPase subunit gamma	Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324_5108147_3_611	0.00	0.00	0.00	12350000.00	12257000.00	7662100.00	0.00	4355400.00	0.00	0.00	0.00	0.00	KO:K02115	F-type H+-transporting ATPase subunit gamma	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfonema;Desulfonema limicola;Desulfonema limicola Jadebusen, DSM 2076
Ga0586324_0065220_427_2157	0.00	0.00	0.00	15295000.00	8178200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02117	V/A-type H+-transporting ATPase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0104853_1_1302	0.00	0.00	0.00	0.00	10506000.00	11195400.00	0.00	0.00	0.00	6583500.00	0.00	9075000.00	KO:K02117	V/A-type H+-transporting ATPase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0402888_898_1803	0.00	1319200.00	0.00	3876000.00	0.00	3505100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02117	V/A-type H+-transporting ATPase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0485266_448_1662	76800000.00	48212000.00	27024000.00	42493500.00	41509000.00	26837200.00	29868000.00	30012000.00	22275000.00	25117400.00	26514400.00	13950000.00	KO:K02117	V/A-type H+-transporting ATPase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0893277_3_1274	70500000.00	47600000.00	89954000.00	46075000.00	39449000.00	67887000.00	87780000.00	52277000.00	45441000.00	0.00	31680000.00	7132500.00	KO:K02117	V/A-type H+-transporting ATPase subunit

Ga0586324_0116474_74_2173	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10368000.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0120170_319_2421	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2895200.00	0.00	KO:K02355	elongation factor G
Ga0586324_0141084_1_285	0.00	0.00	0.00	0.00	0.00	0.00	1666228.56	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0156429_523_2613	1770000.00	0.00	0.00	2344228.55	0.00	0.00	0.00	0.00	0.00	0.00	617607.76	0.00	KO:K02355	elongation factor G
Ga0586324_0189057_206_2308	0.00	0.00	0.00	1786000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0267521_564_2165	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	589220.17	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0274046_488_2140	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14344000.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0276490_401_2134	0.00	0.00	0.00	0.00	0.00	332736.36	0.00	14580000.00	370443.15	2200191.84	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0315069_223_2010	0.00	0.00	0.00	0.00	0.00	0.00	2394000.00	1525000.00	18249300.00	4620000.00	4074400.00	3600000.00	KO:K02355	elongation factor G
Ga0586324_0342349_378_1937	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1049119.39	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0370950_69_1871	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4650000.00	KO:K02355	elongation factor G
Ga0586324_0380749_105_1847	2250000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0422089_2_1606	6420000.00	3910000.00	0.00	3363000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0465687_3_1691	0.00	0.00	0.00	0.00	10180525.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0617102_196_1497	0.00	3182400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_0802749_2_1336	0.00	0.00	1784214.56	0.00	894671.39	1177112.94	0.00	0.00	0.00	0.00	1047200.00	0.00	KO:K02355	elongation factor G
Ga0586324_0988683_3_1220	0.00	0.00	0.00	0.00	704083.47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_1029262_2_1198	5610000.00	306461.72	0.00	0.00	3594700.00	0.00	7259000.00	2138400.00	13013000.00	4109600.00	454110.75	KO:K02355	elongation factor G
Ga0586324_1262453_149_1099	0.00	0.00	0.00	1130500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_1632543_1_983	0.00	601449.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_1773358_1_951	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	954800.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_1831390_1_936	1230000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_1945670_1_915	0.00	0.00	0.00	0.00	0.00	0.00	5862100.00	0.00	7931000.00	0.00	3727500.00	0.00	KO:K02355	elongation factor G
Ga0586324_1947165_240_914	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7816500.00	19250000.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_2200466_1_867	0.00	0.00	0.00	0.00	0.00	0.00	835700.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_2483055_2_598	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1402500.00	KO:K02355	elongation factor G
Ga0586324_3086151_1_753	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5588000.00	2302500.00	0.00	KO:K02355	elongation factor G
Ga0586324_3113699_2_751	3140000.00	2006000.00	1633049.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_3483467_1_717	0.00	0.00	0.00	0.00	1555300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_4281919_2_523	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14274000.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_5846687_3_578	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11700000.00	KO:K02355	elongation factor G
Ga0586324_6113768_1_567	0.00	0.00	0.00	0.00	0.00	4674000.00	0.00	0.00	4811400.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_6432521_1_555	0.00	0.00	0.00	0.00	7344500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_6489451_2_553	1560000.00	1856400.00	0.00	0.00	0.00	1068410.28	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_7190281_2_532	0.00	0.00	0.00	0.00	0.00	0.00	4141900.00	0.00	0.00	0.00	0.00	0.00	KO:K02355	elongation factor G
Ga0586324_8159089_2_502	0.00	0.00	0.00	0.00	1191746.36	0.00	0.00	3562647.73	0.00	0.00	0.00	0.00	KO:K02357	elongation factor Ts
Ga0586324_0000002_83549_84430	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1794100.00	1900800.00	3540000.00	KO:K02357	elongation factor Ts
Ga0586324_0157707_373_1272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1516900.00	22321B.16	0.00	KO:K02357	elongation factor Ts
Ga0586324_0000041_15170_16360	6400000.00	8976000.00	5713492.90	0.00	1421400.00	0.00	103740000.00	9613600.00	86427000.00	140910511.28	230612800.00	3665625000.00	KO:K02358	elongation factor Tu
Ga0586324_0000456_3956_5158	0.00	0.00	0.00	1045000.00	369723.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0000999_14115_15305	0.00	0.00	0.00	0.00	0.00	0.00	1235570.76	1250500.00	0.00	1339800.00	695794.88	0.00	KO:K02358	elongation factor Tu
Ga0586324_0000154_10230_11162	0.00	0.00	0.00	0.00	2090900.00	0.00	3988212.48	5050800.00	11250000.00	7476700.00	10665600.00	6015000.00	KO:K02358	elongation factor Tu
Ga0586324_0008218_7620_8807	31890000.00	20073600.00	0.00	33250000.00	25853000.00	1559209.56	63156000.00	6319600.00	28552500.00	25656400.00	20451200.00	25477500.00	KO:K02358	elongation factor Tu
Ga0586324_0008657_3_1193	0.00	0.00	0.00	0.00	2245400.00	1071602.25	4035600.00	2494900.00	0.00	388615.15	0.00	1455000.00	KO:K02358	elongation factor Tu
Ga0586324_0010172_8833_10120	0.00	5195200.00	1949376.24	0.00	6169700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0010668_6209_7411	0.00	1271600.00	0.00	0.00	0.00	5637400.00	0.00	0.00	2085937.68	0.00	3814000.00	9112500.00	KO:K02358	elongation factor Tu
Ga0586324_0011800_2_679	0.00	0.00	0.00	0.00	0.00	117206.31	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0014164_1_1161	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	713996.36	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0014646_1_1056	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	396654.75	KO:K02358	elongation factor Tu
Ga0586324_0018236_7661_7759	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4898300.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0018881_25_1212	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1274900.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0018840_8255_7457	0.00	548793.32	0.00	6517000.00	0.00	0.00	0.00	6272000.00	7420060.44	3026100.00	2138400.00	2617500.00	KO:K02358	elongation factor Tu
Ga0586324_0021799_4714_5904	0.00	2822000.00	0.00	5909000.00	0.00	5081600.00	0.00	0.00	3555900.00	0.00	0.00	2152500.00	KO:K02358	elongation factor Tu
Ga0586324_0047980_3796_4875	722041.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0059348_3_245	0.00	1128800.00	0.00	0.00	191580000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0059428_1_1005	0.00	0.00	0.00	3952000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0060081_2771_3955	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16897000.00	0.00	0.00	867517.20	0.00	KO:K02358	elongation factor Tu
Ga0586324_0060324_2_788	0.00	0.00	0.00	860898.65	13905000.00	0.00	0.00	206613.71	197067.33	292321.26	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0063855_3442_4248	0.00	0.00	0.00	0.00	2616200.00	4506283.48	1185800.64	26437313.38	23093100.00	2163700.00	58185600.00	13200000.00	KO:K02358	elongation factor Tu
Ga0586324_0070664_1_507	0.00	0.00	0.00	0.00	4470200.00	0.00	0.00	0.00	3539700.00	0.00	0.00	1215000.00	KO:K02358	elongation factor Tu
Ga0586324_0074758_204_1394	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	361403.25	KO:K02358	elongation factor Tu
Ga0586324_0086296_824_2017	0.00	16660000.00	44871100.00	18525000.00	40067000.00	18778100.00	15636472.56	12200000.00	16953300.00	3888500.00	2736800.00	16275000.00	KO:K02358	elongation factor Tu
Ga0586324_0090903_2260_3450	0.00	1190000.00	0.00	0.00	0.00	0.00	9758400.00	3208600.00	33210000.00	13706000.00	16720000.00	35917500.00	KO:K02358	elongation factor Tu
Ga0586324_0096831_1803_2996	0.00	1135600.00	0.00	10640000.00	0.00	1932596.00	3438780.36	3855200.00	1530900.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0099327_2339_3442	0.00	0.00	0.00	969000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0100004_2_1030	0.00	0.00	0.00	0.00	5211800.00	0.00	0.00	0.00	0.00	6514200.00	1249600.00	3015000.00	KO:K02358	elongation factor Tu
Ga0586324_0107466_2550_3314	0.00	1013200.00	295684.79	0.00	0.00	634624.35	0.00	0.00	0.00	0.00	0.00	129314.25	KO:K02358	elongation factor Tu
Ga0586324_0109337_331_1521	0.00	979200.00	0.00	0.00	0.00	0.00	0.00	9057585	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0111284_213_1406	3220000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0113572_2468_3226	0.00	0.00	0.00	1567500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0113861_2259_3224	0.00	0.00	0.00	0.00	1761300.00	0.00	2543700.00	2705400.00	2764300.00	1267200.00	2257500.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0131316_2325_3011	0.00	0.00	0.00	0.00	0.00	0.00	0.00	416309.22	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0132574_333_1526	0.00	2509200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1003200.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0133138_2400_2801	0.00	0.00	0.00	0.00	0.00	0.00	3534000.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0165287_683_1876	11700000.00	909100.84	14963256.36	2071000.00	2529925.14	251392.31	1762100.28	2181939.50	2848759.47	3028414.62	1575200.00	2411313.75	KO:K02358	elongation factor Tu
Ga0586324_0174598_3_1148	0.00	93808.04	446909.40	0.00	0.00	0.00	453341.52	182466.86	0.00	0.00	278931.84	213942.00	KO:K02358	elongation factor Tu
Ga0586324_0195300_568_1758	0.00	0.00	0.00	0.00	0.00	0.00	592401.00	467815.71	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0226515_210_1400	0.00	918000.00	0.00	0.00	0.00	0.00	0.00	0.00	238936.23	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0244091_372_1562	0.00	0.00	0.00	0.00	0.00	0.00	9530400.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0263949_954_2150	0.00	0.00	0.00	0.00	2266000.00	642822.40	3009600.00	2574200.00	2802600.00	0.00	0.00	433640.00	KO:K02358	elongation factor Tu
Ga0586324_0275321_1_1206	0.00	843200.00	37270600.00	861406.80	2327800.00	0.00	1079865.00	0.00	552612.78	230254.64	9592000.00	765000.00	KO:K02358	elongation factor Tu
Ga0586324_0303876_609_1808	0.00	0.00	0.00	0.00	4377500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0315005_804_1994	0.00	0.00	0.00	0.00	0.00	2700886.28	0.00	9760000.00	3199500.00	34804000.00	0.00	3667500.00	KO:K02358	elongation factor Tu
Ga0586324_0319557_431_1630	0.00	0.00	8050900.00	3410500.00	0.00	3970000.00	0.00	1653100.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0322626_1102_1989	0.00	958800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0360213_3_818	0.00	0.00	7319000.00	2403500.00	2224800.00	444933.78	1239385.20	22643200.00	6439500.00	18788000.00	22352000.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0412238_1_771	0.00	0.00	421161.16	0.00	0.00	0.00	1735080.00	1500600.00	3321000.00	26740105.70	21278400.00	20400000.00	KO:K02358	elongation factor Tu
Ga0586324_0420737_392_1582	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1597616.52	0.00	0.00	2387000.00	1020000.00	KO:K02358	elongation factor Tu
Ga0586324_0430907_827_1751	0.00	782000.00	0.00	0.00	0.00	0.00	0.00	0.00	1879200.00	4912600.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0462246_472_1662	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	715900.73	KO:K02358	elongation factor Tu
Ga0586324_0474890_1_849	0.00	0.00	0.00	0.00	0.00	0.00	848907.84	561073.12	0.00	2387000.00	1020800.00	1020000.00	KO:K02358	elongation factor Tu
Ga0586324_0553052_76_1299	0.00	0.00	0.00	0.00	0.00	0.00	1211687.76	0.00	6058800.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0557875_124_1380	9560000.00	0.00	0.00	0.00	0.00	0.00	3716400.00	1982500.00	0.00	3003000.00	2103336.40	2167500.00	KO:K02358	elongation factor Tu
Ga0586324_0571466_676_1545	396960.00	0.00	0.00	0.00	0.00	8932500.00	0.00	0.00	0.00	2541000.00	2261600.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0607632_1_1268	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1239700.00	613202.48	522109.50	KO:K02358	elongation factor Tu
Ga0586324_0616387_3_431	324839.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1360800.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0621617_730_1491	5720000.00	6405600.00	0.00	0.00	0.00	0.00	0.00	1884900.00	0.00	3711400.00	2191200.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0641539_1_966	0.00	0.00	0.00	0.00	0.00	0.00	0.00	388551.09	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0665990_424_1446	38400000.00	22848000.00	0.00	12350000.00	3234200.00	38231100.00	19106400.00	2159400.00	2721600.00	3426500.00	5227200.00	2625000.00	KO:K02358	elongation factor Tu
Ga0586324_0666247_475_1446	1910000.00	0.00	0.00	26573600.00	1586500.00	0.00	13061300.00	16416000.00	0.00	0.00	0.00	12075000.00	KO:K02358	elongation factor Tu
Ga0586324_0684112_844_1431	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	216627.84	0.00	KO:K02358	elongation factor Tu
Ga0586324_0710007_2_1084	1890000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0723597_210_1394	35100000.00	23800000.00	56300000.00	32015000.00	37492000.00	43670000.00	45600000.00	32513000.00	31185000.00	36806000.00	40040000.00	36225000.00	KO:K02358	elongation factor Tu
Ga0586324_0734915_1_972	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2420000.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0758457_91_1299	0.00	165992.76	0.00	0.00	151958.22	125138.82	0.00	0.00	0.00	0.00	1126400.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0768978_3_1124	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2122500.00	KO:K02358	elongation factor Tu
Ga0586324_0776234_145_1344	0.00	0.00	0.00	0.00	1757500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0793950_2_1117	0.00	0.00	0.00	0.00	120690.85	0.00	0.00	166850.40	69268.55	104340.96	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0809346_3_854	0.00	0.00	0.00	0.00	0.00	0.00	5198400.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0817487_3_1190	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	915300.00	0.00	0.00	1290000.00	KO:K02358	elongation factor Tu
Ga0586324_0820679_491_1321	0.00	0.00	0.00	0.00	311062.06	0.00	0.00	0.00	0.00	8624000.00	8976000.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0829184_118_1317	0.00	0.00	0.00	0.00	0.00	250238.12	1128500.00	2867400.00	0.00	0.00	0.00	10125000.00	KO:K02358	elongation factor Tu
Ga0586324_0841095_538_1308	0.00	0.00	0.00	6773500.00	5356000.00	0.00	0.00	1433500.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0849243_619_1302	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2074000.00	0.00	4173400.00	0.00	2572500.00	KO:K02358	elongation factor Tu
Ga0586324_0872283_1_873	0.00	0.00	0.00	0.00	0.00	0.00	571586.88	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0946863_37_1227	0.00	0.00	0.00	0.00	0.00	0.00	8322000.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0958063_22_1212	0.00	0.00	1252928.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	219819.75	KO:K02358	elongation factor Tu
Ga0586324_0966178_3_485	4810000.00	4032400.00	0.00	0.00	0.00	0.00	0.00	5343600.00	2794500.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0973139_2_796	0.00	0.00	0.00	0.00	0.00	0.00	4354800.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_0975914_339_1226	0.00	0.00	0.00	0.00	1928500.00	1359600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1046966_3_1148	1390000.00	24888000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1091670_75_1184	25800000.00	4865743.40	0.00	2014000.00	0.00	0.00	226836.81	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1088278_143_1171	0.00	0.00	0.00	0.00	294231.15	0.00	0.00	0.00	2656800.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1124674_289_1155	0.00	1428000.00	0.00	0.00	4768900.00	0.00	0.00	1116300.00	1077300.00	1740200.00	1645600.00	1402500.00	KO:K02358	elongation factor Tu
Ga0586324_1173361_264_1133	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14409600.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1183476_2_379	0.00	0.00	0.00	0.00	0.00	0.00	2394000.00	0.00	2608200.00	0.00	2393600.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1197804_24_1124	2010000.00	2196400.00	0.00	9329000.00	9383300.00	0.00	19516800.00	14588071.92	16888581	16478000.00	29128000.00	16125000.00	KO:K02358	elongation factor Tu
Ga0586324_1203313_3_917	0.00	1652400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1220788_464_1114	0.00	131376.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1255136_3_998	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19764000.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1296494_2_466	0.00	0.00	0.00	0.00	0.00	2579074.77	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1306920_1_918	0.00	292447.60	0.00	0.00	0.00	0.00	387862.20	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1330242_3_1061	0.00	788800.00	2797271.13	917681.00	1025405.17	782804.60	1825356.60	1476200.00	1482300.00	1393700.00	1944800.00	1425000.00	KO:K02358	elongation factor Tu
Ga0586324_1359412_1_1049	0.00	0.00	0.00	1890500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1361116_161_1063	0.00	0.00	0.00	0.00	0.00	0.00	657791.40	0.00	1385100.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1373314_451_1059	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	333486.75	KO:K02358	elongation factor Tu
Ga0586324_1377567_203_1057	0.00	0.00	0.00	0.00	0.00	2004120.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1379963_752_1	8230000.00	0.00	6418200.00	0.00	4367200.00	0.00	6224400.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu
Ga0586324_1392737_2_1054	7780000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	985600.00	0.00	KO:K02358	elongation factor Tu

Ga0586324_0116474_74_2173	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalbus;Thioalbus denitrificans DSM 26407
Ga0586324_0120170_319_2421	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylbium;Methylbium sp. Pch-M;Methylbium sp. Pch-M
Ga0586324_0141084_1_285	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;

Ga0586324_1409165_164_1048	418166.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Ch-K
Ga0586324_1413137_1_828	0.00	0.00	0.00	12445000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfurispora;Desulfurispora thermophila;Desulfurispora thermophila DSM 16022
Ga0586324_1440916_1_1038	533325.00	20196000.00	35469000.00	1111500.00	5294200.00	18341400.00	49476000.00	38918000.00	27297000.00	30954000.00	25432000.00	378866.25	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea butyrativorans;Desulfatitalea butyrativorans DSM 18734
Ga0586324_1475361_35_1027	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	638945.12	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_1495606_3_1010	5970000.00	0.00	0.00	7932500.00	8219400.00	0.00	5312400.00	0.00	0.00	13090000.00	11352000.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Nitrosoirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324_1507400_2_850	0.00	1475600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324_1578087_3_515	9000000.00	4862000.00	1940154.30	0.00	2266000.00	499973.86	1951151.04	1012600.00	0.00	2579500.00	1566400.00	2130000.00	KO:K02358	elongation factor Tu	Bacteria;Planctomycetes;Phycisphaerae;Sedimentisphaerales;Anaerohalosphaeraceae;Anaerohalosphaera;Anaerohalosphaera lusitana;Phycisphaerae bacterium ST-NAGAB-D1
Ga0586324_1582051_2_997	2240000.00	2359600.00	2143994.08	0.00	0.00	1034252.49	0.00	582761.06	2146500.00	1332100.00	0.00	526178.25	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So ce374
Ga0586324_1700817_227_967	0.00	252392.88	0.00	0.00	0.00	0.00	0.00	0.00	601685.82	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Acidithiobacillia;Acidithiobacillales;Acidithiobacillaceae;Acidithiobacillus;Acidithiobacillus ferrooxidans;Acidithiobacillus ferrooxidans ATCC 53993
Ga0586324_1745882_1_957	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4495500.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324_1786871_688_948	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5535000.00	KO:K02358	elongation factor Tu	Bacteria;Firmicutes;Clostridia;Eubacteriales;Syntrophococcaceae;Tepidibacter;Tepidibacter mesophilus;Tepidibacter mesophilus JCM 16806
Ga0586324_1838165_3_488	0.00	0.00	0.00	0.00	0.00	2918400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_1881162_3_926	0.00	0.00	0.00	0.00	0.00	0.00	0.00	192303.72	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_1901859_182_922	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5271200.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Acidobacteria;Solibacteres;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_1971198_1_819	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	311955.75	KO:K02358	elongation factor Tu	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_2015636_2_514	2670000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324_2060391_3_893	0.00	136202.64	168576.28	231949.15	189005.00	153939.53	426834.24	1531100.00	1004400.00	124740.00	197403.36	38243.40	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea butyrativorans;Desulfatitalea butyrativorans DSM 18734
Ga0586324_2166573_1_873	0.00	42187200.00	12821182.11	3885500.00	12051000.00	18215051.18	41991153.52	2781600.00	4511700.00	83160000.00	18057600.00	5670000.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraninereducens;Geobacter uraninereducens Rf4
Ga0586324_2168160_3_755	0.00	0.00	0.00	2498500.00	0.00	0.00	0.00	775154.40	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobateraceae;Syntrophobater;Syntrophobater fumaroxidans;Syntrophobater fumaroxidans MPOB
Ga0586324_2204828_3_830	0.00	0.00	0.00	0.00	3512300.00	0.00	569398.08	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Nitrosoirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324_2307868_1_849	0.00	0.00	0.00	1776500.00	1833400.00	0.00	7273200.00	1982500.00	1198800.00	6260100.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. HYN0024;Dechloromonas sp. HYN0024
Ga0586324_2352092_2_703	1790000.00	0.00	0.00	0.00	0.00	0.00	0.00	1775100.00	765284.76	3708228.37	143484.88	765000.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Alcanivoracaceae;Ketobacter;Ketobacter alkanivorans;Ketobacter alkanivorans GI5
Ga0586324_2357244_2_724	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	501334.92	0.00	3109400.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_2378363_64_840	0.00	0.00	0.00	0.00	812214.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324_2388044_2_754	24900000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	23409000.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea butyrativorans;Desulfatitalea butyrativorans DSM 18734
Ga0586324_2394157_3_836	0.00	311905.80	0.00	22610000.00	368207.49	0.00	3625200.00	4178500.00	0.00	4365900.00	16456000.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Pseudorhodoplanes;Pseudorhodoplanes sinuspersici;Pseudorhodoplanes sinuspersici RIP1110
Ga0586324_2475114_1_825	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2017400.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraninereducens;Geobacter uraninereducens Rf4
Ga0586324_2505788_1_822	0.00	0.00	33273300.00	0.00	0.00	3434427.15	3990000.00	565723.15	0.00	30338000.00	2596000.00	2482500.00	KO:K02358	elongation factor Tu	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Cellulomonadaceae;Cellulomonas;Cellulomonas massiliensis;Cellulomonas massiliensis JC225
Ga0586324_2519003_3_818	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	674210.79	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes bacterium SCGC AAA252-G04;Aminicenantes bacterium SCGC AAA252-G04 (contamination screened)
Ga0586324_2524486_3_818	3760000.00	4331600.00	30042646.36	5671500.00	20600000.00	32831900.00	26858400.00	37698000.00	30067200.00	27558300.00	0.00	17932500.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Solemya velum endosymbiont;Solemya velum endosymbiont WH
Ga0586324_2537147_2_817	3250000.00	2733600.00	2800440.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas;Pseudoxanthomonas taiwanensis;Pseudoxanthomonas taiwanensis DSM 22914
Ga0586324_2635218_2_805	139355.00	482124.76	0.00	0.00	0.00	973183.14	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_2649834_3_803	4330000.00	0.00	0.00	0.00	649562.21	0.00	8116800.00	2647400.00	2008800.00	1593900.00	1557600.00	1027500.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. Pch-M;Methylibium sp. Pch-M
Ga0586324_2656034_3_800	0.00	0.00	0.00	0.00	774929.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanerobaculum;Thermoanerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_2951950_142_768	0.00	884000.00	0.00	1681500.00	0.00	0.00	0.00	0.00	5483900.00	523354.77	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324_2982324_1_762	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1030900.00	0.00	0.00	0.00	527639.25	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Pelobacter;Pelobacter oroosnicus;Pelobacter oroosnicus DSM 2379
Ga0586324_3294157_3_761	0.00	0.00	3679807.41	8407500.00	9051600.00	6270000.00	5880000.00	5175900.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_3004817_3_761	0.00	0.00	0.00	6013500.00	7374800.00	1544330.00	0.00	7198000.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Thermophagus;Thermophagus xiamenensis;Thermophagus xiamenensis HS1
Ga0586324_3058439_79_756	0.00	0.00	0.00	0.00	0.00	0.00	2031468.60	494367.18	0.00	0.00	0.00	668584.50	KO:K02358	elongation factor Tu	Bacteria;Caldithrichaeota;Caldithrichae;Caldithrichales;Caldithrichaceae;Caldithrix;Caldithrix abysii;Caldithrix abysii LF13, DSM 13497
Ga0586324_3058645_15_755	0.00	11288000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Anaerophaga;Anaerophaga thermohalophila;Anaerophaga thermohalophila Fru22, DSM 12881
Ga0586324_3077947_1_753	0.00	0.00	0.00	2657400.00	0.00	2118416.40	2507100.00	0.00	4851000.00	0.00	1057500.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Nitrosoirae;Nitrosoirales;Nitrosoirales;Nitrosoirae;Candidatus Maenetobacterium;Candidatus Maenetobacterium casensis;Candidatus Maenetobacterium casensis MYR-1
Ga0586324_3092868_3_752	0.00	0.00	0.00	0.00	0.00	2313350.76	0.00	2555900.00	40064000.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia sp. URHD0060;Dongia sp. URHD0060
Ga0586324_3112545_1_750	4800000.00	0.00	0.00	1411500.00	21630000.00	8575200.00	17328000.00	11834000.00	9072000.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324_3126758_1_564	0.00	0.00	0.00	4655000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-01, DSM 14535
Ga0586324_3185260_3_743	0.00	3556400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta lutea;Spirochaeta lutea JC230
Ga0586324_3202370_3_740	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1155000.00	0.00	687897.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_3234912_2_739	0.00	0.00	0.00	3049500.00	0.00	0.00	0.00	0.00	0.00	1012842.92	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_3292188_3_734	0.00	8364000.00	14243900.00	0.00	2595600.00	13617100.00	0.00	0.00	0.00	0.00	8412800.00	10125000.00	KO:K02358	elongation factor Tu	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3417209_2_721	0.00	5684000.00	0.00	7201000.00	0.00	0.00	0.00	0.00	0.00	17117000.00	1997600.00	5707500.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. Root404;Rhizobacter sp. Root404
Ga0586324_3486306_1_714	0.00	2543200.00	6868600.00	1596000.00	0.00	0.00	0.00	0.00	2754000.00	0.00	0.00	4305000.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodovulum;Rhodovulum sp. PH10;Rhodovulum sp. PH10
Ga0586324_3521286_1_618	0.00	0.00	0.00	2071000.00	0.00	0.00	0.00	0.00	3693600.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_3523156_2_631	0.00	5324400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobateraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_3529048_1_711	0.00	1196800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. JS666;Polaromonas sp. JS666
Ga0586324_3607285_3_704	0.00	11084000.00	0.00	13870000.00	15244000.00	0.00	11764800.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobateraceae;Syntrophobater;Syntrophobater fumaroxidans;Syntrophobater fumaroxidans MPOB
Ga0586324_3608113_2_706	0.00	965600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium;Phenylobacterium parvum;Phenylobacterium parvum HYN0004
Ga0586324_3629384_196_699	0.00	4630800.00	0.00	0.00	9661400.00	0.00	0.00	0.00	0.00	101842.92	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Candidatus Parcubacteria;unclassified Candidatus Parcubacteria;unclassified Candidatus Parcubacteria;unclassified Candidatus Parcubacteria;unclassified Candidatus Parcubacteria;Parcubacteria bacterium SCGC AAA011-A09;Parcubacteria bacterium SCGC AAA011-A09 (contamination screened)
Ga0586324_3692397_137_700	0.00	61822.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Algisphaera;Algisphaera agarilytica;Algisphaera agarilytica DSM 103725
Ga0586324_3719442_399_698	0.00	409000.28	434273.99	1026000.00	983365.72	892289.26	399914.28	0.00	0.00	0.00	0.00	207323.25	KO:K02358	elongation factor Tu	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Carboxydothermus;Carboxydothermus pertinax;Carboxydothermus pertinax Ug1
Ga0586324_3736786_1_347	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	212955.88	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324_3751055_3_695	2510000.00	583795.64	0.00	6422000.00	0.00	0.00	0.00	0.00	0.00	2125200.00	6538400.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella sp. OAS946;Reyranella sp. OAS946
Ga0586324_3800375_3_689	1930000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_3821217_1_618	13010000.00	0.00	0.00	6684700.00	0.00	0.00	0.00	8723000.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum psychrotolerans;Methylovulum psychrotolerans HV10_M2
Ga0586324_3928200_3_680	3090000.00	1421200.00	0.00	9253000.00	7519000.00	1988410.23	0.00	1457900.00	6374700.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_3967737_2_679	0.00	0.00	0.00	1985500.00	0.00	0.00	0.00	0.00	1494500.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas sp. Nm51;Nitrosomonas sp. 51 Nm51
Ga0586324_3971095_2_679	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1079700.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Acidobacteria;Ticaribacteria;Ticaribacteraceae;Lutellaea;Lutellaea pratensis;Lutellaea pratensis DSM 100886
Ga0586324_3990035_1_678	0.00	5528400.00	0.00	0.00	0.00	0.00	0.00	2482700.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Sinobacteraceae;Solimonas;Solimonas sp. K1W22B-7;Solimonas sp. K1W22B-7
Ga0586324_4044449_54_674	0.00	1217200.00	0.00	1396500.00	2244829.59	0.00	1516145.28	0.00	1555200.00	0.00	2305600.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;Latescibacteria bacterium SCGC AAA252-D10;Latescibacteria bacterium SCGC AAA252-D10 (contamination screened)
Ga0586324_4237593_169_660	0.00	0.00	0.00	0.00	611602.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Firmicutes;Clostridia;Eubacteriales;unclassified Eubacteriales;Clostridiales bacterium oral taxon 876;Clostridiales sp. oral taxon 876 F0540
Ga0586324_4397857_89_649	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7800000.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_4489457_75_644	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	243182.94	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-01, DSM 14535
Ga0586324_4548196_1_555	4360000.00	2366400.00	0.00	0.00	0.00	1853990.00	0.00	1110200.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324_4564079_1_639	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1128500.00	0.00	0.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Pseudoclostridium;Pseudoclostridium thermosuccinogenes;Pseudoclostridium thermosuccinogenes DSM 5806
Ga0586324_4634240_1_636	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	595223.25	KO:K02358	elongation factor Tu	Bacteria;Caldithrichaeota;Caldithrichae;Caldithrichales;Caldithrichaceae;Caldithrix;Caldithrix abysii;Caldithrix abysii LF13, DSM 13497
Ga0586324_4701906_1_633	0.00	0.00	0.00	2261000.00	2760400.00	0.00	0.00	0.00	0.00	2510200.00	0.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_4723038_1_630	0.00	0.00	1324902.27	0.00	0.00	528960.00	0.00	0.00	0.00	0.00	2675200.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified beta proteobacterium;unclassified betaproteobacterium EN84
Ga0586324_4865977_2_625	0.00	433765.88	887749.66	0.00	0.00	675169.96	0.00	719800.00	0.00	877800.00	648177.20	665154.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_4885423_1_624	24400000.00	0.00	0.00	0.00	3193000.00	38866300.00	1933278.12	0.00	0.00	0.00	21736000.00	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobateraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_4914512_1_512	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	619169.32	672975.60	0.00	KO:K02358	elongation factor Tu	Bacteria;Proteobacteria;Gammaproteobacteria;Vulgatibacterales;Vulgatibacteraceae;Vulgatibacter;Vulgatibacter incomptus;Vulgatibacter incomptus DSM 27710
Ga0586324_5026077_3_590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1279800.00	1054900.00	824850.40	1425000.00	KO:K02358	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter lithotrophicus;Ramlibacter lithotrophicus RBP-1
Ga0586324_5225748_98_607	0.00	0.00	0.00	0.00	0.00	0

Ga0586324 0472512 358 1230	0.00	0.00	0.00	6545500.00	0.00	0.00	4263600.00	0.00	325730.97	0.00	2032800.00	162277.50	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta smaragdinae DSM 11293
Ga0586324 0506385 2 799	0.00	0.00	0.00	0.00	1277200.00	2063558.36	0.00	0.00	1036800.00	1894200.00	1724800.00	2520000.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta smaragdinae;Sediminispirochaeta smaragdinae DSM 11293
Ga0586324 0683272 2 592	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	210056.25	KO:K02406	flagellin		Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 0834616 244 1050	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2552000.00	0.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Ideonella;Ideonella sakaiensis;Ideonella sp. 201-F6
Ga0586324 1013116 2 1183	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	99278.96	0.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 1077790 416 1177	648101.00	1441172.28	629068.05	638457.00	605402.07	0.00	2130703.32	520400.15	566987.04	2979900.00	2418503.12	363504.75	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 1082882 401 1174	488603.00	382404.12	0.00	1130500.00	1627400.00	0.00	649195.80	195433.02	0.00	0.00	0.00	176558.25	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema primitia;Treponema primitia ZAS-2
Ga0586324 1089907 218 1069	0.00	707200.00	1296589.00	894202.70	0.00	543048.36	0.00	0.00	0.00	0.00	145200.00	1942500.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Leptonema;Leptonema illini;Leptonema illini 3055, DSM 21528
Ga0586324 1152088 1 561	1120000.00	1489200.00	1260607.67	1206500.00	4861600.00	1768956.57	2163250.32	34709000.00	0.00	0.00	2410100.00	2103200.00	3236227.50	KO:K02406	flagellin	Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Leptonema;Leptonema illini;Leptonema illini 3055, DSM 21528
Ga0586324 1154575 235 1089	0.00	1346400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	493370.57	0.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 1159252 1 609	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	722344.70	2200000.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema primitia;Treponema primitia ZAS-2
Ga0586324 1160102 3 377	4850000.00	0.00	0.00	177244.35	462551.37	2061247.82	8755200.00	0.00	0.00	0.00	0.00	221116.50	KO:K02406	flagellin		Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324 1357795 274 1065	3210000.00	2770878.96	1171867.61	2907000.00	2600582.11	2030083.32	11754204.84	603803.01	340193.52	0.00	683749.44	662008.50	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 1492833 187 1023	0.00	1319200.00	0.00	5238985.24	0.00	13736200.00	0.00	0.00	0.00	10824000.00	6600000.00	0.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema primitia;Treponema primitia ZAS-1
Ga0586324 1712498 3 875	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2926000.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;unclassified Treponema;Treponema sp. RmG30
Ga0586324 1763445 1 708	9840000.00	24451663.04	8276100.00	602968.80	14382967.38	9101522.75	12426000.00	1554701.51	3393900.00	2256100.00	12707200.00	3787500.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;unclassified Treponema;Treponema sp. RmG30
Ga0586324 1821147 530 940	0.00	0.00	0.00	1795500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatibacillum;Desulfatibacillum aliphaticivorans;Desulfatibacillum aliphaticivorans DSM 15576
Ga0586324 1911584 2 850	0.00	1938849.32	600174.89	587698.50	1583862.93	1128491.16	3792365.04	547185.25	781497.72	546900.97	473638.88	1400841.75	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 1977685 1 885	869412.00	327605.64	720172.71	1957953.80	1631969.08	1048306.29	6292800.00	250658.15	1115578.98	1108800.00	1777600.00	2466333.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema primitia;Treponema primitia ZAS-2
Ga0586324 1980998 190 906	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1070300.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Oligoflexia;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio;Bdellovibrio bacteriovorus;Bdellovibrio bacteriovorus W
Ga0586324 2071280 80 889	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	501214.23	0.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 2328423 2 844	789000.00	1798570.08	0.00	1360841.75	1437315.56	2150080.54	0.00	302803.39	0.00	0.00	128861.04	527804.25	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema primitia;Treponema primitia ZAS-2
Ga0586324 2598338 153 809	0.00	0.00	0.00	1111500.00	0.00	0.00	0.00	0.00	0.00	1654400.00	1402500.00	0.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Leptospirales;Leptospiraceae;Leptonema;Leptonema illini;Leptonema illini 3055, DSM 21528
Ga0586324 2721266 35 793	0.00	0.00	0.00	0.00	0.00	0.00	32832000.00	0.00	0.00	0.00	8888000.00	2362500.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Leptospirales;Leptospiraceae;Leptonema;Leptonema illini;Leptonema illini 3055, DSM 21528
Ga0586324 2929914 349 768	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	271412.24	0.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Methylohalea;Methylohalea fragoieri;Methylohalea fragoieri JAM7
Ga0586324 3019156 2 682	0.00	0.00	464853.90	0.00	0.00	1579651.09	0.00	0.00	0.00	2494800.00	0.00	543148.50	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 3878996 3 680	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2655000.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Leptonema;Leptonema illini;Leptonema illini 3055, DSM 21528
Ga0586324 4206317 2 391	619242.10	0.00	1169111.73	755592.00	439017.93	446986.27	1244618.48	433781.98	176691.78	0.00	0.00	429729.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta smaragdinae;Sediminispirochaeta smaragdinae DSM 11293
Ga0586324 4455547 2 646	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1110000.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Mizugakiibacter;Mizugakiibacter sediminis;Mizugakiibacter sediminis sbMP5
Ga0586324 4466875 1 441	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1557600.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 4844448 2 625	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	353607.75	KO:K02406	flagellin		Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 146;Acidobacteriaceae sp. KBS 146
Ga0586324 5042307 153 614	0.00	5895600.00	0.00	0.00	9187600.00	0.00	0.00	0.00	0.00	0.00	1986600.00	0.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 5055430 1 576	4570000.00	0.00	540575.71	0.00	0.00	585237.55	812842.80	401292.16	0.00	281758.40	429260.48	314274.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta bajacaliforniensis;Sediminispirochaeta bajacaliforniensis DSM 16054
Ga0586324 5327804 243 602	0.00	0.00	0.00	188606.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta smaragdinae;Sediminispirochaeta smaragdinae DSM 11293
Ga0586324 5617555 3 305	2310000.00	1713600.00	2489377.69	2945000.00	0.00	3021372.47	3625200.00	969900.00	0.00	0.00	0.00	2437500.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta cellobiosiphila;Spirochaeta cellobiosiphila DSM 17781
Ga0586324 5646073 3 494	0.00	35428000.00	9289500.00	0.00	0.00	4049400.00	0.00	0.00	0.00	1101100.00	7867200.00	2017500.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema primitia;Treponema primitia ZAS-2
Ga0586324 5748241 2 280	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5985900.00	0.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 6039014 3 569	0.00	3420400.00	17284100.00	4256000.00	8858000.00	0.00	16963200.00	9028000.00	4025700.00	8085000.00	11088000.00	12225000.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema azotonutricium;Treponema azotonutricium ZAS-9
Ga0586324 6201053 2 445	1570000.00	0.00	1638300.00	418444.60	1452300.00	2004800.00	18126000.00	1331000.00	0.00	11781000.00	10984000.00	17775000.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 7545593 2 409	851071.00	1108400.00	1859161.12	679441.90	872679.86	0.00	595490.40	0.00	0.00	235372.06	369415.20	682749.75	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta smaragdinae;Sediminispirochaeta smaragdinae DSM 11293
Ga0586324 7905929 1 405	0.00	0.00	0.00	0.00	1514100.00	0.00	0.00	0.00	0.00	0.00	994400.00	0.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Thauera;unclassified Thauera;Thauera sp. SYD-3
Ga0586324 7995422 2 508	1720000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema azotonutricium;Treponema azotonutricium ZAS-9
Ga0586324 8070674 3 464	0.00	0.00	0.00	0.00	0.00	1769000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02406	flagellin		Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Mizugakiibacter;Mizugakiibacter sediminis;Mizugakiibacter sediminis sbMP5
Ga0586324 7848707 1 267	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	722983.80	0.00	0.00	KO:K02433	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit A		Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 0443573 910 1728	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3960000.00	0.00	KO:K02434	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B		Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus bourgensis;Methanoculleus bourgensis MS2
Ga0586324 0002384 12117 14750	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	885500.00	0.00	0.00	KO:K02453	general secretion pathway protein D		Bacteria;Actinobacteria;Coriobacteriia;Eggerthellales;Eggerthellaceae;Vitrinhabitans;Lutetiella;Lutetiella pratensis;Lutetiella pratensis DSM 100886
Ga0586324 0110436 1990 3270	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4312000.00	4505600.00	4215000.00	KO:K02453	general secretion pathway protein D		Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0126024 19 2535	0.00	0.00	0.00	0.00	449624.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02453	general secretion pathway protein D		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324 0526384 980 1540	4520000.00	661289.80	0.00	6279500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02453	general secretion pathway protein D		Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 1417054 2 1045	0.00	0.00	0.00	0.00	2029100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02453	general secretion pathway protein D		Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Soranium;Soranium cellulosum;Soranium cellulosum So ce1T47
Ga0586324 2875339 2 775	0.00	0.00	0.00	0.00	0.00	0.00	3007300.00	0.00	0.00	0.00	0.00	0.00	KO:K02453	general secretion pathway protein D		Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 4107999 1 669	0.00	0.00	0.00	2224800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02453	general secretion pathway protein D		Bacteria;Verrucomicrobia;Spartobacteria;Chthoniobacteria;Chthoniobacter;Chthoniobacter flavus;Chthoniobacter flavus Ellin428
Ga0586324 4121904 3 668	0.00	0.00	0.00	0.00	7026900.00	0.00	0.00	0.00	0.00	1668600.00	0.00	0.00	KO:K02453	general secretion pathway protein D		Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermogutturaceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324 4574299 1 639	0.00	1196800.00	0.00	0.00	0.00	0.00	3534000.00	49931.12	0.00	0.00	0.00	0.00	KO:K02453	general secretion pathway protein D		Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0000005 69806 72388	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	339332.49	4423640.76	0.00	817500.00	KO:K02469	DNA avrase subunit A		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324 0056296 1 1635	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2244000.00	0.00	KO:K02469	DNA gyrase subunit A		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324 0075607 1800 3917	0.00	0.00	0.00	0.00	0.00	0.00	164458.44	0.00	0.00	0.00	0.00	0.00	KO:K02469	DNA gyrase subunit A		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324 0234429 1 1317	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11016000.00	0.00	0.00	0.00	0.00	KO:K02469	DNA gyrase subunit A		Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Acetobacteroides;Acetobacteroides hydrogenigenes;Acetobacteroides hydrogenigenes DSM 24657
Ga0586324 7009357 1 537	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	584003.02	0.00	0.00	0.00	KO:K02469	DNA gyrase subunit A		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparu;Thiobacillus thioparu DSM 505
Ga0586324 0000524 3 1208	0.00	0.00	0.00	0.00	0.00	1649826.24	279327.54	8424000.00	0.00	0.00	0.00	0.00	KO:K02470	DNA avrase subunit B		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparu;Thiobacillus thioparu DSM 505
Ga0586324 0115811 749 3064	0.00	0.00	2222090.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02470	DNA gyrase subunit B		Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 0184807 1 1689	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1566400.00	0.00	0.00	KO:K02470	DNA gyrase subunit B		Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324 3191729 1 741	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	128066.40	0.00	KO:K02470	DNA gyrase subunit B		Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run_B_J11
Ga0586324 0102272 2233 3270	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	598869.04	0.00	0.00	KO:K02473	UDP-N-acetylglucosamine 4-epimerase		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324 0202144 1 744	0.00	1230800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02473	UDP-N-acetylglucosamine 4-epimerase		Bacteria;Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;Victivallis;Victivallis vadensis;Victivallis vadensis ATCC BAA-548
Ga0586324 0809280 81 1331	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6860700.00	0.00	0.00	KO:K02482	two-component system NtrC family sensor kinase		Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 3124758 132 749	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	244008.75	KO:K02482	two-component system NtrC family sensor kinase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB	
Ga0586324 4640124 1 637	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1155000.00	KO:K02482	two-component system NtrC family sensor kinase		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rivibacter;Rivibacter subsaxonicus DSM 19570	
Ga0586324 2353385 486 842	0.00	0.00	0.00	7191500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02483	two-component system OmpR family response regulator		Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0079881 1781 2173	0.00	0.00	0.00	0.00	1648000.00	0.00	0.00	0.00	2373300.00	0.00	0.00	0.00	KO:K02490	two-component system response reaulator (staee 0 sporulation protein F)		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324 0000013 69686 70936	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	915000.00	KO:K02492	glutamyl-tRNA reductase		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324 0001370 9202 11841	0.00	0.00	0.00	0.00	0.00	0.00	2574200.00	1027953.99	0.00	0.00	0.00	7462500.00	KO:K02519	translation initiation factor IF-2		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324 0077755 1 1722	0.00	0.00	0.00	0.00	3337200.00	0.00	1939800.00	1952100.00	0.00	0.00	0.00	0.00	KO:K02519	translation initiation factor IF-2		Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0124026 1051 3096	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	574986.75	KO:K02519	translation initiation factor IF-2		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus SB	
Ga0586324 0165355 1 2250	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1724800.00	0.00	0.00	KO:K02519	translation initiation factor IF-2		Bacteria;Firmicutes;Clostridia;Eubacteriales;Peotococcaceae;Desulfotomaculum;Desulfotomaculum hydrothermale;Desulfotomaculum hydrothermale LamS
Ga0586324 0230444 1 636	0.00	0.00	0.00	0.00	799461.28	0.00	3374400.00	3501400.00	0.00	0.00	0.00	0.00	KO:K02519	translation initiation factor IF-2		Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Azonexus;Azonexus hydrophilus;Azonexus hydrophilus DSM 23864
Ga0586324 0223454 103 2310	2900000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02519	translation initiation factor IF-2		Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalbus;Thioalbus denitrificans;Thioalbus denitrificans DSM 26407
Ga0586324 0327199 1 1977	0.00	452868.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02519	translation initiation factor IF-2		Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified Bacteroidales;unclassified Bacteroidales;Bacteroidales bacterium 6E;Bacteroidales bacterium 6E
Ga0586324 0859498 2 1297	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3292500.00	KO:K02519	translation initiation factor IF-2		Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 2597510 2 808	0.00	0.00	0.00	0.00	0.00	0.00	0.00	754695.63	0.00	0.00	0.00	0.00	KO:K02519	translation initiation factor IF-2		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira lacus;Nitrosospira lacus APG 3
Ga0586324 3989823 177 677	0.00	0.00	0.00	0.00	0.00	2715618.95	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02519	translation initiation factor IF-2		Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6288122 3 560	0.00	6800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	K

Ga0586324_0003249_11808_14147	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1124200.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0008939_1796_3274	0.00	6514400.00	0.00	5044500.00	3862500.00	0.00	0.00	0.00	939600.00	0.00	0.00	982500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Planctomycetes;Phycisphaerae;Sedimentisphaerales;Anaerohalosphaeraceae;Anaerohalosphaera;Anaerohalosphaera lusitana;Phycisphaerae bacterium ST-NAGAB-D1
Ga0586324_0015478_1276_3417	0.00	0.00	0.00	0.00	0.00	0.00	1470586.32	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylobacillus;Methylobacillus sp. MM3;Methylobacillus sp. MM2
Ga0586324_0016778_6904_8067	655054.00	1407600.00	0.00	0.00	3275400.00	2674842.33	0.00	3928400.00	0.00	5505500.00	3053600.00	802500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazoonensis;Gemmatimonadetes bacterium KBS708
Ga0586324_0022280_2961_5720	0.00	0.00	0.00	0.00	0.00	0.00	0.00	646600.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_0023027_3196_5898	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2065500.00	19789000.00	3713600.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfofaba;Desulfofaba hansenii;Desulfofaba hansenii DSM 12642
Ga0586324_0023547_4357_6492	0.00	795600.00	3838922.47	2641000.00	0.00	2854279.14	1453627.68	933300.00	0.00	15076600.00	13252800.00	11167500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Ferrigenium;Ferrigenium ammiciola;Ferrigenium ammiciola OYT1
Ga0586324_0033140_3261_5339	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1146800.00	0.00	703188.64	2376000.00	5647500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0033725_3242_5440	0.00	0.00	0.00	0.00	5613500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;unclassified Alteromonadaceae;Alteromonadaceae bacterium 2719K.STB50.0a.01;Alteromonadaceae bacterium 2719K.STB50.0a.01
Ga0586324_0034996_365_2491	3930000.00	0.00	6924900.00	0.00	8579900.00	5915300.00	0.00	6002400.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0034994_1162_3804	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1042500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfocella;Desulfocella halotolerans;Desulfocella halotolerans HAS
Ga0586324_0041710_1_1551	0.00	0.00	1253739.07	0.00	0.00	0.00	0.00	1736676.00	0.00	0.00	0.00	597207.75	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-F06;Aminicenantes bacterium SCGC AAA255-F06 (contamination screened)
Ga0586324_0049645_2432_4786	0.00	5310800.00	6587100.00	6716500.00	6962800.00	7423900.00	5654400.00	4800700.00	8181000.00	3903900.00	7858400.00	6052500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_0051811_473_3052	7180000.00	5807200.00	0.00	2764500.00	3038500.00	0.00	1409179.08	1500600.00	3450600.00	2387000.00	1997600.00	1035000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas sp. DDH964;Desulfuromonas sp. DDH964
Ga0586324_0055790_1_1644	1420000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira jaonica;Nitrospira jaonica NJ11
Ga0586324_0073164_2140_3774	0.00	0.00	0.00	0.00	0.00	0.00	5016000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Cupidesulfovibrio;Cupidesulfovibrio termitidis;Desulfovibrio termitidis H1
Ga0586324_0092509_474_2831	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4627500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldaria;Desulfosoma caldaria DSM 22027
Ga0586324_0092904_1684_3552	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	553673.88	4027100.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_0110299_2711_3271	1630000.00	0.00	0.00	2327500.00	3120900.00	0.00	0.00	4782400.00	0.00	197354.08	383650.96	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-F06;Aminicenantes bacterium SCGC AAA255-F06 (contamination screened)
Ga0586324_0111280_1_1083	2250000.00	0.00	10544220.18	0.00	0.00	0.00	658924.72	0.00	0.00	0.00	0.00	3608000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-F06;Aminicenantes bacterium SCGC AAA255-F06 (contamination screened)
Ga0586324_0112968_1661_3235	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	469237.50	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Noviherbaspirillum;Noviherbaspirillum denitrificans;Noviherbaspirillum denitrificans TSA40
Ga0586324_0114907_160_2370	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3806400.00	0.00	4004000.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0123409_1394_3103	0.00	0.00	5109783.63	0.00	8157600.00	4089100.00	0.00	356600.51	0.00	3796100.00	4734400.00	3480000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0156759_1110_2771	0.00	2223600.00	0.00	3581500.00	1812800.00	0.00	0.00	2269200.00	2875500.00	2541000.00	2666400.00	2992500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;unclassified Comamonadaceae;Comamonadaceae bacterium URHA0028;Comamonadaceae bacterium URHA0028
Ga0586324_0162750_1676_2225	0.00	481633.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-8D6;Aminicenantes bacterium SCGC AAA252-K06 (contamination screened)
Ga0586324_0166836_1088_2692	14300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0171803_3_1733	0.00	298117.44	0.00	0.00	0.00	0.00	0.00	0.00	1093500.00	2887500.00	0.00	2141523.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans Rg
Ga0586324_0184509_373_2499	0.00	0.00	0.00	2764500.00	0.00	0.00	1134600.00	4171500.00	0.00	1100000.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0187591_462_2549	0.00	0.00	0.00	0.00	0.00	0.00	0.00	208070.39	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_0188911_1588_2541	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2835000.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0198823_1423_2481	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1056000.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324_0199306_3_692	0.00	0.00	0.00	0.00	0.00	432702.21	1079397.60	0.00	4349700.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-F06;Aminicenantes bacterium SCGC AAA255-F06 (contamination screened)
Ga0586324_0213249_1_1947	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1101600.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0224130_58_2298	0.00	775200.00	0.00	304989.90	0.00	0.00	0.00	0.00	0.00	12089000.00	3044800.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0229359_1_1098	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8060800.00	780000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriflexus;Sulfuriflexus sp. JOSH_001;Sulfuriflexus sp. JOSH_001
Ga0586324_0239778_2_2095	577271.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSH_001;Burkholderiales sp. JOSH_001
Ga0586324_0296842_611_2065	0.00	2414000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas sp. TF;Desulfuromonas sp. TF
Ga0586324_0330647_3_404	0.00	4052800.00	6080400.00	6602500.00	6118200.00	4089100.00	0.00	2690100.00	10044000.00	2718100.00	225844.08	2175000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324_0374955_3_1622	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4471200.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_0436619_3_944	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2389500.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Ferrigenium;Ferrigenium ammiciola;Ferrigenium ammiciola OYT1
Ga0586324_0443912_489_1727	0.00	0.00	0.00	0.00	0.00	0.00	7182000.00	7893400.00	7816500.00	19188400.00	18286400.00	10650000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_0455004_2_1651	0.00	0.00	0.00	4322500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP65;Rubrivivax sp. AAP65
Ga0586324_0532439_853_1593	0.00	0.00	90080000.00	4275000.00	0.00	0.00	0.00	1579900.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-A06;Aminicenantes bacterium SCGC AAA255-A06 (contamination screened)
Ga0586324_0776277_2_1354	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8289600.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0820576_525_1322	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	704676.51	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. SG708;Dechloromonas sp. SG708
Ga0586324_0900498_1_822	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	664378.88	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_1061725_2_1183	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6172500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_1172854_322_1134	0.00	0.00	0.00	1510500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_1280324_1_1091	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	696960.11	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_1295531_3_1046	5140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_1357044_448_1065	0.00	0.00	0.00	1168500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-A06;Aminicenantes bacterium SCGC AAA255-A06 (contamination screened)
Ga0586324_1437669_2_1027	1150000.00	5018400.00	0.00	0.00	0.00	1254500.00	0.00	0.00	6998400.00	8393000.00	6415200.00	7575000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_1535831_103_1011	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	789137.36	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_1560463_501_1004	0.00	1516400.00	0.00	0.00	0.00	0.00	0.00	2433900.00	0.00	2849000.00	4259200.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324_1572625_2_1000	2830000.00	4712400.00	4833838.22	7980000.00	1812800.00	5280100.00	6592891.32	1788900.00	1547100.00	0.00	9125600.00	1387500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324_1580150_338_997	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5156800.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans sk8.26
Ga0586324_1769505_348_950	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1757700.00	0.00	1821600.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Pelobacter;Pelobacter propionicus;Pelobacter propionicus DSM 2379
Ga0586324_1890692_3_926	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2354600.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Marinobacterium;Marinobacterium mangrovicola;Marinobacterium mangrovicola DSM 27697
Ga0586324_1993157_3_905	0.00	2434400.00	0.00	0.00	4583500.00	0.00	0.00	0.00	0.00	0.00	1578500.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas denitrificans;Dechloromonas denitrificans ATCC BAA-841
Ga0586324_2032986_179_898	0.00	1550400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_2241801_3_860	0.00	0.00	0.00	0.00	0.00	0.00	0.00	695400.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas;Gemmatimonas phototrophica;Gemmatimonas phototrophica AP64
Ga0586324_2444409_616_831	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1952000.00	1960200.00	0.00	0.00	1642500.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;Dasania;Dasania marina;Dasania marina DSM 21967
Ga0586324_2659560_3_551	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1328800.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP65;Rubrivivax sp. AAP65
Ga0586324_2703861_2_625	433172.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_2798705_2_784	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13932000.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_2865296_3_776	935736.00	9860000.00	0.00	5329500.00	9682000.00	0.00	0.00	5276500.00	8027100.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So ce0T47
Ga0586324_2977274_1_765	0.00	1258000.00	2208136.67	1273000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324_3023377_1_567	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1170000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324_3545900_3_575	0.00	0.00	26742500.00	20235000.00	24411000.00	23148800.00	0.00	0.00	20574000.00	11627000.00	0.00	9525000.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas sp. TF;Desulfuromonas sp. TF
Ga0586324_4429383_59_649	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8456800.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithrichaeae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_4487674_394_624	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1347500.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_5211268_3_605	0.00	0.00	0.00	0.00	0.00	0.00	0.00	963800.00	0.00	0.00	0.00	0.00	0.00	KO:K02666	type IV pilus assembly protein PilQ	Bacteria;Proteobacteria;Betaproteobacteria;Chromatiales;unclassified Chromatiales;Thiohalobacter;Thiohalobacter thiocyanaticus;Thiohalobacter thiocyanaticus FOKN1
Ga0586324_5353168_1_498	0.00	0.00

Ga0586324_0665822_3_818	0.00	5922800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02886	large subunit ribosomal protein L2
Ga0586324_2502136_225_821	0.00	0.00	0.00	0.00	0.00	0.00	7774800.00	0.00	0.00	0.00	0.00	0.00	KO:K02886	large subunit ribosomal protein L2
Ga0586324_7151541_3_470	0.00	0.00	0.00	0.00	21424000.00	0.00	13497600.00	0.00	10206000.00	0.00	0.00	0.00	KO:K02890	large subunit ribosomal protein L22
Ga0586324_0273353_133_438	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9600000.00	0.00	KO:K02892	large subunit ribosomal protein L23
Ga0586324_4754146_1_345	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3857700.00	0.00	0.00	KO:K02892	large subunit ribosomal protein L23
Ga0586324_0000041_18556_19176	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3586800.00	3653100.00	8239000.00	7708800.00	9375000.00	KO:K02897	large subunit ribosomal protein L25
Ga0586324_1459098_176_841	0.00	1135600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02897	large subunit ribosomal protein L25
Ga0586324_1935596_412_915	0.00	1890400.00	0.00	0.00	0.00	0.00	0.00	0.00	792211.59	2040500.00	0.00	1312500.00	KO:K02897	large subunit ribosomal protein L25
Ga0586324_0004880_465_1109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6001600.00	0.00	KO:K02906	large subunit ribosomal protein L3
Ga0586324_0412238_1181_1786	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4458300.00	0.00	3037500.00	KO:K02906	large subunit ribosomal protein L3
Ga0586324_4396748_171_623	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1053000.00	0.00	0.00	0.00	KO:K02907	large subunit ribosomal protein L30
Ga0586324_6602247_3_398	9690000.00	0.00	7150100.00	0.00	0.00	7146000.00	7911600.00	4892200.00	5119200.00	1593900.00	5209600.00	4447500.00	KO:K02907	large subunit ribosomal protein L30
Ga0586324_0000703_28153_28419	0.00	0.00	0.00	1406000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02910	large subunit ribosomal protein L31e
Ga0586324_0009625_1230_1847	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1821600.00	0.00	KO:K02926	large subunit ribosomal protein L4
Ga0586324_1067142_992_1180	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2085000.00	KO:K02926	large subunit ribosomal protein L4
Ga0586324_1623249_341_988	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	962500.00	0.00	1567500.00	KO:K02926	large subunit ribosomal protein L4
Ga0586324_8096821_3_473	0.00	0.00	0.00	0.00	0.00	0.00	0.00	309330.42	0.00	0.00	0.00	0.00	KO:K02926	large subunit ribosomal protein L4
Ga0586324_5846873_38_577	0.00	0.00	0.00	0.00	0.00	0.00	889708.44	4398100.00	0.00	0.00	377109.04	0.00	KO:K02927	large subunit ribosomal protein L40e
Ga0586324_0022337_3365_3904	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2147200.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_0121247_637_1185	0.00	19652000.00	0.00	1615000.00	13596000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_0229206_1040_1582	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1093900.00	0.00	0.00	0.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_0345493_626_1171	0.00	0.00	0.00	0.00	8270900.00	0.00	0.00	969900.00	0.00	0.00	0.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_0517442_3_623	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	534088.89	0.00	0.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_0614228_1060_1500	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1421300.00	1320300.00	0.00	0.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_1353544_203_919	0.00	0.00	0.00	0.00	5108800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_1502234_111_803	0.00	3413000.00	36876500.00	17195000.00	0.00	0.00	0.00	0.00	1085400.00	0.00	0.00	1387500.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_1633704_617_985	0.00	0.00	0.00	1216000.00	0.00	15880000.00	11126400.00	1342000.00	27378000.00	0.00	0.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_2189888_245_841	0.00	0.00	0.00	0.00	0.00	4247900.00	0.00	0.00	0.00	0.00	0.00	1597500.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_3603896_1_642	0.00	26044000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_4068264_192_671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2147200.00	14925000.00	KO:K02931	large subunit ribosomal protein L5
Ga0586324_0056322_1368_1901	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3757600.00	0.00	14553000.00	0.00	0.00	KO:K02933	large subunit ribosomal protein L6
Ga0586324_0073520_1450_1980	15700000.00	0.00	0.00	0.00	0.00	0.00	0.00	1017706.14	0.00	0.00	0.00	0.00	KO:K02933	large subunit ribosomal protein L6
Ga0586324_0189738_233_766	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1561600.00	0.00	0.00	0.00	0.00	KO:K02933	large subunit ribosomal protein L6
Ga0586324_0259631_1570_2103	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12150000.00	KO:K02933	large subunit ribosomal protein L6
Ga0586324_0521636_967_1509	0.00	2148800.00	0.00	0.00	0.00	1846435.09	1864939.68	1134600.00	1385100.00	2440900.00	0.00	1740000.00	KO:K02933	large subunit ribosomal protein L6
Ga0586324_2439466_71_604	0.00	0.00	7600500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02933	large subunit ribosomal protein L6
Ga0586324_0021444_3733_4122	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4560000.00	KO:K02935	large subunit ribosomal protein L7/L12
Ga0586324_0031827_3300_3680	0.00	0.00	0.00	0.00	0.00	0.00	166304.57	0.00	0.00	0.00	0.00	0.00	KO:K02935	large subunit ribosomal protein L7/L12
Ga0586324_0559483_948_1331	0.00	0.00	0.00	0.00	9452000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02935	large subunit ribosomal protein L7/L12
Ga0586324_5059289_111_614	0.00	0.00	0.00	0.00	0.00	0.00	0.00	194875.02	0.00	0.00	0.00	0.00	KO:K02935	large subunit ribosomal protein L7/L12
Ga0586324_5891342_3_311	0.00	0.00	0.00	0.00	0.00	0.00	3078000.00	3440400.00	0.00	0.00	0.00	0.00	KO:K02935	large subunit ribosomal protein L7/L12
Ga0586324_6609144_1_360	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1944800.00	0.00	KO:K02935	large subunit ribosomal protein L7/L12
Ga0586324_1013208_966_1208	0.00	0.00	0.00	7438500.00	0.00	0.00	8800800.00	0.00	4527900.00	0.00	0.00	0.00	KO:K02936	large subunit ribosomal protein L7Ae
Ga0586324_0017533_2815_3264	0.00	5093200.00	8670200.00	0.00	0.00	0.00	12015600.00	17019000.00	14418000.00	25179000.00	36080000.00	29550000.00	KO:K02939	large subunit ribosomal protein L9
Ga0586324_0062236_1548_2000	0.00	0.00	0.00	647629.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02939	large subunit ribosomal protein L9
Ga0586324_7232787_3_455	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5767300.00	0.00	0.00	KO:K02939	large subunit ribosomal protein L9
Ga0586324_0000005_59155_60876	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4800700.00	18225000.00	25579166.69	56408000.00	40500000.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0013812_4351_6111	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4734400.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0024907_2186_3925	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	802023.93	0.00	0.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0033439_2325_4367	0.00	6868000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0040568_4504_5292	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11528000.00	5250000.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0167923_1_654	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3711400.00	0.00	3052500.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0171902_306_2033	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2842500.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0264411_153_1832	2610000.00	0.00	0.00	0.00	0.00	0.00	0.00	3855200.00	0.00	0.00	0.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0328459_1_836	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6344000.00	0.00	0.00	0.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0444810_2_1198	0.00	0.00	0.00	0.00	2907000.00	4233300.00	0.00	108663.57	0.00	0.00	0.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0487175_2_946	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	715978.50	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0636937_2_550	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1474200.00	0.00	0.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_4342793_2_652	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1296000.00	0.00	0.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_7672759_2_517	0.00	0.00	0.00	0.00	0.00	6247200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02945	small subunit ribosomal protein S1
Ga0586324_0000625_102_410	0.00	8840000.00	0.00	0.00	0.00	0.00	0.00	4959300.00	0.00	0.00	0.00	0.00	KO:K02946	small subunit ribosomal protein S10
Ga0586324_0284109_618_956	0.00	979200.00	0.00	0.00	0.00	0.00	219268.46	0.00	0.00	0.00	0.00	0.00	KO:K02946	small subunit ribosomal protein S10
Ga0586324_0108714_462_1139	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2033100.00	0.00	0.00	KO:K02948	small subunit ribosomal protein S11
Ga0586324_0493077_764_1153	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3355000.00	1239300.00	0.00	0.00	0.00	KO:K02948	small subunit ribosomal protein S11
Ga0586324_0080445_569_1261	0.00	2808400.00	4069994.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02948	small subunit ribosomal protein S11
Ga0586324_1302095_704_1084	0.00	0.00	0.00	3933000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02948	small subunit ribosomal protein S11
Ga0586324_1403350_631_1050	0.00	0.00	0.00	0.00	0.00	0.00	2001746.52	0.00	0.00	0.00	0.00	0.00	KO:K02948	small subunit ribosomal protein S11
Ga0586324_1329514_2_415	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3393900.00	0.00	0.00	0.00	0.00	KO:K02952	small subunit ribosomal protein S13
Ga0586324_0105668_1750_2019	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1676700.00	0.00	0.00	0.00	0.00	KO:K02956	small subunit ribosomal protein S15
Ga0586324_0230444_2027_2296	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5136200.00	4398300.00	0.00	719624.40	0.00	KO:K02956	small subunit ribosomal protein S15
Ga0586324_0541534_591_866	0.00	0.00	0.00	0.00	0.00	0.00	219268.46	0.00	0.00	0.00	0.00	3101988.50	KO:K02956	small subunit ribosomal protein S15
Ga0586324_2119580_488_757	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1215000.00	KO:K02956	small subunit ribosomal protein S15
Ga0586324_2129319_469_735	0.00	0.00	0.00	0.00	201254.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02956	small subunit ribosomal protein S15
Ga0586324_2006676_3_323	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3348900.00	0.00	0.00	0.00	0.00	KO:K02965	small subunit ribosomal protein S19
Ga0586324_1604790_356_973	0.00	0.00	0.00	0.00	1071200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02966	small subunit ribosomal protein S19e
Ga0586324_0000002_84505_85251	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4057500.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_0000532_20643_21521	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1587600.00	994400.00	0.00	2055000.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_0021125_2968_3846	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2033100.00	0.00	0.00	0.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_0024658_3_521	0.00	0.00	0.00	0.00	8672600.00	0.00	0.00	0.00	0.00	7353500.00	7955200.00	5925000.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_0028830_3893_4636	7040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_0041203_845_1585	0.00	0.00	0.00	0.00	0.00	0.00	1409100.00	5467500.00	0.00	0.00	0.00	0.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_0111210_884_1624	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2810500.00	0.00	0.00	3592500.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_1136853_38_757	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5661900.00	0.00	0.00	0.00	0.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_2909193_2_772	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	993300.00	0.00	0.00	0.00	KO:K02967	small subunit ribosomal protein S2
Ga0586324_5052952_477_614	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3115200.00	0.00	KO:K02970	small subunit ribosomal protein S21
Ga0586324_0000625_3621_4325	6530000.00	0.00	0.00	0.00	0.00	11764800.00	14213000.00	11340000.00	5975200.00	7594400.00	0.00	4710000.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0004880_3511_4215	0.00	0.00	0.00	0.00	0.00	7729200.00	6771000.00	5207600.00	3207600.00	0.00	12249000.00	10425000.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0007546_9543_10241	0.00	0.00	0.00	0.00	0.00	0.00	2165710.43	0.00	0.00	0.00	0.00	0.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0038998_772_1419	0.00	6398800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1624700.00	2032800.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0005838_371_1051	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2633400.00	0.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0053090_613_1515	0.00	0.00	6812300.00	3572000.00	2482300.00	0.00	5244000.00	0.00	4884300.00	3934700.00	16984000.00	4477500.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0156257_1158_1985	0.00	4943600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0222240_3_578	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11100000.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0351197_425_1522	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6388800.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0832530_360_1070	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4102500.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_1201587_3_908	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6330000.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_1274316_100_804	0.00	0.00	10246600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_2022549_176_892	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4536000.00	0.00	0.00	0.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_3249001_75_728	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3769800.00	0.00	0.00	0.00	0.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_7009238_34_137	0.00	0.00	0.00	0.00	7107000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02982	small subunit ribosomal protein S3
Ga0586324_0217532_1958_2380	2140000.00	1292000.00	1552326.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02984	small subunit ribosomal protein S3Ae
Ga0586324_0301255_90_722	0.00	0.00	0.00	0.00	8260600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02984	small subunit ribosomal protein S3Ae
Ga0586324_0000625_15965_16585	0.00	0.00	0.00	5434000.00	6921600.00	6629900.00	0.00	0.00	12798000.00	17941000.00	34408000.00	10425000.00	KO:K02986	small subunit ribosomal protein S4
Ga0586324_0004880_11844_12473	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3117100.00	0.00	0.00	0.00	0.00	KO:K02986	small subunit ribosomal protein S4
Ga0586324_0077492_1524_2150	0.00	3780800.00	1955208.92	6507500.00	5685600.00	0.00	0.00	0.00	4519800.00	5759600.00	0.00	0.00	KO:K02986	small subunit ribosomal protein S4
Ga0586324_0081877_36_656	0.00	4311200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02986	small subunit ribosomal protein S4
Ga0586324_1158782_454_1074	0.00	6670800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02986	small subunit ribosomal protein S4
Ga0586324_1776657_327_950	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6588000.00	0.00	0.00	0.00	0.00	KO:K02986	small subunit ribosomal protein S4
Ga0586324_2370642_346_840	0.00	0.00	0.00	0.00	2149167.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02986	small subunit ribosomal protein S4
Ga0586324_8093762_69_506	4690000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02986	small subunit ribosomal protein S4
Ga0586324_0000625_8227_8736	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	531034.35	0.00	627732.75	KO:K02988	small subunit ribosomal protein S5
Ga0586324_0028887_9631_10158	221488.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02988	small subunit ribosomal protein S5
Ga0586324_0316962_618_1130	0.00	0.00	0.00	3885500.00	0.00	0.00	0.00	2379000.00	0.00	0.00	0.00	0.00	KO:K02988	small subunit ribosomal protein S5
Ga0586324_1215072_554_1075	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1455300.00	0.00	0.00	KO:K02988	small subunit ribosomal protein S5
Ga0586324_1521632_278_790	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3795000.00	KO:K02988	small subunit ribosomal protein S5
Ga0586324_2326824_2_379	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	509400.43	0.00	355980.75	KO:K02988	small subunit ribosomal protein S5
Ga0586324_2264057_1_510	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1316700.00	0.00	0.00	KO:K02988	small subunit ribosomal protein S5
Ga0586324_0014756_2928_3398	0.00	0.00	0.00	1396500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_0029351_2028_2498	9720000.00	35156000.00	0.00	6773500.00	6530200.00	6947500.00	0.00	0.00	31104000.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_0070025_3270_3740	0.00	4488000.00	0.00	3021000.00	2863400.00	5240400.00	0.00	0.00	1749600.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_0076619_2088_2558	2420000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2355000.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_0106192_2308_2778	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2130300.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_0109811_2278_2748	0.00	0.00	640057.81	0.00	0.00	968799.10	4810800.00	26352000.00	0.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_1462107_163_633	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	35112000.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_1869360_2_397	0.00	2373200.00	0.00	2223000.00	0.00	0.00	2952400.00	1263600.00	0.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_1958213_202_672	0.00	0.00	518972.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_1990641_1_366	0.00	1863200.00	0.00	0.00	0.00	0.00	5111800.00	0.00	0.00	970200.00	0.00	713592.75	KO:K02992	small subunit ribosomal protein S7
Ga0586324_2382597_2_343	0.00	0.00	0.00	0.00	0.00	1424336.75	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_2901822_270_740	567712.00	0.00	0.00	0.00	0.00	0.00	4218000.00	2257000.00	2292300.00	1332100.00	2763200.00	2970000.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_6121896_222_566	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7177500.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_6721465_96_545	0.00	0.00	0.00	0.00	0.00	0.00	173597.38	0.00	0.00	0.00	0.00	0.00	KO:K02992	small subunit ribosomal protein S7
Ga0586324_0004880_6809_7204	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6093900.00	0.00	2541000.00	0.00	1672500.00	KO:K02994	small subunit ribosomal protein S8
Ga0586324_0593228_119_517	0.00	0.00	0.00	0.00	0.00	1126519.26	0.00	0.00	0.00	0.00	0.00	0.00	KO:K02994	small subunit ribosomal protein S8
Ga0586324_2642244_533_802	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	365411.21	KO:K02994	small subunit ribosomal protein S8
Ga0586324_0017457_7199_7591	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8239000.00	9504000.00	9075000.00	KO:K02996	small subunit ribosomal protein S9
Ga0586324_1212739_170_562	0.00	0.00

Ga0586324 0001419 12543 13592	0.00	1564000.00	0.00	868613.50	2853100.00	0.00	0.00	0.00	0.00	0.00	2288000.00	2280000.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazoonesis;Gemmatimonadetes bacterium KBS708
Ga0586324 0004880 12503 13483	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19943000.00	17424000.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0005242 3 878	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1101600.00	1609300.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 0010273 8451 9428	0.00	0.00	0.00	3078000.00	4892500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324 0049551 1002 2003	0.00	4841600.00	0.00	0.00	0.00	0.00	0.00	1403000.00	0.00	854700.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 9736;Geobacter sp. DSM 9736
Ga0586324 0062358 566 1555	0.00	5174800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;Candidatus Latescibacter;Candidatus Latescibacter anaerobius;Candidatus Latescibacter anaerobius SCGC AAA252-E07 (contamination screened)
Ga0586324 0080266 2914 3807	0.00	0.00	0.00	2536500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium canariense;Bradyrhizobium canariense GAS369
Ga0586324 0089833 614 1666	0.00	0.00	0.00	0.00	0.00	2660666.21	1439343.48	0.00	0.00	1601600.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio yellowstonii;Thermodesulfovibrio yellowstonii DSM 11347
Ga0586324 0102437 3 344	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	400059.75	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0142810 1201 2244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	947100.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas;Gemmatimonas phototrophica;Gemmatimonas phototrophica AP64
Ga0586324 0170406 1714 2667	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	359123.22	2394700.00	21032000.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324 0177767 1510 2613	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10692000.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Planctomycetes;unclassified Planctomycetes;unclassified Planctomycetes;unclassified Planctomycetes;unclassified Planctomycetes;unclassified Planctomycetes;Planctomycetes bacterium P3
Ga0586324 0268605 259 1290	9080000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7476300.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0312883 369 1352	13600000.00	13396000.00	0.00	0.00	0.00	0.00	0.00	10492000.00	0.00	6922300.00	2930400.00	3232500.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium GJ-E10;Burkholderiales bacterium GJ-E10
Ga0586324 0687966 426 1409	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2985000.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Aquabacterium;Aquabacterium sp. NJ1;Aquabacterium sp. NJ1
Ga0586324 0751316 64 1077	0.00	0.00	0.00	7961000.00	0.00	0.00	0.00	0.00	891000.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0772478 1 759	3580000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PB90-1
Ga0586324 0861856 502 1293	2790000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geothermobacter;Geothermobacter sp. HR-1;Geothermobacter sp. HR-1
Ga0586324 1416361 3 836	0.00	0.00	0.00	0.00	0.00	0.00	0.00	524459.09	0.00	725191.39	782864.72	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira lacus;Nitrosospira lacus APG3
Ga0586324 1472390 1 975	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10318000.00	8659200.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324 1478632 1 456	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1838700.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 1773531 3 806	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5929000.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 2729846 3 416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1320000.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 2775532 2 460	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6414100.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. SG708;Dechloromonas sp. SG708
Ga0586324 4959282 1 549	0.00	0.00	0.00	0.00	0.00	2211464.68	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Granulicella;Granulicella mallensis;Granulicella mallensis MP5ACTX8
Ga0586324 4968328 3 617	4260000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03040	DNA-directed RNA polymerase subunit alpha	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0004064 1 2667	773185.00	0.00	0.00	0.00	0.00	1721280.84	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03041	DNA-directed RNA polymerase subunit A'	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0202702 1370 2461	0.00	0.00	0.00	0.00	0.00	0.00	2850000.00	0.00	0.00	0.00	0.00	0.00	KO:K03042	DNA-directed RNA polymerase subunit A''	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 2013075 1 852	1240000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03042	DNA-directed RNA polymerase subunit A''	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 3770164 1 588	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1177300.00	0.00	0.00	0.00	0.00	KO:K03042	DNA-directed RNA polymerase subunit A''	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0000041 7465 11538	0.00	0.00	0.00	0.00	0.00	0.00	30232800.00	18428100.00	30990600.00	96222577.99	72424000.00	73012500.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0000999 2 3871	0.00	0.00	0.00	0.00	0.00	0.00	2049637.92	0.00	0.00	0.00	1636800.00	583347.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 0003508 10697 14827	0.00	0.00	5079110.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324 0003932 7424 11326	0.00	0.00	0.00	0.00	0.00	2026089.50	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter soli;Geobacter soli GSS01
Ga0586324 0004831 5256 9554	0.00	1128800.00	4063660.81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1305000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0005554 6819 11324	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2147200.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324 0005930 4964 9367	2600000.00	0.00	0.00	5158500.00	0.00	0.00	0.00	3556300.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium capsulatum;Acidobacterium capsulatum ATCC 51196
Ga0586324 0009648 4284 8567	0.00	0.00	0.00	969000.00	4511400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-L10;Aminicenantes bacterium SCGC AAA252-L10 (contamination screened)
Ga0586324 0010304 3 3698	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	612650.50	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0012298 2681 6967	0.00	1142400.00	0.00	68422.71	236208.87	0.00	0.00	8052000.00	2032991.46	1621325.86	9011200.00	478338.75	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azospira;unclassified Azospira;Azospira sp. ZAP
Ga0586324 0012818 2566 6678	0.00	3882800.00	0.00	0.00	9939500.00	0.00	0.00	294609.87	3466800.00	0.00	0.00	1147500.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 0013269 2142 6431	0.00	0.00	0.00	0.00	0.00	0.00	5494800.00	0.00	0.00	0.00	0.00	634048.50	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0015541 2978 7069	0.00	0.00	0.00	0.00	404792.06	0.00	0.00	0.00	0.00	0.00	0.00	3345000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter superfactus;Methyloceanibacter superfactus R-67175
Ga0586324 0018288 3 3830	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1830600.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. K;Anaeromyxobacter sp. K
Ga0586324 0020773 908 5389	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	75086.24	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 0021851 4216 7131	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	640457.25	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp2;Nitrosospira sp. Nsp2
Ga0586324 0026123 2 2638	0.00	0.00	0.00	363342.70	483208.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0029393 1761 6191	0.00	5052400.00	2497586.23	14060000.00	3069400.00	7384200.00	1285267.92	0.00	0.00	0.00	0.00	1207500.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324 0029753 1021 5010	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3120000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira japonica;Nitrospira japonica NJ11
Ga0586324 0030633 4710 6071	3140000.00	0.00	0.00	0.00	0.00	0.00	0.00	203954.72	0.00	0.00	1188000.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0031827 3831 5960	0.00	0.00	0.00	0.00	0.00	0.00	5472000.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp2;Nitrosospira sp. Nsp2
Ga0586324 0035080 702 5174	0.00	0.00	0.00	0.00	0.00	626215.89	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 0042280 1106 5191	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3203200.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter metallireducens;Geobacter metallireducens GS-15
Ga0586324 0045809 2 1258	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1860500.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;unclassified Alteromonadaceae;Alteromonadaceae bacterium 2719K.STB50.0a.01;Alteromonadaceae bacterium 2719K.STB50.0a.01
Ga0586324 0049905 2 1978	0.00	0.00	0.00	0.00	0.00	867036.09	0.00	652700.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfonema;Desulfonema limicola;Desulfonema limicola Jadebusen, DSM 2076
Ga0586324 0050188 2 4033	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2948400.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324 0055913 2 4090	0.00	0.00	0.00	0.00	0.00	31005700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324 0059637 1094 4390	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3249400.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0065165 1393 4209	0.00	279744.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfurifustis;Sulfurifustis variabilis;Sulfurifustis variabilis skN76
Ga0586324 0068948 2486 4096	11300000.00	483683.32	0.00	1282500.00	0.00	0.00	0.00	0.00	766831.86	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0087308 442 3660	0.00	0.00	0.00	0.00	0.00	0.00	0.00	428665.91	7969020.57	5536300.00	1980000.00	5332500.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324 0093062 1374 3551	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1061100.00	0.00	4637600.00	1935000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfurifustis;Sulfurifustis variabilis;Sulfurifustis variabilis skN76
Ga0586324 0094866 2 2008	0.00	5344800.00	0.00	7210500.00	402277.83	0.00	0.00	243275.93	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324 0105937 3 3107	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2308500.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira defluvii;Nitrospira defluvii
Ga0586324 0121695 3 3125	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1773900.00	839300.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 0132650 3 2990	13100000.00	0.00	0.00	17575000.00	487133.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa marina;Thiocapsa marina 5811, DSM 5653
Ga0586324 0136197 2 2557	13100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0140329 3 2921	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2310000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324 0177995 1 1692	2653896.00	562683.68	0.00	2128000.00	1040300.00	0.00	0.00	1528901.56	623778.57	2733500.00	2040438.40	1575000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0186705 2 1606	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	321555.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 0188912 2 2227	0.00	0.00	525342.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Propionivibrio;Propionivibrio dicarboxylicus;Propionivibrio dicarboxylicus DSM 5885
Ga0586324 0191241 1 2526	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	737758.56	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 0225608 1 2340	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	352280.72	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium URHE0068;Acidobacteriaceae bacterium URHE0068
Ga0586324 0237184 3 2234	0.00	0.00	0.00	700292.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0247920 1 2241	0.00	0.00	0.00	0.00	1905500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis sp. ATCC 49242;Methylocystis sp. Rockwell, ATCC 49242
Ga0586324 0262898 3 2015	0.00	0.00	0.00	0.00	2719200.00	0.00	0.00	437313.27	3021300.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax sp. GW101-3H11;Acidovorax sp. GW101-3H11
Ga0586324 0265284 3 1403	0.00	0.00	0.00	0.00	0.00	0.00	0.00	301573.63	0.00	0.00	0.00	236494.50	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Codakia orbicularis gill symbiont;Codakia orbicularis gill symbiont
Ga0586324 0276179 3 2135	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4123600.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-O11;Aminicenantes bacterium SCGC AAA252-O11 (contamination screened)
Ga0586324 0282802 1 2109	0.00	2427600.00	0.00	0.00	0.00	0.00	0.00	0.00	173952.36	22022000.00	67341355.84	434130.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0290038 3 2087	0.00	0.00	0.00	0.00	0.00	0.00	2576400.00	3619887.62	2409921.72	5176576.02	4866400.00	10875000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0308649 3 2030	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15488000.00	2115000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324 0321205 2 1993	3920000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324 0338571 3 1946	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2748900.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324 0339513 1 1944	0.00	0.00	0.00	0.00	0.00	0.00	381145.32	45750000.00	0.00	4412100.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0349055 1 1920	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	481170.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 0363190 2 1888	0.00	0.00	0.00	0.00	0.00	0.00	0.00	516690.13	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0371120 3 1868	0.00	0.00	0.00	8008500.00	0.00	0.00	0.00	0.00	2681100.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;unclassified Chitinophagaceae;Chitinophagaceae bacterium PMP191F;Chitinophagaceae bacterium PMP191F
Ga0586324 0406136 2 1795	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18975000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0499644 2 1639	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	345798.72	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum miyakonense;Methylovulum miyakonense HT12
Ga0586324 0525378 2 1603	0.00	1224000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0549030 3 1574	0.00	0.00	0.00	7847000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0561001 3 1559	3480000.00	0.00	0.00	0.00	0.00	2122663.72	1975029.48	0.00	1344600.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinifilaceae;Labilibaculum;Labilibaculum filiforme;Labilibaculum filiforme 59.16B
Ga0586324 0566469 3 1553	16000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 0568462 237 1550	0.00	0.00	0.00	0.00	908450.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0572898 3 1544	0.00	0.00	0.00	0.00	941247.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0611569 3 1502	0.00	0.00	0.00	0.00	22351000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus olearius;Azoarcus olearius DQS4
Ga0586324 0626760 1 1485	0.00	17000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324 0735286 2 1387	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2063600.00	0.00	146250000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0741365 1 1380	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	160568.73	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0752773 3 1373	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	410998.50	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324 0861056 2 1294	0.00	0.00	0.00	24415000.00	0.00	0.00	0.00	890600.00	0.00	27258000.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 0890709 96 1277	0.00	0.00	0.00	0.00	0.00	0.00	119708.44	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Deferrisoma;Deferrisoma camini;Deferrisoma camini S3R1
Ga0586324 0977322 3 1226	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5412000.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Pseudanabaenaceae;Pseudanabaena;Pseudanabaena biceps;Pseudanabaena biceps PCC 7429
Ga0586324 1036849 1 1194	0.00	3393200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 1055973 153 1187	0.00	0.00	0.00	0.00	4253900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Thioalkalispiraceae;Sulfurivermis;Sulfurivermis fontis;Sulfurivermis fontis JG42
Ga0586324 1125115 2 1153	0.00	6024800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 1136729 1 1149	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1147300.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 1176960 1 1131	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	655303.44	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp13;Nitrosospira sp. Nsp13
Ga0586324 1284616 3 1091	22200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalbus;Thioalbus denitrificans;Thioalbus denitrificans DSM 26407
Ga0586324 1325799 3 1076	0.00	0.00	0.00	827694.15	0.00	0.00	0.00	884500.00	0.00	1216600.00	1425600.00	5325000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 1366171 3 1061	0.00	4148000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Trinickia;Trinickia caryophylli;Trinickia caryophylli Ballard 720
Ga0586324 1384769 181 1056	0.00	0.00	0.00	188983.50	0.00	20485200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 1444826 3 1037	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1024100.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 1455312 2 637	0.00	0.00	0.00	0.00	0.00	564343.44	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 1473755 2 1027	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1134600.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 1487310 3 1025	0.00	0.00	0.00	1463000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324 1497240 1 1020	0.00	5032000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosovibrio;Nitrosovibrio tenuis;Nitrosovibrio tenuis Nv1
Ga0586324 1572000 1 999	0.00	0.00	3717719.83	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 1703739 134 967	0.00	2781200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 2018130 3 899	1140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324 2269883 1 855	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	576865.50	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 2481688 3 824	0.00	0.00	0.00	0.00	0.00	0.00	0.00	233894.74	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Planctomycetes;Planctomycetia;Isosphaerales;Isosphaeraceae;Singulisphaera;Singulisphaera sp. GP187;Singulisphaera sp. GP187
Ga0586324 2528978 2 817	0.00	0.00	0.00	0.00	0.00	0.00	4149600.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Roseiarcaceae;Roseiarcus;Roseiarcus fermentans;Roseiarcus fermentans DSM 24875
Ga0586324 2626439 3 806	0.00	0.00	8445000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1222500.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geoalkalibacter;Geoalkalibacter subterraneus;Geoalkalibacter subterraneus Red1
Ga0586324 2655744 1 801	0.00	8296000.00	35018600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324 2699008 2 796	0.00	0.00	0.00	0.00	0.00	0.00	4035600.00	2568100.00	2754000.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324 2725374 311 793	0.00	0.00	0.00	0.00	0.00	0.00	6247200.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324 2916066 3 677	0.00	0.00	0.00	453401.75	0.00	0.00	0.00	646600.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 2988866 255 764	0.00	0.00	0.00	736098.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324 3163912 3 746	0.00	0.00	0.00	0.00	0.00	0.00	1161174.36	1195600.00	0.00	0.00	4276800.00	9825000.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324 3169337 1 744	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	417501.54	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 3190288 2 742	938454.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 3271569 2 505	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5032500.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Cellulomonadaceae;Cellulomonas;Cellulomonas sp. Root137;Cellulomonas sp. Root137
Ga0586324 3274325 1 735	0.00	0.00	0.00	0.00	1967300.00	0.00	0.00	0.00	12312000.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324 3274693 1 735	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2446400.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Novimethylophilus;Novimethylophilus kurashikiensis;Novimethylophilus kurashikiensis La2-4
Ga0586324 3282739 3 734	0.00	0.00	3167516.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Algisphaera;Algisphaera agarilytica;Algisphaera agarilytica DSM 103725
Ga0586324 3449859 2 718	0.00	0.00	0.00	0.00	0.00	0.00	372588.48	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified Myxococcales;Enhygromyxa;Enhygromyxa salina;Enhygromyxa salina SWB007
Ga0586324 3838485 1 687	0.00	251500.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	501141.52	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfofaba;Desulfofaba hansenii;Desulfofaba hansenii DSM 12642
Ga0586324 3899046 2 682	0.00	0.00	0.00	0.00	1472900.00	0.00	0.00	1000400.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26

Ga0586324_4191247_2_619	0.00	0.00	0.00	0.00	0.00	9567700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_5309910_2_601	0.00	0.00	0.00	0.00	0.00	0.00	1935332.40	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_5435181_1_597	0.00	0.00	0.00	0.00	0.00	0.00	12790800.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_5448681_3_587	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1150200.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_6209471_3_563	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15147000.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_6413088_1_555	2990000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1717100.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_6832363_1_543	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	422726.92	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_6896119_3_539	0.00	0.00	0.00	0.00	1781900.00	0.00	0.00	1433500.00	0.00	1871100.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_7096828_2_535	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4941000.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_7240534_1_528	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4963200.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_7737983_3_515	0.00	0.00	6464307.00	0.00	0.00	0.00	0.00	0.00	2130300.00	0.00	0.00	0.00	KO:K03045	DNA-directed RNA polymerase subunit B'
Ga0586324_7947334_1_510	6970000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_7974502_2_508	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	362374.56	6013700.00	0.00	0.00	KO:K03043	DNA-directed RNA polymerase subunit beta
Ga0586324_0004575_3698_5113	0.00	0.00	3418220.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03045	DNA-directed RNA polymerase subunit B'
Ga0586324_0000041_3247_7443	0.00	0.00	0.00	0.00	0.00	0.00	63181066.32	36844000.00	81793800.00	117949617.17	212555200.00	117454440.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0000999_22808_26107	0.00	30736000.00	0.00	0.00	0.00	555708.69	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0004540_5735_9976	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1159000.00	0.00	1955800.00	3599200.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0004831_9734_13906	0.00	0.00	14919500.00	11495000.00	0.00	0.00	0.00	0.00	8967000.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0005412_3_1244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6309900.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0005533_4648_8826	0.00	829600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0005930_718_4947	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	477279.44	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0011414_442_4626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	203741.23	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0023828_1_1461	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1061400.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0024299_2940_6776	1210000.00	0.00	188967.57	0.00	0.00	0.00	0.00	2464400.00	1142100.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0024940_5721_6695	0.00	0.00	0.00	0.00	0.00	0.00	0.00	445581.82	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0025854_3_3323	0.00	0.00	0.00	19760000.00	0.00	0.00	0.00	0.00	0.00	2209900.00	932800.00	8662500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0026673_1_2085	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1747500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0029965_1_1818	0.00	0.00	0.00	0.00	633461.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0030633_253_4653	0.00	0.00	0.00	0.00	0.00	0.00	271950.81	207572.22	0.00	283134.72	124500000.00	12450000.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0034086_1965_4427	0.00	11560000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0041135_299_4357	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1109700.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0043882_1_4107	0.00	0.00	0.00	0.00	1442000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0047152_1_3006	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	367959.13	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0048057_501_4628	0.00	0.00	0.00	10488000.00	0.00	0.00	0.00	0.00	0.00	3403400.00	3208289.92	1732500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0061072_176_4342	0.00	979200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0061429_1739_4330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3238400.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0065235_640_4209	0.00	0.00	0.00	0.00	0.00	0.00	0.00	878400.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0070025_1_1944	0.00	308918.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0072813_588_3992	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3503500.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0084505_845_2440	0.00	1863200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0087505_1_2406	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15127500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0094864_2111_3517	0.00	1190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0099463_3_3083	0.00	0.00	0.00	3040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0101714_1744_3402	0.00	0.00	0.00	0.00	0.00	883932.41	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0102658_602_3388	0.00	0.00	0.00	0.00	0.00	0.00	1140700.00	0.00	0.00	1751200.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0102740_2_3142	21920000.00	4073200.00	0.00	1064000.00	1030000.00	0.00	977727.84	0.00	4033800.00	877800.00	0.00	2722500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0112931_3_3236	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1188000.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0112984_580_3234	11900000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0117182_72_1379	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8775000.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0131073_1_594	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0143001_1_2073	0.00	0.00	0.00	0.00	558213.65	0.00	2172087.60	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0151544_4_2817	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2075500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0158425_3_2711	0.00	0.00	1045254.54	0.00	0.00	0.00	9188400.00	1744600.00	0.00	0.00	2445782.57	2913761.84	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0162708_1_2724	0.00	0.00	0.00	0.00	0.00	0.00	7546800.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0166453_3_2138	0.00	0.00	0.00	0.00	0.00	2214500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0179164_1019_2605	0.00	0.00	0.00	0.00	13081000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0182722_1_2031	0.00	0.00	12611200.00	0.00	0.00	0.00	830391.96	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0183173_2_2230	0.00	0.00	18860500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0186705_1668_2555	0.00	0.00	0.00	0.00	0.00	0.00	163193.05	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0200681_2_730	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1102500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0233636_3_2291	0.00	0.00	0.00	2555500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0239232_1_1428	0.00	0.00	0.00	1957000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0255139_2_2212	0.00	0.00	0.00	0.00	1328700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0272321_3_2147	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1335000.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0329912_1_2122	0.00	0.00	0.00	0.00	0.00	0.00	1140700.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0283283_1_2109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6029100.00	0.00	4582500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0284341_775_2106	0.00	0.00	0.00	0.00	0.00	0.00	0.00	805200.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0315267_2_2017	0.00	0.00	2087609.15	0.00	0.00	0.00	509834.95	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0315286_1_2010	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	686191.50	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0322439_3_596	20800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19976000.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0340966_1_1959	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4175500.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0341079_1_1940	0.00	0.00	0.00	0.00	0.00	0.00	3025600.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0350861_3_1916	1560000.00	0.00	0.00	0.00	0.00	0.00	2543700.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0359799_2_1576	1960000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	683124.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0362543_1_1890	1050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0374844_3_1862	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2340900.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0381259_1_1848	0.00	0.00	0.00	0.00	0.00	0.00	3190300.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0421618_2_1471	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1798200.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0425918_330_1760	0.00	686800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0438627_1_1737	0.00	0.00	0.00	0.00	0.00	2845811.13	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0472170_1_1680	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1635000.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0474974_2_1648	4880000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0493355_2_1648	0.00	0.00	0.00	0.00	0.00	553944.24	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0499075_1_1527	0.00	0.00	0.00	0.00	0.00	0.00	474899.03	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0502996_2_1633	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	915200.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0508665_1_1626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	419985.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0632886_3_1478	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2482500.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0638808_2_1474	0.00	0.00	0.00	0.00	0.00	29457400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0676222_599_1438	0.00	0.00	0.00	1855198.00	0.00	0.00	0.00	0.00	0.00	401512.95	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0683597_2_1432	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8262000.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0696536_3_1418	0.00	0.00	0.00	0.00	0.00	19572100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0717797_3_1400	0.00	6868000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0760132_92_1366	0.00	0.00	0.00	0.00	0.00	17054400.00	0.00	0.00	0.00	0.00	14520000.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0820050_177_1322	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	259706.89	61037.87	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0827692_1_789	0.00	0.00	0.00	0.00	0.00	795619.76	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0832007_3_1314	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	527881.97	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0868050_2_1291	0.00	0.00	0.00	6792500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0876120_1_1275	0.00	0.00	0.00	0.00	0.00	0.00	0.00	738100.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0885538_1_1278	0.00	5392400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5336100.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0908922_1_1266	0.00	0.00	0.00	0.00	1854000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_0940523_3_1247	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	46036.95	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1058510_2_1186	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2647500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1066771_2_1182	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	865993.92	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1083258_23_1174	882875.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1107008_3_1163	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3287900.00	63828000.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1124602_2_1153	0.00	0.00	0.00	0.00	0.00	9408900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1215831_3_1115	0.00	0.00	0.00	0.00	0.00	43273000.00	746269.08	738100.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1270998_3_1094	0.00	2951200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1272497_2_1096	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2197500.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1389484_2_1054	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6758400.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1399002_117_1052	0.00	0.00	0.00	0.00	1843700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1409022_1_1047	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	150335.19	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1443986_1_1038	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1522800.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1460379_3_1031	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1871100.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1477842_1_1028	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2632500.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1499868_1_1020	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1469600.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1561734_1_1002	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	255828.65	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1577031_132_998	0.00	210802.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1662363_1_737	0.00	0.00	0.00	0.00	0.00	0.00	440888.16	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1735193_2_958	0.00	0.00	0.00	0.00	547646.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1827468_1_938	0.00	9452000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1842474_326_856	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3210000.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1863417_3_932	0.00	1400800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1958610_2_910	0.00	0.00	0.00	0.00	35329000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_1981991_3_908	0.00	0.00	0.00	0.00	0.00	595697.88	0.00	0.00	448554.51	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_2000655_3_902	0.00	0.00	0.00	0.00	0.00	0.00	1120536.47	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_2093746_3_887	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	950400.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_2147048_1_801	0.00	0.00	0.00	0.00	0.00	4486100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_2247596_2_859	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2086700.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_2327775_2_847	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1380000.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_2328348_1_848	0.00	10744000.00	0.00	5614500.00	0.00	0.00	0.00	0.00	573400.00	0.00	0.00	4515000.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_2422874_3_833	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Ga0586324_2820932_2_781	0.00	0.00	0.00	0.00	0.00	0.00	1016731.80	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3016108_3_761	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1116500.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3225190_2_739	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3596400.00	0.00	0.00	2242500.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3228420_2_739	0.00	0.00	0.00	0.00	0.00	0.00	0.00	640500.00	10692000.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3294827_3_731	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	545988.52	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3544914_1_711	0.00	128957.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3579279_1_708	0.00	0.00	0.00	126350000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3624590_1_705	0.00	0.00	0.00	0.00	2966400.00	1519033.16	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3779671_2_691	0.00	0.00	0.00	0.00	0.00	0.00	8344800.00	5660800.00	6666300.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3799574_3_689	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3580200.00	9240000.00	11000000.00	7275000.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3809298_3_689	0.00	0.00	0.00	0.00	2888538.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3906820_3_683	0.00	0.00	0.00	0.00	0.00	0.00	93171.40	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_3922992_1_681	0.00	0.00	0.00	0.00	7385100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_4010210_119_676	0.00	0.00	0.00	0.00	0.00	385066.97	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_4095715_3_668	0.00	0.00	0.00	11948000.00	0.00	0.00	0.00	0.00	0.00	14168000.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_4321259_1_654	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1020600.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_4338508_3_485	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6362400.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_4409811_1_648	0.00	0.00	0.00	0.00	0.00	2291940.55	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_4600995_3_638	0.00	8500000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	994400.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_4763141_2_628	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1416800.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_5028611_3_614	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1216600.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_5059105_1_462	0.00	637277.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_5326224_2_601	2990000.00	0.00	0.00	0.00	0.00	0.00	472509.05	6415200.00	13706000.00	18128000.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_5411395_3_596	0.00	0.00	0.00	0.00	0.00	249951.84	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_5414752_1_597	1360000.00	0.00	0.00	0.00	0.00	4742400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_5672553_1_585	0.00	0.00	0.00	0.00	271368.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_5989644_2_571	0.00	0.00	0.00	0.00	0.00	0.00	0.00	37584000.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_6538825_3_551	0.00	0.00	14806900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_6757903_3_545	0.00	8636000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_6846465_2_541	810803.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_7320526_1_528	0.00	0.00	0.00	0.00	0.00	2791958.08	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_7498646_1_522	0.00	0.00	0.00	0.00	0.00	0.00	1310297.76	1360000.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_8065653_3_506	0.00	0.00	0.00	0.00	487496.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_8096508_3_506	0.00	0.00	0.00	0.00	0.00	0.00	0.00	210232.23	0.00	0.00	0.00	0.00	KO:K03046	DNA-directed RNA polymerase subunit beta'
Ga0586324_2330632_3_680	0.00	2522800.00	0.00	0.00	0.00	0.00	2037400.00	1879200.00	0.00	1443200.00	0.00	0.00	KO:K03047	DNA-directed RNA polymerase subunit D
Ga0586324_0000001_150384_153125	0.00	0.00	0.00	0.00	0.00	0.00	5477800.00	4919700.00	10857000.00	21939800.00	12307500.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0001856_14405_17110	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	947100.00	3088800.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0014099_3730_6516	0.00	0.00	0.00	15200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0029083_2217_5396	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1732500.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0042548_1245_3770	0.00	0.00	2145249.57	0.00	0.00	1879310.66	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0048742_1002_3749	0.00	0.00	0.00	0.00	0.00	0.00	0.00	980100.00	0.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0179639_1_1048_3006	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5032500.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0179639_1_2601	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8991000.00	0.00	0.00	7725000.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0380759_3_1574	0.00	0.00	0.00	0.00	0.00	0.00	0.00	477692.64	0.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0960870_2_1234	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	557818.03	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_1041362_165_1193	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3187800.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_1522958_3_1013	0.00	0.00	0.00	0.00	0.00	0.00	683200.00	0.00	0.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_1755049_3_689	0.00	0.00	0.00	0.00	0.00	0.00	439311.02	0.00	1162700.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_1739528_2_790	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2340000.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_3557908_508_708	0.00	0.00	0.00	0.00	0.00	0.00	0.00	766417.95	0.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_7292770_3_527	0.00	0.00	0.00	0.00	0.00	430591.07	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03070	preprotein translocase subunit SecA
Ga0586324_0000184_30477_32324	1810000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03072	preprotein translocase subunit SecD
Ga0586324_0018538_1094_2992	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3344000.00	0.00	KO:K03072	preprotein translocase subunit SecD
Ga0586324_0148906_204_1808	0.00	0.00	0.00	0.00	2268960.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03072	preprotein translocase subunit SecD
Ga0586324_0955773_2_1237	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	298524.18	0.00	0.00	0.00	KO:K03072	preprotein translocase subunit SecD
Ga0586324_0000013_37084_39024	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5613300.00	549083.92	1073600.00	215876.25	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0000896_12618_14537	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1155000.00	4320800.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0004570_6493_8109	0.00	1795200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0017128_6460_7992	7570000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0069687_2132_3997	0.00	0.00	0.00	0.00	0.00	750330.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0260081_57_1928	3270000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0376135_1_1518	0.00	0.00	0.00	0.00	1843700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0388704_3_1802	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	211175.25	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0644646_2_1303	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1612500.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0733831_3_1403	0.00	0.00	0.00	0.00	0.00	0.00	2446100.00	0.00	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_1443534_125_1036	0.00	0.00	0.00	2869000.00	0.00	0.00	1634800.00	0.00	2502500.00	1777600.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_1485074_1_1026	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6415200.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_1993803_3_677	0.00	0.00	0.00	0.00	0.00	0.00	0.00	423258.99	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_4351224_2_652	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	175544.01	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_5572127_1_591	0.00	0.00	0.00	3933000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_7009892_1_535	0.00	0.00	0.00	0.00	1792200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03086	RNA polymerase primary sigma factor
Ga0586324_0966245_1_339	0.00	0.00	0.00	249431.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03088	RNA polymerase sigma-70 factor (ECF subfamily)
Ga0586324_0076874_576_1907	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1417500.00	KO:K03106	signal recognition particle subunit SRP54
Ga0586324_0559778_349_840	6370000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03111	single-strand DNA-binding protein
Ga0586324_1600869_534_992	0.00	0.00	0.00	0.00	0.00	0.00	3836900.00	0.00	0.00	0.00	0.00	0.00	KO:K03111	single-strand DNA-binding protein
Ga0586324_1861409_1_336	3110000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03111	single-strand DNA-binding protein
Ga0586324_2543436_13_525	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3405000.00	0.00	KO:K03111	single-strand DNA-binding protein
Ga0586324_2950203_218_727	18700000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03111	single-strand DNA-binding protein
Ga0586324_0031419_5668_5773	0.00	0.00	0.00	0.00	0.00	0.00	439261.00	0.00	0.00	0.00	0.00	0.00	KO:K03113	translation initiation factor 1
Ga0586324_0112303_464_722	0.00	0.00	0.00	0.00	0.00	0.00	1207800.00	0.00	0.00	0.00	0.00	0.00	KO:K03113	translation initiation factor 1
Ga0586324_0001460_8476_9027	965600.00	0.00	0.00	7125000.00	4810100.00	2925310.38	0.00	1750700.00	1895400.00	1201200.00	0.00	0.00	KO:K03120	transcription initiation factor TFIID TATA-box-binding protein
Ga0586324_0110194_1683_2348	0.00	0.00	0.00	0.00	8435700.00	2745060.47	0.00	5215500.00	5961600.00	0.00	0.00	0.00	KO:K03120	transcription initiation factor TFIID TATA-box-binding protein
Ga0586324_4175700_121_663	0.00	0.00	0.00	0.00	0.00	0.00	4993200.00	0.00	0.00	0.00	0.00	0.00	KO:K03120	transcription initiation factor TFIID TATA-box-binding protein
Ga0586324_0056120_195_1157	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1513600.00	0.00	0.00	KO:K03124	transcription initiation factor TFIIB
Ga0586324_0000004_138971_141025	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4620000.00	0.00	0.00	0.00	KO:K03147	phosphomethylpyrimidine synthase
Ga0586324_0000001_98751_101249	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2685000.00	0.00	KO:K03168	DNA topoisomerase-1
Ga0586324_0000524_4708_6354	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	690662.28	0.00	0.00	0.00	KO:K03217	Wz/Opa1 family membrane protein insertase
Ga0586324_0000672_18076_19347	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9240000.00	0.00	0.00	KO:K03231	elongation factor 1-alpha
Ga0586324_0060050_563_1837	0.00	938400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03231	elongation factor 1-alpha
Ga0586324_1375135_3_908	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	436631.58	0.00	0.00	0.00	KO:K03231	elongation factor 1-alpha
Ga0586324_1504889_2_1018	4990000.00	1706800.00	3096145.31	2793000.00	3687400.00	3107636.60	1574276.16	1640900.00	0.00	0.00	1185800.00	1531200.00	KO:K03231	elongation factor 1-alpha
Ga0586324_1919221_2_853	0.00	9248000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03231	elongation factor 1-alpha
Ga0586324_2439614_1_648	4140000.00	4624000.00	0.00	2897500.00	0.00	0.00	0.00	2250000.00	0.00	0.00	4851000.00	4857600.00	KO:K03231	elongation factor 1-alpha
Ga0586324_2958575_1_765	3770000.00	1944800.00	0.00	0.00	0.00	0.00	0.00	2415600.00	2519100.00	0.00	0.00	0.00	KO:K03231	elongation factor 1-alpha
Ga0586324_3719607_1_681	34400000.00	26200400.00	949234.89	1444000.00	1843700.00	1943549.23	1159742.52	1494500.00	1101600.00	713673.73	915200.00	0.00	KO:K03231	elongation factor 1-alpha
Ga0586324_5129529_3_611	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10530000.00	0.00	0.00	0.00	KO:K03231	elongation factor 1-alpha
Ga0586324_0007595_96_2291	7270000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03234	elongation factor 2
Ga0586324_0007291_2967_3638	0.00	0.00	0.00	0.00	0.00	1565600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03264	translation initiation factor 6
Ga0586324_0000013_2227_2766	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	907500.00	KO:K03273	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase
Ga0586324_0000065_53244_54236	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1455300.00	0.00	KO:K03274	ADP-L-glycero-D-manno-heptose 6-epimerase
Ga0586324_0181661_3_740	6580000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1698400.00	2265000.00	KO:K03285	GBP family porin
Ga0586324_1695197_70_969	0.00	5793600.00	0.00	0.00	0.00	3613033.48	2553600.00	3891800.00	0.00	4704700.00	0.00	4462500.00	KO:K03285	GBP family porin
Ga0586324_3185886_162_743	0.00	0.00	0.00	2365500.00	0.00	0.00	1436400.00	0.00	0.00	0.00	9675000.00	0.00	KO:K03285	GBP family porin
Ga0586324_3757314_1_693	0.00	0.00	0.00	0.00	4717400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03285	GBP family porin
Ga0586324_3766956_1_693	0.00	0.00	0.00	0.00	0.00	0.00	5959700.00	5329800.00	0.00	0.00	0.00	0.00	KO:K03285	GBP family porin
Ga0586324_4819245_2_595	25300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03285	GBP family porin
Ga0586324_5775323_53_580	4030000.00	2781200.00	0.00	5605000.00	8116400.00	0.00	0.00	9522100.00	1117800.00	9933000.00	21049600.00	261318.75	KO:K03285	GBP family porin
Ga0586324_7769628_3_329	0.00	0.00	0.00	0.00	0.00	2926255.24	6178800.00	0.00	1611900.00	0.00	0.00	0.00	KO:K03285	GBP family porin
Ga0586324_0000013_80642_81916	0.00	0.00	0.00	0.00	0.00	567686.18	27968294.98	27558800.00	25725000.00	65288300.00	75153000.00	70575000.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0001111_10242_11330	17450000.00	13246400.00	16552200.00	25935000.00	25193800.00	8495800.00	18992400.00	5965800.00	13851000.00	26634300.00	15884000.00	9022500.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0003059_9306_10331	50350000.00	2441200.00	0.00	731623.50	15244000.00	0.00	0.00	1958100.00	882900.00	0.00	2411200.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0005017_13082_13606	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6364000.00	6844400.00	9525000.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0005137_11010_12122	0.00	0.00	3828720.91	3458000.00	4387800.00	4565500.00	1385790.84	2818200.00	5516100.00	4458300.00	0.00	8032500.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0013780_8050_8826	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	171092.25	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0016029_2848_3417	0.00	1128800.00	0.00	0.00	0.00	6034400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0053180_5306_5677	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9394000.00	7594400.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0037943_4331_5104	0.00	4107200.00	8670200.00	0.00	5242700.00	4208200.00	0.00	2799900.00	2980800.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0049924_4111_4704	0.00	7004000.00	0.00	0.00	0.00	0.00	15982800.00	12261000.00	14175000.00	12243000.00	14432000.00	15675000.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0058018_482_1684	0.00	0.00	0.00	0.00	0.00	3946481.72	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0064503_3_767	0.00	0.00	0.00	1616114.02	0.00	1472900.00	0.00	2822200.00	6173200.00	248930.82	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0068986_1406_2113	0.00	0.00	0.00	0.00	0.00	0.00	3670800.00	11956000.00	13608000.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0070884_174_749	8200000.00	4426800.00	3818052.06	0.00	4841000.00	15205100.00	8367600.00	0.00	2583900.00	8600900.00	5033600.00	8977500.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0076904_321_1415	104734527.00	11900000.00	15325265.36	5709500.00	22557000.00	13180400.00	8983200.00	19611500.00	67675500.00	27704600.00	21648000.00	48900000.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0077996_1214_2287	4310000.00	2087600.00	0.00	0.00	3728600.00	2564473.11	1871188.04	1165100.00	1903500.00	0.00	2164800.00	1057500.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0085121_3187_3702	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2537600.00	3102300.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0100598_1564_2730	5430000.00	4719200.00	2605918.69	2109000.00	0.00	2712701.00	3146400.00	4361500.00	3369600.00	4288900.00	3942400.00	1147500.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0105595_3_695	0.00	5168000.00	14412800.00	6507500.00	5582600.00	0.00	4058400.00	0.00	5483700.00	3026100.00	3986400.00	3855000.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0113325_1749_2777	0.00	6120000.00	0.00	0.00	0.00	0.00	267747.24	13359000.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0113751_399_1553	61900000.00	75072000.00	42788000.00	7210500.00	85314900.00	33784700.00	0.00	19379700.00	33645406.59	59444000.00	72714400.00	17257500.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0128495_129_953	0.00	0.00	0.00	0.00	0.00	2121800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0144946_1269_2414	0.00	0.00	0.00	0.00	0.00	0.00	1295343.24	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0147021_1094_2242	0.00	0.00	0.00	0.00	0.00	2726357.80	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0204555_25_846	0.00	1559465.08	0.00	1330000.00	1915800.00	1157493.20	2872800.00	0.00	1579500.00	823900.00	0.00	368249.25	KO:K03286	OOP family OmpA-OmpF porin
Ga0586324_0338286_1_531	0.00	0.00	9402100.00	0.00	0.00	0.00	6178

Ga0586324_0823863_193_1320	8380000.00	1829200.00	0.00	0.00	0.00	6550500.00	0.00	0.00	0.00	0.00	3349500.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324_0908926_1_444	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3546400.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus sp. KH32C;Azoarcus sp. KH32C
Ga0586324_0935192_450_1250	0.00	2611200.00	0.00	0.00	0.00	2812534.59	3351600.00	9821000.00	1514700.00	0.00	12408000.00	11550000.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_1129502_414_1136	0.00	3325200.00	7825700.00	2508000.00	3265100.00	0.00	2118304.68	8723000.00	1790100.00	3210900.00	2675200.00	2130000.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus sp. KH32C;Azoarcus sp. KH32C
Ga0586324_1131382_2_733	0.00	0.00	0.00	0.00	0.00	0.00	142803.92	0.00	1717100.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Lysobacter;Lysobacter sp. URHA0019;Lysobacter sp. URHA0019
Ga0586324_1425363_1_1044	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3402000.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_1744562_2_958	32900000.00	13056000.00	0.00	16150000.00	20497000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-DMM
Ga0586324_1773197_2_436	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2947500.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Altererythrobacter;Altererythrobacter sp. Root672;Altererythrobacter sp. Root672
Ga0586324_1801935_1_525	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	195021.20	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_1834686_649_936	5170000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas denitrificans;Methylomonas denitrificans FIG1
Ga0586324_2162696_36_875	0.00	0.00	39860400.00	3030500.00	5273600.00	35213900.00	99636000.00	640500.00	0.00	1378300.00	14071200.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_2254824_2_850	12700000.00	4467600.00	0.00	0.00	0.00	60939500.00	0.00	0.00	11210400.00	0.00	0.00	7335000.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_2265959_207_857	0.00	0.00	0.00	0.00	0.00	0.00	0.00	774700.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Solitalea;Solitalea canadensis;Solitalea canadensis USAM 9D, DSM 3403
Ga0586324_2307112_1_849	135500000.00	12308000.00	137372000.00	59185000.00	129471000.00	93930200.00	1282983.36	35190900.00	78302700.00	14553000.00	46816000.00	44550000.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324_2445312_1_600	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	874800.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_2538409_265_546	0.00	5664400.00	0.00	0.00	2348400.00	0.00	0.00	628300.00	0.00	5544000.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324_3044170_2_757	139900000.00	56358400.00	0.00	8163500.00	111739000.00	117008000.00	69157600.00	71740067.76	68906000.00	49491000.00	62662600.00	82280000.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324_3679994_3_563	0.00	0.00	0.00	0.00	0.00	0.00	6452400.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Tsuneonella;Tsuneonella troitsensis;Altererythrobacter troitsensis JCM 17037
Ga0586324_3686422_72_698	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6622000.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_4014842_178_675	0.00	6800000.00	0.00	0.00	0.00	2759666.30	4833600.00	4373700.00	0.00	5305300.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324_4303462_1_657	0.00	12008800.00	0.00	3439000.00	0.00	0.00	0.00	3373300.00	0.00	5074300.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_4425237_1_618	0.00	0.00	0.00	0.00	0.00	0.00	1277826.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324_4812962_1_354	0.00	0.00	0.00	211850000.00	0.00	0.00	0.00	0.00	187920000.00	241010000.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Marichromatium;Marichromatium gracile;Marichromatium gracile YL28
Ga0586324_5053675_3_506	0.00	336406.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas sp. MK1;Methylomonas sp. MK1
Ga0586324_5267729_3_605	0.00	3298000.00	0.00	0.00	0.00	1996477.27	0.00	732000.00	1393200.00	0.00	0.00	1627500.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_6107673_1_567	0.00	6555200.00	0.00	0.00	4892500.00	6015200.00	12716307.00	17841531.24	11663200.00	5605200.00	11234300.00	15435200.00	13084272.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_6130599_3_566	15300000.00	0.00	0.00	0.00	0.00	0.00	5472000.00	0.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Humitalea;Humitalea rosea;Humitalea rosea DSM 24525
Ga0586324_6314408_2_559	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18483000.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Lysobacter;Lysobacter sp. URHA0019;Lysobacter sp. URHA0019
Ga0586324_6361437_1_558	0.00	0.00	0.00	0.00	0.00	2267322.58	2243681.88	0.00	2324700.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_6818286_1_333	0.00	0.00	0.00	0.00	11021000.00	0.00	0.00	0.00	0.00	0.00	0.00	690000.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Burkholderiales;Aquabacterium;Aquabacterium sp. NJ1;Aquabacterium sp. NJ1
Ga0586324_6835114_3_542	32100000.00	0.00	97962000.00	0.00	0.00	46449000.00	21112800.00	44225000.00	36288000.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AMS-C10
Ga0586324_6852716_1_231	0.00	2924000.00	0.00	0.00	0.00	0.00	0.00	1488400.00	1417500.00	0.00	0.00	3135000.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas denitrificans;Methylomonas denitrificans FIG1
Ga0586324_6979936_3_536	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1680000.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfosporosinus;Desulfosporosinus orientis;Desulfosporosinus orientis DSM 10085
Ga0586324_7375952_164_526	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5868200.00	0.00	0.00	0.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas denitrificans;Methylomonas denitrificans FIG1
Ga0586324_8072570_1_504	0.00	0.00	0.00	1425000.00	0.00	0.00	0.00	0.00	3175200.00	2271500.00	1346400.00	0.00	KO:K03286	OOP family OmpA-OmpF porin	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomeanum;Methylomeanum ishizawai;Methylomeanum ishizawai 175
Ga0586324_0723264_340_1398	0.00	0.00	0.00	0.00	0.00	0.00	5472000.00	0.00	0.00	0.00	0.00	0.00	KO:K03307	SSS family sodium/ Na+ symporter	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila 528bF
Ga0586324_0000033_70987_72519	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12123731.28	7381000.00	6196500.00	4912600.00	2992000.00	KO:K03320	Amt family ammonium transporter	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaurus;Thiobacillus thiopaurus DSM 505
Ga0586324_0121849_1324_2763	0.00	0.00	0.00	0.00	0.00	0.00	10168800.00	0.00	0.00	0.00	0.00	0.00	KO:K03385	nitrite reductase (cytochrome c-552)	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0349273_150_1920	0.00	0.00	0.00	2840000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03385	nitrite reductase (cytochrome c-552)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio magneticus;Desulfovibrio cf. magneticus FRC170
Ga0586324_3053575_178_756	0.00	0.00	0.00	0.00	11910000.00	0.00	2403400.00	0.00	0.00	0.00	0.00	0.00	KO:K03385	nitrite reductase (cytochrome c-552)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio aiaas;Desulfovibrio aiaas DSM 1382. ATCC 19364
Ga0586324_5455826_3_596	0.00	0.00	10753300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03385	nitrite reductase (cytochrome c-552)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila 528bF
Ga0586324_6436786_1_555	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2189900.00	2097900.00	0.00	0.00	0.00	KO:K03385	nitrite reductase (cytochrome c-552)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio magneticus;Desulfovibrio magneticus RS-1
Ga0586324_7922908_2_508	0.00	0.00	0.00	0.00	0.00	3205913.95	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03385	nitrite reductase (cytochrome c-552)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio gigas;Desulfovibrio gigas DSM 1382, ATCC 19364
Ga0586324_0003220_5845_6438	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1522800.00	0.00	0.00	0.00	KO:K03386	peroxiredoxin (alkyl hydroperoxide reductase subunit C)	Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;Thermosulfuriphilus;Thermosulfuriphilus ammonigenes;Thermosulfuriphilus ammonigenes DSM 102941
Ga0586324_0925640_296_901	0.00	0.00	6474500.00	0.00	0.00	0.00	0.00	1116300.00	1992600.00	0.00	0.00	3270000.00	KO:K03386	peroxiredoxin (alkyl hydroperoxide reductase subunit C)	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545889
Ga0586324_1355851_1_232_828	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8100000.00	KO:K03386	peroxiredoxin (alkyl hydroperoxide reductase subunit C)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. OR-1;Geobacter sp. OR-1
Ga0586324_3641298_302_703	20300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03386	peroxiredoxin (alkyl hydroperoxide reductase subunit C)	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylotuvimicrobium;Methylotuvimicrobium alcaliphilum;Methylomicrobium alcaliphilum 20Z
Ga0586324_7965539_3_509	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3233000.00	0.00	0.00	0.00	0.00	KO:K03387	alkyl hydroperoxide reductase subunit F	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Sporomusaceae;Propionispora;Propionispora sp. 2/2-37;Propionispora sp. Iso2/2
Ga0586324_0000236_34308_37688	0.00	0.00	0.00	0.00	0.00	0.00	0.00	957700.00	0.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0006360_416_3463	0.00	0.00	0.00	2033000.00	0.00	2515634.17	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_0014051_1_755	0.00	0.00	0.00	0.00	0.00	0.00	0.00	250486.13	0.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0101791_10_3039	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1935900.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_0173665_899_2641	0.00	0.00	9683600.00	0.00	0.00	0.00	0.00	0.00	257975.28	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324_0348560_1_1350	0.00	5263200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324_0584882_2_1633	0.00	0.00	0.00	0.00	0.00	0.00	0.00	187534.74	0.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila 528bF
Ga0586324_0650577_1_1461	0.00	0.00	0.00	0.00	0.00	5443302.28	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324_1050805_2_1189	0.00	0.00	0.00	1672000.00	0.00	0.00	0.00	1628700.00	0.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila 528bF
Ga0586324_1804249_3_944	0.00	0.00	0.00	0.00	0.00	156814.49	0.00	0.00	0.00	0.00	0.00	1237500.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_2754519_3_788	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	585460.26	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfocucumis;Desulfocucumis palustris;Desulfocucumis palustris NAW-5
Ga0586324_3416112_1_723	0.00	0.00	0.00	0.00	0.00	3591770.16	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03388	heterodisulfide reductase subunit A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_0021934_2769_3680	0.00	0.00	0.00	0.00	0.00	0.00	3374400.00	2482700.00	2843100.00	1678600.00	2411200.00	2205000.00	KO:K03389	heterodisulfide reductase subunit B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324_0096786_2180_3484	0.00	0.00	0.00	0.00	2987000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03405	magnesium chelatase subunit I	Bacteria;Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;Thermobaculum;Thermobaculum terrenum;Thermobaculum terrenum YNP1, ATCC BAA-798
Ga0586324_0001778_12274_13515	0.00	897600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Moorella;Moorella thermoacetica;Moorella thermoacetica DSM 21394
Ga0586324_0008150_5773_7467	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	808500.00	0.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Gemmatimonadetes;Longimicrobia;Longimicrobiales;Longimicrobiaceae;Longimicrobium;Longimicrobium terrae;Longimicrobium terrae CECT 8660
Ga0586324_0033426_2102_4516	0.00	0.00	0.00	0.00	0.00	0.00	14797200.00	2165550.00	0.00	0.00	6529600.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_0086484_1927_3555	0.00	0.00	0.00	0.00	0.00	0.00	0.00	652700.00	0.00	0.00	0.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Rhodocyclus;Rhodocyclus tenuis;Rhodocyclus tenuis DSM 109
Ga0586324_0360046_1_895	0.00	918000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. PSR-1;Anaeromyxobacter sp. PSR-1
Ga0586324_0872221_1_1287	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2848700.00	0.00	0.00	0.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_1218318_896_1115	0.00	0.00	5227702.72	0.00	0.00	6709300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Candidatus Magnetomorum;Candidatus Magnetomorum sp. HK-1;Candidatus Magnetomorum sp. HK-1
Ga0586324_1573718_3_740	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1575000.00	0.00	KO:K03406	methyl-acceptine chemotaxis protein	Bacteria;Lenavibacteria;Lenavibacteriales;Lenavibacteriaceae;Lenavibacterium;Lenavibacterium album;Lenavibacterium album Mat9-16. JCM 16511
Ga0586324_2842284_1_782	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	213305.84	2850000.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_3076864_1_753	0.00	0.00	0.00	0.00	0.00	1626517.80	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Caldisericaceae;unclassified Caldisericaceae;unclassified Caldisericaceae;unclassified Caldisericaceae;unclassified Caldisericaceae;Caldisericaceae bacterium JGI 0000059-M03;Caldisericaceae bacterium JGI 0000059-M03 (contamination screened)
Ga0586324_4077155_2_670	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5605600.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_5935507_2_574	0.00	0.00	0.00	0.00	0.00	949797.44	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03406	methyl-accepting chemotaxis protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_8244583_2_502	0.00	0.00	24096400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03406	methyl-acceptine chemotaxis protein	Bacteria;Firmicutes;Bacilli;Bacillales;unclassified Bacillales;Exiguobacterium;Exiguobacterium sp. S17;Exiguobacterium sp. S17
Ga0586324_0002033_923_1357	0.00	0.00	0.00	0.00	1514100.00	0.00	0.00	1464000.00	0.00	2556400.00	2270400.00	2340000.00	KO:K03413	two-component system chemotaxis response regulator CheY	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira lenta;Nitrospira lenta N. lenta BS10
Ga0586324_0011884_4165_4914	13900000.00	0.00	0.00	3752500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03432	proteasome alpha subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri 3
Ga0586324_0213878_2_541	0.00	0.00	0.00	1805000.00	0.00	0.00	0.00	0.00	0.00	9702000.00	0.00	0.00	KO:K03432	proteasome alp

Ga0586324_0302658_3_293	1390000.00	471038.04	0.00	0.00	0.00	0.00	0.00	319804.70	191452.41	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0386824_303_590	0.00	0.00	0.00	0.00	12154000.00	0.00	0.00	0.00	11421000.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0410610_1420_1692	0.00	0.00	0.00	0.00	13184000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324_0486259_897_1199	0.00	0.00	0.00	0.00	0.00	11195400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Actinobacteria;Rubrobacteria;Rubrobacterales;Rubrobacteraceae;Rubrobacter;Rubrobacter radiotolerans;Rubrobacter radiotolerans DSM 5868
Ga0586324_0503738_267_566	0.00	0.00	0.00	0.00	0.00	24653700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0516562_311_610	0.00	0.00	0.00	7486000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. URHD0069;Bradyrhizobium sp. URHD0069
Ga0586324_0588826_713_994	0.00	0.00	0.00	0.00	423623.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0610780_670_978	4690000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium sp. 99;Hyphomicrobium sp. 99
Ga0586324_0827137_658_945	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2534400.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Candidatus Nitrospira inopinata;Candidatus Nitrospira inopinata ENR4
Ga0586324_0876849_311_618	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4312700.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_0999817_211_519	0.00	0.00	0.00	1406000.00	0.00	973761.60	0.00	0.00	1117800.00	0.00	0.00	6570000.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324_1130445_737_1024	0.00	0.00	0.00	0.00	0.00	390609.99	0.00	0.00	155113.24	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira lenta;Nitrospira lenta N. lenta B510
Ga0586324_1717853_283_582	0.00	0.00	0.00	8863500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Brycella;Brycella elongata;Brycella elongata DSM 22489
Ga0586324_1776165_367_663	2580000.00	0.00	0.00	0.00	0.00	595424.57	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_1909042_373_702	0.00	0.00	0.00	0.00	0.00	7146000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira marina;Nitrospira marina Nb-295
Ga0586324_2120252_360_656	0.00	0.00	0.00	0.00	1026412.51	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_2489142_644_823	0.00	18156000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2509125_117_416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	780714.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_2803374_507_809	1910000.00	0.00	0.00	0.00	0.00	1022711.70	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2842562_120_428	0.00	0.00	0.00	0.00	7014300.00	5161000.00	0.00	14653800.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_3019090_381_695	0.00	0.00	11654100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithricaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_3595290_295_594	0.00	0.00	0.00	1928500.00	2873700.00	0.00	0.00	1891000.00	1255500.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_4979010_2_268	1570000.00	0.00	0.00	8170000.00	2678000.00	1392668.06	0.00	1274900.00	1701000.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_7041576_129_428	1080000.00	0.00	0.00	0.00	516766.45	1310223.07	10693200.00	537544.81	700854.12	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_7201329_237_530	0.00	2652000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03530	DNA-binding protein HU-beta	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0002388_13112_14203	0.00	4311200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03531	cell division protein FtsZ	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei 6A8
Ga0586324_0022020_3_1781	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	959200.00	0.00	0.00	KO:K03531	cell division protein FtsZ	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324_0236545_219_1436	0.00	0.00	0.00	0.00	1442000.00	0.00	0.00	0.00	0.00	1900800.00	0.00	0.00	KO:K03531	cell division protein FtsZ	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfallas;Desulfallas thermosapovorans;Desulfallas thermosapovorans DSM 6562
Ga0586324_0527912_674_1600	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1012500.00	0.00	0.00	0.00	KO:K03531	cell division protein FtsZ	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324_1072379_402_1178	0.00	2883200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03531	cell division protein FtsZ	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermosulfurimonas;Thermosulfurimonas dismutans;Thermosulfurimonas dismutans DSM 9736
Ga0586324_1958013_115_912	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2032800.00	0.00	0.00	KO:K03531	cell division protein FtsZ	Bacteria;Chlorflexi;Ktedonobacteria;Ktedonobacterales;Dictyobacteraceae;Dictyobacter;Dictyobacter aurantiacus;Dictyobacter aurantiacus 527
Ga0586324_0000137_35427_36695	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1399200.00	0.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0036515_80_1315	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1636200.00	0.00	0.00	0.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira defluvii;Nitrospira defluvii
Ga0586324_0048196_560_1828	0.00	10132000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylobacillus;Methylobacillus sp. MM3;Methylobacillus sp. MM2
Ga0586324_0980937_3_1013	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	537218.00	0.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Actinobacteria;Actinomycetia;Streptomycetales;Streptomycetaceae;Streptomyces;Streptomyces thermoautotrophicus;Streptomyces thermoautotrophicus H1
Ga0586324_1034443_45_1196	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5082000.00	0.00	0.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Thermosulfurispirillum;Thermosulfurispirillum;Thermosulfurispirillum;Thermosulfurispirillum ammonigenes;Thermosulfurispirillum ammonigenes;Thermosulfurispirillum ammonigenes DSM 102941
Ga0586324_3062471_3_602	0.00	0.00	0.00	0.00	0.00	3442800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_3387301_3_725	0.00	0.00	0.00	0.00	500220.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Niastella;Niastella sp. CF465;Niastella sp. CF465
Ga0586324_6556995_2_550	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3037500.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 9736;Geobacter sp. DSM 9736
Ga0586324_7532543_2_520	0.00	0.00	16439600.00	0.00	0.00	1948702.29	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfofoaia;Desulfoofia aestuarii;Desulfoofia aestuarii DSM 18488
Ga0586324_0010606_8431_9729	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1104100.00	1077300.00	0.00	0.00	2167500.00	KO:K03545	trigger factor	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaeus;Thiobacillus thiopaeus DSM 505
Ga0586324_0413225_223_1524	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2217600.00	0.00	2505000.00	KO:K03545	trigger factor	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella massiliensis;Reyranella massiliensis 521, DSM 23428
Ga0586324_5819185_1_579	0.00	0.00	0.00	0.00	0.00	0.00	0.00	511677.00	0.00	0.00	0.00	0.00	KO:K03545	trigger factor	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella massiliensis;Reyranella massiliensis 521, DSM 23428
Ga0586324_0000114_59366_60475	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2008800.00	5859700.00	4769600.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0002949_2468_3535	0.00	0.00	0.00	0.00	0.00	0.00	261427.70	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0004734_1788_2852	0.00	0.00	0.00	4959000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album MarS-16, JCM 16511
Ga0586324_0182688_335_1669	0.00	0.00	0.00	0.00	0.00	0.00	1817910.12	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithricaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_0184112_449_1534	0.00	0.00	3108200.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0215791_321_1358	0.00	474433.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Chlorflexi;Dehalococcoidia;Dehalococcoides mccartyi;Dehalococcoides mccartyi CBDB1
Ga0586324_0227339_1231_2331	0.00	0.00	0.00	0.00	5623800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Syntrophotaleaceae;Syntrophotalea;Syntrophotalea acetylenica;Pelobacter acetylenicus DSM 3247
Ga0586324_0234758_688_1722	1780000.00	0.00	0.00	1776500.00	1452300.00	0.00	2576400.00	933300.00	1296000.00	0.00	0.00	2415000.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_0245548_85_1110	11100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0250913_1_756	0.00	2216800.00	0.00	0.00	0.00	0.00	397577.28	0.00	2567700.00	3388000.00	3458400.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Azonexus;Azonexus hydrophilus;Azonexus hydrophilus Z502
Ga0586324_0257114_1076_2104	3860000.00	1882914.09	1909500.00	0.00	6431400.00	1600728.72	1958100.00	1182600.00	3026100.00	0.00	4957500.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Azonexus;Azonexus hydrophilus;Azonexus hydrophilus Z502
Ga0586324_0287493_1431_2096	39382.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0337892_3_1100	0.00	0.00	0.00	0.00	0.00	7900300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas sp. DDH964;Desulfuromonas sp. DDH964
Ga0586324_0477497_531_1610	0.00	0.00	4831283.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Alkaliphilus;Alkaliphilus oronensis;Alkaliphilus sp. LacV
Ga0586324_0714473_22_1119	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10032000.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Actinobacteria;Actinomycetales;Intrasporangiaceae;Ornithinibacter;Ornithinibacter aureus;Ornithinibacter aureus DSM 23364
Ga0586324_0743996_619_1380	0.00	0.00	0.00	1961773.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithricaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_0815187_752_1327	0.00	2264400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_1133749_2_1045	0.00	0.00	0.00	0.00	0.00	0.00	11764800.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Syntrophotaleaceae;Syntrophotalea;Syntrophotalea acetylenica;Pelobacter acetylenicus DSM 3247
Ga0586324_1170839_272_1135	0.00	0.00	21112500.00	0.00	0.00	57168000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Firmicutes;Clostridia;Eubacteriales;Thermohalobacteraceae;Thermohalobacter;Thermohalobacter berrensis;Thermohalobacter berrensis CTT3
Ga0586324_1244973_475_1104	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2464000.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Clostridium;Clostridium sp. CT4;Clostridium sp. CT4
Ga0586324_1815020_3_512	0.00	0.00	0.00	0.00	0.00	3381137.84	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Azonexus;Azonexus fungilophilus;Azonexus fungilophilus DSM 23841
Ga0586324_1889744_3_824	0.00	1040400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10425000.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_2551207_2_319	0.00	0.00	0.00	0.00	0.00	7843200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_3093301_3_518	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10044000.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta americana;Alkalispirochaeta americana ASpG1
Ga0586324_3594184_1_723	0.00	487963.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_4274426_2_658	0.00	0.00	0.00	0.00	0.00	4049400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas acetexigens;Desulfuromonas acetexigens DSM 1397
Ga0586324_4526023_3_401	0.00	0.00	0.00	0.00	0.00	0.00	0.00	596454.34	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. YR605;Methylibium sp. YR605
Ga0586324_5266064_43_603	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3262500.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Syntrophotaleaceae;Syntrophotalea;Syntrophotalea acetylenica;Pelobacter acetylenicus DSM 3247
Ga0586324_6795281_2_544	0.00	0.00	0.00	1491500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_7902177_142_510	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1490400.00	0.00	0.00	0.00	KO:K03553	recombination protein RecA	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Nannocystaceae;Plesiocystis;Plesiocystis pacifica;Plesiocystis pacifica SIR-1
Ga0586324_0001547_1350_2258	0.00	0.00	13455700.00	0.00	7539600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03554	recombination associated protein RdgC	Bacteria;Firmicutes;Clostridia;Eubacteriales;Methanosarcinaceae;Methanococcoides;Methanococcoides burtonii;Methanococcoides burtonii DSM 6242;Methylobacter tundripaludum SV96
Ga0586324_0066197_3_500	0.00	0.00	10528100.00	12635000.00	15656000.00	8416400.00	0.00	14213000.00	16767000.00	0.00	0.00	26100000.00	KO:K03561	biopolymer transport protein ExbB	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96. DSM 24297
Ga0586324_0535034_45_707	0.00	0.00	0.00	0.00	0.00	411197.63	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03561	biopolymer transport protein ExbB	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Pelmatobacter;Pelmatobacter sp. URHD0036;Pelmatobacter sp. URHD0036
Ga0586324_0558049_2_1183	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2256100.00	0.00	0.00	0.00	KO:K03561	biopolymer transport protein ExbB	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Hydrocarboniphaga;Hydrocarboniphaga daqingensis;Hydrocarboniphaga daqingensis CGMCC 1.7049
Ga0586324_6331835_155_559	0.00	0.00	0.00	19190000.00	22660000.00	0.00	0.00	11773000.00	0.00	15169000.00	10472000.00	6570000.00	KO:K03561	biopolymer transport protein ExbB	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_7790552_274_513	0.00	0.00	0.00	11590000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03561	biopolymer transport protein ExbB	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324_0244094_1279_1791	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	529064.28	0.00	0.00	KO:K03564	aeroxireductase Q/BCP	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum miyakonense;Methylovulum miyakonense HT12
Ga0586324_1313787_219_713	0.00	2590800.00	0.00	0.00	0.00	0.00	3281800.00	0.00

Ga0586324_0498213_3_1439	1930000.00	0.00	0.00	1415500.00	1720100.00	0.00	0.00	1769000.00	2203200.00	1755600.00	2173600.00	1267500.00	KO:K03628	transcription termination factor Rho	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;TSM 7334
Ga0586324_0529161_31_1599	0.00	0.00	0.00	2156500.00	0.00	0.00	0.00	0.00	8210279.88	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sedimnisipirochaeta;Sedimnisipirochaeta bajacaliforniensis;Sedimnisipirochaeta bajacaliforniensis DSM 16054
Ga0586324_0591387_1_1281	0.00	34612000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7059718.05	13024000.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Woeseiaceae;Woeseia;Woeseia oceani;Woeseia oceani XK5
Ga0586324_0623691_3_1151	0.00	0.00	296764.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324_0663161_937_1449	0.00	0.00	0.00	588617.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0668712_2_751	0.00	0.00	0.00	0.00	0.00	0.00	104632.56	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium EN84
Ga0586324_0699079_2_841	0.00	2060400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0800807_208_1335	0.00	1686400.00	0.00	0.00	0.00	0.00	262511.67	1701000.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea anilini;Desulfatitalea anilini DSM 4660
Ga0586324_0812221_527_1327	0.00	0.00	2886123.79	5006500.00	0.00	0.00	0.00	1762900.00	939600.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_0874693_1_801	0.00	4569600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Planctomycetes;Planctomycetia;Gemmatales;Gemmataceae;Zavarzinella;Zavarzinella formosa;Zavarzinella formosa DSM 19928
Ga0586324_0953964_474_1238	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1381600.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Bryobacteraceae;Bryobacter;Bryobacter agaricicola;Bryobacter agaricicola DSM 18758
Ga0586324_1021362_1_1002	0.00	0.00	0.00	0.00	7931000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-N07;Aminicenantes bacterium SCGC AAA252-N07 (contamination screened)
Ga0586324_1071377_171_1178	0.00	0.00	0.00	0.00	0.00	3100800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_1223574_203_1114	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2006400.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfoferrobacter;Desulfoferrobacter aminophilus;Desulfoferrobacter aminophilus DSM 2059
Ga0586324_1333834_2_1042	6750000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Gemmatimonadetes;Longimicrobia;Longimicrobiales;Longimicrobiaceae;Longimicrobium;Longimicrobium terrae;Longimicrobium terrae CECT 8660
Ga0586324_1342636_3_1070	13200000.00	0.00	0.00	9690000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_1632540_27_983	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4509600.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_1698989_2_967	0.00	0.00	7206400.00	0.00	5915300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_1731014_3_959	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2357100.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_1853003_2_934	2700000.00	0.00	0.00	1643500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Bryobacteraceae;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_1942700_1_915	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17700000.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2000243_3_902	21300000.00	18428000.00	0.00	9053500.00	0.00	0.00	401387.32	0.00	0.00	0.00	4635000.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfurbacter;Dissulfurbacter thermophilus;Dissulfurbacter thermophilus S69
Ga0586324_2374843_1_759	0.00	1496000.00	1323033.11	0.00	0.00	0.00	0.00	0.00	854700.00	1047200.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfonema;Desulfonema limicola;Desulfonema limicola Jadebusen, DSM 2076
Ga0586324_2509953_2_820	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7238000.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_2637317_140_805	0.00	0.00	0.00	0.00	0.00	0.00	2859300.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas thiophila;Desulfuromonas thiophila DSM 8987
Ga0586324_2698847_1_795	0.00	0.00	11147400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Chromobacteriaceae;Chromobacterium;Chromobacterium haemolyticum;Chromobacterium haemolyticum DSM 19808
Ga0586324_2978979_3_650	0.00	0.00	0.00	4665900.00	0.00	0.00	12627000.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_3768232_3_692	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	283586.38	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_3893138_3_683	1920000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter soli;GS021
Ga0586324_4003261_1_675	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11440000.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_4553477_3_641	0.00	0.00	6756000.00	4303500.00	1884900.00	2923654.89	2197491.36	0.00	1522800.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_4638229_21_635	0.00	3604000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sedimnisipirochaeta;Sedimnisipirochaeta bajacaliforniensis;Sedimnisipirochaeta bajacaliforniensis DSM 16054
Ga0586324_4719614_1_630	1340000.00	0.00	37495800.00	0.00	50022000.00	0.00	21777000.00	2592000.00	0.00	32296000.00	22575000.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus;Chloroflexus aurantiacus;Chloroflexus aurantiacus J-10-fl
Ga0586324_5073820_3_614	8150000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfoccoccus;Desulfoccocus multivorans;Desulfoccocus multivorans DSM 2059
Ga0586324_5296757_1_603	0.00	0.00	0.00	0.00	0.00	15549600.00	0.00	0.00	0.00	0.00	15300000.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_5657434_1_585	0.00	0.00	0.00	0.00	0.00	0.00	2446100.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_6327739_3_560	0.00	0.00	0.00	0.00	0.00	0.00	3428200.00	4074300.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_6353864_96_560	0.00	0.00	0.00	0.00	0.00	13474800.00	9394000.00	352891.89	0.00	0.00	11100000.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter delicatus;Curvibacter delicatus NBRC 14919
Ga0586324_7231725_3_530	0.00	0.00	0.00	0.00	868723.63	956543.71	0.00	579495.06	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_7265169_35_529	0.00	0.00	0.00	0.00	0.00	0.00	7068000.00	0.00	0.00	0.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-N07;Aminicenantes bacterium SCGC AAA252-N07 (contamination screened)
Ga0586324_7450882_1_411	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3590400.00	0.00	0.00	KO:K03628	transcription termination factor Rho	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_0000007_13442_14023	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	680046.75	KO:K03640	outer membrane lipoprotein carrier protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhizobacteraceae;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0000007_37429_38478	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4320800.00	3052500.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Proteobacteria;Alphaproteobacteria;Magnetococcales;Magnetococcaceae;Magnetofaba;Magnetofaba australis;Magnetofaba australis IT-1
Ga0586324_0000014_33858_34454	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6029100.00	1293600.00	2715000.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhizobacteraceae;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0000018_45120_45743	0.00	0.00	0.00	0.00	0.00	1785344.44	4788500.00	0.00	3003000.00	3176800.00	3090000.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0003399_133_747	0.00	0.00	0.00	0.00	0.00	0.00	2153300.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio aminophilus;Desulfovibrio aminophilus DSM 12254
Ga0586324_0010725_7348_7983	0.00	0.00	6530800.00	21356000.00	16171000.00	7503300.00	11924400.00	9766100.00	3126151.26	7376600.00	5060000.00	4830000.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-K06;Aminicenantes bacterium SCGC AAA252-K06 (contamination screened)
Ga0586324_0042117_4318_4959	0.00	1271600.00	0.00	0.00	1575900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0084632_3262_3777	0.00	0.00	0.00	0.00	4367200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-K06;Aminicenantes bacterium SCGC AAA252-K06 (contamination screened)
Ga0586324_0111645_223_723	0.00	13464000.00	0.00	22230000.00	0.00	0.00	0.00	8235000.00	0.00	0.00	7500000.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_0128718_1307_1828	5690000.00	0.00	0.00	0.00	7704400.00	0.00	0.00	5538800.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0133927_1171_2800	0.00	0.00	0.00	9661400.00	1214489.61	0.00	3092700.00	3564000.00	0.00	0.00	4027500.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Bryobacteraceae;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0146844_362_910	0.00	0.00	0.00	871066.40	0.00	0.00	0.00	8235000.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324_0218162_1_432	0.00	2856000.00	0.00	0.00	0.00	4674000.00	1817800.00	0.00	2002000.00	1346400.00	2872500.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_0263885_1013_1597	0.00	6630000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Pelobacter;Pelobacter propionicus;Pelobacter propionicus DSM 2379
Ga0586324_0284806_1412_1960	0.00	0.00	0.00	0.00	0.00	0.00	2293659.56	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324_0491891_1006_1620	0.00	0.00	3617579.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0942529_29_799	0.00	1033600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Holophagae;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_2111835_1_579	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2527200.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_2682751_46_687	0.00	0.00	0.00	2821500.00	0.00	0.00	2417251.44	1994700.00	1150200.00	0.00	1170000.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_3991914_1_480	0.00	5453600.00	0.00	3857000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324_5340973_3_377	0.00	5344800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_6658165_50_547	696316.00	348697.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Acidobacteria;Bryobacteriales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_7557939_172_519	431630.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6136900.00	0.00	0.00	0.00	KO:K03640	peptidoglycan-associated lipoprotein	Bacteria;Acidobacteria;Acidobacteria;Bryobacteriales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0053475_7168_8187	1220000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03651	lcc protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa marina;Thiocapsa marina 5811, DSM 5653
Ga0586324_0031225_2796_3815	3440000.00	0.00	3617579.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03651	lcc protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa marina;Thiocapsa marina 5811, DSM 5653
Ga0586324_2087096_2_886	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3141600.00	0.00	0.00	KO:K03655	ATP-dependent DNA helicase RecG	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0000007_102210_102449	0.00	0.00	0.00	0.00	0.00	0.00	184200.00	0.00	0.00	2232200.00	1155000.00	KO:K03666	host factor-I protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhizobacteraceae;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0161510_1893_2159	0.00	4508400.00	2667640.38	0.00	0.00	0.00	4105300.00	5135400.00	6645100.00	0.00	14850000.00	KO:K03666	host factor-I protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Alicycliphilus;Alicycliphilus denitrificans;Alicycliphilus denitrificans BC
Ga0586324_0177936_2027_2266	0.00	0.00	0.00	0.00	727889.67	0.00	0.00	0.00	3248100.00	777700.00	0.00	0.00	KO:K03666	host factor-I protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_1428553_745_996	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	175567.50	0.00	0.00	0.00	KO:K03666	host factor-I protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Gammaproteobacteria bacterium;Codakia orbicularis gill symbiont;Codakia orbicularis gill symbiont
Ga0586324_5284408_58_603	13200000.00	8280419.16	4633219.76	21793000.00	10718323.17	14689000.00	2433900.00	16686000.00	33325116.44	10864802.96	5400000.00	KO:K03666	host factor-I protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax sp. 56;Acidovorax sp. 56	
Ga0586324_0578699_1029_1538	0.00	11764000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03667	ATP-dependent HslUV protease ATP-binding subunit HslU	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae SM 8423
Ga0586324_1237739_613_1107	0.00	0.00	0.00	0.00	4511400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03667	ATP-dependent HslUV protease ATP-binding subunit HslU	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_1659100_1_891	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	264075.00	KO:K03667	ATP-dependent HslUV protease ATP-binding subunit HslU	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324_2385056_3_482	35000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03667	ATP-dependent HslUV protease ATP-binding subunit HslU	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium allaiui;Acidobacterium allaiui PMMR2
Ga0586324_3273139_3_734	0.00	0.00	0.00	0.00	107836.88	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03667	ATP-dependent HslUV protease ATP-binding subunit HslU	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM

Ga0586324_0175763_865_2628	0.00	0.00	0.00	0.00	0.00	0.00	0.00	165158.72	0.00	0.00	0.00	0.00	KO:K03701	excinuclease ABC subunit A
Ga0586324_0633053_3_1478	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	574255.17	0.00	0.00	0.00	KO:K03701	excinuclease ABC subunit A
Ga0586324_0968060_1_1230	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	120946.77	0.00	0.00	0.00	KO:K03701	excinuclease ABC subunit A
Ga0586324_1279881_3_1091	0.00	0.00	1953024.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03701	excinuclease ABC subunit A
Ga0586324_4442304_3_647	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1117800.00	0.00	0.00	0.00	0.00	KO:K03701	excinuclease ABC subunit A
Ga0586324_6414830_2_556	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2623000.00	0.00	0.00	0.00	0.00	KO:K03701	excinuclease ABC subunit A
Ga0586324_0000117_24110_24313	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2357100.00	2587200.00	0.00	0.00	KO:K03704	CspA family cold shock protein
Ga0586324_0015773_4519_4722	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	637140.00	0.00	KO:K03704	CspA family cold shock protein
Ga0586324_0033969_2940_3143	0.00	0.00	0.00	0.00	2954500.00	0.00	0.00	3721000.00	0.00	0.00	3792800.00	3480000.00	KO:K03704	CspA family cold shock protein
Ga0586324_1065815_207_419	0.00	0.00	460973.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03704	CspA family cold shock protein
Ga0586324_1076035_46_240	0.00	5487600.00	0.00	0.00	8341000.00	12772000.00	0.00	0.00	0.00	0.00	0.00	5865000.00	KO:K03704	CspA family cold shock protein
Ga0586324_1393523_160_360	0.00	0.00	0.00	0.00	0.00	0.00	0.00	478473.63	0.00	0.00	0.00	0.00	KO:K03704	CspA family cold shock protein
Ga0586324_6292025_113_307	0.00	0.00	0.00	454661.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03704	CspA family cold shock protein
Ga0586324_0001326_15141_15560	2650000.00	0.00	0.00	2688500.00	0.00	0.00	0.00	1250500.00	0.00	0.00	0.00	0.00	KO:K03711	Fur family ferric uptake transcriptional regulator
Ga0586324_0014321_4646_5551	0.00	0.00	0.00	808118.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03717	LysR family transcriptional activator of nhaA
Ga0586324_0020400_2389_3747	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1077300.00	0.00	0.00	0.00	KO:K03732	ATP-dependent RNA helicase RhlB
Ga0586324_0002180_10959_14609	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3159000.00	0.00	0.00	1777500.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0002552_243_3764	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2733500.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0004169_11826_14822	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	372209.58	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0005236_5091_8669	0.00	6201600.00	3300950.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0030562_1_3510	4730000.00	0.00	0.00	0.00	0.00	0.00	0.00	2208200.00	469010.25	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0038731_566_4138	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1142100.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0048202_838_4416	0.00	0.00	0.00	0.00	371216.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0054740_846_4364	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1039500.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0132153_3_2579	1150000.00	904400.00	0.00	681346.65	787713.10	0.00	729034.56	552211.65	484738.83	549300.29	444708.00	702576.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0173739_1_1362	0.00	0.00	1375544.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0331790_1_1497	9460000.00	7187600.00	0.00	8664000.00	7652900.00	7265100.00	0.00	4428600.00	972000.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0347227_1_1926	0.00	0.00	0.00	3068500.00	2389600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0447207_342_1721	0.00	4066400.00	0.00	8227000.00	3440200.00	0.00	0.00	0.00	5613300.00	2348500.00	0.00	1500000.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0903673_2_1267	0.00	0.00	0.00	769389.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0978715_387_1226	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	378206.82	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_1203942_2_1120	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2982900.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_1674169_3_974	0.00	0.00	0.00	0.00	9094900.00	0.00	0.00	0.00	0.00	0.00	0.00	8550000.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_2288989_1_852	0.00	0.00	0.00	0.00	10001300.00	0.00	0.00	12322000.00	0.00	11011000.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_2373394_1_840	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6030000.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_2435074_1_834	10200000.00	0.00	13737200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_3340306_3_728	0.00	0.00	8501300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_4770104_3_629	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5636400.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_5307293_3_602	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	356785.56	644956.62	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_6737928_1_546	0.00	0.00	0.00	3258500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_7441022_58_522	0.00	0.00	0.00	0.00	0.00	0.00	0.00	474577.56	0.00	0.00	0.00	0.00	KO:K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase
Ga0586324_0002651_50_1876	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6999300.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0002615_13233_15059	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2464400.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0004973_2278_4014	0.00	2964800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0015092_3346_5088	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10549000.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0015054_3706_5448	4620000.00	3638000.00	0.00	1121000.00	0.00	0.00	0.00	1893000.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0025956_3644_5485	0.00	1944800.00	760202.01	0.00	0.00	0.00	944106.96	0.00	0.00	343670.04	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0033238_2305_4047	3710000.00	5004800.00	12386000.00	2004500.00	0.00	2808830.58	3397200.00	2592500.00	2956500.00	4173400.00	2543200.00	2340000.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0044817_445_2181	9910000.00	1101600.00	1778595.82	2365500.00	2018800.00	0.00	0.00	0.00	2405700.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0043321_3173_5026	403357.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0067656_286_2118	1760000.00	1394000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0069864_1398_3137	0.00	0.00	0.00	0.00	0.00	0.00	3784800.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0079436_2282_3826	0.00	1591200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0258389_2_1516	0.00	0.00	0.00	0.00	1545000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0283847_1_2046	0.00	0.00	0.00	0.00	384791.52	0.00	567083.88	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0305596_653_2038	0.00	1931200.00	2612578.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1216600.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0317164_690_2003	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	924000.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0320023_1_626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	557847.34	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0376333_560_1858	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2843100.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0386115_1_1407	0.00	0.00	0.00	0.00	3388700.00	11116000.00	0.00	3324500.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0402987_1_1122	0.00	0.00	0.00	464782.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0403295_43_1785	1890000.00	870400.00	2699596.26	0.00	0.00	1391580.28	0.00	768600.00	0.00	0.00	1293600.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0408835_831_1790	3830000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0424214_1_1707	9770000.00	10608000.00	10031513.40	0.00	0.00	0.00	6156645.24	1640900.00	4738500.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0442884_630_1730	1410000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0533063_24_1592	354892.00	0.00	892067.87	0.00	0.00	0.00	275488.62	0.00	205824.98	0.00	0.00	717075.04	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0570795_206_1546	0.00	0.00	0.00	0.00	0.00	0.00	3426550.67	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0627982_1_1464	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	694114.08	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0644457_1_1467	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1185800.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0762491_2_1288	0.00	0.00	0.00	3771500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0779744_1_498	0.00	1047200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0889247_2_1207	0.00	573174.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0918255_2_1087	0.00	992800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0960373_2_1041	0.00	0.00	0.00	3100300.00	0.00	0.00	0.00	0.00	0.00	0.00	4417600.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0965852_2_790	0.00	0.00	0.00	5025500.00	0.00	0.00	0.00	1506700.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0967776_3_1232	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4515000.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_1121105_1_1155	0.00	0.00	0.00	3600500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_1157792_3_971	0.00	3162000.00	10302900.00	0.00	0.00	1690914.31	0.00	1335900.00	0.00	2487100.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_1227206_3_458	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	346743.75	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_1269480_1_1095	5290000.00	0.00	13117900.00	0.00	0.00	5716800.00	0.00	0.00	0.00	0.00	3528800.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_1503857_61_993	0.00	401036.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_1653824_1_978	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1001000.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_1855350_1_933	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1740200.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_1919096_3_920	0.00	5378800.00	0.00	0.00	3790400.00	0.00	0.00	0.00	3977100.00	0.00	1355200.00	280966.50	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_2008555_3_368	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	625323.75	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_2155592_2_874	3050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_2304584_174_851	9020000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_2544968_224_817	778830.00	10676000.00	457104.77	7923000.00	11845000.00	5835900.00	209395.66	713700.00	10854000.00	7130200.00	440934.56	4462500.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_2961559_322_765	6960000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4489600.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_3204579_159_740	5220000.00	3488400.00	0.00	6756000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_3412484_3_722	1800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_3420085_3_680	0.00	0.00	0.00	0.00	0.00	0.00	4149600.00	0.00	0.00	0.00	2508000.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_3467340_3_716	0.00	1081200.00	0.00	3097000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_3646399_2_703	0.00	1577600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_3891870_233_685	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4904400.00	5200200.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_4046597_2_673	0.00	0.00	0.00	0.00	0.00	113300000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_4067416_1_672	0.00	0.00	8163500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_6065322_3_398	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3080500.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_7204752_1_522	5130000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	569739.42	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0000824_8142957_3_503	0.00	0.00	0.00	0.00	0.00	1619760.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03738	aldehyde:ferredoxin oxidoreductase
Ga0586324_0000018_10707_11357	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	481998.60	7777000.00	6916800.00	6517500.00	KO:K03744	LemA protein
Ga0586324_0001984_549_1151	0.00	0.00	0.00	1263500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_0001845_9572_10174	0.00	1591200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6727700.00	KO:K03744	LemA protein
Ga0586324_0008208_9452_10078	0.00	1686400.00	0.00	0.00	4861600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_0011087_1165_1791	0.00	0.00	0.00	0.00	0.00	5518300.00	0.00	0.00	0.00	2024000.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_0053378_1605_2318	1170000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2340900.00	2579500.00	2298800.00	1590000.00	KO:K03744	LemA protein
Ga0586324_0145676_708_1325	0.00	0.00	0.00	0.00	0.00	6657600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_0181647_1367_2047	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3757600.00	0.00	KO:K03744	LemA protein
Ga0586324_0273503_593_1207	0.00	0.00	0.00	0.00	2201149.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_0376151_203_790	0.00	0.00	0.00	0.00	0.00	0.00	7022400.00	0.00	0.00	0.00	9328000.00	0.00	KO:K03744	LemA protein
Ga0586324_0454029_695_1267	0.00	0.00	0.00	3591388.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_0575745_728_1369	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2745500.00	0.00	KO:K03744	LemA protein
Ga0586324_0759944_326_934	0.00	0.00	0.00	0.00	0.00	0.00	759983.28	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_0775764_60_650	0.00	0.00	0.00	0.00	4202400.00	0.00	0.00	0.00	2089800.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_0820605_18_668	0.00	0.00	0.00	2707500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_1879726_185_844	0.00	0.00	0.00	0.00	0.00	0.00	0.00	945500.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_2868672_2_661	0.00	0.00	0.00	0.00	0.00	0.00	4195200.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_3106489_334_750	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6906900.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_4420883_313_648	0.00	0.00	0.00	0.00	0.00	0.00	0.00	829600.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_5585494_124_588	0.00	0.00	0.00	0.00	0.00	9156700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_5771405_246_581	0.00	0.00	0.00	0.00	0.00	0.00	0.00	945500.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_6298602_53_562	0.00	0.00	0.00	0.00	9142800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_7090431_3_533	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1037000.00	0.00	0.00	0.00	0.00	KO:K03744	LemA protein
Ga0586324_1177975_792_1130	2240000.00	0.00	0.00	5804500.00	0.00	0.00	0.00	0.00	0.00	4543000.00	17776000.00	0.00	KO:K03746	DNA-binding protein H-NS
Ga0586324_7496189_91_492	0.00	0.00	0.00	5757000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03746	DNA-binding protein H-NS
Ga0586324_0000586_9077_9874	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2261600.00	0.00	KO:K03769	peptidyl-prolyl cis-trans isomerase C
Ga0586324_0001823_5280_6098	0.00	0.00	0.00	0.00	0.00	2895600.00	0.00	0.00	0.00	10241000.00	0.00	3802500.00	KO:K03769	peptidyl-prolyl cis-trans isomerase C
Ga0586324_1609368_244_993	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3142500.00	0.00	KO:K03769	peptidyl-prolyl cis-trans isomerase C
Ga0586324_1634701_1_414	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4276800.00	KO:K03769	peptidyl-prolyl cis-trans isomerase C
Ga0586324_2277036_2_793	0.00	0.00	0.00	5491000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03769	peptidyl-prolyl cis-trans isomerase C
Ga0586324_3195464_1_414	2720000.00	2019600.00	2757534.59	0.00	0.00	2668117.90	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03769	peptidyl-prolyl cis-trans isomerase C
Ga0586324_0000137_30238_32133	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2013000.00	939600.00	5243700.00	5271200.00	9997500.00	KO:K03770	peptidyl-prolyl cis-trans isomerase D
Ga0586324_0026215_2521_4437	0.00	0.00	0.00	0.00	0.00

Ga0586324_0009240_1_1878	15000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanococcoides;Methanococcoides methylutens;Methanococcoides methylutens DSM 2657
Ga0586324_0035016_4086_5690	0.00	0.00	0.00	0.00	6571400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanococcoides;Methanococcoides methylutens;Methanococcoides methylutens MM1
Ga0586324_0052523_1347_3515	0.00	0.00	3145351.51	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_0073750_1661_3853	0.00	0.00	0.00	0.00	0.00	0.00	4093100.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_0079361_1593_3785	0.00	289478.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Firmicutes;Neoatividcutes;Selenomonadales;Sporomusaceae;Dendrosporobacter;Dendrosporobacter quercicolus;Dendrosporobacter quercicolus DSM 1736
Ga0586324_0091325_245_2458	0.00	0.00	0.00	8664000.00	0.00	0.00	0.00	13315200.00	0.00	0.00	6850500.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0088;Rhodospirillales bacterium URHD0088
Ga0586324_0126621_1_1056	0.00	0.00	3364049.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. JS666;Polaromonas sp. JS666
Ga0586324_0137830_181_2370	0.00	0.00	0.00	0.00	0.00	25884400.00	16826400.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Chromobacterium;Chromobacterium piscinae;Chromobacterium piscinae ND17
Ga0586324_0163020_2126_2222	0.00	277708.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri 227
Ga0586324_0257437_1_1097	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	404437.05	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri MS
Ga0586324_0335083_479_1957	0.00	4807600.00	0.00	0.00	0.00	13259800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina sp. WH1;Methanosarcina sp. WH1
Ga0586324_0399200_3998_1988	3250000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	997500.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina sp. WH1;Methanosarcina sp. WH1
Ga0586324_0810207_806_1330	0.00	0.00	0.00	0.00	0.00	0.00	1697143.08	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;unclassified Peptococcaceae;Peptococcaceae bacterium DCMP;Peptococcaceae bacterium DCMP
Ga0586324_0826282_1001_1318	0.00	12172000.00	0.00	0.00	567246.75	0.00	1165935.00	0.00	773424.45	278073.95	0.00	469189.50	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia;Ralstonia solanacearum;Ralstonia solanacearum bv. 2 SL2312
Ga0586324_0972235_2_1228	0.00	761600.00	0.00	0.00	0.00	432817.34	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Nitrosomonadales;Rhodocyclales;Rhodocyclaceae;Ragoibacter;Ragoibacter aromaticivorans;Ragoibacter aromaticivorans PG1-Ca6
Ga0586324_0974593_1_1227	0.00	0.00	0.00	0.00	0.00	10004400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoreulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c DSM 19958
Ga0586324_1413144_163_1047	0.00	0.00	2430324.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Chromobacterium;Chromobacterium sp. MWU13-2610;Chromobacterium sp. MWU13-2610
Ga0586324_1501991_637_1020	0.00	26724000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina sp. WH1;Methanosarcina sp. WH1
Ga0586324_1699822_526_969	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3248100.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324_2109125_1_882	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5137500.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanobacteria;Methanobacteriales;Methanobacteriaceae;Methanobacterium;Methanobacterium paludis;Methanobacterium paludis SWAN-1
Ga0586324_2337394_3_845	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8393000.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfomonadales;Syntrophotalaceae;Syntrophotalea;Syntrophotalea acetylenivorans;Pelobacter sp. SF893
Ga0586324_2460739_3_827	0.00	0.00	0.00	0.00	0.00	532289.66	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. JS666;Polaromonas sp. JS666
Ga0586324_2835918_126_779	0.00	0.00	17734500.00	3543500.00	6046100.00	0.00	3602400.00	1884900.00	2033100.00	862400.00	0.00	2375500.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia;Ralstonia solanacearum;Ralstonia solanacearum bv. 2 SL2312
Ga0586324_2838472_2_778	0.00	0.00	0.00	0.00	2832500.00	0.00	3078000.00	0.00	1636200.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanococcoides;Methanococcoides methylutens;Methanococcoides methylutens MM1
Ga0586324_2920269_2_769	4940000.00	0.00	0.00	0.00	0.00	10004400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri MS
Ga0586324_3183868_1_744	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	915000.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Rhizobium;Rhizobium sp. BK333;Rhizobium sp. BK333
Ga0586324_5717742_2_583	0.00	0.00	0.00	0.00	0.00	0.00	0.00	619290.36	0.00	0.00	0.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Meiothermus;Meiothermus granaticius;Meiothermus granaticius NBRC 107808
Ga0586324_6013406_86_571	0.00	0.00	0.00	0.00	0.00	0.00	1268800.00	1514700.00	0.00	0.00	3052500.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Meiothermus;Meiothermus granaticius;Meiothermus granaticius NBRC 107808
Ga0586324_7726725_99_515	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9225000.00	0.00	KO:K03782	catalase-peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio putealis;Desulfovibrio putealis DSM 16056
Ga0586324_0000004_99744_100274	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1755600.00	2100000.00	0.00	KO:K03786	3-dehydroquinate dehydratase-2	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanococcoides;Methanococcoides burtonii;Methanococcoides burtonii DSM 6242
Ga0586324_0000290_20935_22278	0.00	0.00	0.00	0.00	1154434.68	646600.00	826200.00	1878800.00	1496000.00	1845000.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324_0008696_9198_10613	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4347200.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaeus;Thiobacillus thiopaeus DSM 505
Ga0586324_0001297_9517_11940	0.00	0.00	0.00	0.00	0.00	0.00	902800.00	0.00	0.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Labilithrix tuleyla;Labilithrix tuleyla DSM 27948
Ga0586324_0009890_8501_9868	2710000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0172381_1306_2640	0.00	0.00	0.00	0.00	0.00	0.00	485067.73	226813.77	0.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324_0239560_168_1502	0.00	0.00	0.00	11742000.00	0.00	0.00	1134600.00	0.00	0.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Gammaproteobacteria;Geobacterales;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0248273_1153_2241	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	606750.76	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_0429509_344_1687	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	906400.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter daltoni;Geobacter daltoni FRC-32
Ga0586324_0429509_758_1687	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	351486.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodovulum;Rhodovulum sp. PH10;Rhodovulum sp. PH10
Ga0586324_0591133_1_876	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4792500.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_1099797_82_1164	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2907900.00	6252400.00	3062400.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GA5499
Ga0586324_1238469_1_935	2730000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_1650723_1_981	0.00	0.00	0.00	0.00	0.00	0.00	564348.21	0.00	0.00	1188000.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_1961461_3_629	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1139600.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0088;Rhodospirillales bacterium URHD0088
Ga0586324_2899178_1_624	0.00	7480000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter whitterburii;Methylobacter whitterburii ACM 3310
Ga0586324_3383039_1_723	7200000.00	0.00	0.00	0.00	0.00	0.00	7729200.00	0.00	0.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_5088416_2_613	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5111100.00	0.00	0.00	0.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-DMM
Ga0586324_6470024_3_554	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2865000.00	0.00	KO:K03797	carboxyl-terminal processing protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_0316181_3_1832	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4889500.00	0.00	0.00	0.00	KO:K03798	cell division protease FtsH	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;Novherbaspirillum;Novherbaspirillum huminicola;Novherbaspirillum huminicola U15
Ga0586324_0535252_1_1026	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1335000.00	0.00	KO:K03798	cell division protease FtsH	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. Ai1a-2;Bradyrhizobium sp. Ai1a-2
Ga0586324_0774536_512_1354	0.00	0.00	0.00	0.00	0.00	0.00	774700.00	0.00	0.00	0.00	0.00	0.00	KO:K03798	cell division protease FtsH	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324_0941976_3_1247	0.00	1224000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03798	cell division protease FtsH	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter whitterburii;Methylobacter whitterburii ACM 3310
Ga0586324_6208373_136_564	0.00	0.00	0.00	790496.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03832	protein TonB	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Rhodanobacter;Rhodanobacter sp. K2T2;Rhodanobacter sp. K2T2
Ga0586324_0033085_5231_5854	2490000.00	1978800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03841	fructose-1,6-bisphosphatase I	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0184544_642_1661	0.00	0.00	0.00	0.00	997323.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03841	fructose-1,6-bisphosphatase I	Bacteria;Proteobacteria;Gammaproteobacteria;Candidatus Comeitbacteria;Candidatus Comeitbacter;Candidatus Comeitbacter dentirificans;Candidatus Comeitbacter dentirificans Run_A_D11
Ga0586324_1897278_1_612	0.00	720800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03841	fructose-1,6-bisphosphatase I	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run_B_J11
Ga0586324_2229137_1_756	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1316700.00	0.00	0.00	KO:K03841	fructose-1,6-bisphosphatase I	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazoonensis;Gemmatimonadetes bacterium KB5708
Ga0586324_0303894_1034_2044	0.00	0.00	0.00	0.00	0.00	0.00	902800.00	0.00	0.00	0.00	1252500.00	0.00	KO:K03856	3-deoxy-7-phosphoheptulonate synthase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_1838141_24_935	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2478600.00	0.00	0.00	0.00	KO:K03856	3-deoxy-7-phosphoheptulonate synthase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0000075_37944_38981	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1894200.00	0.00	0.00	KO:K03924	MurR-like ATPase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaeus;Thiobacillus thiopaeus DSM 505
Ga0586324_0001512_6702_7700	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4860000.00	0.00	KO:K03924	MurR-like ATPase	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazoonensis;Gemmatimonadetes bacterium KB5708
Ga0586324_0010432_6412_7401	0.00	0.00	0.00	0.00	0.00	0.00	6405000.00	0.00	0.00	0.00	0.00	0.00	KO:K03924	MurR-like ATPase	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_0710031_2_1042	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10875000.00	0.00	KO:K03924	MurR-like ATPase	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Blastopirellula;Blastopirellula cremea;Blastopirellula cremea HEX PIRIS-MGV
Ga0586324_1221701_3_455	0.00	6364800.00	0.00	0.00	0.00	0.00	0.00	9639000.00	0.00	0.00	0.00	0.00	KO:K03924	MurR-like ATPase	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinifilaceae;Labilibaculum;Labilibaculum antarcticum;Labilibaculum antarcticum SPP2
Ga0586324_1329123_3_437	0.00	0.00	0.00	0.00	0.00	0.00	7808800.00	0.00	0.00	0.00	0.00	0.00	KO:K03924	MurR-like ATPase	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Phycicoccus;Phycicoccus sp. Soil802;Phycicoccus sp. Soil802
Ga0586324_2795672_76_783	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1724800.00	0.00	KO:K03924	MurR-like ATPase	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinifilaceae;Labilibaculum;Labilibaculum filiforme;Labilibaculum filiforme 59.16B
Ga0586324_7914247_2_511	14000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03924	MurR-like ATPase	Bacteria;Candidatus Hydrogenedentes;unclassified Candidatus Hydrogenedentes;unclassified Candidatus Hydrogenedentes;unclassified Candidatus Hydrogenedentes;unclassified Candidatus Hydrogenedentes bacterium JGI 0000077-D07;Hydrogenedentes bacterium JGI 0000077-D07 (contamination screened)
Ga0586324_0113376_3_1700	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1347500.00	0.00	0.00	KO:K03929	para-nitrobenzyl esterase	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas;Pseudomonas geniculata;Pseudomonas geniculata CL-AP6
Ga0586324_0269651_2_1615	0.00	0.00	0.00	1121000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03929	para-nitrobenzyl esterase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Neorhizobium;Neorhizobium galegae;Neorhizobium galegae bv. orientalis HAMBI 2605
Ga0586324_0284597_140_1768	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1486100.00	0.00	0.00	KO:K03929	para-nitrobenzyl esterase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GA5499
Ga0586324_1379989_1_1056	0.00	782000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03929	para-nitrobenzyl esterase	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas;Pseudomonas fluorescens;Pseudomonas fluorescens ICMP 18415
Ga0586324_0005739_3132_3812	1540000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1179200.00	0.00	0.00	KO:K03969	phage shock protein A	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0048011_3442_4146	1400000.00	1115200.00	1489039.29	2308500.00	2276300.00	2145816.76	1590160.92	0.00	939600.00	2163700.00	0.00	0.00	KO:K03969	phage shock protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_0092820_3732_4436	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	31833.74	0.00	KO:K03969	phage shock protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_0121675_2_667	0.00	0.00	0.00	0.00	887317.19	0.00	0.00	0.00	371018.07	0.00	0.00	0.00	KO:K03969	phage shock protein A	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0159344_3_686	0.00	0.00	0.00	0.00	0.00	0.00	1061400.00	0.00	0.00	0.00	0.00	0.00	KO:K03969	phage shock protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_1678869_192_974	0.00	0.00	1394370.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K03969	phage shock protein A	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Micrococcaceae;Compostimonas;Compostimonas suwonensis;Compostimonas suwonensis DSM 25625
Ga0586324_0000002_223334_224398	0.00	0.00	0.00	0.00	0.00	0.00	1323700.00	1749600.00	0.00	0.00	0.00	0.00	KO:K03979	GTP-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_2264078_227_505	15900000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04027	ethanolamine utilization protein EutM	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_2592728_3_278	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10087000.00	0.00	0.00	0.00	KO:K04027	ethanolamine utilization protein EutM	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sp. GM2;Paenibacillus sp. GM2
Ga0586324_5203960_500_607	0.00	0.00	0.00	0.00	514055

Ga0586324_0357604_3_1484	0.00	0.00	0.00	1719500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Archangiaceae;Vitiosangium;Vitiosangium sp. GDMCC 1.1324;Vitiosangium sp. GDMCC 1.1324
Ga0586324_0357786_3_1205	0.00	0.00	0.00	0.00	1287500.00	0.00	0.00	0.00	358931.25	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0372044_920_1867	0.00	0.00	0.00	0.00	0.00	1554528.93	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina cetonica;Desulfosarcina cetonica JCM 12296
Ga0586324_0388513_186_1832	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	186309.20	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324_0389708_1_023	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9943000.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324_0464587_339_1694	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1552500.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324_0466820_3_1148	0.00	625349.08	0.00	1168500.00	0.00	0.00	0.00	0.00	0.00	2679600.00	4444000.00	5640000.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-1
Ga0586324_0489999_1_1530	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	231522.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_0501856_153_1637	0.00	0.00	0.00	0.00	0.00	38826600.00	0.00	0.00	0.00	0.00	0.00	26850000.00	KO:K04043	molecular chaperone DnaK	Bacteria;Chlorflexi;unclassified Chlorflexi;unclassified Chlorflexi;unclassified Chlorflexi;unclassified Chlorflexi;unclassified Chlorflexi;Chlorflexi sp. G233
Ga0586324_0520638_3_1610	8750000.00	3230000.00	20549500.00	6165500.00	0.00	0.00	0.00	0.00	5397700.00	8078400.00	10950000.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_0544565_504_1580	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4544100.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Chlorflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Anaerolinea;Anaerolinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_0564369_892_1554	0.00	0.00	2103334.22	6783000.00	5047000.00	0.00	0.00	1393200.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324_0592008_524_1522	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1036800.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run_A_D11
Ga0586324_0604577_2_1252	0.00	0.00	18353800.00	0.00	0.00	0.00	1329800.00	2438100.00	23177000.00	6177600.00	18375000.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0650832_1_1056	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	292500.67	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae;Halomonas;Halomonas huaneheensis;Halomonas huaneheensis BIGMM-B45
Ga0586324_0690175_738_1424	0.00	0.00	11823000.00	0.00	0.00	0.00	0.00	6161000.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Chlorflexi;Ktedonobacteria;Thermogemmatisporales;Thermogemmatisporaceae;Thermogemmatispora;Thermogemmatispora carboxidivorans;Thermogemmatispora carboxidivorans PMS
Ga0586324_0788616_344_1345	0.00	0.00	0.00	0.00	28767900.00	0.00	4719600.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324_0803187_3_1334	0.00	2046800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1031800.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus sp. KH32C;Azoarcus sp. KH32C
Ga0586324_0827555_1_435	0.00	0.00	0.00	5339000.00	0.00	9250100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0851005_2_1285	0.00	3699200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Chlorflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0873210_2_1288	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1335000.00	KO:K04043	molecular chaperone DnaK	Bacteria;Nitrospinae;Nitrospinia;Nitrospinales;Nitrospinaceae;Nitrospina;Nitrospina gracilis;Nitrospina gracilis 3/211
Ga0586324_0877683_1_1239	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1262700.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324_0892667_591_1274	0.00	0.00	0.00	0.00	1761300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0929413_764_1252	0.00	0.00	0.00	0.00	0.00	2911848.11	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0931821_1_735	0.00	0.00	0.00	0.00	0.00	3397871.39	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0990497_1_1218	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5135900.00	0.00	1147500.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1049109_3_1190	0.00	0.00	0.00	0.00	0.00	2809926.30	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_1063667_2_1183	0.00	0.00	647697.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	538884.72	650748.75	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_1159132_2_1138	0.00	0.00	0.00	0.00	968784.01	3111142.11	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1239010_2_1108	0.00	0.00	0.00	0.00	0.00	0.00	6042000.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodobacter;Rhodobacter sp. Z2-YC6860;Rhodobacter sp. Z2-YC6860
Ga0586324_1297123_2_1087	0.00	0.00	0.00	0.00	0.00	8614900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Candidatus Caldatribacteria;Caldatribacteria;Caldatribacteraceae;Caldatribacter;Caldatribacter abyssi;Caldatribacter abyssi LF13, DSM 13497
Ga0586324_1364225_2_1063	0.00	0.00	0.00	0.00	0.00	0.00	6840000.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas thiophila;Desulfuromonas thiophila DSM 8987
Ga0586324_1382540_3_1058	0.00	6099600.00	1289016.65	0.00	0.00	4128800.00	1129527.96	0.00	0.00	0.00	43817.36	462672.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1389786_1_1053	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1830400.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geothermobacter;Geothermobacter ehrlichii;Geothermobacter ehrlichii DSM 15274
Ga0586324_1510683_1_1017	7020000.00	2298400.00	6996125.13	969000.00	4902800.00	3951571.26	0.00	0.00	0.00	3819200.00	4171200.00	4327500.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_1584969_88_996	0.00	0.00	0.00	2109000.00	0.00	0.00	2237035.68	2793800.00	580756.23	2294600.00	4048000.00	15427500.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas thiophila;Desulfuromonas thiophila DSM 8987
Ga0586324_1620689_2_988	0.00	0.00	0.00	0.00	0.00	0.00	0.00	523847.87	381731.13	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1630116_1_984	0.00	9316000.00	0.00	0.00	0.00	0.00	8662000.00	10044000.00	22407000.00	21296000.00	750000.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus sp. KH32C;Azoarcus sp. KH32C
Ga0586324_1692915_501_968	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	231206.40	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Chlorflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas formicexedens;Dehalogenimonas formicexedens NSZ-14
Ga0586324_1762837_1_953	0.00	0.00	0.00	0.00	10300000.00	0.00	0.00	0.00	0.00	9009000.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_1868420_2_931	1160000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Planctomycetes;Planctomycetia;Isosphaerales;Isosphaeraceae;Singulisphaera;Singulisphaera sp. GP187;Singulisphaera sp. GP187
Ga0586324_2143314_1_876	4650000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Gammaproteobacteria;Gammatimonadales;Gammatimonadaceae;Gemmatirosa;Gemmatirosa kalamazoonensis;Gemmatimonadetes bacterium KBS708
Ga0586324_2187565_3_644	0.00	8772000.00	0.00	0.00	1781900.00	0.00	0.00	0.00	53541000.00	0.00	105336000.00	73200000.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithricaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_2193286_1_870	0.00	1496000.00	0.00	2688500.00	3357800.00	0.00	2485200.00	2702300.00	2867400.00	0.00	0.00	1687500.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324_2320017_2_847	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5978000.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia carboxidovorans;Oligotropha carboxidovorans OM4
Ga0586324_2383137_1_840	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	140349.51	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;Candidatus Latescibacteria;Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;Latescibacteria bacterium SCGC AAA252-B13;Latescibacteria bacterium SCGC AAA252-B13 (contamination screened)
Ga0586324_2444977_2_829	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	825000.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas thiophila;Desulfuromonas thiophila DSM 8987
Ga0586324_2514667_401_820	0.00	0.00	0.00	0.00	0.00	141321.92	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_2658627_3_800	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3241700.00	7682400.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Gammaproteobacteria;Gallionellales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_2711771_1_795	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2907900.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_2744255_2_790	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4815000.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_2756411_2_790	0.00	0.00	0.00	0.00	0.00	0.00	8052000.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Nitrospirae;Nitrospiria;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira japonica;Nitrospira japonica N1I1
Ga0586324_2787856_214_786	0.00	0.00	22040000.00	11948000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_2817946_1_750	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1701000.00	6737500.00	7832000.00	8175000.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas eutropha;Nitrosomonas eutropha C91
Ga0586324_2823731_3_782	0.00	0.00	0.00	6293300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2880462_3_776	0.00	0.00	0.00	0.00	0.00	666343.68	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_2887459_1_774	0.00	0.00	0.00	2090000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2898878_1_774	0.00	0.00	0.00	0.00	13081000.00	0.00	0.00	0.00	3742200.00	0.00	4162400.00	3105000.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324_2935005_3_770	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5289000.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Archaea;Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;Thaumarchaeota archaeon sp. BS1
Ga0586324_3252826_1_495	0.00	0.00	0.00	903458.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1822500.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_3380985_2_724	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1188000.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Rhizobium;Rhizobium wallis;Rhizobium wallis LMG 25295
Ga0586324_3383724_265_723	0.00	210136.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_3433946_3_719	0.00	0.00	0.00	0.00	0.00	2485200.00	0.00	603415.98	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_3603920_1_705	0.00	2774400.00	0.00	0.00	3574100.00	0.00	3876000.00	7688000.00	0.00	5405400.00	4725600.00	4132500.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dechlorobacter;Dechlorobacter hydrogenophilus;Dechlorobacter hydrogenophilus LT-1
Ga0586324_3622014_168_704	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	816200.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Leptothrix;Leptothrix mobilis;Leptothrix mobilis DSM 10617
Ga0586324_3689066_2_700	0.00	0.00	0.00	2935500.00	2533800.00	2061569.39	1493363.52	0.00	581313.51	511695.80	4558400.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_3879465_1_684	0.00	0.00	0.00	0.00	0.00	0.00	2804400.00	0.00	1539000.00	0.00	1443200.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dechlorobacter;Dechlorobacter hydrogenophilus;Dechlorobacter hydrogenophilus LT-1
Ga0586324_4007573_1_674	0.00	3148400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	550369.01	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324_4074325_1_492	430684.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatibacillum;Desulfatibacillum alkenivorans;Desulfatibacillum alkenivorans DSM 16219
Ga0586324_4143192_3_665	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5235000.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_4224241_39_662	4270000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Gammaproteobacteria;Beyerellales;Beyerellaceae;Beyerella;Beyerella sp. OA5946;Beyerella sp. OA5946
Ga0586324_4373246_3_653	0.00	829600.00	42562800.00	0.00	0.00	0.00	0.00	0.00	0.00	73920000.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_4564431_2_640	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14322000.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Chlorflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_4681333_1_633	0.00	1700000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1818000.00	1447500.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324_4964823_3_617	2000000.00	0.00	0.00	4503000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus sp. GAS368;Opitutus sp. GAS368
Ga0586324_5125027_1_363	0.00	1122000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatibacillum;Desulfatibacillum alkenivorans;Desulfatibacillum alkenivorans DSM 16219
Ga0586324_5214014_206_607	0.00	3862400.00	0.00	0.00	0.00	0.00	0.00	0.00	542118.42	234193.96	0.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI_001;Burkholderiales sp. JOSHI_001
Ga0586324_5552180_50_592	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	416721.36	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_5789712_1_579	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4327400.00	4012800.00	0.00	KO:K04043	molecular chaperone DnaK	Bacteria;Proteobacteria;Gammaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423

Ga0586324_0011956_6215_7846	0.00	610455.72	0.00	0.00	0.00	0.00	0.00	0.00	730804.68	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;Omnitrophica bacterium SCGC AAA011-L16;Omnitrophica bacterium SCGC AAA011-L16 (contamination screened)
Ga0586324_0014375_4921_6552	0.00	1060800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0015151_2916_4538	0.00	0.00	0.00	2061500.00	3481400.00	0.00	0.00	61000000.00	64314000.00	71456000.00	75328000.00	55950000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0016019_1_1248	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1242693009.78	8725211.76	353861.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methylocoleaceae;Methylocella;Methylocella sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_0017301_1331_2965	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	324220.32	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0017747_5165_6823	2270000.00	10064000.00	0.00	0.00	1823100.00	0.00	0.00	0.00	12960000.00	10010000.00	13200000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_0018000_3579_5201	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5178900.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So0157-25
Ga0586324_0018662_1203_2864	0.00	0.00	0.00	4512732.75	0.00	0.00	2895600.00	3135297.52	2269274.13	4693609.69	8107640.64	1116534.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracius;Sandaracius amylolyticus;Sandaracius amylolyticus DSM 53668
Ga0586324_0018690_4476_6143	0.00	0.00	0.00	0.00	0.00	0.00	3767530.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;Rickettsiella;Rickettsiella grylli;Rickettsiella grylli
Ga0586324_0018927_1127_2261	0.00	0.00	0.00	1045570000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	51750000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_0019147_4693_6353	0.00	0.00	39691500.00	0.00	1823100.00	0.00	0.00	9680700.00	5564700.00	10271800.00	10560000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0019973_6190_7440	607400.00	10360347.20	1073089.26	1102021.90	1388982.81	528867.52	5118141.26	15743058.73	2217839.13	6506500.00	15202665.28	16996899.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP51;Betaproteobacteria bacterium AAP51
Ga0586324_0020129_1177_2847	0.00	2590800.00	0.00	1120949.65	183279.23	0.00	0.00	0.00	2956500.00	496715.45	1170400.00	757500.00	KO:K04077	chaperonin GroEL	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sedimnispirochaeta;Sedimnispirochaeta bajacaliforniensis;Sedimnispirochaeta bajacaliforniensis DSM 16054
Ga0586324_0020832_4280_5917	0.00	0.00	6024100.00	0.00	0.00	3282368.21	4446000.00	0.00	0.00	5459300.00	4787200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Actinomycetia;unclassified Actinomycetia;unclassified Actinomycetia;unclassified Actinomycetia;unclassified Actinomycetia;Actinobacteria bacterium IMCC26256;Actinobacteria bacterium IMCC26256
Ga0586324_0021034_1_1116	16200000.00	3424505.84	74203400.00	0.00	3371190.00	0.00	8857328.04	39888230.01	6018300.00	99476300.00	122427470.88	116865000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324_0021252_339_1973	0.00	0.00	0.00	997500.00	0.00	0.00	16963200.00	0.00	22599000.00	0.00	0.00	1695000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324_0021327_2_1243	0.00	0.00	0.00	6507500.00	6386000.00	0.00	0.00	0.00	0.00	6806800.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_0022153_3214_4857	0.00	0.00	3932577.52	5633500.00	5335400.00	1506063.17	1293323.16	2342400.00	1628100.00	0.00	0.00	1875000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methylocoleaceae;Methylocella;Methylocella sp. Root1462;Methylocella sp. Root1462
Ga0586324_0025186_4403_6061	28200000.00	38692000.00	131404200.00	62320000.00	71791000.00	0.00	67032000.00	30317000.00	76140000.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;Corallococcus;Corallococcus sp. H22C18031201;Corallococcus sp. H22C18031201
Ga0586324_0025299_5639_6652	0.00	741200.00	0.00	10355000.00	8930100.00	0.00	0.00	0.00	4017600.00	0.00	4488000.00	481500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Gammatimonadales;Gammatimonadaceae;Gammatimonas;Gammatimonas ohototrophica;Gammatimonas ohototrophica AP64
Ga0586324_0025519_532_2172	0.00	0.00	0.00	0.00	0.00	23780300.00	2553600.00	0.00	947700.00	7777000.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_0026287_959_2599	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11528000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_0026425_1541_3172	0.00	943132.12	0.00	0.00	19000000.00	256715.14	0.00	0.00	221253.10	49161.01	0.00	1196800.00	7140000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Haliangium;Haliangium ochraceum;Haliangium ochraceum SMP-2, DSM 14365
Ga0586324_0026669_3259_4893	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	280141.74	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0026724_4734_6350	0.00	9996000.00	5964821.73	15637000.00	22072900.00	3534784.78	12813600.00	8314300.00	12328200.00	16085300.00	19711068.88	11895000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp1;Nitrosospira sp. 1 Nsp1
Ga0586324_0027924_1013_2626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4989600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;Tepidiphilus;Tepidiphilus thermophilus;Tepidiphilus thermophilus JCM 19170
Ga0586324_0027423_1255_2865	0.00	0.00	3932577.52	5633500.00	5335400.00	1506063.17	1293323.16	2342400.00	1628100.00	0.00	0.00	630438.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0027819_3539_5164	0.00	1285200.00	0.00	1463000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1942500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina cetonica;Desulfosarcina cetonica JCM 12296
Ga0586324_0028147_3702_5330	0.00	2502400.00	0.00	0.00	0.00	0.00	0.00	0.00	3248100.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_0028606_533_2161	0.00	505446.04	0.00	0.00	0.00	0.00	6815649.60	1079700.00	21878.55	1326635.31	1091200.00	795000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Binatia;Binatales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0028829_2_1129	0.00	0.00	0.00	2935500.00	0.00	0.00	155268000.00	1794422.97	0.00	1432200.00	0.00	945000.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Acetobacteroides;Acetobacteroides hydrogenigenes;Acetobacteroides hydrogenigenes DSM 24657
Ga0586324_0029790_1643_3292	17045926.00	135164333.72	89507184.66	5760268.00	132849400.00	8416400.00	85028759.57	72038860.04	85817597.31	109671100.00	81566549.68	73065000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0029939_792_2420	0.00	0.00	0.00	6013500.00	8404800.00	2564650.00	0.00	0.00	0.00	1423100.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_0030182_128_1768	0.00	466260.36	784399.75	350578.50	549601.82	271968.03	1114803.72	884500.00	1385100.00	1254300.00	3616800.00	3345000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_0031737_3_1337	0.00	0.00	0.00	0.00	0.00	0.00	4286400.00	4117500.00	0.00	4573800.00	5051200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga;Hydrogenophaga taeniospiralis;Hydrogenophaga taeniospiralis NBRC 102512
Ga0586324_0031994_486_2135	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	145455.75	0.00	1038400.00	1365000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS138
Ga0586324_0033740_3853_4671	0.00	0.00	0.00	0.00	542810.00	0.00	5950800.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324_0033897_1_1062	0.00	0.00	0.00	3619500.00	4521700.00	3407383.51	2004120.00	1329800.00	0.00	0.00	1487200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0034450_4134_5735	0.00	2930800.00	3931000.62	3039810000.00	831571.35	1294800.75	14638847.13	1186692.55	2060800.00	41210400.00	0.00	102300000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geoalkalibacter;Geoalkalibacter ferrihydriticus;Geoalkalibacter ferrihydriticus DSM 17813
Ga0586324_0034806_3170_4843	53000.08	1876800.00	0.00	0.00	28016000.00	3784188.12	0.00	2543700.00	2673000.00	0.00	541293.28	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira moscoviensis;Nitrospira moscoviensis NSP M-1
Ga0586324_0034930_3448_5076	278326.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	165904.75	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_0035645_1330_2973	8380000.00	0.00	0.00	2698000.00	0.00	0.00	0.00	0.00	0.00	1223100.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_0035654_3_1145	0.00	945200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1223100.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Desulfurifbacter;Desulfurifbacter thermophilus;Desulfurifbacter thermophilus S69
Ga0586324_0036009_30_1658	0.00	0.00	0.00	173062.45	0.00	0.00	0.00	0.00	805200.00	674716.23	314399.47	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0036117_4874_5605	2370000.00	3311600.00	844556.30	1605500.00	1818232.21	3693600.00	4370176.64	955800.00	4802664.02	11749429.60	6286932.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. NZG;Methylibium sp. NZG
Ga0586324_0039106_3035_4663	0.00	0.00	0.00	0.00	0.00	3169200.00	1531100.00	1693900.00	0.00	1883200.00	2677500.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0039504_4532_5365	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	939600.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA255-E10 (contamination screened)
Ga0586324_0041652_1584_3218	2640000.00	0.00	0.00	0.00	0.00	125205800.00	7273200.00	0.00	10854000.00	0.00	7726400.00	718068.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_0042533_4440_5174	0.00	0.00	0.00	2907000.00	14008000.00	2878781.88	3169200.00	1692551.75	1798200.00	0.00	8869031.68	336498.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0043595_472_2103	0.00	0.00	0.00	0.00	15429400.00	1591120.42	0.00	0.00	2664900.00	378757.61	0.00	269497.50	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_0044217_1_1592	0.00	0.00	0.00	3914000.00	0.00	0.00	0.00	461702.29	216232.74	421139.95	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosovibrio;Nitrosovibrio sp. Nv4;Nitrosovibrio sp. Nv4
Ga0586324_0044644_724_2352	260000000.00	0.00	0.00	9319500.00	0.00	0.00	0.00	0.00	442123.92	0.00	1135200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Sorangiineae;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So ce56;Sorangium cellulosum So ce56
Ga0586324_0047047_910_2565	0.00	4766800.00	8276100.00	0.00	1421400.00	100441000.00	0.00	0.00	0.00	0.00	0.00	301485.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Haliangium;Haliangium ochraceum;Haliangium ochraceum SMP-2, DSM 14365
Ga0586324_0049017_1534_3177	961440.00	580653.36	1774891.28	4275000.00	2863400.00	0.00	2000800.00	1917270.81	1901900.00	3696000.00	1627500.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira lacus;Nitrosospira lacus AP63
Ga0586324_0052118_1669_3309	11000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodobacter;Rhodobacter sp. Z2-YC6860;Rhodobacter sp. Z2-YC6860
Ga0586324_0054127_839_2476	0.00	7004000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_0056786_1822_3465	0.00	0.00	0.00	2916500.00	11608100.00	0.00	0.00	1720200.00	7200900.00	0.00	4532000.00	5880000.00	KO:K04077	chaperonin GroEL	Bacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga;Hydrogenophaga taeniospiralis;Hydrogenophaga taeniospiralis NBRC 102512
Ga0586324_0058586_3532_4428	107000000.00	7004000.00	0.00	1877853.31	1235000.00	2533800.00	3831050.00	2915800.00	2875500.00	3203200.00	1777600.00	1140000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodobacter;Rhodobacter sp. Z2-YC6860;Rhodobacter sp. Z2-YC6860
Ga0586324_0060597_507_2153	32641702.00	10737200.00	2159054.33	10800084.50	1593410.00	1119501.88	14250000.00	11459441.09	15860653.74	34973400.00	21832800.00	2284500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0060706_2_1198	186477.00	399245.00	10584400.00	2913118.95	0.00	0.00	4537200.00	969900.00	9420300.00	0.00	4540800.00	13035000.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Calescamantes bacterium JGI 0000106-H18;Calescamantes bacterium JGI 0000106-H18 (contamination screened)
Ga0586324_0064131_3163_4239	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8025000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosovibrio;Nitrosovibrio sp. Nv17;Nitrosovibrio sp. Nv17
Ga0586324_0065559_853_2487	0.00	0.00	0.00	0.00	336883.13	7979700.00	0.00	0.00	0.00	0.00	947100.00	982500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324_0070909_3_761	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	29727000.00	0.00	166672.00	40125000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Ardenticateria;Ardenticateraceae;Ardenticateraceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Ch-K
Ga0586324_0071657_1720_3360	4000000.00	5372000.00	6361900.00	10865513.85	9213685.78	5298516.83	3602400.00	5794024.61	6659982.81	5197500.00	1751200.00	1777500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0071895_1_1194	7360000.00	11036578.16	150940000.00	105811000.00	79134900.00	185720367.53	53557200.00	61494100.00	164909179.80	107030000.00	7118741.52	190756420.25	8700000.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfatibacillalesb;Desulfatibacillaceae;Desulfatibacillum;Desulfatibacillum aliphaticivorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0075324_2475_3926	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0075963_1126_2769	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3194400.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfopurpuratum;Desulfopurpuratum benzoelyticum;Desulfopurpuratum benzoelyticum DSM 28570
Ga0586324_0076692_2598_3893	0.00	0.00	0.00	0.00	0.00	0.00	116052000.00	54595000.00	329097.33	182958.93	415669.44	462000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_0077424_137_1762	4840000.00	5242800.00	5352699.98	0.00	2307200.00	4089100.00	1965617.64	0.00	3677400.00	2941400.00	1768800.00	1477500.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0077725_2197_3843	0.00	0.00	0.00	0.00	0.00	6193200.00	0.00	0.00	0.00	0.00	3660800.00	1788750.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324_0077925_3075_3703	0.00	0.00	8050900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	787500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga;Hydrogenophaga taeniospiralis;Hydrogenophaga taeniospiralis DSM 100886
Ga0586324_0084587_2866_3714	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3127500.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas sp. WBC-2;Dehalogenimonas sp. WBC-2
Ga0586324_0085943_2151_3686	3540000.00	112514.84	0.00	723980.75	0.00	0.00	0.00	0.00	218119.53	3175200.00	1509200.00	0.00	129069.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Woeseiaceae;Woeseiales;Woeseia oceani;Woeseia oceani XK5
Ga0586324_0087456_2910_3656	0.00	741200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	573802.04	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Steroibacteraceae;Sulfuriso;Sulfurisoma sedimnicola;Sulfurisoma sedimnicola DSM 26916
Ga0586324_0089538_701_2317	6730000.00	1550400.00	10217794.11	1102000.00	7900100.00	31659034.96	4012800.00	26516700.00	6270907.41	342700.82	8712000.00	18344241.75	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA255-E10 (contamination screened)
Ga0586324_0089599_1971_3617	0.00	0.00	0.00	9458400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter daltoni;Geobacter daltoni FRC-32

Ga0586324_0186985_315_1973	0.00	0.00	0.00	247894.90	0.00	0.00	344391.72	0.00	405292.41	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium GJ-E10;Burkholderiales bacterium GJ-E10
Ga0586324_0188679_3_560	0.00	16184000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	31185000.00	1777600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_0190138_730_2355	0.00	0.00	0.00	0.00	0.00	97265000.00	2488688.40	37232370.53	219012.66	0.00	777209.84	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina cetonica;Desulfosarcina cetonica JCM 12296
Ga0586324_0191407_1_1530	1870000.00	1149200.00	0.00	0.00	0.00	0.00	0.00	18727000.00	0.00	0.00	0.00	2040000.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospiria;Nitrospirales;Nitrospiraceae;Candidatus Magnetobacterium;Candidatus Magnetobacterium casensis;Candidatus Magnetobacterium casensis MYR-1
Ga0586324_0193010_1_1098	0.00	0.00	0.00	0.00	0.00	0.00	261144.36	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Firmicutes;Neoaticvicates;Selenomonadales;Sporomusaceae;Sporomusa;Sporomusa acidovorans;Sporomusa acidovorans DSM 3132
Ga0586324_0195824_1_984	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4788500.00	0.00	3780700.00	4628800.00	4027500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea anilini;Desulfatitalea anilini DSM 4660
Ga0586324_0196005_456_2096	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	75735000.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Methylacidiphilae;Methylacidiphilales;Methylacidiphilaceae;Methylacidiphilum;Methylacidiphilum infernorum;Methylacidiphilum infernorum V4
Ga0586324_0197204_528_2144	0.00	608948.84	0.00	1263500.00	0.00	8732400.00	1836100.00	7748513.29	0.00	2692800.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA255-E10 (contamination screened)
Ga0586324_0197688_838_2469	0.00	0.00	0.00	26362967.40	8425400.00	0.00	0.00	15121900.00	7209000.00	3503500.00	11176000.00	12690000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0201697_566_2212	0.00	0.00	0.00	0.00	0.00	0.00	0.00	235219.05	0.00	396231.99	0.00	509960.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium GJ-E10;Burkholderiales bacterium GJ-E10
Ga0586324_0203051_942_2459	0.00	6704800.00	1175572.15	593202.80	0.00	0.00	0.00	4770200.00	0.00	977414.85	877800.00	215966.96	8662500.00	KO:K04077	chaperonin GroEL
Ga0586324_0203282_2_1087	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	835026.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_0206080_1253_2440	5290000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0207531_3_953	0.00	0.00	11260000.00	4113500.00	3986100.00	0.00	0.00	5758400.00	0.00	0.00	0.00	2775000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0210491_144_1775	4480000.00	3658400.00	0.00	0.00	1184500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Archangiaceae;Vitiosanalim;Vitiosanalim sp. GDMCC 1.1324;Vitiosanalim sp. GDMCC 1.1324
Ga0586324_0216558_2_1639	0.00	0.00	0.00	0.00	0.00	0.00	0.00	197454.56	763908.57	367179.12	549236.16	242507.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_0216662_3_1439	0.00	0.00	0.00	0.00	0.00	1239079.68	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_0221696_989_2359	0.00	0.00	0.00	2736000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	765000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_0224332_866_2347	2640000.00	7848092.16	3305115.71	3249000.00	4418700.00	22630099.69	113638373.76	2769400.00	5653800.00	2326264.71	318147.28	28020141.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 6L1, DSM 198
Ga0586324_0234920_881_1299	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1689600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes DSM 22220
Ga0586324_0238716_564_2192	14110000.00	16639600.00	5506849.38	4180000.00	8971300.00	2104564.89	14353714.92	13877500.00	9009209.61	17509800.00	11017600.00	24915000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0242391_1209_2264	0.00	0.00	0.00	0.00	0.00	0.00	777039.96	4001600.00	17901000.00	37191000.00	3238400.00	877500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_0244757_942_2255	0.00	652537.52	10865900.00	0.00	0.00	0.00	667342.32	3092221.92	0.00	2012908.59	3320697.60	5002500.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;Spartobacteria bacterium LR76;Spartobacteria bacterium LR76
Ga0586324_0244974_1220_2254	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6405000.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;unclassified Verrucomicrobiae;unclassified Verrucomicrobiae;unclassified Verrucomicrobiae;Verrucomicrobiae bacterium DG1235;Verrucomicrobiales sp. DG1235
Ga0586324_0247739_1_1142	0.00	0.00	0.00	0.00	0.00	0.00	6093990.00	1401300.00	0.00	0.00	2200000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0250220_3_1472	0.00	0.00	2098133.67	1197000.00	0.00	0.00	1145278.20	0.00	230806.26	218175.65	302638.16	238101.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Woeseiaceae;Woeseia;Woeseia oceani;Woeseia oceani XK5
Ga0586324_0251325_1083_2228	0.00	2339200.00	0.00	0.00	0.00	0.00	0.00	0.00	891000.00	1948100.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0252067_1231_2226	451644.00	339205.76	0.00	2831000.00	520961.64	0.00	0.00	289534.06	1327130.73	1239700.00	0.00	900000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run_A_D11
Ga0586324_0253786_757_2217	0.00	197376.12	0.00	0.00	0.00	0.00	0.00	20496000.00	12231000.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina cetonica;Desulfosarcina cetonica JCM 12296
Ga0586324_0255038_3_1109	1260000.00	668926.88	568061.37	4579000.00	0.00	1253059.24	2280000.00	1085800.00	0.00	2471700.00	3845600.00	4575000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Archaeoglobaceae;Archaeoglobus;Archaeoglobus sp. Ch G35;Archaeoglobus sp. Ch G35
Ga0586324_0255394_513_2177	0.00	0.00	0.00	0.00	915583.40	623139.70	0.00	5767195.25	336573.60	481991.87	9548000.00	15224000.00	3562500.00	KO:K04077	chaperonin GroEL
Ga0586324_0255474_1_1278	0.00	0.00	0.00	0.00	43985000.00	1318400.00	2881426.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324_0256513_355_2007	7560000.00	536200.00	10077900.00	2555500.00	2080600.00	2687600.00	4560000.00	4306000.00	4268700.00	4935700.00	6608000.00	2850000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylococcus;Methylococcus sp. EBS1547;Methylococcus sp. EBS1547
Ga0586324_0268138_1251_2162	0.00	0.00	0.00	1415500.00	4336300.00	0.00	0.00	0.00	383317.11	8085000.00	4802156.48	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticateniaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324_0268820_2_1663	30620000.00	58076151.40	53354158.80	15571341.70	8933698.82	26732963.68	15526800.00	136926700.00	65634633.72	177089973.06	113152044.72	106404489.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodoplanes;unclassified Rhodoplanes sp. LVNP
Ga0586324_0271979_325_1989	0.00	4773600.00	0.00	0.00	0.00	6629900.00	0.00	0.00	13688900.00	0.00	580247.36	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Archangiaceae;Vitiosanalim;Vitiosanalim sp. GDMCC 1.1324;Vitiosanalim sp. GDMCC 1.1324
Ga0586324_0273975_860_2140	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	486205.74	0.00	763757.36	669987.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_0278594_34_1668	0.00	0.00	5798900.00	0.00	0.00	0.00	2690400.00	2989000.00	0.00	0.00	5324000.00	3465000.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolibacteraceae;Draconibacterium;Draconibacterium sediminis;Draconibacterium sediminis JN14CK-3
Ga0586324_0281552_1_585	508000.00	0.00	0.00	4158373.95	3429900.00	12267300.00	2280000.00	4270000.00	6147900.00	2140600.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-01, DSM 14535
Ga0586324_0285424_1_963	851544.00	5888800.00	1121580.45	6042000.00	5850400.00	0.00	1283961.48	7143100.00	5880520.62	3734500.00	4840000.00	5632500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324_0288273_527_2092	0.00	0.00	0.00	0.00	0.00	1729019.98	0.00	0.00	0.00	293132.05	244124.28	6152300.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43
Ga0586324_0289271_925_2088	1610000.00	4259690.00	0.00	1576000.00	22243882.06	8309250.00	867692.76	1028435.55	0.00	5074300.00	0.00	7529532.12	1545000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea butyrativorans;Desulfatitalea butyrativorans DSM 18734
Ga0586324_0294719_1_876	0.00	178652.32	0.00	4370000.00	0.00	14530200.00	10225533.24	9760000.00	0.00	12236370.21	19289600.00	6517500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea anilini;Desulfatitalea anilini DSM 4660
Ga0586324_0298000_908_2062	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas oligotropha;Nitrosomonas oligotropha Nm75
Ga0586324_0299974_849_2057	0.00	836400.00	0.00	8426500.00	3203300.00	7304800.00	0.00	6421701.80	4625100.00	6457260.81	109195737.84	1567500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_0300965_375_2051	0.00	0.00	0.00	2118500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;unclassified Methylophilaceae;unclassified Methylophilaceae;Betaproteobacterium LSUCC0135;Betaproteobacterium LSUCC0135
Ga0586324_0301154_3_1535	6010000.00	6181200.00	0.00	0.00	0.00	0.00	0.00	1354200.00	1182600.00	1447600.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_0301327_140_1774	0.00	0.00	0.00	0.00	0.00	1555800.00	1716912.96	0.00	2697300.00	0.00	541200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Acetobacteroides;Acetobacteroides hydrogenigenes;Acetobacteroides hydrogenigenes DSM 24657
Ga0586324_0303950_1137_2042	1680000.00	1530680.68	6892595.06	5089334.30	4933700.00	20615431.88	5694746.88	2477860.05	10824652.89	14814800.00	17864000.00	29392500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thiotrichales;Candidatus Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324_0304269_2_598	0.00	0.00	0.00	0.00	132870000.00	1838110.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;unclassified Rhodothermaceae;Rhodothermaceae bacterium RA;Halothermothamnus malaysiensis RA
Ga0586324_0304465_2_1222	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2921600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Kuenenia;Candidatus Kuenenia stuttgartiensis;Candidatus Kuenenia stuttgartiensis MBR1
Ga0586324_0306696_812_2035	0.00	0.00	2521890.94	0.00	0.00	1271420.29	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Alkaliflexus;Alkaliflexus sapovilacus;Alkaliflexus sapovilacus DSM 24412
Ga0586324_0307071_3_1106	11800000.00	199144.12	0.00	0.00	0.00	0.00	0.00	0.00	297592.77	589637.88	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0307573_2_791	0.00	0.00	0.00	0.00	150380000.00	10361700.00	0.00	0.00	0.00	0.00	3819200.00	6067500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0308523_3_1625	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1539000.00	121184.92	5359200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_0309156_416_2026	0.00	0.00	0.00	0.00	0.00	0.00	0.00	106475.50	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0319856_1711_1998	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9477000.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticateniaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324_0322866_1217_1972	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1085800.00	0.00	0.00	0.00	5820000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Francisellaceae;Francisella;unclassified Francisella;Francisella bacterium MT45;Francisella bacterium GJ-E10
Ga0586324_0329337_1_852	0.00	1475600.00	77131000.00	0.00	0.00	0.00	21888000.00	0.00	12393000.00	12243000.00	17512000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0336642_267_1901	0.00	0.00	0.00	2698000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-B84
Ga0586324_0337707_137_1783	5280000.00	1774800.00	2618832.16	2356000.00	0.00	0.00	0.00	2831882.91	510483.06	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;unclassified Methylophilaceae;unclassified Methylophilaceae;Betaproteobacterium LSUCC0135;Betaproteobacterium LSUCC0135
Ga0586324_0337906_1_852	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1390800.00	0.00	0.00	9240000.00	2092500.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0338879_627_1946	0.00	0.00	0.00	0.00	0.00	10602000.00	149858.09	3904200.00	1116500.00	4400000.00	1927500.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas;Gemmatimonas phototrophica;Gemmatimonas phototrophica AP64
Ga0586324_0340705_160_1815	0.00	0.00	0.00	0.00	7601400.00	0.00	1451001.12	23234900.00	2162700.00	1062600.00	5112800.00	1207500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0342123_230_1861	0.00	152651.16	0.00	18620000.00	0.00	0.00	0.00	573872.14	122319000.00	0.00	815760.00	7950000.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Caldithrix abscisiibacillus;Candidatus Caldithrix abscisiibacillus;Candidatus Caldithrix abscisiibacillus LP13, DSM 14397
Ga0586324_0342624_1_1392	4050000.00	0.00	0.00	17423000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	610888.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Vulgatibacteraceae;Vulgatibacter;Vulgatibacter incomptus;Vulgatibacter incomptus DSM 27710
Ga0586324_0342965_1_1509	0.00	0.00	0.00	438310.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Actinomycetia;Frankiales;unclassified Frankiales;unclassified Frankiales;Frankineae bacterium MT45;Frankineae sp. MT45
Ga0586324_0344243_1_1283	0.00	0.00	0.00	0.00	0.00	0.00	933330.00	1806300.00	0.00	1763300.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_0347510_2_1060	0.00	0.00	0.00	0.00	0.00	0.00	361388.40	0.00	0.00	3957800.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0347958_166_1800	0.00	1006400.00	0.00	0.00	0.00	0.00	0.00	634400.00	0.00	468413.33	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Methylacidiphilae;Methylacidiphilales;Methylacidiphilaceae;Methylacidiphilum;Methylacidiphilum kamchatkense;Methylacidiphilum kamchatkense Kam1
Ga0586324_0348744_1_1600	5370000.00	656600.20	3687650.00	6517000.00	7498400.00	7536139.84	40128000.00	0.00	6439500.00	4342800.00	0.00	6315000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0350606_3_1484	13767478.00	22459076.72	834990.93	3553000.00	3203300.00	5994700.00	0.00	19276000.00	20266883.18	17463600.00	12311914.56	14025000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324_0351186_114_1766	0.00	0.00	2043740.67	879629.70	0.00	0.00	0.00	1138907.88	683200.00	0.00	434125.23	1091200.00	409173.75	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Isosphaerales;Isosphaeraceae;Paludisphaera;Paludisphaera borealis;Paludisphaera borealis PX4
Ga0586324_0352498_775_1914	940000.00	0.00	0.00	0.00	0.00	299680.56	0.00	0.00	0.00	0.00	2625700.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Myxococcales;Polyangiaceae;Chondromyces;Chondromyces apiculatus;Chondromyces apiculatus DSM 436
Ga0586324_0353656_1_855	0.00	0.00	0.00	0.00	0.00	0.00	17578800.00	0.00	2413800.00	0.00	0.00	6285000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0355604_459_1904	262770.00	0.00	0.00	0.00	0.00	0.00	0.00	5514400.00	0.00	0.00	5632000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0355713_300_1904	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2047400.00	0.00	2302300.00	369908.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;shellaceae;Hahella;Hahella sp. KA22;Hahella sp. KA22
Ga0586324_0364283_323_1885	1910000.00	0.00	3797975.48	2802500.00	0.00	542290.09	0.00	915000.00	826200.00	0.00	1257857.92	1072710.75	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Cand

Ga0586324_0590606_2_1177	0.00	5827600.00	6136700.00	6317500.00	1545000.00	0.00	0.00	6466000.00	4827600.00	3880800.00	6644000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324_0590866_3_209	0.00	1455200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	364746.69	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324_0592122_1_480	13320000.00	3338800.00	5614331.71	4493500.00	4274500.00	0.00	0.00	0.00	7030800.00	5058900.00	0.00	5730000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis parvus;Methylocystis parvus OBBP
Ga0586324_0593990_3_1520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22176000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;unclassified Chlorflexi;unclassified Chlorflexi;unclassified Chlorflexi;unclassified Chlorflexi;Chlorflexi bacterium TB1;Chlorflexi bacterium TB1
Ga0586324_0594172_1_521	16900000.00	16728000.00	0.00	34295000.00	19055000.00	0.00	7090800.00	25010000.00	12186702.72	21406000.00	23144000.00	11325000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0594969_390_1520	0.00	433130.76	0.00	639070.70	0.00	0.00	838910.04	0.00	0.00	0.00	906400.00	723330.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Haliangium;Haliangium ochraceum;Haliangium ochraceum SMP-2, DSM 14365
Ga0586324_0595215_143_1519	0.00	0.00	0.00	0.00	336634.90	0.00	0.00	768600.00	7727400.00	17248000.00	665041.52	14325000.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospiria;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira marina;Nitrospira marina Nb-295
Ga0586324_0595394_42_1520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4373600.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_0595560_376_1515	3450000.00	2267800.00	744618.17	0.00	389971.39	0.00	996360.00	2257000.00	7371687.69	17871700.00	14064417.84	13389162.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0600642_3_1292	898158.00	0.00	0.00	30020000.00	0.00	0.00	480391.44	0.00	3442500.00	3349500.00	3212000.00	3607500.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0608322_391_1506	0.00	0.00	0.00	0.00	456917.27	0.00	0.00	0.00	0.00	793100.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;Desulfobacter;Desulfobacter thermophilus;Desulfurlbacter thermophilus;Desulfurlbacter thermophilus S69
Ga0586324_0608632_526_1506	0.00	829600.00	0.00	0.00	0.00	0.00	0.00	7455600.00	0.00	3183300.00	7854000.00	6661600.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_0611607_1_825	0.00	0.00	0.00	1168500.00	538757.98	508032.96	1093975.92	224265.89	626140.53	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daeninsii;Thermanaerothrix daeninsii GN5-1
Ga0586324_0614064_386_1498	0.00	0.00	514472.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;alpha proteobacterium BAL199;Nisaea sp BAL199
Ga0586324_0615025_1_1497	0.00	0.00	0.00	10640000.00	0.00	2611831.24	3237600.00	2763300.00	4576500.00	2502500.00	3238400.00	2797500.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0617535_2_1066	0.00	0.00	0.00	22610000.00	0.00	0.00	0.00	16457800.00	0.00	0.00	1179200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospiria;Nitrospirales;Nitrospiraceae;Nitrospira;Candidatus Nitrospira nitrosa;Candidatus Nitrospira nitrosa COMA1
Ga0586324_0618976_803_1495	0.00	3141600.00	0.00	0.00	613598.84	0.00	11445600.00	10400500.00	8181000.00	8470000.00	13200000.00	7800000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0619927_590_1492	3620000.00	0.00	2067088.28	7058500.00	5139700.00	10599900.00	4400400.00	9272000.00	0.00	3264800.00	1540000.00	802500.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0627245_188_1486	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9240000.00	2085000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0647813_3_818	379256.00	0.00	0.00	626183.00	0.00	0.00	1984783.32	647784.01	3967025.22	1940400.00	386962.88	3702549.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;mitochondriales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium macuxiense;Bradyrhizobium macuxiense BR 10303
Ga0586324_0654544_3_1457	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3256000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Hydrogenophilalia;Hydrogenophilales;Hydrogenophilaceae;Tepidiphilus;Tepidiphilus margaritifer;Tepidiphilus margaritifer DSM 15129
Ga0586324_0658756_145_1455	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	310336.40	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0671001_3_752	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2138010.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Novimethylophilus;Novimethylophilus kurashikiensis;Novimethylophilus kurashikiensis La2-4
Ga0586324_0671889_265_1440	30800000.00	15388400.00	20211700.00	47405000.00	14729000.00	0.00	12448800.00	11699800.00	11421000.00	16454900.00	14872000.00	12750000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324_0675008_100_1437	0.00	0.00	0.00	3876000.00	0.00	3081447.04	1180759.56	17019000.00	8675100.00	5959800.00	20011200.00	17175000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium UKL13-2;Betaproteobacteria bacterium UKL13-2
Ga0586324_0675796_1_1437	17700000.00	0.00	1684507.26	0.00	0.00	19214800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;Myxococcus;Myxococcus xanthus;Myxococcus xanthus KF3.2.8c11
Ga0586324_0680857_121_1434	1380000.00	2951200.00	30876198.01	4474500.00	1740700.00	782887.97	7660800.00	2324100.00	2663280.00	2539200.51	26274167.04	3187500.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Calescamantes bacterium JGI 0000106-H18;Calescamantes bacterium JGI 0000106-H18 (contamination screened)
Ga0586324_0686531_421_1428	608459.00	1747844.80	277774.63	15038500.00	0.00	0.00	528966.84	658764.62	0.00	0.00	0.00	410624.25	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0687455_1_894	0.00	0.00	0.00	0.00	1266900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Leptolinea;Leptolinea saccharolytica;Leptolinea saccharolytica DSM 16555
Ga0586324_0690043_3_512	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	668852.64	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Acidithiobacillales;Acidithiobacillaceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola SA4;Sulfuricaulis limicola HAS
Ga0586324_0690260_240_1424	1780000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;Dehalococcidia;Dehalococcoidales;Dehalococcoidaceae;Dehalococcoides;Dehalococcoides mccartyi;Dehalococcoides mccartyi V5
Ga0586324_0692247_1_422	0.00	30117200.00	0.00	8892000.00	13493000.00	3384795.21	1331007.00	4441434.30	0.00	53284000.00	7568000.00	1560000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0693023_763_1422	0.00	4619753.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11704000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luciae;Methylobacter luciae OJ-12
Ga0586324_0695674_3_1304	0.00	521773.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324_0703513_634_1413	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1012000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Oleomonas;Oleomonas sp. K1W22B-8;Oleomonas sp. K1W22B-8
Ga0586324_0703705_2_1381	0.00	754800.00	0.00	0.00	0.00	0.00	14174301.72	2122800.00	19148400.00	1478400.00	2646029.76	514486.50	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0703887_3_1346	0.00	0.00	0.00	1463000.00	8044300.00	236215000.00	0.00	1018700.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0706076_3_1412	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15525000.00	KO:K04077	chaperonin GroEL	Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;Thermosulfurimonas;Thermosulfurimonas dismutans 595
Ga0586324_0712577_3_1235	3404781.00	935800.00	0.00	537196.50	5339972.17	12113258.91	2781600.00	5207404.08	6601500.00	0.00	0.00	960000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Haliangium;Haliangium ochraceum;Haliangium ochraceum SMP-2, DSM 14365
Ga0586324_0712784_3_1406	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	459375.84	607992.88	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0719302_3_734	0.00	3005600.00	0.00	0.00	0.00	0.00	597360.00	0.00	0.00	0.00	0.00	616787.25	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0725488_3_1395	6817704.00	0.00	0.00	4921000.00	0.00	0.00	0.00	25131.39	0.00	0.00	0.00	692658.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324_0729127_51_1391	0.00	0.00	0.00	3097000.00	0.00	9131000.00	0.00	0.00	1571400.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Draconibacterium;Draconibacterium sediminis;Draconibacterium sediminis JN14CK-3
Ga0586324_0730369_19_1389	0.00	0.00	0.00	0.00	0.00	0.00	0.00	499178.64	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Coriobacteriia;Eggerthellales;Eggerthellaceae;Slackia;Slackia isoflavoniconvertens;Slackia isoflavoniconvertens DSM 22006
Ga0586324_0734697_2_1387	0.00	4644400.00	0.00	0.00	813600.09	0.00	3853200.00	16958000.00	256094.27	5944400.00	5500000.00	4957500.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospiria;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira marina;Nitrospira marina Nb-295
Ga0586324_0734236_3_1361	0.00	0.00	0.00	732513.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_0756070_529_1368	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2276100.00	0.00	4628800.00	5272500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter tataouinensis;Ramlibacter tataouinensis 5-10
Ga0586324_0763000_2_1363	0.00	294189.76	0.00	2470000.00	0.00	7026900.00	15367280.00	12566000.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS478
Ga0586324_0770063_3_1223	0.00	0.00	0.00	0.00	53148000.00	67093000.00	1507567.00	38186000.00	193517.10	723930.13	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospiria;Nitrospirales;Nitrospiraceae;Leptospirillum;Leptospirillum;Leptospirillum sp. Group II 'C75';Leptospirillum sp. Group II 'C75'
Ga0586324_0777149_2_565	22130000.00	0.00	0.00	49305000.00	259033.67	49625000.00	0.00	0.00	0.00	572128.48	0.00	6712500.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324_0779977_357_1352	0.00	167241.92	1851605.66	0.00	0.00	0.00	0.00	1525000.00	0.00	2579500.00	2490400.00	1147500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyratrovans;Desulfatirhabdium butyratrovans DSM 18734
Ga0586324_0795904_3_707	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2335722.22	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_0797336_376_1338	1840000.00	986000.00	0.00	5538500.00	1639760.00	39303000.00	0.00	10695463.06	8879602.32	2033067.19	0.00	1762500.00	KO:K04077	chaperonin GroEL	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_0802506_604_1335	0.00	0.00	0.00	0.00	2296900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0803740_385_1335	0.00	2556800.00	1854189.84	3154000.00	3162100.00	0.00	3420000.00	1762900.00	14836291.29	7279914.11	1478400.00	1415500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Sebetemonadales;Sebetemonadaceae;Sebetemonas;Sebetemonas sp. oral taxon 149;Sebetemonas sp. oral taxon 149 67H29BP
Ga0586324_0812340_3_1025	0.00	0.00	0.00	7552500.00	6911300.00	6272600.00	0.00	0.00	5386500.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfopyrunum;Desulfopyrunum benzoelyticum;Desulfopyrunum benzoelyticum DSM 28570
Ga0586324_0813017_1_858	14270000.00	2721194.76	6129409.15	45163000.00	44454800.00	10912132.56	13520400.00	23180000.00	20047500.00	7977200.00	8395200.00	14227500.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Leptolinea;Leptolinea saccharolytica;Leptolinea saccharolytica DSM 16555
Ga0586324_0814458_3_890	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	722877.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Idonella;Idonella dinghuensis;Idonella dinghuensis JS 201-F6
Ga0586324_0822566_1_1320	0.00	7752000.00	0.00	0.00	0.00	19776000.00	201297111.14	23028000.00	6588000.00	193249800.00	8470000.00	10032000.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0823359_297_1319	0.00	0.00	3756482.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	516715.76	862500.00	KO:K04077	chaperonin GroEL	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0828992_586_1317	0.00	0.00	0.00	0.00	0.00	0.00	644902.56	489307.84	0.00	0.00	606650.88	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Archangiaceae;Stigmatella;Stigmatella erecta;Stigmatella erecta DSM 16858
Ga0586324_0829534_2_1243	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16120836.36	0.00	0.00	0.00	190152.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Thauera;unclassified Thauera;Thauera sp. SYD-3
Ga0586324_0850166_1_1302	0.00	0.00	0.00	0.00	7972200.00	0.00	0.00	3580700.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_0857779_3_1235	0.00	0.00	0.00	0.00	0.00	1961529.36	0.00	0.00	0.00	0.00	0.00	700482.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Desulfobacter;Desulfobacter thermophilus;Desulfurlbacter thermophilus;Desulfurlbacter thermophilus S69
Ga0586324_0860265_1_924	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2365200.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Anaerohalosinonia;Anaerohalosinonia thermotolerans;Anaerohalosinonia thermotolerans DSM 19859
Ga0586324_0862477_1_1278	0.00	7820000.00	6080400.00	5244000.00	4944000.00	3590793.54	82422000.00	5032500.00	8553600.00	73319400.00	9680000.00	7800000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0864860_465_1292	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1223200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_0868892_3_365	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2125200.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;Omnitrophica bacterium SCGC AAA257-O07;Omnitrophica bacterium SCGC AAA257-O07 (contamination screened)
Ga0586324_0869957_1_1083	0.00	0.00	1574716.63	1567500.00	443201.79	0.00	1033760.24	1939454.74	133702.65	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324_0870498_2_1288	0.00	0.00	0.00	455956.30	0.00	395010.24	0.00	0.00	424388.16	0.00	0.00	479955.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_0876795_1_1149	0.00	0.00	0.00	842549.30	0.00	0.00	0.00	0.00	156674.25	2879800.00	0.00	3382500.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Flavobriia;Flavobriales;Flavobriaceae;Flavihumibacter;Flavihumibacter sp. J0627;Flavihumibacter sp. J0627 CCTCC AB2013368
Ga0586324_0879792_3_1283	0.00	3978000.00	1381720.23	7913500.00	1596500.00	7582700.00	1388953.20	1335900.00	681632.82	777700.00	1496000.00	1185000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0883946_279_1280	0.00	5875200.00	540281.26	0.00	5133455.11	0.00	0.00	13395600.00	1927800.00	0.00	2965600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium GJ-E10;Burkholderiales bacterium GJ-E10
Ga0586324_0888712_2_784	4600000.00	965600.00	0.00	13300000.00	0.00	0.00	0.00	2879200.00	0.00	1232000.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira briensis;Nitrosospira briensis C-128
Ga0586324_0890796_3_485	0.00	0.00	0.00	0.00	0.00	475209.00	0.00	0.00	253601.28	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0891336_2_691	1000000.00	3474800.00	0.00	0.00	8631338.97	0.00	0.00	622200.00	0.00	4535300.00	0.00	298197.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324_0905080_619_1266	14400000.00	2080800.00	3195242.88	734541.90	3481689.43	438581.78	64888346.80	41324.28	7188541.02	6360200.00	2233200.00	51975000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Acidophilum;Acidophilum cryptum;Acidophilum cryptum JF-5
Ga0586324_0905420_3_791	0.00	1040400.00	1973247.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1240800.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Thermodesulfovibrionia;Th

Ga0586324_1237710_1_969	0.00	0.00	0.00	0.00	0.00	0.00	0.00	354390.48	603245.88	0.00	0.00	642671.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324_1244784_3_524	0.00	0.00	0.00	0.00	0.00	9210400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Solitalea;Solitalea canadensis;Solitalea canadensis USAM 9D, DSM 3403
Ga0586324_1244792_2_898	4820000.00	0.00	0.00	1388124.80	2274918.77	0.00	2872800.00	29896100.00	1801783.44	24101000.00	26928000.00	19425000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;Chloroflexi bacterium T81;Chloroflexi bacterium T81
Ga0586324_1250253_2_692	0.00	659776.12	0.00	0.00	0.00	0.00	647928.12	0.00	0.00	0.00	0.00	817500.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermogutataceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324_1255417_2_733	0.00	0.00	0.00	0.00	0.00	0.00	0.00	595988.30	450357.57	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1268121_1_1095	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6269400.00	3141600.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324_1271641_621_1094	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	465783.01	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;endosymbiont of Riftia pachyptila;endosymbiont of Riftia pachyptila (vent Mk28)
Ga0586324_1272245_3_713	0.00	0.00	0.00	54075000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;unclassified Bradyrhizobium;Bradyrhizobium sp. HAMBI 2127
Ga0586324_1279677_3_755	0.00	54377.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermogutataceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324_1284848_1_1089	0.00	775200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Pirellula;Pirellula staleyi;Pirellula staleyi DSM 6068
Ga0586324_1285596_3_1091	0.00	0.00	1268985.11	0.00	0.00	2064722.40	0.00	3661200.00	2548700.00	0.00	0.00	3735000.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Pseudobacter;Pseudobacter ginsenosidimutans;Pseudobacter ginsenosidimutans DSM 18116
Ga0586324_1294808_515_1087	1590000.00	0.00	0.00	6031585.15	3573995.97	0.00	0.00	2698477.74	2795457.42	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_1316497_3_1079	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2130947.28	1638945.44	5814103.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Trinickia;Trinickia caryophylli;Trinickia caryophylli Ballard 720
Ga0586324_1318742_1_1077	1390000.00	0.00	3291680.84	2147000.00	0.00	2810363.00	2986800.00	1482300.00	0.00	1689600.00	4515000.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Acidimicrobiaceae;Luteiluna;Luteiluna pratensis;Luteiluna pratensis DSM 100886
Ga0586324_1324643_2_886	0.00	4467600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehaloeneimonas;Dehaloeneimonas sp. WBC-2;Dehaloeneimonas sp. WBC-2
Ga0586324_1326564_3_1076	4270000.00	0.00	11823000.00	0.00	0.00	0.00	0.00	9089000.00	7865100.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Pirellula;Pirellula sp. SH-Sr6A;Pirellula sp. SH-Sr6A
Ga0586324_1332878_3_1073	0.00	0.00	0.00	0.00	0.00	0.00	379093.32	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas lykanthroparepellens;Dehalogenimonas lykanthroparepellens BL-DC-9
Ga0586324_1333931_609_1073	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3269600.00	2924100.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_1339613_3_1070	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	353035.52	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;Omnitrophica bacterium SCGC AAA257-O07;Omnitrophica bacterium SCGC AAA257-O07 (contamination screened)
Ga0586324_1357176_3_1064	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	738474.88	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatalea;Desulfatalea anilini;Desulfatalea anilini DSM 4660
Ga0586324_1358918_2_1048	0.00	4458774.96	0.00	0.00	41251500.00	0.00	0.00	0.00	665598.06	2394700.00	2420000.00	1305000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithrichaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_1359163_3_863	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1355200.00	1072500.00	KO:K04077	chaperonin GroEL	Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;Thermodesulfatator;Thermodesulfatator autotrophicus;Thermodesulfatator autotrophicus S606
Ga0586324_1365126_1_1062	0.00	312200.24	966136.15	12445000.00	0.00	7185700.00	0.00	24156000.00	2883600.00	0.00	0.00	14925000.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermogutataceae;Thermogutta;Thermogutta terrifontis;Thermogutta terrifontis R1
Ga0586324_1369567_1_1062	0.00	0.00	0.00	0.00	0.00	3267099.59	1936066.56	6649000.00	5151600.00	0.00	1592800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobculales;Thermoanaerobculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_1369892_1_1062	0.00	0.00	0.00	11127653.05	491449.05	5637400.00	14250000.00	5166700.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_1371484_3_1061	5030000.00	17061200.00	14537862.32	4807000.00	29355000.00	5121300.00	5677200.00	5544900.00	26073900.00	30030000.00	26144800.00	6075927.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run_A_D11
Ga0586324_1382410_3_848	0.00	5807200.00	0.00	2128000.00	0.00	0.00	0.00	2696200.00	0.00	2541000.00	4144800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324_1407468_3_650	10800000.00	500537.12	2134608.87	1843000.00	2070300.00	8337000.00	2895600.00	2379000.00	2268000.00	763521.22	1152800.00	1290000.00	KO:K04077	chaperonin GroEL	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_1421778_1_1026	0.00	0.00	1053046.46	9690000.00	5644400.00	709716.90	0.00	2281400.00	5162422.16	4959144.11	22149600.00	4317594.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp4;Nitrosospira sp. Nsp44
Ga0586324_1427317_1_1044	0.00	123711.72	658710000.00	0.00	0.00	25098089.89	0.00	26162900.00	205740000.00	17171000.00	0.00	3412500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdus;Desulfatirhabdus butyrativorans;Desulfatirhabdus butyrativorans DSM 18734
Ga0586324_1446228_3_1037	0.00	132402800.00	5742600.00	3543500.00	0.00	0.00	1910475.84	385202800.00	383826600.00	368060000.00	446652800.00	403995000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_1446626_3_1037	0.00	0.00	0.00	0.00	0.00	0.00	1770586.44	0.00	0.00	0.00	0.00	426674.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_1446785_3_992	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4629900.00	2732042.09	0.00	0.00	68260.95	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidimicrobiia;Acidimicrobiales;Acidimicrobiaceae;Luteiluna;Luteiluna pratensis;Luteiluna pratensis DSM 100886
Ga0586324_1461475_2_613	0.00	0.00	0.00	0.00	0.00	0.00	459315.12	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_1468437_3_1031	1570000.00	0.00	0.00	0.00	907740.03	0.00	0.00	0.00	0.00	307116.81	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-P13 (contamination screened)
Ga0586324_1474597_3_1028	0.00	112850.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_1474646_413_1027	0.00	0.00	0.00	0.00	0.00	1026233.09	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Pandoraea;Pandoraea thiooxydans;Pandoraea thiooxydans DSM 25325
Ga0586324_1474991_1_1029	0.00	0.00	0.00	0.00	0.00	961224.34	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_1486277_166_1023	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	300161.70	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Donga;Donga sp. UHH00060;Donga sp. UHH00060
Ga0586324_1503966_3_1019	0.00	0.00	0.00	0.00	0.00	727994.78	866003.28	4593330.00	2247511.05	0.00	0.00	601467.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1506514_430_1017	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1416800.00	1144000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Ktedonobacteria;Ktedonobacterales;Ktedonobacteraceae;Ktedonosporobacter;Ktedonosporobacter rubrisoli;Ktedonosporobacter rubrisoli JCM 18351
Ga0586324_1513989_3_1016	5162000000.00	14422800.00	27812200.00	23180000.00	262135000.00	29497000.00	31830500.00	253700000.00	279450000.00	293049902.55	235840000.00	259950000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324_1514848_250_1017	0.00	0.00	0.00	443882.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfaciculum;Desulfaciculum infernum;Desulfaciculum infernum DSM 9756
Ga0586324_1522268_2_586	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4197600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324_1525582_340_1014	0.00	0.00	0.00	0.00	83430000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfiburnum;Desulfiburnum benzoelyticum;Desulfiburnum benzoelyticum DSM 28570
Ga0586324_1528050_2_715	0.00	0.00	0.00	0.00	0.00	0.00	1055195.40	0.00	1296000.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadaceae;Gemmatimonas;Gemmatimonas aurantiaca;Gemmatimonas aurantiaca T-27T
Ga0586324_1541617_127_1008	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1611900.00	0.00	1592800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Selenomonadaceae;Selenomonas;Selenomonas ruminantium;Selenomonas ruminantium ATCC 12561
Ga0586324_1542576_2_880	0.00	1101600.00	0.00	0.00	0.00	0.00	0.00	10699400.00	0.00	24178000.00	10208000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324_1553882_3_1004	8230000.00	0.00	0.00	0.00	4109700.00	0.00	0.00	0.00	2972700.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium amorphae CCNWGS0123
Ga0586324_1557960_1_1005	0.00	0.00	0.00	0.00	0.00	0.00	0.00	713700.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_1562043_2_664	0.00	0.00	0.00	0.00	0.00	0.00	0.00	847900.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Calescamantes bacterium JGI 0000106-H18;Calescamantes bacterium JGI 0000106-H18 (contamination screened)
Ga0586324_1563381_71_1003	0.00	0.00	3714500.00	0.00	0.00	0.00	0.00	3446500.00	0.00	3988600.00	2939200.00	2272500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Archangiaceae;Vitioangium;Vitioangium sp. GDMCC 1.1324;Vitioangium sp. GDMCC 1.1324
Ga0586324_1566228_3_1001	0.00	0.00	0.00	0.00	0.00	2060000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Nitririuptoria;Nitririuptorales;Nitririuptoraceae;Nitririuptor;Nitririuptor alkaliphilus;Nitririuptor alkaliphilus DSM 45188
Ga0586324_1569823_11_1000	0.00	0.00	0.00	8284000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_1573006_1_999	0.00	2271200.00	2145030000.00	0.00	7931000.00	2863803.43	1526811.12	9146607.75	1036800000.00	636251.77	473366.96	14100000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_1574824_240_1001	0.00	0.00	0.00	0.00	0.00	1203648.42	0.00	572912.61	0.00	0.00	449738.08	477342.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_1576138_1_999	1830000.00	0.00	0.00	0.00	0.00	0.00	4377600.00	0.00	0.00	0.00	0.00	5047500.00	KO:K04077	chaperonin GroEL	Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Leptospira;Leptospira santarosai;Leptospira santarosai LV160
Ga0586324_1582416_268_999	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	959200.00	1252500.00	1175000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methylocoenaceae;Methylocoenaibacter;Methylocoenaibacter caenitepidi;Methylocoenaibacter caenitepidi Gela4
Ga0586324_1584219_2_997	0.00	0.00	0.00	3213600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324_1584744_3_890	887797.00	1686400.00	0.00	4123000.00	7083333.69	0.00	1557985.56	1030900.00	2405700.00	1309000.00	550693.44	370681.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azoneaceae;Dechloromonas;Dechloromonas aromatica;Dechloromonas aromatica RCB
Ga0586324_1586773_3_644	0.00	0.00	0.00	0.00	478950000.00	491934.61	0.00	171114.15	127170000.00	0.00	0.00	300623.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium alkanii;Bradyrhizobium alkanii WSM1741
Ga0586324_1586944_155_997	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1378600.00	0.00	2279200.00	0.00	1507500.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_1587390_2_772	9340000.00	0.00	0.00	3334500.00	0.00	3001585.99	0.00	0.00	4203900.00	6183100.00	437552.72	5385000.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_1587845_3_995	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3742500.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;unclassified Solirubrobacterales;unclassified Solirubrobacterales;Solirubrobacterales;Solirubrobacterales bacterium URHD0059;Solirubrobacterales bacterium URHD0059
Ga0586324_1588119_3_995	1020000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosovibrio;Nitrosovibrio tenuis;Nitrosovibrio tenuis Nv1
Ga0586324_1616324_3_794	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2490000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_1618843_304_987	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	741179.67	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324_1632142_69_986	753385.00	0.00	1559500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2520000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_1633705_1_984	0.00	0.00	0.00	73438.33	0.00	109275.38	0.00	0.00	0.00	0.00	0.00	4335000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_1644817_1_981	0.00	383282.00	0.00	0.00	0.00	0.00	0.00	0.00	171114.15	0.00	0.00	300623.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_1647724_3_982	0.00	0.00	0.00	4418700.00	0.00	0.00	0.00	3751500.00	0.00	4750900.00	3564000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfaciculum;Desulfaciculum infernum;Desulfaciculum infernum DSM 9756
Ga0586324_1653429_1_978	0.00	0.00	0.00	0.00	0.00	6247200.00	0.00	0.00	0.00	1355200.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Calescamantes bacterium JGI 0000106-H18;Calescamantes bacterium JGI 0000106-H18 (contamination screened)
Ga0586324_1667162_121_975	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	194188.61	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Draconiibacterium;Draconiibacterium sediminis;Draconiibacterium sediminis JN14CK-3
Ga0586324_1671387_3_974	0.00	0.00	0.00	0.00	0.00	0.00	0.00	615634.83	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_1689956_368_970	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3960000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96. DSM 24297
Ga0586324_1697695_2_967	339383.00	8432000.00	0.00	0.00	0.00	0.00	0.00	327652.29	550019.47	2955704.40	565038.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_1698841_195_968	0.00	357763.64	0.00	0.00	0.00	2122512.28	5166700.00	3086100.00	0.00	0.00	7436000.00	636576.00	KO:K04077	chaperonin GroEL	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melliorbacteraceae;Melliorbacter;Melliorbacter roseus;Melliorbacter roseus P3M
Ga0586324_1701721_126_968	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	207911.44	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;

Ga0586324_2129619_1_879	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1082400.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazooensis;Gemmatimonadetes bacterium KB5708
Ga0586324_2141489_1_545	0.00	0.00	6305600.00	0.00	1751000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_2144220_2_778	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2037400.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_2146879_142_876	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	847000.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sinica;Candidatus Brocadia sinica JPN1
Ga0586324_2182224_2_871	0.00	6269600.00	0.00	387559.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324_2187491_2_742	0.00	6371600.00	2837570.67	0.00	1225700.00	0.00	0.00	1367991.49	19388285.90	26719000.00	3493600.00	18525000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. NI5;Nitrosospira sp. NI5
Ga0586324_2190598_208_870	0.00	0.00	0.00	0.00	0.00	5319800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Baggiatoa;Baggiatoa leptomitoformis;Baggiatoa leptomitoformis D-402
Ga0586324_2195520_1_744	0.00	0.00	0.00	175380136.50	0.00	222488863.95	5494800.00	1756800.00	4479300.00	8778000.00	133654400.00	108750000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_2197386_1_867	0.00	0.00	0.00	0.00	0.00	0.00	0.00	744200.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosovibrio;Nitrosovibrio tenuis;Nitrosovibrio tenuis Nv1
Ga0586324_2202714_1_867	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2257000.00	1142100.00	2787400.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324_2204249_1_867	0.00	3264000.00	0.00	0.00	0.00	0.00	0.00	0.00	6002100.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_2205265_3_866	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4459100.00	0.00	0.00	1724800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_2208977_1_489	0.00	0.00	0.00	0.00	1730400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_2214622_1_864	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7931000.00	8060800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio thiophilus;Thermodesulfovibrio thiophilus DSM 17215
Ga0586324_2217974_115_864	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3794200.00	0.00	0.00	2490400.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Dysgonomonadaceae;Dysgonomonas;Dysgonomonas sp. HGC4;Dysgonomonas sp. HGC4
Ga0586324_2230193_337_864	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1762500.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetodovum;Candidatus Magnetodovum chiemensis;Candidatus Magnetodovum chiemensis CS-04
Ga0586324_2230913_1_863	11700000.00	2699600.00	8332400.00	4208500.00	5304500.00	16658092.21	6680400.00	1195600.00	4681800.00	9209200.00	6744600.00	4012500.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2237233_1_831	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4250400.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriales;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_2250524_1_858	0.00	1700000.00	2244714.78	3239500.00	5500200.00	893111.05	3304039.20	3001200.00	5710500.00	2979900.00	2798400.00	19087500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. K;Anaeromyxobacter sp. K
Ga0586324_2252934_1_858	0.00	0.00	813315.43	0.00	0.00	0.00	454476.96	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;Chloroflexi sp. G233
Ga0586324_2270428_3_857	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1262700.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S2Bbf
Ga0586324_2279052_1_854	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	160344.36	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Actinomycetia;Motilibacterales;Motilibacteraceae;Motilibacter;Motilibacter peucedani;Motilibacter peucedani DSM 45328
Ga0586324_2284182_221_853	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8052000.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_2294525_2_853	0.00	0.00	0.00	0.00	0.00	0.00	0.00	872300.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Caldithrichaeota;Caldithrichae;Caldithrichales;Caldithrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324_2297552_1_851	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6645100.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Dehalococcoidia;Dehalococcoidales;Dehalococcoidaceae;Dehalococcoides;Dehalococcoides mccartyi;Dehalococcoides mccartyi VS
Ga0586324_2306912_1_849	0.00	5698400.00	0.00	0.00	0.00	825291.54	0.00	505639.37	20898000.00	28105000.00	1240800.00	1972773.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Pigmentiphaga;Pigmentiphaga sp. MWL080357;Pigmentiphaga sp. MWL080357
Ga0586324_2320362_66_848	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1498500.00	0.00	1214400.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2332701_3_845	11250000.00	2951200.00	774840.01	2377850.00	57401900.00	1431101.63	42499200.00	54210700.00	13365000.00	7422800.00	18392000.00	12204199.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_2340090_3_845	0.00	0.00	1120505.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	333864.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. K;Anaeromyxobacter sp. K
Ga0586324_2348218_132_845	0.00	0.00	0.00	0.00	15367600.00	959473.57	0.00	1923900.00	3410100.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_2343943_3_845	0.00	320208.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PB90-1
Ga0586324_2356242_1_843	0.00	0.00	0.00	0.00	0.00	0.00	0.00	382169.27	0.00	0.00	0.00	195524.25	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2367919_1_821	0.00	0.00	0.00	0.00	0.00	0.00	2095037.28	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324_2368979_1_408	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4611600.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;Thermodesulfobacterium;Thermodesulfobacterium commune;Thermodesulfobacterium commune DSM 2178
Ga0586324_2376545_1_840	0.00	83082.40	110548.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Thermomicrobiales;Thermomicrobiaceae;Thermomicrobium;Thermomicrobium roseum;Thermomicrobium roseum DSM 5159
Ga0586324_2379158_1_840	1030000.00	8092000.00	18871600.00	10640000.00	0.00	23764159.86	183084000.00	16581600.00	0.00	17941000.00	15400000.00	15123750.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2385775_1_837	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2778300.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_2396465_1_836	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3167100.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324_2400886_1_834	0.00	3107600.00	0.00	0.00	6327000.00	0.00	6153500.00	8344800.00	0.00	0.00	9009000.00	10736000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2415240_3_605	0.00	0.00	1959572.17	0.00	0.00	24534600.00	1375856.88	17995000.00	626102.46	0.00	0.00	1095000.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Prolixibacter;Prolixibacter denitrificans;Prolixibacter denitrificans DSM 27267
Ga0586324_2419001_3_833	0.00	0.00	0.00	928317.20	0.00	0.00	5580162.92	0.00	5378400.00	3226300.00	2235200.00	3555000.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324_2421592_452_832	0.00	0.00	0.00	3562500.00	32960000.00	2911923.54	1050142.92	2982900.00	1441800.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_2437204_1_396	0.00	0.00	0.00	819051.05	0.00	0.00	0.00	11102000.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_2437365_3_728	5450000.00	0.00	34624500.00	27170000.00	0.00	8138500.00	1416484.20	3660000.00	456281.10	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methylocaenaceae;Methylocaenaceae;Methylocaenaceae caenitepidi;Methylocaenaceae caenitepidi Gela4
Ga0586324_2437845_84_830	0.00	0.00	0.00	6707000.00	0.00	0.00	0.00	6649000.00	5427000.00	15323000.00	932800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_2445890_1_744	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1445700.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_2448631_313_828	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1240800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_2454760_1_828	3020000.00	0.00	0.00	0.00	0.00	14212600.00	8299200.00	11468000.00	11421000.00	0.00	0.00	6427500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2462045_2_826	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7774800.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_2462393_1_828	3660000.00	2917200.00	5572613.41	3771500.00	2327800.00	6267943.19	3214800.00	2793800.00	5645700.00	6075300.00	0.00	2145000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324_2464544_3_827	0.00	304579.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	862400.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas;Roseomonas lacus;Roseomonas lacus DSM 19439
Ga0586324_2476185_2_826	0.00	604983.08	0.00	0.00	1598873.93	0.00	0.00	169425.06	1077300.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324_2482722_25_825	0.00	0.00	0.00	0.00	1792200.00	0.00	0.00	0.00	0.00	0.00	2736800.00	5542500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2490866_2_823	731086.00	6800000.00	0.00	0.00	1668600.00	0.00	3488400.00	0.00	2762100.00	5374600.00	10208000.00	4755000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas sp. AL212;Nitrosomonas sp. AL212
Ga0586324_2500628_1_821	0.00	72000.00	6812000.00	4351000.00	0.00	0.00	0.00	0.00	0.00	3511200.00	5257500.00	3124000.00	KO:K04077	chaperonin GroEL	Bacteria;Archaea;Euryarchaeota;Methanococcales;Methanococcaceae;Methanococcus;Methanococcus vannielii;Methanococcus vannielii SB;GOMCC1.1324;Methanococcus vannielii SB;GOMCC1.1324
Ga0586324_2506557_338_820	19700000.00	8092000.00	0.00	5485647.70	10437970.56	0.00	0.00	4556700.00	5375842.83	3834600.00	14344000.00	37650000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2529825_3_818	0.00	2985200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7348000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324_2532019_3_710	0.00	0.00	0.00	10355000.00	0.00	0.00	2508000.00	0.00	1490400.00	3126200.00	1869600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Dehalococcoidia;Dehalococcoidales;Dehalococcoidaceae;Dehalococcoides;Dehalococcoides mccartyi;Dehalococcoides mccartyi VS
Ga0586324_2534706_3_818	2250000.00	469943.92	0.00	0.00	529901.01	1746919.10	0.00	0.00	282956.49	3287900.00	0.00	3427500.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacteriales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_2535689_1_816	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10241000.00	7964000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aseroeatus;Bryobacter aseroeatus DSM 18758
Ga0586324_2538623_267_818	0.00	0.00	0.00	5073000.00	0.00	5915300.00	4286400.00	1282000.00	0.00	1008700.00	1689600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_2547692_116_814	0.00	0.00	0.00	0.00	552581.61	2386021.61	1482166.44	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_2551134_150_815	23900000.00	6759200.00	1443284.28	1387000.00	8435700.00	1120341.94	8504400.00	18605000.00	24057000.00	11627000.00	6468000.00	5340000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas;Pseudomonas putida;Pseudomonas putida PC2
Ga0586324_2555285_3_566	0.00	1054000.00	2833229.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324_2558552_1_813	0.00	0.00	0.00	9690000.00	8549000.00	0.00	10009200.00	0.00	7921800.00	6221600.00	6230400.00	5580000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_2561104_240_815	0.00	979200.00	2005912.70	0.00	0.00	0.00	0.00	456243.96	957488.94	413410.23	535074.54	543292.64	1642500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;Dasania;Dasania marina;Dasania marina DSM 21967
Ga0586324_2568076_3_812	0.00	0.00	0.00	771547.25	0.00	0.00	0.00	386546.64	1052623.32	354386.34	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_2577060_3_812	0.00	2000207.76	0.00	8160500.00	0.00	0.00	5722800.00	0.00	2069444.65	0.00	1513600.00	2925000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_2585345_3_755	0.00	7752000.00	0.00	6640500.00	3625600.00	0.00	0.00	0.00	4714200.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_2592073_2_811	0.00	0.00	0.00	7324500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5122500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_2594150_1_810	0.00	0.00	0.00	0.00	1524400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_2598219_50_808	0.00	850000.00	0.00	0.00	0.00	2274559.92	0.00	0.00	0.00	0.00	0.00	1702500.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira moscoviensis;Nitrospira moscoviensis NSP M-1
Ga0586324_2608977_3_806	0.00	3060000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	323808.84	576326.52	2252800.00	3180000.00	KO:K04077	chaperonin GroEL	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema calidum;Treponema calidum DSM 7334
Ga0586324_2611224_1_807	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2543200.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PB90-1
Ga0586324_2614839_1_806	13600000.00	2468400.00	0.00	11495000.00	0.00	0.00	0.00	17556000.00	7759800.00	2094400.00	0.00	7950000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter daltonii;Geobacter daltonii FRC-32
Ga0586324_2626164_1_804	0.00	0.00	0.00	0.00	0.00	188773.25	0.00	0.00	0.00	144689.49	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Caldithrichaeota;Caldithrichae;Caldithrichales;Caldithrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324_2627420_1_354	0.00	0.00	0.00	657867.15	867278.54	0.00	0.00	921100.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_2644344_2_802	0.00	0.00	0.00	1320500.00	510262.00	1611033.94	0.00	0.00	3312900.00	0.00	0.00	174421.50	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Conexibacteraceae;Conexibacter;Conexibacter woese;Conexibacter woese! Iso977N
Ga0586324_2644627_1_804	0.00	0.00	0.00	1444000.00	3780100.00	0.00	0.00	0.00	0.00	3141600.00	3238400.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Planctomycetales;Planctomycetaceae;Planctomyces;Planctomyces sp. SH-PL62;Planctomyces sp. SH-PL62
Ga0586324_2648884_1_803

Ga0586324_3111926_3_749	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	779134.40	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;propionivibrio;propionivibrio pelophilus;Propionivibrio pelophilus DSM 12018
Ga0586324_3117329_278_748	0.00	1020008.16	1462116.63	1125646.45	1165451.18	0.00	0.00	1624370.76	2849000.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio sp. DMSS-1;Desulfovibrio sp. DMSS-1
Ga0586324_3120268_1_750	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2226500.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_3121543_3_749	0.00	0.00	0.00	9690000.00	10609000.00	7900300.00	0.00	5429000.00	40743000.00	0.00	0.00	2227500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324_3130054_1_747	0.00	0.00	4216211.29	0.00	0.00	393808.12	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;Chloroflexi sp. G233
Ga0586324_3131039_471_749	0.00	0.00	0.00	0.00	0.00	0.00	0.00	415677.79	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Methylacidiphilae;Methylacidiphilales;Methylacidiphilaceae;Methylacidiphilum;Methylacidiphilum fumariolicum;Methylacidiphilum fumariolicum SolV
Ga0586324_3137428_2_748	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1409100.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Planctomycetales;Planctomycetaceae;Planctopirus;Planctopirus limnophila;Planctopirus limnophila DSM 3776
Ga0586324_3140418_19_747	5470000.00	13219200.00	15622062.07	23710770.70	5026400.00	4724300.00	4651200.00	8506654.11	27564300.00	6135480.12	12034360.80	6804111.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3164199_1_744	0.00	0.00	0.00	0.00	0.00	592174.81	0.00	0.00	513171.65	0.00	8162000.00	6080800.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Calescamantes bacterium JGI 0000106-H18;Calescamantes bacterium JGI 0000106-H18 (contamination screened)
Ga0586324_3178178_2_742	0.00	0.00	0.00	5339000.00	3110600.00	0.00	0.00	1775100.00	1919700.00	0.00	0.00	937500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tasiolohila;Desulfatitalea tasiolohila SZBdF
Ga0586324_3186407_3_743	0.00	0.00	0.00	0.00	72718000.00	0.00	0.00	158517.65	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. NIS;Nitrosospira sp. NIS
Ga0586324_3189150_1_741	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	571809.70	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_3208261_2_742	0.00	157107.20	876838.72	0.00	0.00	0.00	0.00	668853.22	0.00	0.00	0.00	410690.25	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Calescamantes bacterium JGI 0000106-H18;Calescamantes bacterium JGI 0000106-H18 (contamination screened)
Ga0586324_3211431_3_740	0.00	0.00	0.00	0.00	0.00	6907800.00	0.00	3586800.00	4827600.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Calescamantes bacterium JGI 0000106-H18;Calescamantes bacterium JGI 0000106-H18 (contamination screened)
Ga0586324_3225670_3_740	0.00	0.00	0.00	13870000.00	6656581.00	9611830.52	0.00	6478200.00	7970400.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_3232492_1_738	42700000.00	49000800.00	1632942.09	3667000.00	0.00	0.00	72276000.00	559166.26	8594835.48	52062692.99	62840800.00	3863491.50	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3232943_117_737	0.00	77342.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1927500.00	KO:K04077	chaperonin GroEL	Bacteria;Fibrobacteres;Fibrobacteria;Fibrobacterales;Fibrobacteraceae;Fibrobacter;Fibrobacter sp. UWH2;Fibrobacter sp. UWH2
Ga0586324_3235615_3_737	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1056000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Gemmatimonadetes;Longimicrobia;Longimicrobiales;Longimicrobiaceae;Longimicrobium;Longimicrobium terrae;Longimicrobium terrae CECT 8660
Ga0586324_3239191_75_737	26600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga;Hydrogenophaga sp. Root209;Hydrogenophaga sp. Root209
Ga0586324_3262186_141_734	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	839300.00	0.00	2647500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_3262600_3_464	0.00	0.00	0.00	1168500.00	0.00	0.00	0.00	494744.16	1441800.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_3264575_3_734	0.00	0.00	22294800.00	0.00	0.00	11790900.00	0.00	0.00	0.00	0.00	0.00	2454298.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_3282396_1_732	64000000.00	144368.76	0.00	0.00	0.00	7189400.00	0.00	0.00	0.00	0.00	0.00	891054.75	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteraceae;unclassified Vicinamibacteraceae;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_3285694_3_734	0.00	32912000.00	0.00	0.00	0.00	0.00	0.00	966891.00	2531500.00	2081700.00	4073300.00	3176800.00	3195000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium denitrificans;Hyphomicrobium denitrificans 1NES1
Ga0586324_3285726_1_732	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	683200.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoalkalia;Desulfoalkalia alkanexedens;Desulfoalkalia alkanexedens ALDC
Ga0586324_3287112_3_734	0.00	0.00	0.00	0.00	0.00	0.00	587765.76	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324_3297900_239_733	0.00	0.00	0.00	0.00	0.00	0.00	0.00	606982.33	0.00	0.00	0.00	209139.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3305414_2_730	0.00	0.00	0.00	6745000.00	7210519.65	0.00	0.00	3757600.00	4374000.00	1809500.00	2393600.00	1252500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_3314464_3_731	0.00	795600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324_3321163_3_731	0.00	0.00	0.00	0.00	3162100.00	345022.38	0.00	0.00	0.00	631580.95	275813.12	0.00	0.00	chaperonin GroEL	Bacteria;Actinobacteria;Micromonosporales;Micromonosporaceae;Catenulospora;Catenulospora tetraspora;Catenulospora tetraspora TL-X7
Ga0586324_3323387_115_729	0.00	4807600.00	4349265.08	0.00	0.00	4406700.00	1968214.56	5331400.00	3766500.00	5135900.00	2226400.00	6907500.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Acidimicrobia;Acidimicrobiales;Acidimicrobiaceae;Acidithrix;Acidithrix ferroxidans;Acidithrix ferroxidans Py-F3
Ga0586324_3323437_1_729	0.00	1054000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	594512.38	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Myxococcales;Labilithriceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_3331374_1_729	1060000.00	2271200.00	0.00	19095000.00	14420000.00	18976600.00	0.00	2763000.00	0.00	3340445.60	0.00	19260000.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Deferribacterales;Deferribacteraceae;Deferribacter;Deferribacter desulfuricans;Deferribacter desulfuricans SSM1
Ga0586324_3335780_166_729	0.00	0.00	0.00	0.00	0.00	0.00	0.00	292726.80	0.00	0.00	5227200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Myxococcales;Labilithriceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_3342009_1_720	0.00	843200.00	214171.39	851439.40	51244110.92	0.00	3214800.00	0.00	107730000.00	426879.53	816800.16	1129702.50	KO:K04077	chaperonin GroEL	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Deferribacter;Deferribacter desulfuricans;Deferribacter desulfuricans SSM1
Ga0586324_3344261_1_729	0.00	0.00	399081.42	0.00	0.00	0.00	0.00	6470.74	0.00	0.00	103942.88	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter thermophilus;Desulfobacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324_3344582_1_729	0.00	0.00	0.00	0.00	927546.93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea anilini;Desulfatitalea anilini DSM 4660
Ga0586324_3355633_2_727	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2657600.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP51;Betaproteobacteria bacterium AAP51
Ga0586324_3361432_1_350	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3727500.00	0.00	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_3371734_147_725	0.00	924800.00	6136700.00	1881000.00	0.00	8535500.00	4560000.00	1134600.00	0.00	0.00	4681600.00	567057.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_3377017_1_726	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1884900.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_3398575_2_724	1870000.00	2808400.00	6193000.00	4978000.00	6715600.00	5983600.58	1133300.58	4922700.00	3863700.00	5905900.00	5744640.00	5317500.00	5744000.00	chaperonin GroEL	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium DSM 7334
Ga0586324_3400072_2_724	24081504.00	27472000.00	14697887.44	10317000.00	18231000.00	5597700.00	20100337.24	43693258.12	36155151.90	3938409.09	1570754.24	6855000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. HYN0024;Dechloromonas sp. HYN0024
Ga0586324_3400951_1_699	0.00	0.00	0.00	0.00	0.00	520371.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. UNP
Ga0586324_3414522_214_723	395330.00	0.00	0.00	0.00	0.00	0.00	21386400.00	0.00	0.00	0.00	682144.54	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Citriformentans;Citriformentans bemidjiense;Geobacter bemidjiensis Bem. DSM 16622
Ga0586324_3419838_3_692	7800000.00	5074378.84	0.00	7562000.00	22763000.00	0.00	0.00	1250500.00	826200.00	35805000.00	416334.16	7080000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea anilini;Desulfatitalea anilini DSM 4660
Ga0586324_3420012_1_720	0.00	0.00	0.00	0.00	0.00	1422538.34	1299260.28	0.00	1992600.00	1771000.00	2543200.00	604921.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium canariense;Bradyrhizobium canariense GAS369
Ga0586324_3425726_3_722	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	251043.76	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_3430765_2_721	0.00	0.00	0.00	0.00	7159834.19	1883082.16	2394000.00	3233000.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Actinobacteria;Micrococcales;Micrococcineae;Dermacoccaceae;Dermacoccus;Dermacoccus sp. Ellin074;Dermacoccus sp. Ellin074
Ga0586324_3452042_1_717	0.00	0.00	0.00	11666000.00	16768400.00	0.00	9758400.00	12407400.00	14450400.00	0.00	0.00	7575000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_3452105_3_719	7520000.00	795600.00	1691201.33	4047260.30	2348400.00	392783.07	5571262.08	2366800.00	4479300.00	1355200.00	1664084.40	3352500.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-K07;Aminicenantes bacterium SCGC AAA252-K07 (contamination screened)
Ga0586324_3495019_2_661	0.00	1684400.00	0.00	0.00	0.00	0.00	0.00	0.00	1229100.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3473796_1_717	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4567500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhizomicrobium;Rhizomicrobium sp. SG733;Rhizomicrobium sp. SG733
Ga0586324_3482647_2_715	41280000.00	0.00	6305600.00	28376500.00	0.00	10599900.00	19174800.00	36500507.78	17455500.00	0.00	11744937.68	20992281.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324_3486370_1_714	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	577387.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Sedisaxicola;Saxitoxin biosynthesis;Saxitoxin biosynthesis;unclassified Saxitoxin biosynthesis;Saxitoxin biosynthesis;Saxitoxin biosynthesis bacterium LR76;Saxitoxin biosynthesis bacterium LR76
Ga0586324_3487625_3_716	0.00	0.00	0.00	337749.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324_3498205_2_715	0.00	0.00	0.00	0.00	0.00	0.00	2462400.00	884500.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Chloroflexi;Ktedonobacteria;Thermogemmatispirales;Thermogemmatispiraceae;Thermogemmatispora;Thermogemmatispora carboxidivorans;Thermogemmatispora carboxidivorans PMS
Ga0586324_3529693_3_713	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3095400.00	2305600.00	2872500.00	2872500.00	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium oligotrophicum;Bradyrhizobium oligotrophicum S58
Ga0586324_3531000_1_678	0.00	5582800.00	0.00	0.00	0.00	0.00	0.00	4202900.00	0.00	0.00	0.00	437552.72	0.00	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3533483_3_713	0.00	0.00	0.00	0.00	0.00	0.00	469132.80	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_3535917_216_710	0.00	214574000.00	251817221.24	4788000.00	57577000.00	234687.46	237781840.68	2623000.00	2907900.00	3542000.00	2852200.00	7575000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylocaldum;Methylocaldum szegediense O-12
Ga0586324_3544692_347_712	0.00	0.00	0.00	0.00	0.00	0.00	6490024.99	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Anaerophaga;Anaerophaga thermohalophila;Anaerophaga thermohalophila Fru2;Fru2 DSM 12881
Ga0586324_3552823_3_710	0.00	321051.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithriceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_3565782_40_708	0.00	0.00	0.00	0.00	0.00	0.00	0.00	756400.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter tataouinensis;Ramlibacter tataouinensis 5-10
Ga0586324_3566641_3_710	4900000.00	6596000.00	0.00	6821000.00	23690000.00	0.00	7729200.00	1201700.00	10287000.00	18641833.98	17424000.00	8100000.00	8100000.00	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3581984_3_677	0.00	0.00	0.00	0.00	0.00	0.00	6270000.00	5172800.00	0.00	0.00	0.00	4492500.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Isosphaerales;Isosphaeraceae;Paludisphaera;Paludisphaera borealis;Paludisphaera borealis PX4
Ga0586324_3588271_269_706	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	615008.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Alcanivoracaceae;Ketobacter;Ketobacter alkanivorans;Ketobacter alkanivorans GI5
Ga0586324_3589496_244_708	3510000.00	170325.72	2938860000.00	0.00	0.00	329510000.00	339720000.00	267790000.00	722485.17	0.00	0.00	281250000.00	281250000.00	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium UKL13-2;Betaproteobacteria bacterium UKL13-2
Ga0586324_3606452_3_707	11000000.00	0.00	0.00	0.00	0.00	0.00	3602400.00	29463000.00	30500136.09	34881000.00	94705600.00	4240307.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalkalivibrio;Thioalkalivibrio sulfidiphilus;Thioalkalivibrio sulfidiphilus ALJ17
Ga0586324_3610909_3_704	0.00	0.00	0.00	0.00	214685.69	0.00	0.00	0.00	72425.91	358619.80	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_3620236_3_704	0.00	0.00	0.00	0.00	0.00	0.00	293748.55	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_3621639_2_703	0.00	337231.04	0.00	0.00	0.00	0.00	0.00	329081.58	0.00	0.00	0.00	641472.00	KO:K04077	chaperonin GroEL	Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;Thermosulfuriphilus;Thermosulfuriphilus ammonigenes;Thermosulfuriphilus ammonigenes DSM 102941
Ga0586324_3632849_2_703	0.00	2101200.00	0.00	4759500.00	0.00	856618.81	9325200.00	0.00	990826.02	0.00	0.00	409087.50	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_3645514_1_702	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1195600.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas;Gemmatimonas aurantiaca;Gemmatimonas aurantiaca T-27T
Ga0586324_3654207_2_703	0.00	0.00	0.00	0.00	638749.35	0.00	0.00	0.00	342587.88	0.00	1856800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_3657405_2_700	0.00	1122000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3665444_3_701	0.00	0.00	0.00	0.00	0.00	3990000.00	0.00	0.00	0.00	968000.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324_3678384_2_418	0.00	1795200.00	0.00	0.00	8013400.00	0.00	0.00	9455000.00	0.00	6106100.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula

Ga0586324_4259349_3_554	0.00	0.00	0.00	0.00	68598000.00	2049460.89	75696000.00	6649000.00	59292000.00	10010000.00	7268800.00	7072500.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Granulicella;Granulicella tundricola;Granulicella tundricola MP5ACTX9
Ga0586324_4259535_112_660	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2987600.00	0.00	3435000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_4278833_1_324	0.00	0.00	4173654.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;Spartobacteria bacterium LR76;Spartobacteria bacterium LR76
Ga0586324_4286601_3_656	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	254527.35	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter soli;Solirubrobacter soli DSM 22325
Ga0586324_4301111_56_655	0.00	0.00	0.00	0.00	846718.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_4308896_3_656	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	850407.36	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_4308974_1_657	3880000.00	5084400.00	7769400.00	10715647.55	10650000.00	9766200.00	10129558.92	9636049.83	10068300.00	2156000.00	1082400.00	7312500.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-01, DSM 14535
Ga0586324_4323996_114_656	56700000.00	10812000.00	0.00	676506.40	5057300.00	3802473.94	8572800.00	1903200.00	6868800.00	1208900.00	0.00	5722500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_4334130_2_655	0.00	451908.28	0.00	0.00	0.00	0.00	1527043.68	0.00	1059032.88	0.00	69327.72	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilithrichaeae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324_4342412_22_654	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	406300.40	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Aquamicrobium;Aquamicrobium sp. LC103;Aquamicrobium sp. LC103
Ga0586324_4355537_1_654	0.00	0.00	0.00	551211.85	0.00	0.00	8185200.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorobi;Ignavibacteria;Ignavibacterales;Ignavibacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus mccarthyi VS
Ga0586324_4359722_3_521	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	777388.48	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_4372848_1_653	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	334632.75	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_4383847_2_589	0.00	124104.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Pelobacter;Pelobacter propionicus;Pelobacter propionicus DSM 2379
Ga0586324_4391855_2_649	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	241465.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_4394556_3_650	0.00	19094400.00	0.00	0.00	0.00	0.00	3830400.00	0.00	12636000.00	0.00	0.00	15975000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus sp. RS-1;Roseiflexus sp. RS-1
Ga0586324_4395021_16_651	0.00	0.00	0.00	0.00	0.00	0.00	0.00	553091.27	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter pauli;Solirubrobacter pauli DSM 14954
Ga0586324_4402008_3_650	30500000.00	28696000.00	0.00	9500000.00	7838300.00	0.00	35112000.00	16104000.00	15228000.00	14014000.00	2164800.00	13200000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_4436809_1_648	0.00	0.00	0.00	0.00	0.00	2615662.29	0.00	780800.00	1432903.77	367646.51	0.00	165000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324_4441838_3_482	0.00	0.00	0.00	1678900.00	0.00	2185284.24	0.00	0.00	0.00	0.00	2384800.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chlorobi;unclassified Chlorobi;Ignavibacteria;Caldithrichaeota;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324_4469378_1_645	220452.00	0.00	151578.18	0.00	5445936.51	255260.68	153855.54	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter sp. URHD0082;Solirubrobacter sp. URHD0082
Ga0586324_4474121_3_644	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1532300.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;Myxococcus;Myxococcus stipitatus;Myxococcus stipitatus DSM 14675
Ga0586324_4485548_2_646	0.00	42175.64	0.00	259580.85	1442000.00	0.00	248668.20	240782.25	1344600.00	1416800.00	205018.88	136044.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldaricum;Desulfosoma caldaricum DSM 22027
Ga0586324_4498965_1_645	0.00	0.00	0.00	0.00	0.00	0.00	0.00	568869.53	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_4500219_1_498	0.00	0.00	0.00	0.00	2523500.00	5081600.00	0.00	1848300.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_4514096_3_644	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3172500.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_4517468_3_644	0.00	0.00	0.00	0.00	852664.69	0.00	2074000.00	0.00	0.00	0.00	3132800.00	2287500.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Thermomicrobiales;Thermomicrobiaceae;Thermomicrobium;Thermomicrobium roseum;Thermomicrobium roseum DSM 5159
Ga0586324_4518090_3_644	0.00	467619.00	0.00	0.00	0.00	0.00	0.00	2616900.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina cetonica;Desulfosarcina cetonica JCM 12296
Ga0586324_4523952_1_642	0.00	0.00	0.00	6944500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_4547106_1_642	0.00	2121600.00	0.00	0.00	2544100.00	0.00	0.00	0.00	2690100.00	13851000.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfocapsa;Desulfocapsa sp. DSM 2909;Desulfocapsa sp. DSM 2909
Ga0586324_4549495_2_640	0.00	1878540.80	0.00	0.00	5150000.00	1054842.10	10168800.00	0.00	0.00	8547000.00	5850471.44	6909438.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_4567459_1_639	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	480523.89	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_4573927_2_490	0.00	132283.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Ignavibacteria;Ignavibacterales;Ignavibacteraceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album MarS-16, JCM 16511
Ga0586324_4581071_3_587	0.00	334615.76	0.00	307096.05	0.00	0.00	0.00	1713181.34	0.00	29087537.71	681183.36	19335823.50	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_4585246_1_639	0.00	0.00	0.00	0.00	0.00	2104113.96	3845400.00	0.00	0.00	0.00	0.00	1627500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_4606629_2_637	0.00	1679600.00	0.00	1786000.00	16583000.00	12862800.00	0.00	1256000.00	9072000.00	0.00	0.00	1050000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_4602367_2_637	506025.00	0.00	0.00	1919000.00	0.00	0.00	0.00	788353.32	0.00	0.00	0.00	1328800.00	1282500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324_4603950_1_603	0.00	0.00	0.00	219808245.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter pauli;Solirubrobacter pauli DSM 14954
Ga0586324_4607544_3_637	1340000.00	0.00	2751904.59	0.00	0.00	0.00	1245821.28	591061.94	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_4611682_2_637	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4673700.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tesiidohila;Desulfatitalea tesiidohila S28bF
Ga0586324_4629872_1_636	0.00	0.00	0.00	424421.05	0.00	400970.00	0.00	10614000.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_4647469_3_434	0.00	567120.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium metallidurans;Mesorhizobium metallidurans STM 2683
Ga0586324_4716647_3_632	0.00	8092000.00	2825460.54	25935000.00	4253900.00	1216546.95	936893.04	6527000.00	4463100.00	1393700.00	4963200.00	4732500.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_4716648_3_632	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1963500.00	5139200.00	0.00	0.00	chaperonin GroEL	Bacteria;Verrucomicrobia;Spartobacteria;Chthoniobacterales;Chthoniobacteraceae;Chthoniobacter;Chthoniobacter flavus;Chthoniobacter flavus Ellin428
Ga0586324_4729509_3_632	518021.00	439524.12	0.00	1301613.05	833171.71	0.00	250473.96	0.00	616475.61	291502.75	296303.92	2354713.25	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_4793002_3_632	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2924100.00	0.00	0.00	795000.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Asinibacterium;Asinibacterium sp. OR53;Asinibacterium sp. OR53
Ga0586324_4749751_117_629	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1061100.00	0.00	0.00	0.00	6787500.00	KO:K04077	chaperonin GroEL	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Oscillatoriales;Microcoleaceae;Microcoleus;Microcoleus vaginatus;Microcoleus vaginatus PCC 9802
Ga0586324_4776489_1_627	1200000.00	4624000.00	6924900.00	14706000.00	8415100.00	16396100.00	6311149.44	10040600.00	4568400.00	7623000.00	0.00	3217500.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Rhodopirellula;Rhodopirellula baltica;Rhodopirellula baltica BR-MGV
Ga0586324_4786800_1_627	0.00	2325600.00	0.00	0.00	10609000.00	0.00	0.00	0.00	0.00	9317000.00	15400000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_4797338_3_626	685468.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324_4815664_3_626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7753900.00	2244000.00	0.00	0.00	chaperonin GroEL	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Ilumatobacteraceae;Ilumatobacter;Ilumatobacter coccineus;Ilumatobacter coccineus YM16-304
Ga0586324_4917938_2_238	0.00	0.00	3258500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 83;Acidobacteriaceae bacterium KBS 83;Acidobacteriaceae bacterium KBS 83
Ga0586324_4821613_1_627	0.00	0.00	0.00	14345000.00	0.00	6550500.00	32832000.00	7686000.00	13527000.00	0.00	0.00	41025000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_4869981_3_614	2931662.00	18645600.00	1396493.35	8711500.00	1627400.00	6812889.21	154564373.76	1116300.00	6034500.00	1747900.00	3335200.00	6142500.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324_4876188_3_623	0.00	0.00	0.00	5177500.00	0.00	0.00	0.00	1110200.00	4390200.00	2048200.00	1584000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Caldithrichaeota;Caldithrichaeota;Caldithrichaeotaclasses;Caldithrichaeotaclasses;Caldithrichaeotaclasses;Caldithrichaeotaclasses;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324_4877856_1_624	0.00	918000.00	543259.53	284928.85	902200.69	630332.78	928511.76	0.00	312974.28	487236.75	491801.68	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JAD2
Ga0586324_4900110_3_623	0.00	0.00	0.00	374012.15	0.00	0.00	0.00	6319600.00	4365900.00	0.00	9768000.00	915000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_4923818_2_622	0.00	463816.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2772000.00	0.00	11775000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Perminiibacter;Perminiibacter aggregans;Perminiibacter aggregans DSM 103792
Ga0586324_4929362_3_620	0.00	2080800.00	0.00	0.00	798835.04	0.00	764848.80	501829.92	718896.06	0.00	3499135.20	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_4931654_1_621	0.00	0.00	0.00	1140000.00	0.00	0.00	0.00	2049420.05	0.00	0.00	2490400.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfofaba;Desulfofaba sp. IMCC35005;Desulfofaba sp. IMCC35005
Ga0586324_4961026_1_618	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	274354.50	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-P13;Aminicenantes bacterium SCGC AAA252-P13 (contamination screened)
Ga0586324_4976400_3_617	9160000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12750000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324_4977351_1_618	0.00	0.00	0.00	0.00	0.00	0.00	206268.64	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. K;Anaeromyxobacter sp. K
Ga0586324_4995475_21_616	0.00	0.00	0.00	0.00	2235100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas formicexedens;Dehalogenimonas formicexedens NSZ-14
Ga0586324_5001488_1_618	0.00	0.00	0.00	15675000.00	20394000.00	5994700.00	8572800.00	22509000.00	33939000.00	0.00	0.00	8400000.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_5012340_3_617	0.00	564519.00	0.00	1624500.00	0.00	0.00	0.00	6319600.00	4365900.00	0.00	9768000.00	915000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_5020227_3_617	0.00	0.00	0.00	2280000.00	0.00	1063900.00	0.00	0.00	0.00	2772000.00	0.00	11775000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324_5051796_3_614	5110000.00	4569600.00	5742600.00	4978000.00	4902800.00	11116000.00	20235392.16	16592000.00	17496000.00	10503800.00	17327576.64	42292500.00	KO:K04077	chaperonin GroEL	Bacteria;unclassified Bacteria;candidate division WS3;Aerophobetes;Aerophobetes bacterium RIFOXYA2_FULL_53_18;Aerophobetes bacterium RIFOXYA2_FULL_53_18
Ga0586324_5082657_1_612	0.00	113560000.00	123297000.00	4835500.00	455290.90	10401400.00	1162859.28	2732800.00	3993300.00	80749900.00	1240800.00	1300700.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Haliangium;Haliangium ochraceum;Haliangium ochraceum SMP-2, DSM 14365
Ga0586324_5087721_2_565	0.00	0.00	0.00	347593.60	292683.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_5100556_3_611	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1155000.00	1645600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Solibacterales;Candidatus Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_5106740_2_610	0.00	5274607.00	8235445.77	0.00	0.00	0.00	4719600.00	0.00	0.00	0.00	9847200.00	0.00	0.00	chaperonin GroEL	Bacteria;Caldithrichaeota;Caldithrichae;Caldithrichales;Caldithrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324_5123223_2_610	0.00	1373600.00	28938200.00	4522000.00	14584800.00	4930432.33	2021028.48	8418000.00	1709100.00	7045500.00	20592000.00	3435653.25	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_5144876_1_609	0.00	130576.32	0.00	0.00	0.00	0.00	0.00	1415200.00	3977100.00	2933700.00	591634.32	23302500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira lacus;Nitrosospira lacus APG3
Ga0586324_5147362_3_608	0.00	149946.80	0.00	0.00	0.00	0.00	0.00	115874.99	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira lacus;Nitrosospira lacus APG3
Ga0586324_5179038_28_609	0.00	0.00	0.00	0.00	0.00	0.00	0.00	171453.31	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Woeseiaceae;Woeseia;Woeseia oceani;Woeseia oceani XK5
Ga0586324_5180716_2_607	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	152547.75	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Actinomycetia;Micromonosporales;Micromonosporaceae;unclassified Micromonosporaceae;Micromonosporaceae bacterium URHE0070;Micromonosporaceae bacterium URHE0070
Ga0586324_5184255_2_607	6720000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylocaldum;Methylocaldum szegediense;Methylocaldum szegediense O-12
Ga0586324_5213937_3_605	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	29392000.00	0.00	0.00	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacte

Ga0586324 6068063 3 569	0.00	0.00	1404240.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1650000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp1;Nitrosospira sp. 1 Nsp1
Ga0586324 6069053 2 568	0.00	0.00	0.00	3990000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 6077464 2 568	0.00	0.00	0.00	0.00	0.00	0.00	3351600.00	0.00	1020600.00	0.00	0.00	168988.50	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324 6080026 2 460	0.00	416703.32	409008.24	0.00	278682.98	0.00	1736587.08	0.00	0.00	137850.79	412532.56	429447.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfarculus;Desulfarculus baarsii;Desulfarculus baarsii 2st14, DSM 2075
Ga0586324 6104940 1 567	0.00	620642.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6110030 2 568	0.00	31076000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324 6157797 1 567	0.00	473645.84	0.00	378426.80	0.00	0.00	0.00	250415.37	0.00	0.00	11968000.00	459647.25	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Bipolaricaulota;unclassified Candidatus Bipolaricaulota;unclassified Candidatus Bipolaricaulota;unclassified Candidatus Bipolaricaulota;unclassified Candidatus Bipolaricaulota;Acetothermia bacterium SCGC AAA255-C06;Acetothermia bacterium SCGC AAA255-C06 (contamination screened)
Ga0586324 6160721 50 565	0.00	0.00	0.00	0.00	0.00	0.00	0.00	394542.51	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324 6163184 1 567	1030000.00	0.00	19705000.00	13110000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Haliangium;Haliangium ochraceum;Haliangium ochraceum SMP-2, DSM 14365
Ga0586324 6165917 309 566	0.00	0.00	0.00	6802000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 6169713 1 564	28200000.00	335890.76	0.00	0.00	3821300.00	42885.53	631888.32	915000.00	834300.00	0.00	723562.40	549723.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 6169737 47 565	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1488400.00	1587600.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 6186299 2 565	1320000.00	1341155.16	916890.54	12969268.90	763297.98	389144.56	6657600.00	5715700.00	19311710.58	12080728.66	1874400.00	2632500.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6188187 1 564	308111.00	0.00	0.00	0.00	165220.24	0.00	0.00	0.00	320109.57	1001000.00	915200.00	584372.25	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 6194576 2 565	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1421300.00	0.00	0.00	0.00	832500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS478
Ga0586324 6199609 1 564	7530000.00	355965.04	0.00	0.00	0.00	0.00	256903.56	2067900.00	0.00	0.00	0.00	2062500.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Dehalococcoidia;Dehalococcoidales;Dehalococcoidaceae;Dehalococcoides;Dehalococcoides mccartyi;Dehalococcoides mccartyi VS
Ga0586324 6225363 3 563	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3944700.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Actinomycetia;Kineosporiales;Kineosporiaceae;Quadrisphaera;Quadrisphaera granulorum;Quadrisphaera granulorum DSM 44889
Ga0586324 6232871 3 563	0.00	0.00	10809600.00	0.00	4635000.00	0.00	0.00	0.00	5621400.00	3826900.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax ferrireducens;Rhodoferax ferrireducens T118
Ga0586324 6237511 1 564	3080000.00	1989810.56	5092351.89	5272412.60	2407553.93	2289967.46	3671830.56	2726700.00	26885531.34	6375600.00	0.00	5805000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 6241248 3 563	0.00	0.00	0.00	23560000.00	26368000.00	0.00	0.00	0.00	24786000.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 6251764 1 561	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	126623.42	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas formicexedens;Dehalogenimonas formicexedens NSZ-14
Ga0586324 6255740 3 563	0.00	272127.84	0.00	0.00	0.00	0.00	20998800.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS138
Ga0586324 6262026 1 561	21000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Trinickia;Burkholderia dabaoshanensis;Burkholderia dabaoshanensis GIMN1.004
Ga0586324 6263746 3 563	0.00	0.00	447184.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium sulfonivorans;Hyphomicrobium sulfonivorans S1
Ga0586324 6270258 2 562	120420.00	0.00	0.00	1140000.00	0.00	0.00	1987523.88	0.00	0.00	174106.24	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 6274565 25 561	0.00	0.00	1862494.08	0.00	0.00	736502.49	1552556.88	447973.02	0.00	0.00	976800.00	1350000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324 6292103 2 562	0.00	0.00	0.00	1064000.00	853716.53	719546.62	0.00	1192963.58	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 6347514 2 559	0.00	958800.00	0.00	82175000.00	2389600.00	0.00	1373175.60	9064600.00	1449900.00	3056900.00	1760000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 6405313 3 557	8774003.00	8228000.00	9685960.66	541735.60	0.00	0.00	7476512.16	7191900.00	5653800.00	971730.76	775795.68	840000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 6427977 1 555	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1316700.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324 6430205 1 555	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3625600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6431274 175 555	0.00	0.00	0.00	0.00	0.00	43273000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium ailaaui;Acidobacterium ailaaui PMMR2
Ga0586324 6433814 3 557	0.00	0.00	0.00	80479.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 6456891 3 554	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1891000.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 6468426 2 553	0.00	0.00	283686.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 6482771 3 554	0.00	0.00	0.00	3477000.00	0.00	0.00	0.00	3580700.00	3661200.00	0.00	0.00	5512500.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 6515392 1 552	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	127816.38	0.00	445542.24	559033.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 6528097 2 553	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	670432.07	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Leptospira;Leptospira santarosai;Leptospira santarosai U160
Ga0586324 6529464 1 552	0.00	0.00	0.00	0.00	1802500.00	0.00	0.00	114983.17	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324 6534835 1 552	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17415000.00	0.00	0.00	364927.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium UKL13-2;Betaproteobacteria bacterium UKL13-2
Ga0586324 6580831 2 550	0.00	8903659.56	0.00	0.00	0.00	0.00	22800000.00	6466000.00	1524904.38	498793.68	0.00	453739.50	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;Omnitrophica bacterium SCGC AAA011-L16;Omnitrophica bacterium SCGC AAA011-L16 (contamination screened)
Ga0586324 6589958 2 550	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	477627.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6606580 3 551	0.00	0.00	3430617.98	0.00	0.00	0.00	0.00	1598597.72	2162700.00	1617000.00	707469.84	2055000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 6609767 2 550	1050000.00	0.00	10809600.00	8132000.00	0.00	378508.53	1123130.28	829600.00	0.00	600569.20	985600.00	3217500.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus sp. RS-1;Roseiflexus sp. RS-1
Ga0586324 6649781 1 549	0.00	0.00	1153896.65	1605500.00	0.00	963999.37	0.00	902490.73	1125900.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 6662179 1 549	3340000.00	0.00	0.00	178600000.00	12360000.00	0.00	0.00	124086200.00	71358.08	0.00	0.00	113250000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Steroidobacter;Steroidobacter denitrificans;Steroidobacter denitrificans DSM 18526
Ga0586324 6683545 3 548	0.00	3740000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3395700.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 6691141 3 548	0.00	0.00	361015.31	0.00	15450000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Prolixibacter;Prolixibacter denitrificans;Prolixibacter denitrificans DSM 27267
Ga0586324 6694713 3 548	0.00	0.00	0.00	0.00	0.00	31442400.00	0.00	13054000.00	0.00	0.00	0.00	13350000.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6704468 3 545	0.00	0.00	0.00	0.00	0.00	416703.11	0.00	0.00	0.00	0.00	0.00	840000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 6722068 3 545	320015.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter postgatei;Desulfobacter postgatei 2ac9
Ga0586324 6723171 2 547	0.00	0.00	0.00	0.00	8126700.00	0.00	0.00	0.00	0.00	1509200.00	0.00	164094.75	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 6731884 3 545	0.00	292791.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6764480 1 543	0.00	0.00	0.00	0.00	38728000.00	0.00	0.00	0.00	3045600.00	691801.88	675114.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324 6782897 3 545	0.00	0.00	0.00	0.00	1246300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;Deferribacteraceae;Deferribacter;Deferribacter desulfuricans;Deferribacter desulfuricans SSM1
Ga0586324 6827283 1 543	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3229600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium valentinum;Bradyrhizobium valentinum LmjM6
Ga0586324 6898969 3 539	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18361000.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;Bacteroides graminisolvens;Bacteroides graminisolvens DSM 19988
Ga0586324 6902509 1 540	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3775200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 6926734 2 538	0.00	0.00	0.00	0.00	0.00	1904405.03	0.00	0.00	0.00	0.00	0.00	922500.00	KO:K04077	chaperonin GroEL	Bacteria;Firmicutes;Clostridia;Thermosediminibacterales;Thermosediminibacteraceae;Caldanaerovirga;Caldanaerovirga acetigignens;Caldanaerovirga acetigignens DSM 18802
Ga0586324 6960467 3 329	0.00	0.00	1245249.03	0.00	0.00	0.00	0.00	0.00	1080420.12	0.00	0.00	952500.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 6963065 2 538	0.00	0.00	0.00	0.00	0.00	0.00	0.00	199719.49	0.00	140721.35	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Propionicimonas;Propionicimonas paludicola;Propionicimonas paludicola DSM 15597
Ga0586324 6980858 1 537	0.00	0.00	0.00	0.00	325195.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 6993014 1 537	0.00	0.00	35975700.00	0.00	2472000.00	0.00	36936000.00	17690000.00	0.00	3873100.00	4408800.00	47250000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Prosthecomicrobium;Prosthecomicrobium hirschii;Prosthecomicrobium hirschii ATCC 27832
Ga0586324 7029147 3 536	0.00	1428000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	155865.60	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium UKL13-2;Betaproteobacteria bacterium UKL13-2
Ga0586324 7047159 2 535	62000000.00	584231.52	54048000.00	111055000.00	64313200.00	44148857.43	95463600.00	232562500.00	42006600.00	118903400.00	119539200.00	4995000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilitrichaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324 7087088 2 469	0.00	0.00	0.00	0.00	0.00	6709300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta bajacaliforniensis;Sediminispirochaeta bajacaliforniensis DSM 16054
Ga0586324 7087981 20 535	0.00	0.00	0.00	627854.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324 7135665 3 476	0.00	0.00	30739800.00	0.00	260994.79	1433428.05	307396.44	835700.00	4884300.00	7107100.00	7436000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA255-E10 (contamination screened)
Ga0586324 7138747 3 533	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9801000.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium sulfonivorans;Hyphomicrobium sulfonivorans S1
Ga0586324 7156591 1 531	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1207800.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324 7212010 2 529	0.00	516074.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324 7234226 2 529	0.00	0.00	0.00	0.00	0.00	0.00	0.00	282720.97	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 7284117 2 529	0.00	514882.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Ilumatobacteraceae;Desertimonas;Desertimonas flava;Acidimicrobiales bacterium SYSU D60003
Ga0586324 7300269 2 526	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	874800.00	3711400.00	5112800.00	3915000.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 7329156 3 527	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1670900.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;Porticoccus;Porticoccus hydrocarbonoclasticus;Porticoccus hydrocarbonoclasticus MCTG13d
Ga0586324 7354239 1 525	110690.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Actinomycetia;unclassified Actinomycetia;unclassified Actinomycetia;unclassified Actinomycetia;Actinobacteria bacterium IMCC26256;Actinobacteria bacterium IMCC26256
Ga0586324 7362969 3 524	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	699338.64	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Propionibacteriaceae;Microlunatus;Microlunatus phosphovorus;Microlunatus phosphovorus NM-1
Ga0586324 7369589 3 524	3730000.00	2923475.72	6699700.00	0.00	3605000.00	3518670.55	7341600.00	29456900.00	4673700.00	14606900.00	3748800.00	25605000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 7383262 2 526	0.00	0.00	0.00	911141.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;unclassified Chitinophagaceae;Chitinophagaceae bacterium PMP191F;Chitinophagaceae bacterium PMP191F
Ga0586324 7387731 1 525	0.00	4882400.00	7037500.00	0.00	0.00	0.00	8709600.00	0.00	0.00	5397700.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Sutterellaceae;Sutterella;Sutterella wadsworthensis;Sutterella wadsworthensis 2 1 59BFAA
Ga0586324 7390304 1 525	0.00	0.00	0.00	0.00	0.00	28822200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium zavarzinii;Hyphomicrobium zavarzinii ATCC 27496
Ga0586324 7390395 3 524	0.00	0.00	2982942.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10800000.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Calescamantes bacterium JGI 0000106-H18;Calescamantes bacterium JGI 0000106-H18 (contamination screened)
Ga0586324 7453023 1 522	0.00	0.00	0.00	0.00	0.00	0.00	15481200.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324 7460490 3 521	0.00	264831.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324 7486040 3 521	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2242500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas;Roseomonas gilardii;Roseomonas gilardii rosea ATCC BAA-691
Ga0586324 7504413 1 522	0.00	195178.36	15369900.00	0.00	0.00	0.00	2622000.00	1464000.00	0.00	1162700.00	1826153.12	1425000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324 7531220 2 520	0.00	1353200.00	0.00	2289500.00	0.00	0.00	9943091.40	2305800.00	2203200.00	0.00	5852000.00	5971766.25	KO:K04077	chaperonin GroEL	Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Leptospira;Leptospira santarosai;Leptospira santarosai CBC379
Ga0586324 7539811 3 521	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	802500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Micropepsales;Micropepsaceae;Rhizomicrobium;Rhizomicrobium sp. SG733;Rhizomicrobium sp. SG733
Ga0586324 7547027 3 521	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	429302.72	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosovibrio;Nitrosovibrio sp. Nv17;Nitrosovibrio sp. Nv17
Ga0586324 7552295 2 520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	242704.97	609689.43	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sinica;Candidatus Brocadia sinica JPN1
Ga0586324 7556382 3 521	0.00	2495600.00	2314639.38	4436500.00	4489526.92	0.00	4793412.72	1464000.00	955706.04	0.00	2912800.00	10950000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324 7574551 1 519	4048046.00	5542000.00	2698976.96	4968500.00	13052879.97	0.00	0.00	1061400.00	641042.91	5459300.00	0.00	2512500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilitrichaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324 7588146 2 520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	260086.14	0.00	418093.28	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 7590119 1 519	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2194500.00	1073600.00	885000.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospinae;Nitrospinia;Nitrospinales;Nitrospinaceae;Candidatus Nitromaritima;Candidatus Nitromaritima sp. SCGC AAA799-A02;Candidatus Nitromaritima sp. SCGC AAA799 A02
Ga0586324 7591954 2 520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3836900.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;Omnitrophica bacterium SCGC AAA257-O07;Omnitrophica bacterium SCGC AAA257-O07 (contamination screened)
Ga0586324 7595243 1 339	0.00	0.00	0.00	0.00	7951600.00	6312300.00	0.00	0.00	2802600.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Roseimarinus;Roseimarinus sediminis;Roseimarinus sediminis DSM 28824
Ga0586324 7602981 1 519	0.00	0.00	0.00	0.00	426849.51	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 7669693 3 515	0.00	1319200.00	352358.62	0.00	0.00	0.00	0.00	11102000.00	899100.00	1193500.00	0.00	555947.25	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus sp. ER46;Opitutus sp. ER46
Ga0586324 7683023 28 516	0.00	375146.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	475023.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 7683358 84 515	0.00	0.00	0.00	0.00	0.00	0.00	2416800.00	2372900.00	2567700.00	0.00	3722400.00	4680000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 7714952 3 374	0.00	0.00	0.00	2099500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 7732817 2 478	0.00	1862195.64	1351042.36	2473039.05	0.00	0.00	0.00	1390800.00	689530.32	2040500.00	2340800.00	1290000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilitrichaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324 7766463 1 513	0.00	0.00	0.00	0.00	0.00	0.00	1536763.32	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 7770370 3 515	0.00	123711.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 7774271 1 513	0.00	100357.80	0.00	0.00	0.00	0.00	0.00	179472.37	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 7793056 3 512	11430000.00	0.00	0.00	0.00	2369000.00	0.00	2065376.76	463731.15	0.00	1543523.52	1020800.00	588787.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324 7795577 1 513	0.00	1115200.00	0.00	2878500.00	4253900.00	0.00	0.00	3342800.00	3920400.00	2279200.00	2816000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 7809805 3 512	0.00	0.00	0.00	7343500.00	0.00	7185700.00	7501200.00	5923100.00	6439500.00	3757600.00	4188800.00	3427500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 7822267 3 512	0.00	1142400.00	3399394.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324 7859188 1 510	0.00	0.00	0.00	0.00	0.00	0.00	0.00	563545.45	0.00	0.00	257664.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetoovum;Candidatus Magnetoovum chiemensis;Candidatus Magnetoovum chiemensis CS-04
Ga0586324 7868429 3 512	0.00	0.00	0.00	297992.20	0.00	0.00	0.00	0.00	217425.06	0.00	829023.36	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1pr3, DSM 2032
Ga0586324 7868862 3 512	0.00	0.00	0.00	0.00	0.00	463426.04	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira lenta;Nitrospira lenta N. lenta BS10
Ga0586324 7890952 2 511	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	608166.75	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;unclassified Candidatus Omnitrophica;Omnitrophica bacterium SCGC AAA011-L16;Omnitrophica bacterium SCGC AAA011-L16 (contamination screened)
Ga0586324 7909277 2 511	0.00	357470.56	0.00	0.00	996550.75	0.00	0.00	407423.88	644950.35	808500.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 7915693 25 510	0.00	0.00	0.00	0.00	0.00	0.00	786846.24	0.00	0.00	0.00	568785.36	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 7960933 2 508	0.00	0.00	0.00	0.00	0.00	0.00	22754400.00	505003.14	471121.11	540338.26	24552000.00	29025000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas europaea;Nitrosomonas europaea ATCC 19718
Ga0586324 7982695 153 509	0.00	0.00	0.00	0.00	720062.70	0.00	13360800.00	439555.63	4430700.00	5844300.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Chloroflexi;Thermomicrobia;Sphaerobacterales;Sphaerobacteraceae;Sphaerobacter;Sphaerobacter thermophilus;Sphaerobacter thermophilus 4ac11, DSM 20745
Ga0586324 7993154 3 509	0.00	0.00	0.00	0.00	0.00	0.00	7364400.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;Rhodothermus;Rhodothermus marinus;Rhodothermus marinus R-10, DSM 4252
Ga0586324 8019664 1 507	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	300768.16	0.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 8039779 3 506	0.00	0.00	0.00	0.00	857600.66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Acidihalobacter;Acidihalobacter prosperus;Acidihalobacter prosperus V6
Ga0586324 8061802 1 468	0.00	0.00	0.00	0.00	0.00	0.00	395196.96	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatirosa;Gemmatirosa kalamazoonesis;Gemmatimonadetes bacterium KBS708
Ga0586324 8073518 1 504	0.00	172282.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira moscoviensis;Nitrospira moscoviensis NSP M-1
Ga0586324 8075159 3 506	0.00	0.00	0.00	0.00	3409300.00	0.00	0.00	0.00	2146500.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Methylacidiphilae;Methylacidiphilales;Methylacidiphilaceae;Methylacidiphilum;Methylacidiphilum kamchatkense;Methylacidiphilum kamchatkense Kam1
Ga0586324 8095789 3 506	0.00	0.00	0.00	0.00	0.00	0.00	0.00	988200.00	0.00	3110800.00	7867200.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella sp. OAS946;Reyranella sp. OAS946
Ga0586324 8129441 2 505	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3303300.00	1487200.00	1380000.00	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 8162787 3 503	0.00	0.00	0.00	2175500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiorhodovibrio;Thiorhodovibrio sp. 970;Thiorhodovibrio sp. 970
Ga0586324 8173622 2 502	0.00	0.00	0.00	0.00	0.00	0.00	8094000.00	0.00	0.00	0.00	37224000.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium sp. CS1BSMeth3;Hyphomicrobium sp. CS1BSMeth3
Ga0586324 8188665 1 501	0.00	678983.40	269071.78	53095500.00	56979600.00	83924041.29	79959600.00	12126800.00	13810500.00	66458700.00	403287.28	20910868.50	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 8206217 3 503	0.00	516889.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2393600.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 8209974 3 503	494750.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 8217539 3 503	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	274063.50	KO:K04077	chaperonin GroEL	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 8221951 3 503	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1747900.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 8233794 2 499	0.00	0.00	0.00	579883.80	0.00	793825.32	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. OR-1;Geobacter sp. OR-1
Ga0586324 8234695 2 502	0.00	0.00	4094394.98	0.00	0.00	0.00	0.00	9455000.00	0.00	8767930.71	0.00	8700000.00	KO:K04077	chaperonin GroEL	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA255-E10 (contamination screened)
Ga0586324 8235524 3 500	0.00	0.00	0.00	0.00	0.00	0.00	0.00	37405.63	0.00	0.00	0.00	15975000.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 8263120 3 500	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	707968.80	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas sp. TF;Desulfuromonas sp. TF
Ga0586324 8301710 3 500	0.00	0.00	0.00	1225500.00	0.00	865515.58	6612000.00	0.00	0.00	4150300.00	0.00	5002500.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Elioraeaceae;Elioraea;Elioraea tepidiphila;Elioraea tepidiphila DSM 17972
Ga0586324 8311849 1 498	0.00	4678400.00	542169.00	0.00	0.00	393690.61	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Planctomycetes;Planctomycetia;Planctomycetales;Planctomycetaceae;Planctomyces;Planctomyces sp. SH-PL14;Planctomyces sp. SH-PL14
Ga0586324 8318259 3 500	0.00	0.00	0.00	0.00	0.00	0.00	1781804.04	0.00	0.00	0.00	0.00	1987500.00	KO:K04077	chaperonin GroEL	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334

Ga0586324_8318449_1_498	0.00	0.00	0.00	1282500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_8327149_2_499	0.00	0.00	0.00	1330000.00	6887969.47	0.00	0.00	0.00	0.00	0.00	477605.92	0.00	0.00	KO:K04077	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324_8336586_3_500	0.00	6086000.00	969547.93	23541000.00	18004400.00	1368971.13	5979644.28	20618000.00	20646900.00	22214500.00	20354400.00	20077500.00	KO:K04077	chaperonin GroEL	chaperonin GroEL	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geoalkalibacter;Geoalkalibacter subterraneus;Geoalkalibacter subterraneus Red1
Ga0586324_8343122_1_498	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2098400.00	1093500.00	0.00	0.00	714640.50	KO:K04077	chaperonin GroEL	chaperonin GroEL	Bacteria;Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;Chloroflexi bacterium TB1;Chloroflexi bacterium TB1
Ga0586324_0000709_27603_27890	0.00	0.00	0.00	0.00	0.00	0.00	76836000.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0028606_161_517	2520000.00	972400.00	0.00	0.00	0.00	0.00	0.00	1976400.00	1514700.00	2032800.00	3713600.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0030188_2979_3287	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5175900.00	0.00	0.00	7470000.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Nitrospirae;Nitrospiria;Nitrospiracea;Nitrospira;Nitrospira moscoviensis;Nitrospira moscoviensis NSP M-1
Ga0586324_0035645_3001_3294	0.00	0.00	0.00	12635000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gentianae DSM 8423
Ga0586324_0150273_2075_2392	0.00	340431.12	0.00	0.00	0.00	245166.16	0.00	0.00	232723.53	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Boseaceae;Bosea;Bosea sp. LC85;Bosea sp. LC85
Ga0586324_0216662_1474_1791	306000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Variibacter;Variibacter aotiawaiensis;Variibacter aotiawaiensis GJW-30
Ga0586324_0268820_1804_2124	10200000.00	12920000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodopseudomonas;Rhodopseudomonas palustris;Rhodopseudomonas palustris BisA53;Rhodopseudomonas palustris BisB18;Rhodopseudomonas palustris BisB5;Rhodopseudomonas palustris HaA2;Rhodopseudomonas palustris TIE-1;Rhodopseudomonas palustris BisA53 LVNP
Ga0586324_0355604_95_409	0.00	0.00	655574.09	0.00	0.00	932529.18	0.00	0.00	0.00	0.00	916300.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324_0445115_1065_1427	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	555519.58	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324_0566822_551_844	0.00	0.00	0.00	0.00	0.00	4327300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Verrucomicrobia;Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;Spartobacteria bacterium LR76;Spartobacteria bacterium LR76
Ga0586324_0660567_421_735	830820.00	0.00	0.00	88160000.00	109180000.00	1049374.22	1663200.72	459296.45	533846.70	41888000.00	2270400.00	1815000.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium japonicum;Bradyrhizobium japonicum USDA 6
Ga0586324_0775198_719_1006	0.00	0.00	0.00	0.00	323274.77	0.00	0.00	182390000.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;Thermosulfuriphilus;Thermosulfuriphilus ammonigenes;Thermosulfuriphilus ammonigenes DSM 102941
Ga0586324_0798844_214_528	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1312200.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;unclassified Hyphomicrobiales;Rhizobiales bacterium GAS113;Rhizobiales bacterium GAS113
Ga0586324_0846075_700_1035	0.00	0.00	0.00	4189500.00	4089100.00	0.00	0.00	0.00	0.00	0.00	1214400.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_1476271_583_879	0.00	0.00	1594562.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_1466999_55_372	895955.00	952000.00	0.00	0.00	0.00	813496.67	864550.92	539672.49	0.00	0.00	860474.56	1230000.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodobiaceae;Bradyrhizobium;Bradyrhizobium enthomelanicum;Bradyrhizobium enthrophilki GAS401
Ga0586324_2370034_571_840	0.00	40596000.00	0.00	0.00	0.00	0.00	0.00	41724000.00	0.00	0.00	0.00	34350000.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_2437204_422_709	0.00	15436000.00	0.00	0.00	3841900.00	48434000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_2622444_348_665	0.00	0.00	0.00	0.00	0.00	3712799.58	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Verrucomicrobia;Spartobacteria;unclassified Spartobacteria;unclassified Spartobacteria;Spartobacteria bacterium LR76;Spartobacteria bacterium LR76
Ga0586324_2626729_108_440	0.00	0.00	0.00	4512500.00	4243600.00	4803700.00	0.00	933300.00	0.00	0.00	0.00	1050000.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobiaceae;Rhodobacter;Rhodobacter sp. OAS957;Rhodobacter sp. OAS957
Ga0586324_3097086_267_584	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3547500.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_3310691_474_731	0.00	0.00	0.00	0.00	1256600.00	5121300.00	0.00	6466000.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium sp. CS1B5Meth3;Hyphomicrobium sp. CS1B5Meth3
Ga0586324_3348584_280_591	0.00	123760000.00	502916.64	0.00	46762000.00	252083.88	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Chondromyces;Chondromyces apiculatus;Chondromyces apiculatus DSM 436
Ga0586324_3645227_3_227	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1980000.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_3664227_209_526	0.00	0.00	0.00	226100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;Enhydrobacter;Enhydrobacter aerosaccus;Enhydrobacter aerosaccus ATCC 27094
Ga0586324_3992340_190_480	0.00	0.00	0.00	0.00	0.00	323400.70	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus alkaneexedens;Desulfobulbus alkaneexedens ALDC
Ga0586324_4630004_187_474	3980000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;Dissulfuribacter;Dissulfuribacter thermophilus;Dissulfuribacter thermophilus S69
Ga0586324_5406666_267_557	0.00	0.00	0.00	0.00	734696.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324_5554863_84_485	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1082400.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Acidobacteria;Gammabacteria;Vicinamibacterales;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_5762313_263_583	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium sp. YR577;Mesorhizobium sp. YR577
Ga0586324_6843315_171_461	0.00	0.00	0.00	0.00	0.00	22629000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_7867390_2_376	0.00	0.00	0.00	0.00	8892800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04078	chaperonin GroES	chaperonin GroES	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324_0007904_755_2692	0.00	0.00	0.00	0.00	0.00	8595600.00	0.00	1668600.00	6352500.00	0.00	3007500.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Noviherbaspirillum;Noviherbaspirillum humi;Noviherbaspirillum humi U15
Ga0586324_0008820_3598_5643	0.00	0.00	0.00	3743000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Alkalitalea;Alkalitalea saponilacus;Alkalitalea saponilacus DSM 24412
Ga0586324_0067623_2557_4134	3020000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Thiobacillus;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_0084717_2_925	1450000.00	3175600.00	11541500.00	0.00	0.00	0.00	23592468.72	16226000.00	7857000.00	13244000.00	14344000.00	5850000.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum 31/32
Ga0586324_0750919_339_1373	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8850000.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_0787744_230_1345	0.00	0.00	4505217.10	0.00	0.00	0.00	0.00	0.00	0.00	1082400.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_1410941_421_1047	0.00	0.00	0.00	14725000.00	0.00	0.00	0.00	6771000.00	0.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_1496025_3_1016	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2702300.00	0.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_1542583_422_1009	2040000.00	2305200.00	27530700.00	0.00	0.00	0.00	0.00	0.00	9801000.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324_3630403_2_703	0.00	0.00	0.00	1026000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Gammaproteobacteria;Xenorhabdus;Xenorhabdaceae;Photobacter;Photobacter iverum;Photobacter iverum DSM 26723
Ga0586324_4239470_2_661	0.00	2420800.00	0.00	0.00	8034000.00	0.00	2325600.00	3885700.00	0.00	3003000.00	1795200.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324_4361929_2_652	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	421080.75	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Acidobacteria;Holophagae;Holophagales;Holophagaceae;Holophaga;Holophaga foetida;Holophaga foetida TMB54. DSM 6591
Ga0586324_5219447_45_605	0.00	7888000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_6832212_3_542	0.00	0.00	0.00	0.00	0.00	5121300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. AR865;Bradyrhizobium sp. AR865
Ga0586324_7214041_2_529	2630000.00	2692800.00	1117560.63	4313000.00	0.00	5836800.00	2610800.00	5653800.00	7438200.00	9627200.00	8467500.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_7467836_3_521	0.00	0.00	0.00	0.00	15369900.00	0.00	0.00	0.00	0.00	0.00	6247500.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium lacus;Methylosarcina lacus LW14
Ga0586324_7586862_2_520	2600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04079	molecular chaperone HtpG	molecular chaperone HtpG	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter sp. BBA5.1;Methylobacter sp. BBA5.1
Ga0586324_2734746_3_419	0.00	578677.28	0.00	0.00	0.00	624035.80	0.00	3260400.00	0.00	256851.00	2102100.00	0.00	KO:K04080	molecular chaperone IbpA	molecular chaperone IbpA	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 6111. DSM 198
Ga0586324_6573862_299_550	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1663200.00	0.00	KO:K04080	molecular chaperone IbpA	molecular chaperone IbpA	Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococcaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_0003450_2051_2278	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7259000.00	4981500.00	0.00	0.00	0.00	KO:K04085	tRNA 2-thiouridine synthesizing protein A	tRNA 2-thiouridine synthesizing protein A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaurus;Thiobacillus thiopaurus DSM 505
Ga0586324_0125566_1997_2224	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	767019.78	0.00	0.00	0.00	KO:K04085	tRNA 2-thiouridine synthesizing protein A	tRNA 2-thiouridine synthesizing protein A	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 13892
Ga0586324_0000002_98969_99847	0.00	0.00	0.00	0.00	0.00	6361200.00	4483500.00	0.00	0.00	8008000.00	4500000.00	0.00	KO:K04087	membrane protease subunit HflC	membrane protease subunit HflC	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaurus;Thiobacillus thiopaurus DSM 505
Ga0586324_0002538_3951_4895	0.00	2250800.00	0.00	2061500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04087	membrane protease subunit HflC	membrane protease subunit HflC	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0017662_5620_6474	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1287100.00	0.00	0.00	0.00	772500.00	KO:K04087	membrane protease subunit HflC	membrane protease subunit HflC	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_0045143_3141_4052	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1757700.00	0.00	0.00	0.00	KO:K04087	membrane protease subunit HflC	membrane protease subunit HflC	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium labiatis;Bradyrhizobium labiatis GAS499
Ga0586324_0982345_208_1128	0.00	0.00	0.00	0.00	0.00	0.00	2468021.96	0.00	0.00	0.00	0.00	0.00	KO:K04087	membrane protease subunit HflC	membrane protease subunit HflC	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_0000002_99844_101025	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1077300.00	0.00	0.00	4005000.00	KO:K04088	membrane protease subunit HflK	membrane protease subunit HflK	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0022042_4231_5424	0.00	0.00	0.00	0.00	0.00	0.00	0.00	969900.00	1466100.00	0.00	0.00	0.00	KO:K04088	membrane protease subunit HflK	membrane protease subunit HflK	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaurus;Thiobacillus thiopaurus DSM 505
Ga0586324_0044334_812_2011	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1260000.00	0.00	KO:K04088	membrane protease subunit HflK	membrane protease subunit HflK	Bacteria;Proteobacteria;Gammaproteobacteria;Gallionellales;Gallionellaceae;Gallionella;Gallionella;Gallionella capsoferriformans;Gallionella capsoferriformans ES-2
Ga0586324_0049929_2440_3669	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1267500.00	KO:K04088	membrane protease subunit HflK	membrane protease subunit HflK	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324_0191051_218_1432	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1311500.00	0.00	0.00	0.00	KO:K04088	membrane protease subunit HflK	membrane protease subunit HflK	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosovibrio;Nitrosovibrio sp. Nv17;Nitrosovibrio sp. Nv17
Ga0586324_0192787_1103_2398	0.00	0.00	0.00	0.00	0.00	0.00	3420000.00	0.00	508440.24	0.00	0.00	0.00	KO:K04088	membrane protease subunit HflK	membrane protease subunit HflK	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Dechloromonas;Dechloromonas denitrificans;Dechloromonas denitrificans ATCC BAA-841
Ga0586324_3589602_3_572	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1860000.00	KO:K04088	membrane protease subunit HflK	membrane protease subunit HflK	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_3898795_1_684	0.00	0.00	0.00	1130500.00	1328700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04088	membrane protease subunit HflK	membrane protease subunit HflK	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta thermophila;Spirochaeta thermophila DSM 6192
Ga0586324_0000002_1_315	35600000.00	28696000.00	92895000.00	106400000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04480	methanol–5-hydroxybenzimidazolylcobamide Co-methyltransferase	methanol–5-hydroxybenzimidazolylcobamide Co-methyltransferase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina sp. Kolkaat;Methanosarcina sp. Kolkaat;Methanosarcinales;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324_0127643_196_1572	43600000.00	62689200.00	72232900.00	36366000.00	9434800.00	21914400.00	29252400.00	125652.07	30456000.00	12012000.00	15180000.00	39750000.00	KO:K04480	methanol–5-hydroxybenzimidazolylcobamide Co-methyltransferase	methanol–5-hydroxybenzimidazolylcobamide Co-methyltransferase	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324_0253324_2_1186	194870000.00	85965600.00	69136400.00	55375500.00	89630600.00	176939803.40	10191600.00	15616000.00	0.00	0.00	0.00	0.00	KO:K04480	methanol–5-hydroxybenzimidazolylcobamide Co-methyltransferase	methanol–5-hydroxybenzimidazolylcobamide Co-methyltransferase	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324_0531464_430_1623	765000.00	26560800.00	7818286.55	0.00	2132100.00	2990652.61	3579600.00	6649000.00	3304800.00	6167700.00	0.00	0.00	KO:K04480	methanol–5-hydroxybenzimidazolylcobamide Co-methyltransferase	methanol–5-hydroxybenz

Ga0586324_0052710_1386_1724	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1598200.00	0.00	0.00	0.00	0.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Nitrobacter;Nitrobacter winogradskyi;Nitrobacter winogradskyi Nb-255
Ga0586324_0078374_577_915	0.00	1040400.00	0.00	0.00	2842800.00	0.00	6840000.00	8723000.00	5540400.00	8932000.00	11704000.00	7327500.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriharbulus;Sulfuriharbulus autotrophica;Sulfuriharbulus autotrophica DSM 100309
Ga0586324_0389007_153_491	0.00	0.00	0.00	0.00	0.00	4922800.00	4970400.00	3861300.00	0.00	0.00	7823200.00	0.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. YR681;Bradyrhizobium sp. YR681
Ga0586324_0571820_976_1314	0.00	0.00	0.00	0.00	8229700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azoneaceae;Dechloromonas;Dechloromonas aromatica;Dechloromonas aromatica RCB
Ga0586324_0647447_882_1238	0.00	297759.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-B84
Ga0586324_0832507_386_724	6940000.00	8500000.00	0.00	47120000.00	11536000.00	0.00	0.00	0.00	4195800.00	0.00	0.00	8625000.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii WSM1741
Ga0586324_1432914_244_582	0.00	0.00	0.00	0.00	0.00	4049400.00	0.00	0.00	0.00	0.00	0.00	877500.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_2073087_317_655	0.00	0.00	0.00	0.00	0.00	4605600.00	13481000.00	11745000.00	0.00	0.00	0.00	5805000.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Betaproteobacteria;Ferrovales;Ferrovaceae;Ferrovum;Ferrovum myxofaciens;Ferrovum myxofaciens PN-J185
Ga0586324_2715460_377_715	0.00	0.00	0.00	0.00	0.00	0.00	3629500.00	0.00	0.00	0.00	0.00	7875000.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_3002953_2_250	0.00	7208000.00	0.00	7058500.00	7755900.00	0.00	0.00	0.00	0.00	5582500.00	6617600.00	0.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_3882447_219_557	8670000.00	0.00	0.00	0.00	0.00	0.00	3779600.00	0.00	0.00	0.00	0.00	0.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium sp. 99;Hyphomicrobium sp. 99
Ga0586324_4745892_132_470	0.00	0.00	630498.07	0.00	0.00	0.00	867961.80	0.00	0.00	0.00	515870.96	1185000.00	KO:K04752	nitrogen regulatory protein P-II 2	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. AET1TH-212;Polaromonas sp. AET1TH-212
Ga0586324_0366923_1489_1764	0.00	0.00	0.00	0.00	0.00	8257600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04764	integration host factor subunit alpha	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_0598672_24_308	0.00	0.00	0.00	0.00	8404800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04764	integration host factor subunit alpha	Bacteria;Proteobacteria;Gammaproteobacteria;Vulgatibacterales;Vulgatibacteraceae;Vulgatibacter;Vulgatibacter incomptus;Vulgatibacter incomptus DSM 27710
Ga0586324_3255206_293_592	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1628100.00	0.00	0.00	0.00	0.00	KO:K04764	integration host factor subunit alpha	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Comeetibacteraceae;Candidatus Comeetibacter;Candidatus Comeetibacter denitrificans;Candidatus Comeetibacter denitrificans Run_A_D11
Ga0586324_2285703_245_721	5750000.00	2454800.00	0.00	0.00	7374800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04767	acetoin utilization protein AcuB	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_0000537_26465_27862	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5556600.00	77169400.00	57024000.00	44835000.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax sp. KO-19;Acidovorax sp. KO-19
Ga0586324_0000875_1654_3114	9350000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax citrulli;Acidovorax avenae citrulli AAC00-1
Ga0586324_0003945_12599_14131	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1655500.00	1760000.00	2595000.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Aquabacterium;Aquabacterium commune;Aquabacterium commune DSM 17314
Ga0586324_0006917_4589_6058	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2842400.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Aquabacterium;Aquabacterium parvum;Aquabacterium parvum B8
Ga0586324_0017806_1768_3159	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1031444.22	14213823.36	8362500.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaeus;Thiobacillus thiopaeus DSM 505
Ga0586324_0020619_4878_6272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7427200.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_0033345_1391_2875	0.00	0.00	0.00	0.00	0.00	2599200.00	4074800.00	10481400.00	17440500.00	28520800.00	47610000.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriharbulus;Sulfuriharbulus autotrophica;Sulfuriharbulus autotrophica DSM 100309
Ga0586324_0034773_4882_5709	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	367392.08	0.00	KO:K04771	serine protease Do	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0036983_2056_3486	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1801800.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax citrulli;Acidovorax avenae citrulli AAC00-1
Ga0586324_0139854_588_2024	0.00	0.00	657651.56	0.00	1050600.00	0.00	28044000.00	4068700.00	378456.30	3472700.00	1179200.00	543104.25	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324_0151163_3_1496	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	621093.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatibacillum;Desulfatibacillum alliphaticivorans;Desulfatibacillum alliphaticivorans DSM 15576
Ga0586324_0190409_170_2533	0.00	0.00	0.00	1235000.00	0.00	0.00	0.00	0.00	0.00	3934700.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolinaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324_0219915_223_1740	0.00	2121600.00	0.00	0.00	0.00	0.00	0.00	2681100.00	0.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfotomaculum;Desulfotomaculum sp. Ox39;Desulfotomaculum sp. Ox39
Ga0586324_0259355_520_2001	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1100000.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Aquabacterium;Aquabacterium citratiphilum;Aquabacterium citratiphilum B
Ga0586324_0326660_2_1189	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1832600.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia sp. GAS231;Afipia sp. GAS231
Ga0586324_0498233_1021_1641	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1393700.00	4197600.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0527796_1_1323	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1080000.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;unclassified Nitrosomonadales;Nitrosomonas;unclassified Nitrosomonas;Nitrosomonas bacterium HCH-1;Nitrosomonas bacterium HCH-1
Ga0586324_0514813_59_1543	0.00	0.00	0.00	0.00	0.00	3008133.96	868658.91	527842.98	5020400.00	5156800.00	5167500.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriharbulus;Sulfuriharbulus autotrophica;Sulfuriharbulus autotrophica DSM 100309
Ga0586324_0555492_293_1564	0.00	0.00	0.00	0.00	4962500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatibacillum;Desulfatibacillum alliphaticivorans;Desulfatibacillum alliphaticivorans DSM 15576
Ga0586324_0561483_1_1302	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1845000.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-B84
Ga0586324_0595199_3_1376	0.00	0.00	0.00	0.00	0.00	0.00	1183400.00	0.00	1478400.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_0635925_58_1476	0.00	0.00	0.00	0.00	0.00	0.00	4495700.00	0.00	0.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0724316_912_1394	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2235200.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. YR605;Methylibium sp. YR605
Ga0586324_0727710_1_1368	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1117500.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0851363_159_1325	0.00	0.00	0.00	0.00	416494.92	591438.69	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deferribacteres;Deferribacteraceae;Deferribacter;Deferribacter abyssi;Deferribacter abyssi DSM 11778
Ga0586324_0854317_1_938	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4408096.96	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS401
Ga0586324_0854562_56_1300	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	746511.75	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_0938867_2_889	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1177500.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. OR-1;Geobacter sp. OR-1
Ga0586324_1389803_2_1054	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5040000.00	KO:K04771	serine protease Do	Bacteria;Planctomycetes;Planctomycetia;Planctomycetales;Planctomycetaceae;Fuerestia;Fuerestia marisaermanicae;Fuerestia marisaermanicae NH11
Ga0586324_1634411_3_704	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1894200.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia sp. BH72;Burkholderia sp. BH72
Ga0586324_4373263_261_653	0.00	0.00	0.00	0.00	0.00	155040000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-DMIM
Ga0586324_4701283_1_632	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2257500.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Silvimonas;Silvimonas terrae;Silvimonas terrae DSM 18233
Ga0586324_5106437_3_491	0.00	0.00	2832678.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04771	serine protease Do	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0005837_2814_3998	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3842300.00	0.00	0.00	KO:K04771	serine protease DeaD	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaeus;Thiobacillus thiopaeus DSM 505
Ga0586324_0000007_51755_52693	0.00	0.00	0.00	0.00	0.00	0.00	866200.00	760790.88	0.00	1161600.00	653935.50	KO:K04773	protease-4	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0073775_2587_3582	0.00	0.00	0.00	1567500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K04801	replication factor C small subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_1987579_2_424	3530000.00	1346400.00	2724756.73	1814500.00	1792200.00	2232021.34	2348400.00	1647000.00	1717200.00	0.00	1944800.00	960000.00	KO:K04802	proliferating cell nuclear antigen	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_2184007_238_870	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	169592.25	KO:K04802	proliferating cell nuclear antigen	Archaea;Thaumarchaeota;Nitrososphaeria;Nitrososphaerales;Nitrososphaeraceae;Candidatus Nitrosocosmicus;Candidatus Nitrosocosmicus hydrocola;Candidatus Nitrosocosmicus exaquare G61
Ga0586324_0560751_1_1257	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1501500.00	0.00	0.00	KO:K05301	sulfite dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Limnohabitans;Limnohabitans curvus;Limnohabitans curvus MWH-C5
Ga0586324_1630631_1_984	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	994400.00	0.00	KO:K05301	sulfite dehydrogenase	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Rudaea;Rudaea cellulosilytica;Rudaea cellulosilytica DSM 22992
Ga0586324_1900128_1_279	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5151300.00	0.00	0.00	KO:K05301	sulfite dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylobacteriaceae;Methylobacterium;Methylobacterium nodulans;Methylobacterium nodulans ORS 2060
Ga0586324_6091202_3_569	2850000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05301	sulfite dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Limnohabitans;Limnohabitans curvus;Limnohabitans curvus MWH-C5
Ga0586324_0023761_707_4210	0.00	4834800.00	8951700.00	8996500.00	7571785.44	0.00	0.00	0.00	0.00	6814500.00	0.00	0.00	KO:K05349	beta-glucosidase	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter soli;Solirubrobacter soli DSM 22325
Ga0586324_0032920_1_2448	0.00	0.00	0.00	0.00	351309.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05349	beta-glucosidase	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;Bacteroides ihuae;Bacteroides ihuae Marseille-P2824
Ga0586324_0164974_179_2707	0.00	0.00	0.00	0.00	0.00	0.00	1715323.80	0.00	0.00	0.00	0.00	0.00	KO:K05349	beta-glucosidase	Bacteria;Proteobacteria;Alphaproteobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter aggregans;Edaphobacter aggregans EB153
Ga0586324_0172930_2_1852	0.00	0.00	0.00	0.00	759676.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05349	beta-glucosidase	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas hengshuiensis;Sphingomonas hengshuiensis WHSC-8
Ga0586324_0492407_1_1650	0.00	0.00	4362242.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05349	beta-glucosidase	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalibacter uvarum DSM 26723
Ga0586324_0691323_1_1424	0.00	0.00	0.00	720110.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05349	beta-glucosidase	Bacteria;Proteobacteria;Alphaproteobacteria;Micropepsales;Micropepsaceae;Rhizomicrobium;Rhizomicrobium electricum;Rhizomicrobium electricum DSM 21034
Ga0586324_1632386_3_986	0.00	0.00	0.00	0.00	476709.66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05349	beta-glucosidase	Bacteria;Proteobacteria;Alphaproteobacteria;Micropepsales;Micropepsaceae;Rhizomicrobium;Rhizomicrobium electricum;Rhizomicrobium electricum DSM 21034
Ga0586324_0485554_57_1019	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	164368.82	0.00	0.00	KO:K05516	curved DNA-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_0020341_2534_4174	0.00	14076000.00	0.00	19285000.00	0.00	0.00	0.00	0.00	29808000.00	0.00	0.00	0.00	KO:K05601	hydroxylamine reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0024257_1_1561	0.00	0.00	0.00	0.00	5778300.00	10282800.00	4776300.00	0.00	0.00	0.00	0.00	0.00	KO:K05601	hydroxylamine reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_0536571_1_1590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2681100.00	0.00	0.00	0.00	0.00	KO:K05601	hydroxylamine reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0939143_315_1247	0.00	3026000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05601	hydroxylamine reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_1617287_1_987	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5799600.00	0.00	0.00	0.00	0.00	KO:K05601	hydroxylamine reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_3711326_129_698	6030000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05601	hydroxylamine reductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0025459_5201_6007	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2422500.00	KO:K05772	tungstate transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia sp. YMA4;Massilia sp. YMA4
Ga0586324_3946121_2_679	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2017500.00	KO:K05772	tungstate transport system substrate-binding protein	Bacteria;Proteobacteria;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio islandicus;Thermodesulfovibrio islandicus DSM 12570
Ga0586324_6902250_18_539	0.00	0.00	0.00	0.00	611987.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05772	tungstate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_0011056_4857_5432	0.00	1968831.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05795	tellurium resistance protein TerD	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_4580906_2_403	4310000.00	2958000.00	0.00	1292000.00	2276300.00	0.00	0.00	0.00	1935900.00	2117500.00	3256000.00	2490000.00	KO:K05795	tellurium resistance protein TerD	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_7044410_199_534	0.00	134644.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05795	tellurium resistance protein TerD	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium lacus;Methylosarcina lacus LW14
Ga0586324_1027441_269_796	0.00	822800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K05808	putative sigma-54 modulation protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Moorella;Moorella sp. Hama-1;Moorella sp. Hama-1
Ga0586324_3463375_1_717	0.00	0.00	0.00	0.00	0.00	0.00	254669.09	0.00	0.00	0.00	0.00	0.00	KO:K05813	sn-glycerol 3-phosphate transport system substrate-binding protein	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Selenomonadaceae;Pectinatus;Pectinatus cerevisiiphilus;Pectinatus cerevisiiphilus

Ga0586324_1153130_3_887	0.00	2468400.00	0.00	0.00	0.00	0.00	4856400.00	16116200.00	11161800.00	62631800.00	62383200.00	11572500.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_1153303_2_1141	0.00	0.00	0.00	28310000.00	0.00	0.00	0.00	1140700.00	0.00	0.00	0.00	2025000.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. SG708;Dechloromonas sp. SG708
Ga0586324_1303287_2_1060	415049.00	301605.84	0.00	0.00	0.00	0.00	0.00	403455.83	0.00	1540000.00	0.00	423813.75	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter sp. PAE-UM;Curvibacter sp. PAE-UM
Ga0586324_1532909_2_1012	1480000.00	0.00	0.00	0.00	0.00	40584000.00	80763000.00	167508000.00	104458200.00	171952000.00	132900000.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_1735776_1_960	0.00	12240000.00	0.00	0.00	0.00	0.00	0.00	2786400.00	12782000.00	0.00	0.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montoellier
Ga0586324_1799772_3_800	0.00	0.00	0.00	0.00	0.00	0.00	1238300.00	0.00	0.00	0.00	0.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_2112755_3_881	0.00	234338.20	0.00	465690.95	0.00	0.00	572544.78	0.00	1339800.00	817203.20	1042500.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter lithotrophicus;Ramlibacter lithotrophicus RBP-1
Ga0586324_2307312_1_849	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3528800.00	0.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sterolibacterium;Sterolibacterium denitrificans;Sterolibacterium denitrificans Chol
Ga0586324_2575249_1_813	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2181103.80	3102300.00	8932000.00	12320000.00	12187500.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter lithotrophicus;Ramlibacter lithotrophicus RBP-1
Ga0586324_2754818_187_789	1620000.00	2298400.00	2663018.15	2698000.00	4717400.00	3575763.12	6361200.00	2732800.00	4155300.00	2148300.00	2833600.00	2520000.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. JJ;Dechloromonas sp. JJ
Ga0586324_3091499_1_753	0.00	0.00	0.00	0.00	5459000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. JJ;Dechloromonas sp. JJ
Ga0586324_3243650_3_737	423326.00	1298800.00	0.00	3961500.00	4305400.00	0.00	0.00	1683600.00	0.00	0.00	2868800.00	2820000.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter sp. PAE-UM;Curvibacter sp. PAE-UM
Ga0586324_3380788_2_724	0.00	9778400.00	0.00	6241500.00	9846800.00	0.00	2644800.00	3702700.00	4082400.00	6067600.00	5156800.00	3030000.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. SG708;Dechloromonas sp. SG708
Ga0586324_3965962_2_679	0.00	0.00	0.00	0.00	0.00	4009770.00	0.00	6588000.00	6107400.00	8162000.00	0.00	9525000.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_4382573_12_650	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	462185.19	0.00	3194400.00	0.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_4507868_1_644	0.00	0.00	0.00	0.00	0.00	0.00	592033.68	0.00	0.00	924000.00	0.00	0.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_6399458_3_557	0.00	0.00	955112.61	4740500.00	6571400.00	0.00	42636000.00	34892000.00	7346700.00	8962800.00	89760000.00	81000000.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula multivorans;Sulfuriferula multivorans TTN
Ga0586324_6913809_3_539	10800000.00	11220000.00	14412800.00	14155000.00	10258800.00	5081600.00	0.00	33428000.00	10773000.00	12320000.00	0.00	68100000.00	KO:K06076	long-chain fatty acid transport protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_2016603_3_464	0.00	0.00	0.00	0.00	0.00	0.00	491980.68	0.00	0.00	0.00	0.00	0.00	KO:K06077	outer membrane lipoprotein SlyB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula autotrophica;Sulfuriferula autotrophica DSM 100309
Ga0586324_0005655_10774_11310	0.00	1822400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06142	outer membrane protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas sp. DDH964;Desulfuromonas sp. DDH964
Ga0586324_0009356_7608_8213	0.00	0.00	0.00	0.00	1339000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06142	outer membrane protein	Bacteria;Deferribacteres;Deferribacteres;Deferribacteraceae;Geovibrio;Geovibrio sp. L21-Ace-BES;Geovibrio sp. L21-Ace-BES, DSM 26904
Ga0586324_0524333_873_1394	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4582500.00	KO:K06142	outer membrane protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run_B_J11
Ga0586324_1919152_542_919	0.00	0.00	0.00	0.00	0.00	1061423.17	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06142	outer membrane protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Draconibacterium;Draconibacterium orientale;Draconibacterium orientale FHS
Ga0586324_0088330_115_561	0.00	2305200.00	0.00	9880000.00	0.00	0.00	3328800.00	0.00	1377000.00	1516900.00	0.00	0.00	KO:K06149	universal stress protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0202854_1817_2263	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1635000.00	KO:K06149	universal stress protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_1777363_1_438	0.00	3910000.00	0.00	0.00	4645300.00	0.00	0.00	0.00	0.00	3488100.00	0.00	0.00	KO:K06149	universal stress protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacales;Smithellaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_0008005_7386_9134	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1469600.00	0.00	KO:K06178	23S rRNA pseudouridine2605 synthase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia sp. GV016;Massilia sp. GV016
Ga0586324_0000030_5333_6529	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1751200.00	0.00	KO:K06186	outer membrane protein assembly factor BamE	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0025592_1267_3117	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13041000.00	0.00	0.00	0.00	KO:K06207	GTP-binding protein	Bacteria;Chlorflexi;Chlorflexia;Kallotenuales;Kallotenuaceae;Kallotenue;Kallotenue papyrolyticum;Kallotenue papyrolyticum JKG1
Ga0586324_0002753_1477_3306	0.00	0.00	11541500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06207	GTP-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Xanthobacteraceae;Pseudoalabrus;Pseudoalabrus sp. Root1462;Pseudoalabrus sp. Root1462
Ga0586324_0347668_617_1924	0.00	0.00	0.00	0.00	0.00	0.00	0.00	27360000.00	0.00	0.00	0.00	0.00	KO:K06207	GTP-binding protein	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Candidatus Nitrospira nitrosa;Candidatus Nitrospira nitrosa COMA1
Ga0586324_0396342_1_791	0.00	0.00	0.00	0.00	17716000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06207	GTP-binding protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium allauzi PMMR2
Ga0586324_0479691_1_1299	0.00	8976000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06227	GTP-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacales;Syntrophobacaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0667395_2_1447	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10919000.00	0.00	0.00	0.00	0.00	KO:K06207	GTP-binding protein	Bacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324_5148578_1_609	1900000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06207	GTP-binding protein	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Weeksellaceae;Aeibacter;Aeibacter sp. wk8309;Aeibacter sp. wk8309
Ga0586324_0004492_4501_5399	0.00	0.00	0.00	0.00	0.00	0.00	1067500.00	0.00	0.00	0.00	0.00	0.00	KO:K06215	pyridoxal 5'-phosphate synthase pdxS subunit	Archaea;Euryarchaeota;Methanomicrobia;Methanocellales;Methanocellaceae;Methanocella;Methanocella paludicola;Methanocella paludicola SANAE
Ga0586324_0461921_836_1696	0.00	0.00	0.00	19095000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06215	pyridoxal 5'-phosphate synthase pdxS subunit	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run_B_J11
Ga0586324_0582334_160_1041	0.00	8092000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06215	pyridoxal 5'-phosphate synthase pdxS subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_2166691_2_619	0.00	0.00	0.00	0.00	8569600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06215	pyridoxal 5'-phosphate synthase pdxS subunit	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_4082108_25_669	0.00	0.00	0.00	0.00	0.00	0.00	1543300.00	0.00	0.00	0.00	0.00	0.00	KO:K06215	pyridoxal 5'-phosphate synthase pdxS subunit	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_6208543_3_491	0.00	0.00	0.00	0.00	5778300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06215	pyridoxal 5'-phosphate synthase pdxS subunit	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Iluma tobacteraceae;Desertimonas;Desertimonas flava;Acidimicrobiales bacterium SY5U D60003
Ga0586324_1090001_369_1169	0.00	11832000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06217	phosphate starvation-inducible PhoH-like protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophococcales;Anaerompyobacter;Anaerompyobacter dehalogenans;Anaerompyobacter dehalogenans 2CP-1
Ga0586324_0000005_11964_13721	0.00	0.00	0.00	0.00	0.00	0.00	1000400.00	0.00	6229300.00	14484800.00	6945000.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0000597_2013_3470	0.00	0.00	0.00	0.00	0.00	0.00	9393600.00	0.00	0.00	0.00	0.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1pr3, DSM 2032
Ga0586324_0025429_3523_5223	0.00	0.00	0.00	5301000.00	0.00	0.00	3739300.00	0.00	3888500.00	0.00	5002500.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalbus;Thioalbus denitrificans;Thioalbus denitrificans DSM 26407
Ga0586324_0102811_176_1939	0.00	0.00	0.00	0.00	0.00	364428.36	6405000.00	0.00	0.00	7400800.00	2902500.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0113263_2550_3230	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1036800.00	0.00	0.00	0.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sedimnicola;Sulfurisoma sedimnicola DSM 26916
Ga0586324_0403733_1_1328	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4762500.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Rhodopseudomonas;Rhodopseudomonas palustris;Rhodopseudomonas palustris O.U.11, DSM 7375
Ga0586324_0660996_171_1451	0.00	0.00	0.00	0.00	0.00	4696800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Azoarcus indigens;Azoarcus indigens DSM 12121
Ga0586324_1065884_1_1179	0.00	0.00	0.00	0.00	0.00	357656.76	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Aquaspirillum;Aquaspirillum sp. LM1;Aquaspirillum sp. LM1
Ga0586324_2376205_3_839	0.00	0.00	0.00	0.00	0.00	0.00	1304100.00	0.00	0.00	0.00	0.00	1957500.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1pr3, DSM 2032
Ga0586324_2573607_3_593	0.00	0.00	0.00	0.00	0.00	344048.48	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Mucilaginibacter;Mucilaginibacter gotjawali;Mucilaginibacter gotjawali SA3-7
Ga0586324_3358479_288_728	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2300400.00	0.00	0.00	0.00	0.00	KO:K06281	hydrogenase large subunit	Bacteria;Firmicutes;Clostridia;Eubacteriales;Heliobacteriaceae;Heliomicrobium;Heliomicrobium modesticaldum;Heliomicrobium modesticaldum Ice1
Ga0586324_4059606_45_671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1957500.00	KO:K06281	hydrogenase large subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 611, DSM 198
Ga0586324_0003727_1_1398	0.00	0.00	0.00	0.00	19135400.00	0.00	0.00	10044000.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0010092_6220_8124	24020000.00	5780000.00	26010600.00	22230000.00	7992800.00	12981900.00	0.00	6588000.00	10837800.00	17702300.00	0.00	7290000.00	KO:K06324	spore coat protein A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Abyssisolibacter;Abyssisolibacter fermentans;Abyssisolibacter fermentans MCW03
Ga0586324_0013881_5782_7956	1780000.00	0.00	468215.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0013978_1720_5040	2420000.00	0.00	0.00	2517500.00	2669760.00	19587638.58	4696800.00	9570000.00	14102100.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Nitrosococcus;Nitrosococcus halophilus;Nitrosococcus halophilus Nc4
Ga0586324_0022131_1_2715	0.00	4399600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Chlorflexi;Ktedonobacteria;Ktedonobacterales;Dictyobacteraceae;Dictyobacter;Dictyobacter aurantiacus;Dictyobacter aurantiacus S27
Ga0586324_0045294_2_1810	0.00	0.00	0.00	0.00	4223000.00	0.00	4007700.00	1458000.00	4188800.00	0.00	705665.25	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0105611_1159_3342	0.00	2788000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0113510_3_2096	0.00	1645600.00	2185712.38	2394000.00	2121800.00	0.00	0.00	0.00	475032.62	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0138117_1_1083	0.00	2162400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0160252_1536_2744	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1717500.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0163708_1_1782	12059055.00	14229585.48	4094625.81	15922000.00	14646600.00	6074650.52	6467327.16	9872746.30	9360234.45	9409400.00	7840800.00	8730000.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0177590_3_2153	5910000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0199886_2_1327	12500000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0032496_201_1982	0.00	0.00	0.00	2394000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0393204_2_1564	0.00	0.00	0.00	0.00	0.00	2397117.76	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified Myxococcales;Minicystis;Minicystis rosea;Minicystis rosea DSM 24000
Ga0586324_0701904_3_1415	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	793100.00	624014.16	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sulfurreducens;Geobacter sulfurreducens PCA
Ga0586324_0706127_1_1410	30380000.00	9717200.00	8170210.96	7581000.00	3874565.42	4768093.07	6026931.48	3020816.99	4767377.29	8916600.00	6221600.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_0791572_1_1344	3670000.00	0.00	9120600.00	0.00	0.00	0.00	0.00	0.00	0.00	9702000.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia ubonensis;Burkholderia ubonensis MSMB2120WGS
Ga0586324_0883833_1_1281	0.00	0.00	0.00	0.00	0.00	1690386.30	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324_1182769_3_1130	0.00	2475200.00	0.00	5111000.00	0.00	0.00	9963600.00	0.00	4681800.00	7053200.00	6573600.00	12900000.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_1512860_1_1017	0.00	686800.00	0.00	0.00	0.00	0.00	0.00	1069200.00	1771000.00	0.00	1957500.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sulfurreducens;Geobacter sulfurreducens PCA
Ga0586324_1664191_3_977	0.00	0.00	1189140.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Pseudogulbenkiania;Pseudogulbenkiania sp. MAI-1;Pseudogulbenkiania sp. MAI-1
Ga0586324_2156411_53_874	0.00	0.00	343480.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	930000.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_3383546_2_724	896713.00	2284800.00	0.00	1957000.00	0.00	0.00	0.00	0.00	0.00	0.00	1470000.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. M18;Geobacter sp. M18
Ga0586324_3463910_1_717	13900000.00	0.00	0.00	11020000.00	11330000.00	0.00	0.00	0.00	0.00	11704000.00	0.00	12225000.00	KO:K06324	spore coat protein A	Bacteria;Firmicutes;Clostridia;Eubacteriales;Syntrophomonadaceae;Syntrophomonas;Syntrophomonas zehnderi;Syntrophomonas zehnderi OL-4
Ga0586324_3478110_2_715	4320000.00	1536800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K06324	spore coat protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324_4016040_2_652	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2810500.00

Ga0586324 0085036 2 748	0.00	3828400.00	63056000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0107071 1745 2692	0.00	15436000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10918600.00	8219200.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0206822 1771 2436	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1470000.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0259640 1 927	0.00	0.00	0.00	0.00	2286600.00	0.00	0.00	0.00	2357100.00	0.00	1258400.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0275988 3 443	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7777000.00	0.00	1560000.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 0335257 713 1750	0.00	0.00	2856774.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0400275 1020 1808	0.00	0.00	0.00	0.00	2193900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Prosthecomicrobium;Prosthecomicrobium hirschii;Prosthecomicrobium hirschii ATCC 27832
Ga0586324 0465987 891 1691	0.00	0.00	0.00	0.00	1015184.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter postgatei;Desulfobacter postgatei 2ac9
Ga0586324 1081415 2 1054	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2332000.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Dethiosulfatarculus;Dethiosulfatarculus sandiegensis;Dethiosulfatarculus sandiegensis SPR
Ga0586324 1219603 82 1041	0.00	0.00	0.00	0.00	0.00	3200125.69	0.00	5160600.00	3426300.00	5790400.00	8729600.00	5985000.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dechlorobacter;Dechlorobacter hydrogenophilus;Dechlorobacter hydrogenophilus LT-1
Ga0586324 1274246 1 930	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	29400000.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Noviherbaspirillum;Noviherbaspirillum sp. Root189;Noviherbaspirillum sp. Root189
Ga0586324 2148589 3 875	7910000.00	6310400.00	0.00	540000.90	335294.87	0.00	0.00	7564000.00	4949100.00	8855000.00	9152000.00	5587500.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 2211166 216 866	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1628000.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter tataouinensis;Ramlibacter tataouinensis TTB310
Ga0586324 4940485 3 620	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	104124.69	0.00	0.00	0.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 5567493 3 590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2366800.00	0.00	0.00	0.00	3247500.00	KO:K07080	TRAP transporter TAXI family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter curvatus;Desulfobacter curvatus DSM 3379
Ga0586324 6784031 148 543	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	850500.00	0.00	0.00	0.00	KO:K07092	predicted peroxiredoxin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0390910 2 1696	0.00	0.00	0.00	0.00	0.00	0.00	0.00	192484.89	0.00	0.00	0.00	0.00	KO:K07141	molybdenum cofactor cytidylyltransferase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 0021710 2664 4718	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1263600.00	0.00	0.00	0.00	KO:K07180	serine protein kinase	Bacteria;Planctomycetes;Planctomycetia;Isosphaerales;Isosphaeraceae;Paludisphaera;Paludisphaera borealis;Paludisphaera borealis PX4
Ga0586324 0025633 3 1637	647041.00	506784.28	0.00	3914000.00	3543200.00	0.00	0.00	2592500.00	2681100.00	0.00	0.00	4140000.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rubrivivax;Rubrivivax benzoatilyticus;Rubrivivax benzoatilyticus JA2
Ga0586324 0028345 3591 5666	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1470100.00	2300400.00	0.00	0.00	0.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Sandaracinaceae;Sandaracinus;Sandaracinus amylolyticus;Sandaracinus amylolyticus DSM 53668
Ga0586324 0078599 3 1523	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4507900.00	0.00	0.00	0.00	0.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS401
Ga0586324 0098158 447 2513	0.00	734400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. K;Anaeromyxobacter sp. K
Ga0586324 0171911 750 2654	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1287900.00	0.00	0.00	0.00	KO:K07180	serine protein kinase	Bacteria;Planctomycetes;Planctomycetia;Planctomycetales;Planctomycetaceae;Planctomyces;Planctomyces sp. SH-PL62;Planctomyces sp. SH-PL62
Ga0586324 0179755 3 1628	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4807500.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324 0843379 3 203	1820000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324 1654125 2 979	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4245000.00	KO:K07180	serine protein kinase	Bacteria;Planctomycetes;Planctomycetia;Gemmatales;Gemmataceae;Gemmata;Gemmata massiliana;Gemmata massiliana IIL30
Ga0586324 2355363 3 842	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5121600.00	0.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter tataouinensis;Ramlibacter tataouinensis TTB310
Ga0586324 4058102 3 671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6151200.00	0.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thioflavicoccus;Thioflavicoccus mobilis;Thioflavicoccus mobilis 8321
Ga0586324 4797539 2 628	0.00	484015.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07180	serine protein kinase	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So0157-25
Ga0586324 0094425 798 2783	0.00	0.00	0.00	0.00	2214500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07182	CBS domain-containing protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0998838 3 1214	0.00	1985600.00	0.00	0.00	2667700.00	0.00	0.00	0.00	1741500.00	0.00	0.00	0.00	KO:K07221	phosphate-selective porin OprO/OprP	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324 4613245 3 638	0.00	0.00	0.00	899508.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07221	phosphate-selective porin OprO/OprP	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenotrichaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324 0000049 63473 63832	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2818800.00	0.00	0.00	0.00	KO:K07235	tRNA 2-thiouridine synthesizing protein D	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula multivorans;Sulfuriferula multivorans TTN
Ga0586324 0051016 1616 1975	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10395000.00	10736000.00	11175000.00	KO:K07235	tRNA 2-thiouridine synthesizing protein D	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0283980 189 551	0.00	1434800.00	0.00	0.00	2657400.00	0.00	0.00	0.00	0.00	3457300.00	0.00	2902500.00	KO:K07235	tRNA 2-thiouridine synthesizing protein D	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324 0590777 695 1054	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8418000.00	0.00	0.00	0.00	0.00	KO:K07235	tRNA 2-thiouridine synthesizing protein D	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324 0000003 177176 177472	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1557600.00	0.00	KO:K07237	tRNA 2-thiouridine synthesizing protein B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0051016 2408 2713	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	450508.08	0.00	KO:K07237	tRNA 2-thiouridine synthesizing protein B	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula multivorans;Sulfuriferula multivorans TTN
Ga0586324 0000041 32626 33960	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5412000.00	0.00	KO:K07263	zinc protease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0162431 236 2725	0.00	0.00	0.00	0.00	0.00	19135400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07263	zinc protease	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Draconibacterium;Draconibacterium sediminis;Draconibacterium sediminis JN14CK-3
Ga0586324 0025664 116 946	0.00	0.00	0.00	5966000.00	0.00	7423900.00	6771600.00	6283000.00	5370300.00	4158000.00	6670400.00	4905000.00	KO:K07274	outer membrane protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia timonae;Massilia timonae CCUG 45783
Ga0586324 0000002 75603 77930	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4211900.00	9724000.00	0.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0015454 4236 6536	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5272500.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0030649 2002 4533	0.00	0.00	0.00	0.00	0.00	8138500.00	8937600.00	0.00	0.00	0.00	3150400.00	0.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 0061388 3 2135	7390000.00	1523200.00	0.00	1263500.00	933062.58	2804237.29	0.00	0.00	0.00	2233000.00	3344000.00	4050000.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS401
Ga0586324 0126751 869 3064	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1936000.00	1312500.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0169362 725 2674	0.00	0.00	0.00	4940000.00	4253900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis parvus;Methylocystis parvus OBBP
Ga0586324 0175395 705 2630	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1185000.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324 1900291 3 923	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2452500.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324 2178266 1 870	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4147500.00	KO:K07277	outer membrane protein insertion porin family	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. STM 3843;Bradyrhizobium sp. STM 3843
Ga0586324 0838444 3 656	873271.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07283	putative salt-induced outer membrane protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Labilitrichaceae;Labilithrix;Labilithrix luteola;Labilithrix luteola DSM 27648
Ga0586324 0000002 169139 170242	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4267500.00	KO:K07287	outer membrane protein assembly factor BamC	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324 0808886 2 1324	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	303501.33	0.00	0.00	0.00	KO:K07289	AsmA protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacula;Desulfobacula phenolica;Desulfobacula phenolica DSM 3384
Ga0586324 0010089 1327 3486	0.00	3100800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5407500.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium viridifuturi;Bradyrhizobium viridifuturi SEMIA 690
Ga0586324 0041788 2263 4470	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1609300.00	0.00	0.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Collimonas;Collimonas arenae;Collimonas arenae Cal35
Ga0586324 0044225 1910 4234	6820000.00	0.00	0.00	2992500.00	0.00	5677100.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0088;Rhodospirillales bacterium URHD0088
Ga0586324 0097230 1015 3228	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	880000.00	0.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0180579 588 2594	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4417600.00	0.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS499
Ga0586324 0252780 3 1742	0.00	2291600.00	4981621.05	0.00	0.00	0.00	0.00	0.00	0.00	6131978.93	4206400.00	6240000.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Collimonas;Collimonas arenae;Collimonas arenae Cal35
Ga0586324 0267465 3 2000	0.00	0.00	0.00	0.00	0.00	0.00	0.00	471514.14	0.00	0.00	0.00	0.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Collimonas;Collimonas arenae;Collimonas arenae Cal35
Ga0586324 0309052 726 2027	1570000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax saidenbachensis;Rhodoferax saidenbachensis ED16
Ga0586324 0337560 1 1950	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	638891.33	0.00	0.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0088;Rhodospirillales bacterium URHD0088
Ga0586324 0464292 2 1456	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3832500.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax soli;Variovorax soli NBRC 106424
Ga0586324 3182481 1 744	0.00	0.00	0.00	0.00	34505000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07303	isoquinoline 1-oxidoreductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. BK119;Variovorax sp. BK119
Ga0586324 3926626 168 680	0.00	0.00	3639727.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1732500.00	KO:K07304	peptide-methionine (S)-S-oxide reductase	Bacteria;Deinococcus-Thermus;Deinococci;Thermales;Thermaceae;Calidithermus;Calidithermus timidus;Meiothermus timidus DSM 17022
Ga0586324 0005259 9651 11696	0.00	5902400.00	0.00	0.00	0.00	0.00	0.00	6057300.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus;Chloroflexus aggregans;Chloroflexus aggregans DSM 9485
Ga0586324 0007772 7846 8919	0.00	0.00	0.00	0.00	0.00	1635008.77	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0028479 61 1137	2920000.00	1285200.00	0.00	0.00	0.00	0.00	3739200.00	0.00	0.00	5035800.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 0034050 2873 4954	0.00	0.00	17058900.00	0.00	0.00	0.00	0.00	0.00	14661000.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0041345 988 3102	17630000.00	11689200.00	1270555.88	2764500.00	11845000.00	1643818.20	1648718.16	9723400.00	2041200.00	2456300.00	2323200.00	2655000.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus;Chloroflexus islandicus;Chloroflexus islandicus isl-2
Ga0586324 0045154 3235 4257	0.00	0.00	7544200.00	0.00	0.00	0.00	0.00	0.00	0.00	4797100.00	30509600.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 0061263 3 920	8360000.00	3563200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Leptolyngbyaceae;Leptolyngbya;Leptolyngbya sp. 2LT21S03;Leptolyngbya sp. 2LT21S03
Ga0586324 0062946 2 1876	0.00	0.00	0.00	0.00	0.00	0.00	2177003.28	486717.78	0.00	1863400.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0129895 1566 2612	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1470100.00	1701000.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Actinobacteria;Actinomycetia;Kineosporiales;Kineosporiaceae;Kineosporia;Kineosporia sp. R H 3;Kineosporia sp. R H 3 R H 3
Ga0586324 0137725 1519 2637	0.00	1720400.00	0.00	0.00	0.00	7543000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Coprothermobacterota;Coprothermobacteria;Coprothermobacterales;Coprothermobacteraceae;Coprothermobacter;Coprothermobacter proteolyticus;Coprothermobacter proteolyticus DSM 5265
Ga0586324 0139974 1774 2925	0.00	3182400.00	0.00	0.00	0.00	0.00	0.00	0.00	2810700.00	0.00	3194400.00	2640000.00	KO:K07335	basic membrane protein A	Bacteria;Firmicutes;Limnochordia;Limnochordales;Limnochordaceae;Limnochorda;Limnochorda pilosa;Limnochorda pilosa HC45
Ga0586324 0170651 743 1741	4010000.00	0.00	0.00	0.00	5067600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 0201364 2 262	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1250500.00	1514700.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus castenholzii;Roseiflexus castenholzii HLO8, DSM 13941
Ga0586324 0220593 773 1906	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2138400.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324 0221825 1 690	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2318000.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Leptolyngbyaceae;Leptolyngbya;Leptolyngbya sp. 2LT21S03;Leptolyngbya sp. 2LT21S03
Ga0586324 0330108 703 1968	0.00	2475200.00	0.00	0.00	2698600.00	0.00	0.00	0.00	2624400.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;SAR324 cluster bacterium JCVI-SC AAA005;SAR324 cluster bacterium JCVI-SC AAA005
Ga0586324 0363820 2 1417	0.00	0.00	0.00	0.00	0.00	0.00	0.00	473321.57	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0363862 454 1521	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16401000.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Leptolyngbyaceae;Leptolyngbya;Leptolyngbya sp. 2LT21S03;Leptolyngbya sp. 2LT21S03
Ga0586324 0438842 3 1241	3670000.00	0.00	2828033.45	0.00	0.00	1234662.06	0.00	1769000.00	0.00	1532300.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0448765 1 1116	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4562800.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Leptolyngbyaceae;Leptolyngbya;Leptolyngbya sp. 2LT21S03;Leptolyngbya sp. 2LT21S03
Ga0586324 0461035 82 1146	4280000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3311000.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0487445 937 1656	0.00	0.00	0.00	0.00	269096.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;[Polyangium] brachysporum;Polyangium brachysporum DSM 7029
Ga0586324 0490131 59 1054	741299.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Firmicutes;Clostridia;Eubacteriales;unclassified Eubacteriales;unclassified Eubacteriales;Clostridiales bacterium PH28 bin88;Clostridiales bacterium PH28 bin88
Ga0586324 0491708 2 958	8360000.00	0.00	0.00	0.00	0.00	0.00	0.00	8418000.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0522058 86 1120	0.00	0.00	0.00	0.00	0.00	0.00	3967200.00	2958500.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0591542 25 1200	0.00	0.00	0.00	0.00	0.00	9369200.00	13246800.00	0.00	0.00	0.00	4567200.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Oscillochloridaceae;Oscillochloris;Oscillochloris trichoides;Oscillochloris trichoides DG6
Ga0586324 0719726 2 1156	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2635200.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0752410 3 1373	3230000.00	707200.00	7431600.00	13328500.00	7107000.00	6352000.00	15618000.00	3373300.00	6204600.00	4820200.00	8791200.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Chloroflexaceae;Chloroflexus;Chloroflexus islandicus;Chloroflexus islandicus isl-2
Ga0586324 0763715 3 662	0.00	1496000.00	0.00	0.00	0.00	0.00	0.00	570514.70	0.00	0.00	0.00	1612500.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 0784694 2 1048	0.00	0.00	0.00	5054000.00	3100300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324 0817277 93 1172	0.00	0.00	0.00	0.00	0.00	4168500.00	8846400.00	6649000.00	0.00	2294600.00	0.00	4305000.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 0907826 1 675	0.00	0.00	0.00	0.00	10403000.00	0.00	0.00	0.00	0.00	0.00	5834400.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 1069784 1 891	3930000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Coprothermobacterota;Coprothermobacteria;Coprothermobacterales;Coprothermobacteraceae;Coprothermobacter;Coprothermobacter proteolyticus;Coprothermobacter proteolyticus DSM 5265
Ga0586324 1251084 70 1104	0.00	0.00	4527296.94	0.00	0.00	0.00	0.00	0.00	0.00	2209900.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Actinobacteria;Rubrobacteria;Gaiellales;Gaiellaceae;Gaiella;Gaiella occulta;Gaiella occulta F2-233
Ga0586324 1397295 1 1053	0.00	1278400.00	0.00	0.00	0.00	0.00	0.00	0.00	2502900.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Leptolyngbyaceae;Leptolyngbya;Leptolyngbya sp. 2LT21S03;Leptolyngbya sp. 2LT21S03
Ga0586324 1432183 3 455	0.00	552203.52	0.00	0.00	0.00	0.00	0.00	0.00	2195100.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Firmicutes;Limnochordia;Limnochordales;Limnochordaceae;Limnochorda;Limnochorda pilosa;Limnochorda pilosa HC45
Ga0586324 1882355 3 926	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	701216.67	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 2710134 3 794	0.00	0.00	0.00	0.00	0.00	0.00	8230800.00	3836900.00	34749000.00	17579100.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 3400019 3 722	0.00	0.00	0.00	0.00	0.00	3673226.62	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Leptolyngbyaceae;Leptolyngbya;Leptolyngbya sp. 2LT21S03;Leptolyngbya sp. 2LT21S03
Ga0586324 4478623 67 645	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1915400.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 5134402 3 611	0.00	0.00	0.00	0.00	0.00	4605200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 5251408 1 603	0.00	0.00	0.00	0.00	0.00	2950174.49	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Synergistetes;Synergistia;Synergistales;Synergistaceae;Aminivibrio;Aminivibrio pyruvatiphilus;Aminivibrio pyruvatiphilus DSM 25964
Ga0586324 5799317 62 580	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5499900.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 6011712 1 573	7090000.00	6092800.00	0.00	0.00	0.00	0.00	7296000.00	0.00	8100000.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 6302974 8 559	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2481600.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 6580007 3 308	0.00	0.00	0.00	0.00	0.00	0.00	8846400.00	0.00	0.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 7237484 2 475	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1206900.00	0.00	0.00	0.00	KO:K07335	basic membrane protein A	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0005323 2031 2444	0.00	1931200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07397	putative redox protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatitalea;Desulfatitalea tepidiphila;Desulfatitalea tepidiphila S28bF
Ga0586324 0370071 3 1742	504639.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07407	alpha-galactosidase	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0000182 5669 7510	0.00	0.00	0.00	4474500.00	7580800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07463	RecJ-like exonuclease	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0005330 10500 12881	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14245000.00	0.00	0.00	KO:K07516	3-hydroxyacyl-CoA dehydrogenase	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324 0238143 1 2130	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	462433.05	0.00	0.00	0.00	KO:K07516	3-hydroxyacyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 0387438 1158 1835	0.00	0.00	0.00	514455.40	851701.85	0.00	0.00	30012000.00	0.00	0.00	0.00	0.00	KO:K07516	3-hydroxyacyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0790768 2 1342	2150000.00	0.00	0.00	1624500.00	2605900.00	1138306.19	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07516	3-hydroxyacyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 6097495 69 569	0.00	0.00	0.00	3239500.00	0.00	5478600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07516	3-hydroxyacyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 4092280 168 671	341910.00	0.00	0.00	1301500.00	0.00	473347.07	488948.28	224130.47	0.00	0.00	0.00	0.00	KO:K07537	cyclohexa-1,5-dienecarbonyl-CoA hydratase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324 0021186 1888 3000	2180000.00	3298000.00	0.00	0.00	1781900.00	0.00	0.00	1329800.00	750840.03	0.00	0.00	0.00	KO:K07538	6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0004542 2 1024	3140000.00	0.00	0.00	29830000.00	9960100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 0021186 705 1853	27100000.00	1788400.00	38452900.00	75620000.00	70040000.00	67847300.00	38355170.04	35892400.00	26568000.00	16940000.00	0.00	16500000.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0064950 3305 4216	6620000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324 0141527 3 620	6510000.00	0.00	12329700.00	8303000.00	0.00	12108500.00	11445600.00	0.00	0.00	0.00	0.00	0.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 1375992 2 886	0.00	0.00	0.00	0.00	0.00	0.00	874637.64	0.00	0.00	0.00	0.00	0.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 2116187 1 852	0.00	13532000.00	0.00	0.00	23690000.00	0.00	20360400.00	0.00	12960000.00	12397000.00	13464000.00	2970000.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 2128400 2 880	1480000.00	7208000.00	0.00	3087500.00	1133000.00	0.00	0.00	0.00	6755400.00	0.00	0.00	0.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 2224347 29 865	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	947100.00	0.00	0.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324 2934599 1 768	0.00	0.00	0.00	8122500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324 3154272 1 747	0.00	1387200.00	0.00	0.00	2513200.00	0.00	995438.88	0.00	907200.00	0.00	0.00	0.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324 5082594 3 386	20000000.00	23732000.00	28150000.00	23465000.00	24514000.00	18301700.00	13862400.00	13359000.00	13203000.00	15708000.00	0.00	12150000.00	KO:K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0209238 535 1098	0.00	1863200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07572	putative nucleotide binding protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0002706 2572 3879	0.00	0.00	0.00	0.00	1545000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07662	two-component system response regulator CpxR	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324 0009977 2 739	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1441800.00	0.00	0.00	1200000.00	KO:K07712	two-component system nitrogen regulation response regulator GlnG	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324 0235423 545 1987	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2780800.00	0.00	KO:K07712	two-component system nitrogen regulation response regulator GlnG	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS499
Ga0586324 0362938 871 1632	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	959200.00	0.00	KO:K07736	CarD family transcriptional regulator	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0382876 309 1304	0.00	0.00	0.00	0.00	0.00	0.00	2895600.00	0.00	0.00	0.00	0.00	0.00	KO:K07736	CarD family transcriptional regulator	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii USDA 94

Ga0586324_1032819_332_1198	0.00	0.00	0.00	0.00	0.00	0.00	0.00	262029.33	0.00	0.00	0.00	KO:K07736	CarD family transcriptional regulator		Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii WSM1741
Ga0586324_5240671_209_604	0.00	0.00	0.00	8597500.00	0.00	0.00	0.00	2559600.00	0.00	2340800.00	0.00	KO:K07736	CarD family transcriptional regulator		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0034737_2423_3310	0.00	2278000.00	0.00	2242000.00	0.00	0.00	1677500.00	0.00	0.00	0.00	0.00	KO:K07744	predicted transcriptional regulator		Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_1627179_3_986	0.00	0.00	0.00	0.00	0.00	900643.32	0.00	0.00	0.00	0.00	0.00	KO:K07749	formyl-CoA transferase		Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium icense;Bradyrhizobium icense LMTR 13
Ga0586324_5747967_2_583	0.00	0.00	2135380.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07749	formyl-CoA transferase		Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodopolaneae;Rhodopolaneae sp. Z2-YC6860;Rhodopolaneae sp. Z2-YC6860
Ga0586324_0000626_24085_25089	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8855000.00	0.00	0.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_0008220_8971_9987	0.00	1074400.00	0.00	0.00	0.00	0.00	0.00	0.00	1886500.00	0.00	0.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. EUR3 1.2.1;Polaromonas sp. EUR3 1.2.1
Ga0586324_0020385_2949_3956	0.00	0.00	0.00	0.00	0.00	3373300.00	0.00	5828900.00	6265600.00	5295000.00	0.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hylemonella;Hylemonella gracilis;Hylemonella gracilis Niagara R
Ga0586324_0025491_4548_5561	0.00	0.00	0.00	0.00	0.00	14689000.00	0.00	0.00	0.00	0.00	0.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0028651_2726_3712	2600000.00	3060000.00	0.00	0.00	0.00	0.00	0.00	2527200.00	4034800.00	3916000.00	4665000.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0030312_3287_4288	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1887300.00	0.00	0.00	855000.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0062838_236_1213	0.00	0.00	0.00	0.00	0.00	6976800.00	3788100.00	6407100.00	4412100.00	0.00	8992500.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. YR568;Polaromonas sp. YR568
Ga0586324_0133754_1133_2125	4400000.00	0.00	0.00	0.00	3934600.00	30052900.00	12950400.00	21289000.00	0.00	0.00	23625000.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0686205_3_902	0.00	0.00	0.00	0.00	0.00	0.00	781570.32	0.00	383328.45	1932700.00	1812800.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. YR568;Polaromonas sp. YR568
Ga0586324_0691410_381_1403	0.00	0.00	0.00	0.00	0.00	0.00	5987074.80	4721400.00	4576500.00	5166700.00	6168800.00	7605000.00	KO:K07795	putative tricarboxylic transport membrane protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_1083090_1_489	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11956000.00	10206000.00	0.00	0.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified Oxalobacteraceae;Oxalobacteraceae bacterium;Oxalobacteraceae sp. OA5666
Ga0586324_1721227_2_907	2680000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Polynucleobacter;Polynucleobacter rarus;Polynucleobacter rarus MT-CB6645
Ga0586324_2919013_1_771	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5713400.00	0.00	0.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Polynucleobacter;Polynucleobacter sp. UB-Domo-W1;Polynucleobacter sp. UB-Domo-W1
Ga0586324_5636256_1_585	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4760800.00	0.00	KO:K07795	putative tricarboxylic transport membrane protein		Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0261288_3_2189	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1887300.00	0.00	0.00	0.00	KO:K08086	pilus assembly protein FimV		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriharbadus;Sulfuriharbadus autotrophica;Sulfuriharbadus autotrophica DSM 100309
Ga0586324_0475403_352_1677	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4188800.00	0.00	KO:K08086	pilus assembly protein FimV		Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum DSM 26723
Ga0586324_2612510_145_807	0.00	0.00	0.00	774718.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08086	pilus assembly protein FimV		Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas denitrificans;Dechloromonas denitrificans ATCC BAA-841
Ga0586324_0019659_1823_2464	0.00	0.00	10302000.00	0.00	0.00	0.00	0.00	0.00	3819200.00	0.00	0.00	KO:K08093	3-hexulose6-phosphate synthase		Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Crenothrixaceae;Crenothrix;Crenothrix polyspora;Crenothrix polyspora ERS1545888
Ga0586324_0112735_1290_1985	8720000.00	4338400.00	5079352.22	3344000.00	0.00	0.00	1939800.00	0.00	0.00	0.00	0.00	KO:K08093	3-hexulose6-phosphate synthase		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylovorus;Methylovorus glucosotrophus;Methylovorus glucosotrophus DSM 6874
Ga0586324_1623353_1_561	15300000.00	4624000.00	9176900.00	0.00	0.00	0.00	4453000.00	0.00	8239000.00	15840000.00	9375000.00	KO:K08093	3-hexulose6-phosphate synthase		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylobacillus;Methylobacillus sp. MM3;Methylobacillus sp. MM2
Ga0586324_1625264_2_496	7010000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7110400.00	0.00	KO:K08093	3-hexulose6-phosphate synthase		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylotenera;Methylotenera versatilis;Methylotenera versatilis 301, ICM 17579
Ga0586324_1798020_1_480	0.00	172856000.00	184326200.00	0.00	0.00	0.00	105792000.00	100040000.00	140130000.00	66759000.00	117040000.00	113850000.00	KO:K08093	3-hexulose6-phosphate synthase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-GS3F
Ga0586324_3021936_1_387	603590.00	678090.56	924035.01	0.00	0.00	0.00	0.00	774700.00	5224500.00	0.00	0.00	KO:K08093	3-hexulose6-phosphate synthase		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylobacillus;Methylobacillus sp. MM3;Methylobacillus sp. MM2
Ga0586324_0066885_2307_2852	0.00	0.00	0.00	0.00	0.00	0.00	0.00	23814000.00	0.00	0.00	0.00	KO:K08094	6-phospho-3-hexuloisomerase		Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-GS3F
Ga0586324_1284577_440_973	0.00	2087600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08094	6-phospho-3-hexuloisomerase		Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-GS3F
Ga0586324_3783405_102_647	0.00	952000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08094	6-phospho-3-hexuloisomerase		Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomarinum;Methylomarinum vadi;Methylomarinum vadi IT-4
Ga0586324_0001625_1000_2637	17567035.00	5752800.00	13655441.14	0.00	2142400.00	9616538.94	0.00	6081700.00	5378400.00	25625600.00	6476800.00	11842500.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus aromaticus;Desulfoarcus aromaticus DSM 9756
Ga0586324_0038228_91_1731	638057.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus aromaticus;Desulfoarcus aromaticus DSM 9756
Ga0586324_0060271_800_2479	27800000.00	23364800.00	18701970.46	21261000.00	22972800.00	24949965.22	57729926.04	12627000.00	5227400.00	25025000.00	25432000.00	21675000.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0079167_934_2613	54520000.00	31320800.00	27431060.26	91307389.90	88784463.24	61644987.26	62877110.40	3542700.00	58975537.05	12335400.00	9820800.00	14617500.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0219130_1047_2402	4660000.00	0.00	0.00	0.00	0.00	0.00	0.00	1494500.00	0.00	0.00	0.00	2017500.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0319551_218_1903	13243369.00	10147531.20	10068962.24	0.00	506012.23	11514000.00	5612000.00	8748000.00	0.00	4338400.00	13644832.50	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0342351_1_684	12700000.00	12240000.00	0.00	0.00	1802500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0462544_3_233	0.00	10948000.00	15876600.00	14440000.00	13596000.00	31442400.00	20816400.00	11224000.00	12231000.00	8162000.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0491014_1_687	0.00	0.00	0.00	0.00	0.00	0.00	0.00	200577.15	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0492076_3_578	0.00	4134400.00	0.00	0.00	0.00	1658197.54	0.00	0.00	1158300.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0533033_2_1594	3210000.00	16592000.00	3424241.90	23389000.00	9712900.00	11299867.86	56042400.00	1744600.00	0.00	30415000.00	0.00	3967500.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0668512_2_703	742397.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus inferrunum;Desulfoarcus inferrunum DSM 9756
Ga0586324_0993661_156_1217	1770000.00	3375520.00	0.00	1656800.00	0.00	0.00	1415880.00	8747400.00	8035729.74	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_1055803_1_1187	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4305000.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_1353343_1_1065	73600000.00	44880000.00	0.00	54910000.00	40685000.00	84561000.00	0.00	38613000.00	45603000.00	0.00	2160000.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_1660071_3_977	23700000.00	24024400.00	35469000.00	40204000.00	135033000.00	135518697.24	12403200.00	81270300.00	24364800.00	23716000.00	22352000.00	12300000.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_2053716_149_892	0.00	0.00	0.00	0.00	0.00	0.00	4218000.00	0.00	13932000.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_2073383_1_551	0.00	0.00	0.00	9975000.00	11433000.00	22629000.00	5403600.00	1842200.00	7200900.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_2120516_168_881	0.00	3869200.00	0.00	0.00	4717400.00	0.00	0.00	2745000.00	0.00	0.00	2992500.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_2135944_159_878	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2482700.00	0.00	1270500.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus inferrunum;Desulfoarcus inferrunum DSM 9756
Ga0586324_2242044_1_153	0.00	0.00	0.00	0.00	0.00	153122.50	0.00	0.00	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_3097798_1_384	0.00	0.00	0.00	40660000.00	53457000.00	32315800.00	53808000.00	52216000.00	56538000.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus hydrotrermahe;Desulfoarcus hydrotrermahe DSM 13146
Ga0586324_4205099_2_367	0.00	0.00	0.00	0.00	1668600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_4384196_2_517	2090000.00	2794800.00	0.00	0.00	0.00	5677200.00	2208200.00	2284200.00	0.00	0.00	2490000.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus inferrunum;Desulfoarcus inferrunum DSM 9756
Ga0586324_4977739_3_617	0.00	0.00	0.00	1900000.00	0.00	0.00	0.00	0.00	0.00	565196.72	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_5410732_114_596	33100000.00	30464000.00	37608400.00	7866000.00	85284000.00	72811376.09	46740000.00	40748000.00	35478000.00	27181000.00	23584000.00	22500000.00	KO:K08295	2-aminoenzoate-CoA ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_5764971_1_582	468986.00	1978800.00	0.00	850692.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_5765977_2_580	3160000.00	3774000.00	0.00	0.00	0.00	0.00	0.00	1195600.00	582922.98	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_5826454_101_580	0.00	0.00	0.00	0.00	32445000.00	22946600.00	0.00	13420000.00	16443000.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_5874540_203_577	0.00	1448400.00	0.00	0.00	20291000.00	0.00	0.00	1945900.00	1927800.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_2794566_2_514	0.00	0.00	0.00	0.00	0.00	0.00	1610251.85	0.00	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_8261402_3_500	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1958100.00	0.00	0.00	0.00	KO:K08295	2-aminoenzoate-CoA ligase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoarcus;Desulfoarcus acetoxidans;Desulfoarcus acetoxidans ASR82, DSM 11109
Ga0586324_0000007_46820_49429	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2949100.00	0.00	KO:K08300	ribonuclease E		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0062438_2311_5049	0.00	328780.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	565196.72	0.00	KO:K08300	ribonuclease E		Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;unclassified Rickettsiales;unclassified Rickettsiales;Candidatus Pelagibacter;Candidatus Pelagibacter sp. HIMB1321
Ga0586324_0014901_2418_5192	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1848000.00	0.00	KO:K08300	ribonuclease E		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Chitinimonas;Chitinimonas koreensis;Chitinimonas koreensis DSM 17726
Ga0586324_0033251_2724_5363	0.00	0.00	1102000.00	0.00	0.00	0.00	0.00	2928000.00	3102300.00	0.00	3027200.00	KO:K08300	ribonuclease E		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Steroliibacteriaceae;Methyloversatilis;Methyloversatilis discipulorum;Methyloversatilis discipulorum FAM1
Ga0586324_0048937_1_1647	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4365900.00	0.00	0.00	KO:K08300	ribonuclease E		Bacteria;Candidatus Contendibacter;Candidatus Contendibacter odensis;Candidatus Contendibacter odensis Run_B_J11
Ga0586324_1851278_2_478	0.00	0.00	0.00	0.00	648568.34	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08300	ribonuclease E		Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_0000111_46490_47197	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1463000.00	0.00	0.00	KO:K08355	arsenite oxidase small subunit		Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus sp. KH32;Azoarcus sumilus;Azoarcus sumilus SY39
Ga0586324_0076339_1603_3900	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1455300.00	0.00	0.00	KO:K08356	arsenite oxidase large subunit		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia bryophila;Paraburkholderia bryophila H2C3B
Ga0586324_0181765_630_1403	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7079400.00	0.00	15664000.00	0.00	KO:K08358	tetrathionate reductase subunit B		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriharbadus;Sulfuriharbadus autotrophica;Sulfuriharbadus autotrophica DSM 100309
Ga0586324_0000013_58661_60382	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1047200.00	0.00	0.00	KO:K08483	phosphotransferase system enzyme I (PtsI)		Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0000406_6350_8785	2040000.00	12031192.40	15482500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K08655	thermitase		Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_0015122_4299_5252	11900000.00	0.00	0.00	0.00	0.00	3307081.46	0.00	0.00	0.00	1755600.00	627670.56	KO:K08678	UDP-glucuronate decarboxylase		Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0504955_3_725	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2173600.00	KO:K08678	UDP-glucuronate decarboxylase		Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Janthinobacterium;Janthinobacterium sp. B9-8;Janthinobacterium sp. B9-8
Ga0586324_1757495_1_513	0.00	0.00	0.00	2907000.00	0.00	0.00	0.00	0.00

Ga0586324 0410950 488 1387	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2417800.00	0.00	0.00	KO:K10001	glutamate/aspartate transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. SG703;Rhizobacter sp. SG703
Ga0586324 0100752 935 2041	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	177605.25	KO:K10111	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Devosiaceae;Maritalea;Maritalea mobilis;Maritalea mobilis CGMCC 1.7002
Ga0586324 0004979 12021 13118	10900000.00	4692000.00	0.00	3752500.00	0.00	2150203.61	111720000.00	3983300.00	3345300.00	5844300.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Salinispira;Salinispira pacifica;Salinispira pacifica L21-RPul-D2
Ga0586324 0018862 3212 4411	0.00	6174400.00	606519.90	0.00	0.00	0.00	2964000.00	4892200.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 0028932 1846 2916	0.00	0.00	0.00	0.00	5912200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. NZG;Methylibium sp. NZG
Ga0586324 0050128 3611 4711	0.00	877200.00	0.00	884335.05	0.00	0.00	0.00	1274900.00	0.00	0.00	737073.92	277938.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0058874 3795 4415	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	624570.87	671997.92	817500.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Stellaceae;Stella;Stella humosa;Stella humosa DSM 5900
Ga0586324 0060506 1 1110	0.00	0.00	0.00	0.00	940935.90	0.00	0.00	415822.36	0.00	341388.74	65824000.00	373577.25	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0078451 2156 3256	0.00	0.00	1196825.40	0.00	0.00	0.00	0.00	561017.00	402548.94	0.00	1135200.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0135906 1137 2237	0.00	0.00	0.00	0.00	0.00	218499.27	0.00	0.00	0.00	0.00	773116.96	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0169913 1342 2442	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1293600.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0174299 1276 2433	6430000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;unclassified Chloroflexi;Thermobaculum;Thermobaculum terrenum;Thermobaculum terrenum YNP1, ATCC BAA-798
Ga0586324 0200559 3 950	423176.00	0.00	0.00	0.00	0.00	149193.00	1628727.12	0.00	0.00	0.00	514304.56	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0273290 351 1523	1670000.00	0.00	0.00	0.00	0.00	0.00	0.00	286094.88	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0376035 845 1858	0.00	0.00	13975388.41	3439000.00	9228800.00	10373502.81	0.00	5782800.00	12822300.00	0.00	0.00	5610000.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324 0462852 339 1436	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	426904.72	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax ferrireducens;Rhodoferax ferrireducens T118
Ga0586324 0498261 524 1642	0.00	0.00	0.00	0.00	0.00	0.00	0.00	555875.92	0.00	0.00	0.00	594847.50	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0511540 638 1621	0.00	447557.64	0.00	9129500.00	1472900.00	0.00	1193910.60	768600.00	1134000.00	0.00	1029600.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax ferrireducens;Rhodoferax ferrireducens T118
Ga0586324 0556972 1 1563	0.00	5236000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0823989 256 1320	0.00	775200.00	0.00	0.00	0.00	430856.16	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0904532 1 816	0.00	0.00	0.00	0.00	0.00	2256254.22	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Thermotogae;Thermotogae;Petrotogales;Petrotogaceae;Marinitoga;Marinitoga piezophila;Marinitoga piezophila KA3
Ga0586324 0914960 3 1145	0.00	0.00	0.00	868942.20	0.00	0.00	0.00	0.00	0.00	0.00	693067.76	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 1108834 18 1091	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	387056.56	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. OK202;Variovorax sp. OK202
Ga0586324 1133738 29 1135	9960000.00	16150000.00	17847100.00	16758000.00	17242200.00	0.00	6680400.00	8954800.00	1328400.00	0.00	8140000.00	6802500.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 1292523 3 866	0.00	0.00	0.00	0.00	1658300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Azospirillaceae;Azospirillum;Azospirillum palustre;Azospirillum palustre B2
Ga0586324 1296405 3 1085	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3803800.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Firmicutes;Clostridia;Halanaerobiales;Halanaerobiaceae;Halanaerobium;Halanaerobium saccharolyticum;Halanaerobium saccharolyticum WC1
Ga0586324 1298080 498 1085	3700000.00	0.00	0.00	0.00	0.00	2805340.95	0.00	0.00	0.00	3064600.00	2393600.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 1413896 177 1046	2930000.00	13260000.00	0.00	9082000.00	7735300.00	0.00	3328800.00	4263900.00	4212000.00	15554000.00	13552000.00	6262500.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta thermophila;Spirochaeta thermophila DSM 6192
Ga0586324 1570224 751 1002	0.00	1516400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 1651078 1 729	1660000.00	2699600.00	6924900.00	2052000.00	10557500.00	4499018.38	0.00	1561600.00	1587600.00	1624700.00	1636800.00	1792500.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta bajacaliforniensis;Sediminispirochaeta bajacaliforniensis DSM 16054
Ga0586324 2577840 1 810	0.00	1584400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Chelatococcaceae;Chelatococcus;Chelatococcus sambhunathii;Chelatococcus sambhunathii DSM 18167
Ga0586324 2596184 32 808	0.00	0.00	0.00	0.00	0.00	0.00	0.00	982100.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. OV700;Variovorax sp. OV700
Ga0586324 2812491 3 782	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16831.35	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0088;Rhodospirillales bacterium URHD0088
Ga0586324 3175725 2 745	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	576899.40	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 3285766 1 732	0.00	0.00	0.00	0.00	0.00	1001027.56	0.00	1085800.00	0.00	0.00	0.00	1552500.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PB90-1
Ga0586324 3555070 2 709	0.00	583123.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	446797.12	420727.12	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema lecithinolyticum;Treponema lecithinolyticum ATCC 700332
Ga0586324 4070193 41 670	4110000.00	0.00	6924900.00	4968500.00	4284800.00	0.00	0.00	969900.00	3572100.00	266552.44	0.00	1050000.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 4086459 3 671	0.00	0.00	0.00	0.00	2245400.00	1105577.51	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 4776225 3 629	391415.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	184440.24	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 5021867 2 616	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	21560000.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. EL159;Variovorax sp. EL159
Ga0586324 5355639 1 600	0.00	0.00	0.00	0.00	0.00	0.00	191537.78	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. URHD0069;Bradyrhizobium sp. URHD0069
Ga0586324 6444782 1 555	9740000.00	0.00	3685825.88	6099000.00	8899200.00	1764704.70	3534000.00	6100000.00	4746600.00	4881800.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 7235249 3 530	0.00	1455200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	862500.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Sphaerochaetaceae;Sphaerochaeta;Sphaerochaeta globosa;Sphaerochaeta globosa Buddy
Ga0586324 7358589 3 527	2410000.00	3359200.00	296382.34	0.00	2760400.00	685329.19	2936601.24	680193.92	2625999.75	2841300.00	2411309.12	3945000.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 7570789 1 519	0.00	37060000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10112	multiple sugar transport system ATP-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema maltophilum;Treponema maltophilum ATCC 51939
Ga0586324 0004496 9834 11186	15050000.00	22188400.00	11597800.00	21660000.00	0.00	0.00	10602000.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0004673 4863 6272	9790000.00	2577200.00	0.00	4702500.00	6777400.00	0.00	4035600.00	2769400.00	899100.00	2417800.00	4074400.00	4800000.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0015488 7595 8359	0.00	0.00	0.00	3116000.00	0.00	0.00	0.00	72590000.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0035652 1655 3067	10140000.00	17183600.00	7544200.00	2204000.00	0.00	6510800.00	0.00	2464400.00	0.00	3126200.00	0.00	1650000.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 0040551 2187 3545	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1000400.00	0.00	0.00	1443200.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0073132 587 2020	0.00	0.00	0.00	2783500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0081531 116 1501	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1782000.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Ruminiclostridium;Ruminiclostridium sufflavum;Ruminiclostridium sufflavum DSM 19573
Ga0586324 0148421 55 1470	2330000.00	0.00	3839603.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0210012 940 2334	1200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 0400723 936 1808	0.00	0.00	976658.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium sp. WSM3882;Mesorhizobium sp. WSM3882
Ga0586324 0406488 3 1139	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2782500.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 1356416 3 1064	8360000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 1361864 3 1064	5800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 1603425 2 991	0.00	2427600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 1686914 1 951	0.00	35142400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Firmicutes;unclassified Firmicutes;unclassified Firmicutes;unclassified Firmicutes;Hydrogenispora;Hydrogenispora ethanolica;Hydrogenispora ethanolica DSM 25471
Ga0586324 1752563 369 956	0.00	2271200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 1869002 1 648	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2690100.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 2279545 279 854	0.00	0.00	0.00	2783500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 3014340 84 761	9270000.00	5882000.00	10584400.00	8407500.00	0.00	9210400.00	0.00	5801100.00	0.00	5220600.00	5544000.00	5295000.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 3258692 45 737	0.00	0.00	3078422.07	0.00	0.00	0.00	0.00	0.00	1101600.00	4704700.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Kallotenuales;Kallotenuaceae;Kallotenue;Kallotenue papyrolyticum;Kallotenue papyrolyticum JKG1
Ga0586324 3673999 1 591	0.00	2917200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 3288341 3 734	2610000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10188	lactose/L-arabinose transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 4583003 3 614	0.00	0.00	9627300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10206	LL-diaminopimelate aminotransferase	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Candidatus Methanomassiliicoccus intestinalis;Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1
Ga0586324 0008110 2662 5109	1280000.00	0.00	0.00	0.00	0.00	599819.36	31236000.00	13054000.00	16524000.00	0.00	0.00	12750000.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 0015750 314 2989	0.00	0.00	0.00	0.00	0.00	0.00	10396800.00	7198000.00	8343000.00	0.00	0.00	8925000.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324 0085770 2783 3691	0.00	3638000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 0124223 1532 2953	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	110499.75	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 0595481 1 1485	0.00	3175600.00	7487900.00	0.00	0.00	0.00	0.00	0.00	5629500.00	0.00	0.00	0.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 1385288 1 1056	2350000.00	1468800.00	0.00	0.00	0.00	2628231.31	0.00	0.00	1968300.00	0.00	0.00	665346.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 1784092 56 949	0.00	0.00	0.00	0.00	0.00	0.00	24168000.00	0.00	0.00	0.00	0.00	0.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 1870987 2 928	0.00	0.00	0.00	0.00	0.00	0.00	2462400.00	2555900.00	2924100.00	0.00	0.00	1440000.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324 2547094 3 740	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1409400.00	0.00	0.00	645597.75	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Ardenticatena;Ardenticatena maritima;Ardenticatena maritima 110S
Ga0586324 3102044 1 750	0.00	0.00	0.00	0.00	3254800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Oscillochloridaceae;Candidatus Viridilinea;Candidatus Viridilinea mediisalina;Viridilinea mediisalina Kir15-3F
Ga0586324 5895392 3 575	0.00	0.00	0.00	0.00	0.00	0.00	16210800.00	0.00	0.00	0.00	0.00	0.00	KO:K10232	alpha-glucoside transport system substrate-binding protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sp. MBLB1234;Paenibacillus sp. MBLB1234
Ga0586324 3509841 1 714	0.00	2087600.00	0.00	0.00	0.00	0.00	0.00	0.00	2446200.00	0.00	0.00	0.00	KO:K10236	trehalose/maltose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Halanaerobiales;unclassified Halanaerobiales;Anoxybacter;Anoxybacter fermentans;Anoxybacter fermentans DY22613
Ga0586324 0044188 4110 5078	3080000.00	2713200.00	0.00	0.00	2822200.00	2164189.92	4240800.00	0.00	0.00	0.00	0.00	2332500.00	KO:K10355	actin	Eukaryota;Arthropoda;Insecta;Diptera;Culicidae;Culex;Culex quinquefasciatus;Culex pipiens quinquefasciatus JHB
Ga0586324 0001903 9463 10401	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	826200.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Rhodospirillum;Rhodospirillum rubrum;Rhodospirillum rubrum S1, ATCC 11170
Ga0586324 0007436 5518 7677	4909005.00	0.00	0.00	0.00	0.00	0.00	0.00	2177700.00	437830.92	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0022403 5794 6882	2390000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2032800.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Tepidamorphaceae;Tepidamorphus;Tepidamorphus gemmatus;Tepidamorphus gemmatus DSM 19345
Ga0586324 0025068 2448 3584	0.00	1162800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. OV329;Variovorax sp. OV329
Ga0586324 0025068 874 2022	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1903200.00	0.00	3280200.00	3053600.00	1942500.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Hoeflea;Hoeflea marina;Hoeflea marina DSM 16791
Ga0586324 0028755 3537 5711	0.00	0.00	0.00	0.00	5150000.00	0.00	0.00	0.00	0.00	536124.82	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Devosiaceae;Devosia;Devosia sp. Root105;Devosia sp. Root105
Ga0586324 0030539 3604 4551	0.00	0.00	1789174.59	0.00	0.00	0.00	2394000.00	0.00	0.00	6006000.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Albidiferax sp. OV413;Albidiferax sp. OV413
Ga0586324 0041586 3497 4426	0.00	4569600.00	0.00	0.00	0.00	1621792.64	0.00	0.00	947700.00	0.00	0.00	1557622.50	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermoanaerobacter;Thermoanaerobacter ethanolicus;Thermoanaerobacter ethanolicus JW 200
Ga0586324 0057470 3242 4468	0.00	0.00	1455844.81	0.00	0.00	6312300.00	0.00	0.00	0.00	0.00	0.00	8475000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium loti;Mesorhizobium loti UFLA 01-765
Ga0586324 0058284 2595 3569	375420.00	0.00	4393314.20	499719.95	711849.48	0.00	754349.40	177686.90	1733400.00	527671.76	320876.16	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324 0059902 165 1217	6220000.00	0.00	10779603.36	5282000.00	0.00	2203322.21	0.00	1671400.00	2673000.00	695833.60	4030400.00	825000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta smaragdinae;Sediminispirochaeta smaragdinae DSM 11293
Ga0586324 0108219 1 486	5240000.00	4039200.00	0.00	3401000.00	3399000.00	0.00	0.00	3568500.00	2292300.00	1316700.00	5482400.00	1530000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Petroclostridium;Petroclostridium xylanilyticum;Petroclostridium xylanilyticum SK-Y3
Ga0586324 0129328 1748 2734	0.00	0.00	0.00	0.00	6334500.00	0.00	0.00	2202100.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;Verrucomicrobia bacterium LW23;Verrucomicrobia bacterium LW23
Ga0586324 0196859 622 1629	13200000.00	8160000.00	15595100.00	6897000.00	7539600.00	5955000.00	8755200.00	12846600.00	12425400.00	9625000.00	10296000.00	9900000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324 0227014 107 1135	0.00	1910800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0254225 1 1176	1800000.00	1992400.00	0.00	0.00	0.00	0.00	0.00	616100.00	0.00	854700.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sp. 1 12;Paenibacillus sp. 1 12
Ga0586324 0258796 673 2199	0.00	754800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Anaerobacterium;Anaerobacterium chartisolvens;Anaerobacterium chartisolvens DSM 27016
Ga0586324 0324990 970 1881	0.00	0.00	0.00	0.00	0.00	2578487.21	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-K07;Aminicenantes bacterium SCGC AAA252-K07 (contamination screened)
Ga0586324 0354957 587 1594	0.00	0.00	0.00	0.00	0.00	0.00	2872800.00	0.00	923400.00	0.00	6679200.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Petroclostridium;Petroclostridium xylanilyticum;Petroclostridium xylanilyticum SK-Y3
Ga0586324 0385703 942 1838	6700000.00	7752000.00	9739900.00	0.00	0.00	0.00	4833600.00	6527000.00	7241400.00	5544000.00	8395200.00	5985000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Aquamicrobium;Aquamicrobium aerolatum;Aquamicrobium aerolatum DSM 21857
Ga0586324 0470382 13 996	2410000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Thermotogae;Thermotogae;Kosmotogales;Kosmotogaceae;Kosmotoga;Kosmotoga arenicorallina;Kosmotoga arenicorallina S304
Ga0586324 0536845 336 1589	0.00	0.00	0.00	0.00	0.00	0.00	29868000.00	0.00	0.00	34419000.00	27720000.00	2287500.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Devosiaceae;Devosia;Devosia geojensis;Devosia geojensis BD-c194
Ga0586324 0605420 1 1101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12960000.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324 0614357 1 600	0.00	0.00	0.00	0.00	0.00	0.00	8755200.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Petroclostridium;Petroclostridium xylanilyticum;Petroclostridium xylanilyticum SK-Y3
Ga0586324 0692329 491 1423	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2140600.00	3106400.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia ginsengiterrae;Paraburkholderia ginsengiterrae DCY85-1
Ga0586324 0869601 532 1290	0.00	0.00	441149.35	0.00	0.00	330823.67	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter gummiphilus;Rhizobacter gummiphilus NBRC 109400
Ga0586324 0885194 3 701	1370000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1085700.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium sp. DCY119;Mesorhizobium sp. DCY119
Ga0586324 0945418 3 722	0.00	3073600.00	3967915.34	0.00	8147300.00	486348.82	0.00	0.00	5872500.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermoanaerobacter;Thermoanaerobacter ethanolicus;Thermoanaerobacter ethanolicus JW 200
Ga0586324 1025919 102 1202	12000000.00	2985200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Actinobacteria;Nitriliruptoria;Nitriliruptorales;Nitriliruptoraceae;Nitriliruptor;Nitriliruptor alkaliphilus;Nitriliruptor alkaliphilus DSM 45188
Ga0586324 1115434 35 1084	0.00	607557.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Flexilinea;Flexilinea flocculi;Flexilinea flocculi TC1
Ga0586324 1131061 1 567	0.00	4760000.00	8219800.00	4978000.00	4789500.00	4803700.00	8253600.00	0.00	4941000.00	8239000.00	8888000.00	8400000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324 1256415 2 688	0.00	4338400.00	0.00	347200.30	0.00	5915300.00	608730.36	304865.80	365536.80	0.00	287276.88	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324 1321578 157 1077	0.00	2033200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Moorella;Moorella thermoacetica;Moorella thermoacetica Y72
Ga0586324 1577248 18 998	1650000.00	0.00	1570550.43	0.00	0.00	0.00	0.00	0.00	0.00	3511200.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus alginolyticus;Paenibacillus alginolyticus DSM 5050
Ga0586324 1617947 1 831	0.00	21692000.00	0.00	4417500.00	1163900.00	0.00	0.00	0.00	712250.01	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Nitratireductor;Nitratireductor sp. StC3;Nitratireductor sp. StC3
Ga0586324 2014648 3 899	0.00	0.00	27192900.00	0.00	0.00	0.00	0.00	0.00	25434000.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Rhizobium;Rhizobium azooxidifex;Rhizobium azooxidifex DSM 100211
Ga0586324 2144317 3 878	0.00	0.00	0.00	0.00	2255700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 2207592 3 866	0.00	0.00	4560322.52	0.00	7817700.00	8575200.00	0.00	2348500.00	2259900.00	2748900.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 2521427 265 819	5100000.00	4073200.00	3100716.87	0.00	0.00	0.00	8709600.00	0.00	0.00	14637700.00	0.00	9030000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324 2580631 18 812	0.00	2148800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Atribacterota;unclassified Atribacterota;unclassified Atribacterota;unclassified Atribacterota;Candidatus Caldatribacterium;Candidatus Caldatribacterium saccharofermentans;Candidatus Caldatribacterium saccharofermentans OP9-77CS
Ga0586324 2599157 3 809	1270000.00	5582800.00	1634591.68	0.00	2492600.00	0.00	5266800.00	1628700.00	3734100.00	2695000.00	2728000.00	5700000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Aquamicrobium;Aquamicrobium aerolatum;Aquamicrobium aerolatum DSM 21857
Ga0586324 2672974 2 799	2190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus sp. RS-1;Roseiflexus sp. RS-1
Ga0586324 2742681 538 792	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5491800.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia vietnamiensis;Burkholderia vietnamiensis FL-2-3-10-S1-D7
Ga0586324 3333182 270 728	0.00	0.00	8276100.00	0.00	0.00	568285.65	2713200.00	0.00	0.00	4235000.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus alginolyticus;Paenibacillus alginolyticus DSM 5050
Ga0586324 3709890 144 698	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	530593.91	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Sphaerochaetaceae;Sphaerochaeta;Sphaerochaeta halotolerans;Sphaerochaeta halotolerans 4-11
Ga0586324 4238327 115 660	6160000.00	0.00	0.00	0.00	0.00	0.00	6178800.00	1579900.00	0.00	0.00	0.00	1627500.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus chondroitinus;Paenibacillus chondroitinus OK414
Ga0586324 4624777 261 638	0.00	8840000.00	0.00	0.00	14214000.00	0.00	0.00	7869000.00	0.00	10703000.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324 4975379 2 619	985219.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Geminicoccaceae;Geminicoccus;Geminicoccus roseus;Geminicoccus roseus DSM 18922
Ga0586324 5011108 3 512	0.00	1285200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia tropica;Paraburkholderia tropica LMG 22274
Ga0586324 5184316 3 608	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1324400.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Clostridium;Clostridium sp. D5;Clostridium sp. D5
Ga0586324 5309649 1 603	0.00	0.00	0.00	0.00	0.00	1572052.51	0.00	762500.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Armatimonadetes;unclassified Armatimonadetes;unclassified Armatimonadetes;unclassified Armatimonadetes;unclassified Armatimonadetes;Armatimonadetes bacterium JGI 0000077-K19;Armatimonadetes bacterium JGI 0000077-K19 (contamination screened)
Ga0586324 5741125 2 454	237074.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermoanaerobacter;Thermoanaerobacter ethanolicus;Thermoanaerobacter ethanolicus JW 200
Ga0586324 5766202 3 581	1850000.00	3134800.00	5176565.43	0.00	0.00	0.00	0.00	0.00	0.00	900900.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Candidatus Fervidibacteria;unclassified Candidatus Fervidibacteria;unclassified Candidatus Fervidibacteria;unclassified Candidatus Fervidibacteria;unclassified Candidatus Fervidibacteria;Fervidibacteria bacterium JGI 0000001-G10;Fervidibacteria bacterium JGI 0000001-G10 (contamination screened)
Ga0586324 6853075 2 541	0.00	0.00	0.00	0.00	14729000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Rhizobium;Rhizobium leguminosarum;Rhizobium leguminosarum bv. trifolii WSM2297
Ga0586324 7610324 1 399	503204.00	1475600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1073600.00	2190000.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Petroclostridium;Petroclostridium xylanilyticum;Petroclostridium xylanilyticum SK-Y3
Ga0586324 7653423 3 518	609480.00	0.00	2105062.63	0.00	0.00	0.00	0.00	0.00	0.00	2849000.00	0.00	2602500.00	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Thermotogae;Thermotogae;Kosmotogales;Kosmotogaceae;Kosmotoga;Kosmotoga pacifica;Kosmotoga pacifica SLHLJ1
Ga0586324 8313507 2 499	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	729859.50	KO:K10439	ribose transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylobacteriaceae;Microvirga;Microvirga massiliensis;Microvirga massiliensis JC119
Ga0586324 0015365 3513 4988	0.00	0.00	0.00	0.00	0.00	0.00	20178000.00	3464800.00	0.00	3796100.00	0.00	3277500.00	KO:K10535	hydroxylamine dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax ferrireducens;Rhodoferax ferrireducens T118

Ga0586324_0183225_770_2275	5360000.00	0.00	0.00	0.00	3594700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10535	hydroxylamine dehydrogenase
Ga0586324_2917349_1_771	0.00	0.00	2094213.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10535	hydroxylamine dehydrogenase
Ga0586324_2612995_1_807	0.00	2964800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10537	L-arabinose transport system substrate-binding protein
Ga0586324_3124119_3_749	2430000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10537	L-arabinose transport system substrate-binding protein
Ga0586324_3713389_1_696	0.00	0.00	17171500.00	0.00	0.00	4962500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10537	L-arabinose transport system substrate-binding protein
Ga0586324_0381175_3_911	0.00	616770.88	0.00	0.00	0.00	762708.46	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10540	methyl-galactoside transport system substrate-binding protein
Ga0586324_0001947_5230_6453	3400000.00	19312000.00	18633500.00	5073000.00	0.00	0.00	2690400.00	8479000.00	5062500.00	15053500.00	9240000.00	12075000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0004025_482_1582	38930000.00	30668000.00	29562486.49	2099500.00	0.00	2263801.19	13771200.00	1122400.00	0.00	1692003.39	14828000.00	15037500.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0018461_4815_5852	1250000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0033302_2842_3891	13010000.00	20196000.00	9683600.00	1253050.00	2863400.00	6749000.00	0.00	10132100.00	8002800.00	31231200.00	30483200.00	23055000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0009497_2_1018	771802.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0142194_885_1988	0.00	1774800.00	0.00	1273000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0213301_1590_2402	5700000.00	596078.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0214536_886_2001	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4568900.00	16637400.00	4496800.00	2921600.00	6742500.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0227733_1123_2211	0.00	0.00	0.00	0.00	0.00	0.00	1500600.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0228145_1147_2217	32500000.00	19679200.00	20831000.00	13585000.00	11433000.00	8019400.00	6384000.00	15768500.00	14256000.00	50119300.00	17424000.00	25425000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0226456_1654_2163	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1065000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0305616_1058_2038	7640000.00	2509200.00	864587.84	0.00	0.00	0.00	0.00	3202500.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0391902_125_1252	3010000.00	2407200.00	2661498.05	0.00	0.00	0.00	3146400.00	0.00	2114100.00	2294600.00	3440800.00	1770000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0399781_666_1808	1760000.00	2767600.00	4124419.77	0.00	6257514.70	2902740.93	2667600.00	0.00	0.00	1409100.00	2525600.00	2617500.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0429683_674_1741	0.00	2298400.00	4160744.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0497451_1366_1641	1150000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0512077_553_1623	0.00	1849600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1316700.00	0.00	647589.75	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0645915_112_1122	5690000.00	0.00	3997395.71	0.00	0.00	0.00	0.00	3550200.00	0.00	0.00	3836800.00	4222500.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0680703_310_1434	0.00	1033600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1770000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0701540_412_1416	0.00	0.00	1580690.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0751990_3_581	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	777700.00	0.00	1965000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0765999_81_1259	0.00	0.00	11203700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0940872_158_1246	4620000.00	1713600.00	1674654.76	0.00	0.00	2057801.86	2021058.12	0.00	818100.00	649390.28	485801.36	2887500.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_1404346_1_1040	1290000.00	5773200.00	0.00	0.00	0.00	0.00	17419200.00	0.00	0.00	0.00	0.00	4620000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_1500679_1_1020	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1177500.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_1527816_3_860	10300000.00	13464000.00	9120600.00	16473000.00	0.00	7344500.00	9444864.66	5105700.00	2729700.00	9308904.99	8152513.60	11325000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_1554725_3_1004	0.00	2142000.00	0.00	0.00	0.00	2633563.20	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_1661960_2_871	0.00	0.00	1371107.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_1929304_86_916	0.00	3842000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_1945474_397_876	0.00	0.00	0.00	0.00	0.00	0.00	3146400.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_2153717_3_692	0.00	0.00	0.00	0.00	0.00	1910753.06	0.00	3123200.00	3159000.00	0.00	5024800.00	9112500.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_2539350_400_816	4940000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_2567512_84_812	2550000.00	4182000.00	1368000.00	0.00	0.00	0.00	0.00	0.00	0.00	10703000.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_2608882_199_807	7120000.00	2893257.88	12667500.00	8151000.00	4768900.00	1723710.48	6019200.00	1238300.00	1304100.00	3187800.00	3810400.00	3915000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_2730394_1_792	5650000.00	0.00	0.00	0.00	0.00	0.00	3990000.00	0.00	0.00	0.00	5535200.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_2769154_1_786	6200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2741622.39	2279200.00	287344.64	3765000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_2783461_2_787	948485.00	354770.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_3037131_1_747	0.00	1985600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_3198227_2_730	8530000.00	0.00	0.00	0.00	0.00	7741500.00	0.00	1201700.00	0.00	0.00	0.00	4230000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_3219933_1_626	0.00	1101600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_3423933_1_629	9720000.00	4658000.00	2092845.53	1529500.00	1720100.00	0.00	603707.52	1360300.00	717258.24	2926000.00	6168800.00	2991564.75	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_3812976_2_388	1060000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_3818530_1_690	3560000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1312500.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_3822971_2_688	0.00	1584400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_4186681_2_664	36200000.00	22372000.00	14806900.00	6640500.00	6890700.00	12942200.00	7501200.00	7625000.00	8262000.00	10087000.00	8518400.00	14775000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_4749571_3_629	0.00	2393600.00	0.00	0.00	0.00	2578959.64	0.00	11712000.00	972000.00	0.00	0.00	1560000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_4831903_2_445	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6067600.00	7075200.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_4833877_2_559	11400000.00	12648000.00	16439600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_5064145_2_613	0.00	0.00	4039286.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_5856859_2_577	274365.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_5911029_1_576	4090000.00	3121200.00	0.00	0.00	0.00	342275.14	1202198.40	563709.54	488313.36	0.00	1372800.00	1170000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_5955861_3_575	5890000.00	5236000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3511200.00	4644000.00	5010000.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_6276086_1_561	0.00	4630800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_6808737_130_543	0.00	748000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_6922786_2_538	664874.00	4111187.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1012000.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_7097857_2_532	9460000.00	5059200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10543	D-xylose transport system substrate-binding protein
Ga0586324_0076166_989_3148	0.00	1625200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0092070_724_2733	7490000.00	3413600.00	29670100.00	0.00	0.00	0.00	13953600.00	201331.72	1717200.00	0.00	7207200.00	9450000.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0100428_2_892	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10032800.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0160636_2179_2739	0.00	0.00	6080400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3555200.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0218068_1571_2377	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1347500.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0229262_1_570	748988.00	4488000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5359200.00	6987367.75	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0408164_1_1224	0.00	0.00	20999900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0461461_1_870	525133.00	0.00	1785683.99	0.00	1884900.00	1551900.79	1598268.60	324845.74	1790100.00	823900.00	1716000.00	27676114.50	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0839646_1_1310	0.00	2624800.00	0.00	0.00	18746000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0857332_1_220	0.00	7752000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	690324.25	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_1365953_1_492	0.00	0.00	39072200.00	0.00	0.00	0.00	0.00	0.00	2177700.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_1374434_3_1058	0.00	0.00	0.00	0.00	0.00	0.00	16712400.00	0.00	0.00	0.00	1862600.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_1453070_2_1033	3920000.00	3787600.00	0.00	4066000.00	4161200.00	11790900.00	0.00	2366800.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_1832287_1_714	0.00	0.00	0.00	1016500.00	5376600.00	3583758.70	4651200.00	0.00	0.00	2502500.00	0.00	3637500.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_2427553_3_833	16600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_3242611_1_738	0.00	2053600.00	0.00	0.00	4212700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_3396380_3_701	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15494000.00	13446000.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_4008636_97_675	0.00	0.00	0.00	7001500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_4069835_2_670	0.00	1754400.00	3998307.77	0.00	1462600.00	3612390.34	2690400.00	1683600.00	0.00	2356200.00	3828000.00	3022500.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_4143497_1_666	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3220800.00	339323.25	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_4156032_3_665	9690000.00	2046800.00	17700800.00	0.00	0.00	4486100.00	0.00	1628700.00	6083671.51	4943400.00	9416000.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_4313806_1_654	0.00	0.00	9206759.53	0.00	0.00	0.00	0.00	2670000.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_4536808_3_641	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19096000.00	23100000.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_5071077_144_614	22100000.00	0.00	5798900.00	0.00	0.00	0.00	0.00	0.00	0.00	7361200.00	0.00	1455000.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_5311200_2_592	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	555849.54	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_5579393_1_588	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	713701.53	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_5618460_1_588	0.00	0.00	0.00	0.00	0.00	0.00	21386400.00	0.00	0.00	0.00	0.00	1282500.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_5632112_2_586	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6997627.25	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_6032880_1_570	0.00	0.00	0.00	0.00	0.00	0.00	17100000.00	0.00	0.00	0.00	0.00	11850000.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_6069768_2_568	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5589000.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_6276107_2_562	0.00	5501200.00	9793344.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15300000.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_6472738_3_554	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14094000.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_7105679_2_532	0.00	1883600.00	230830000.00	13205000.00	2049700.00	2913269.37	2667600.00	117120000.00	1287900.00	2987600.00	2895200.00	2122500.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_7378278_3_524	5240000.00	0.00	7037500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_7747234_2_514	0.00	0.00	45490400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10546	putative multiple sugar transport system substrate-binding protein
Ga0586324_0549977_728_1573	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	842400.00	0.00	0.00	KO:K10552	fructose transport system substrate-binding protein
Ga0586324_7115346_2_532	4330000.00	1740800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4252500.00	KO:K10552	fructose transport system substrate-binding protein
Ga0586324_0013139_3804_4903	0.00	10404000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8008000.00	10208000.00	9600000.00	KO:K10559	rhamnose transport system substrate-binding protein
Ga0586324_0464142_3_1271	1120000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2057400.00	0.00	1342500.00	KO:K10559	rhamnose transport system substrate-binding protein
Ga0586324_0670318_280_1443	0.00	1237600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10559	rhamnose transport system substrate-binding protein
Ga0586324_1424544_68_1147	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1311503.88	0.00	0.00	0.00	1267500.00	KO:K10559	rhamnose transport system substrate-binding protein
Ga0586324_2874828_1_774	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	866200.00	0.00	1262800.00	975000.00	KO:K10559	rhamnose transport system substrate-binding protein
Ga0586324_2905479_2_715	11100000.00	6215200.00	0.00	2223000.00	0.00	5319800.00	3876000.00	3876000.00	2629100.00	5483700.00	5536300.00	4180000.00	KO:K10559	rhamnose transport system substrate-binding protein
Ga0586324_4916960_309_620	2740000.00	5963000.00	4269735.70	2831000.00	0.00	2886178.09	4628400.00	0.00	1425600.00	0.00	0.00	4530000.00	KO:K10559	rhamnose transport system substrate-binding protein
Ga0586324_5836699_3_578	0.00	0.00	0.00	0.00	0.00	0.00	1620945.48	0.00	0.00	0.00	1378300.00	0.00	1815000.00	KO:K10559
Ga0586324_0045441_4342_4851	8440000.00	437820.04	6672169.30	0.00	10063100.00	8694300.00	13429200.00	9345200.00	67716600.00	6429500.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_0190629_115_624	8850000.00	5854800.00	4561797.58	5852000.00	0.00	5161000.00	0.00	2763300.00	0.00	8085000.00	5814800.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_0256468_1363_1881	0.00	57868000.00	0.00	0.00	38522000.00	0.00	0.00	0.00	0.00	49329000.00	29040000.00	37200000.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_0475964_772_1272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2736000.00	0.00	1571400.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_0529332_37_618	3190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_0854593_328_843	0.00	0.00	0.00	0.00	0.00	10898400.00	29524000.00	27864000.00	0.00	0.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_1948731_192_761	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2559600.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_2694260_3_386	0.00	14750000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_3127443_3_419	0.00	149011.12	0.00	0.00	0.00	0.00	12227600.00	0.00	0.00	0.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_4700569_1_486	0.00	0.00	0.00	0.00	0.00	0.00	5240400.00	0.00	4227300.00	0.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_4721494_426_632	4700000.00	3536000.00	0.00	0.00	6550800.00	0.00	0.00	0.00	0.00	4650800.00	4963200.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_5820654_1_420	11600000.00	96578600.00	115809100.00	22990000.00	24617000.00	57962000.00	0.00	138470000.00	0.00	0.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_6249212_1_279	0.00	0.00	0.00	0.00	0.00	0.00	4651200.00	774700.00	0.00	0.00	0.00	0.00	KO:K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase
Ga0586324_6042799_2_571	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1814400.00	0.00	0.00	0.00	0.00	KO:K10823	oligopeptide transport system ATP-binding protein
Ga0586324_0145251_280_990	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3126600.00	0.00	0.00	0.00	0.00	KO:K10914	CRP/FNR family cyclic AMP-dependent transcriptional regulator
Ga0586324_0009226_9489_10382	0.00	0.00	0.00	0.00	0.00	0.00	0.00	433941.00	0.00	0.00	0.00	0.00	KO:K10944	methane/ammonia monooxygenase subunit A
Ga0586324_0009226_8227_9492	6800000.00	6786400.00	0.00	0.00	11330000.00	9595116.82	13611600.00	0.00	0.00	1053000.00	0.00	3317600.00	KO:K10945	methane/ammonia monooxygenase subunit B
Ga0586324_0113958_1864_2985	###########	###########	###########	200596000.00	572185000.00	342887000.00	###########	###########	62982500.00	702027000.00	229136000.00	349096000.00	775725000.00	KO:K10945
Ga0586324_0169447_852_2117	0.00	2964800.00	0.00	0.00	0.00	1668600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10945	methane/ammonia monooxygenase subunit B
Ga0586324_0181757_1198_2517	50490000.00	77227600.00	66888425.45	89953704.50	122982000.00	40494000.00	46159327.32	56040700.00	37389600.00	52567900.00	45011521.28	34500000.00	KO:K10945	methane/ammonia monooxygenase subunit B
Ga0586324_0496635_152_1417	0.00	0.00	0.00	0.00	0.00	3430218.95	0.00	0.00	0.00	0.00	0.00	0.00	KO:K10945	methane/ammonia monooxygenase subunit B
Ga0586324_0752065_78_1322	0.00	30668000.00	###########	42085000.00	377701000

Ga0586324_1083067_181_672	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2271500.00	3141600.00	0.00	290614.50	KO:K11065	thiol peroxidase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thiopaeus DSM 5505
Ga0586324_2806457_279_782	0.00	0.00	0.00	0.00	276172.87	0.00	449449.56	562082.06	850500.00	525592.76	0.00	290614.50	KO:K11065	thiol peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324_3087077_1_519	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	302893.83	0.00	0.00	0.00	KO:K11085	subfamily B ATP-binding cassette protein MsbA	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Sporomusaceae;Sporolitus;Sporolitus thermophilus;Sporolitus thermophilus DSM 23256]
Ga0586324_0000003_179518_180810	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6222000.00	11064600.00	23331000.00	24129600.00	23627500.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0000049_60952_62244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1886500.00	0.00	1320000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfurifustis;Sulfurifustis variabilis;Sulfurifustis variabilis sikN76
Ga0586324_0001021_13892_15193	1450000.00	6936000.00	0.00	0.00	0.00	3215600.75	43456800.00	7763000.00	12040650.00	18437650.00	273072800.00	105232500.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_0004429_4006_5301	0.00	0.00	0.00	0.00	0.00	0.00	2094658.44	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Ferrigenasalus;Ferrigenasalus amnicola;Ferrigenasalus amnicola OYT1]
Ga0586324_0019654_7270_7497	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9086000.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter sp. PAE-UM;Curvibacter sp. PAE-UM
Ga0586324_0028735_2326_3567	0.00	0.00	0.00	0.00	1277200.00	0.00	0.00	0.00	1571400.00	1193500.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0028923_1542_2795	0.00	4875600.00	9064300.00	0.00	0.00	0.00	0.00	5660800.00	0.00	0.00	0.00	3555000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_0041780_2638_3918	8640000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter sp. PAE-UM;Curvibacter sp. PAE-UM
Ga0586324_0047188_571_1818	0.00	0.00	0.00	0.00	0.00	8853100.00	4286400.00	1110200.00	2794500.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0069840_2542_3720	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5567100.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetobacterium;Candidatus Magnetobacterium casensis;Candidatus Magnetobacterium casensis MYR-1
Ga0586324_0070982_1658_2959	1290000.00	0.00	0.00	0.00	0.00	0.00	6465090.48	5648600.00	8910000.00	8339000.00	0.00	4245000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_0087561_998_1845	0.00	0.00	11710400.00	0.00	0.00	0.00	0.00	6026800.00	5815800.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0144035_1990_2883	0.00	0.00	0.00	0.00	0.00	2709155.79	0.00	0.00	7055100.00	2533300.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324_0153499_1_282	0.00	0.00	0.00	1483200.00	0.00	0.00	0.00	0.00	714308.22	537543.16	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0156778_602_1900	0.00	0.00	0.00	1287500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Ferrigenasalus;Ferrigenasalus amnicola;Ferrigenasalus amnicola OYT1]
Ga0586324_0187036_755_1933	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3588300.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324_0195715_1299_2498	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	352312.73	325403.76	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Calderihabitans;Calderihabitans maritimus;Calderihabitans maritimus KKC1
Ga0586324_0219864_1_129	2460000.00	0.00	0.00	0.00	0.00	0.00	0.00	634400.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0271695_3_818	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5483900.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324_0349685_3_1079	11800000.00	2094400.00	0.00	4816500.00	705123.58	39700000.00	42567600.00	6527000.00	22680000.00	3234000.00	8395200.00	6435000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0354113_156_1469	7660000.00	0.00	0.00	0.00	0.00	0.00	840729.48	0.00	0.00	0.00	0.00	2925000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignatibadium;Desulfatitalbadium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0374606_2_583	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16958000.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium GJ-E10;Burkholderiales bacterium GJ-E10
Ga0586324_0453890_2_1147	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2763300.00	3418200.00	2918300.00	0.00	2212500.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 10923
Ga0586324_0483529_397_1662	0.00	7684000.00	0.00	0.00	4140600.00	0.00	5722800.00	6527000.00	6933600.00	2394700.00	3194400.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0602559_413_1510	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	351874.60	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter lithotrophicus;Ramlibacter lithotrophicus RBP-1
Ga0586324_0634589_183_1478	20620000.00	33585200.00	27080300.00	35815000.00	39861000.00	46131400.00	39763200.00	4983700.00	46996200.00	50981700.00	68200000.00	27000000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfonema;Desulfonema limicola;Desulfonema limicola Jadibuseh, DSM 2076
Ga0586324_0653338_3_1100	0.00	1822400.00	0.00	3866500.00	0.00	0.00	0.00	0.00	0.00	2525600.00	0.00	2062500.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0663948_1_945	0.00	0.00	8219800.00	2565000.00	1011519.74	0.00	0.00	0.00	2494800.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0752000_3_1046	0.00	0.00	0.00	3458000.00	0.00	1914135.50	0.00	896700.00	1385100.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_1277912_1_621	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	21141000.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_1336663_3_944	577404.00	24548000.00	0.00	1016500.00	0.00	0.00	0.00	0.00	0.00	401149.98	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_1589143_1_926	1730000.00	2380000.00	0.00	0.00	9795300.00	2330461.46	440899.56	530172.35	582846.03	1409100.00	1918400.00	2197500.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_1608571_1_990	0.00	1616000.00	0.00	0.00	0.00	0.00	11058000.00	1610400.00	1611900.00	2748900.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_1701750_3_653	0.00	4229600.00	0.00	0.00	0.00	0.00	0.00	0.00	19359000.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_1713397_472_963	0.00	0.00	0.00	0.00	0.00	0.00	2986800.00	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoarcula;Desulfoarcula anilini;Desulfatiglans anilini DSM 4660
Ga0586324_1793868_3_947	3270000.00	2686000.00	0.00	0.00	0.00	0.00	0.00	1683000.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfoarcula;Desulfoarcula anilini;Desulfatiglans anilini DSM 4660
Ga0586324_1812708_189_941	0.00	10608000.00	0.00	0.00	25750000.00	1272206.35	0.00	15616000.00	22923000.00	12782000.00	9064000.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1or3. DSM 2032
Ga0586324_1956730_573_911	0.00	3950800.00	0.00	0.00	0.00	0.00	0.00	19215000.00	10287000.00	23408000.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_2049332_336_887	4100000.00	0.00	0.00	1786000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_2230265_3_863	6690000.00	7820000.00	0.00	0.00	0.00	5631600.00	7869000.00	7200900.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_2364420_3_581	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4587200.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thioploca;Thioploca ingrica;Thioploca ingrica Lake Okotanpe
Ga0586324_2676346_553_798	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	24462000.00	21175500.00	26224000.00	18825000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_2762681_1_789	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5107500.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324_3094512_1_702	13500000.00	15232000.00	0.00	7191500.00	7148200.00	0.00	0.00	9028000.00	6804000.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_3152047_3_506	0.00	9452000.00	0.00	0.00	13287000.00	7701800.00	1821218.40	0.00	0.00	14091000.00	14960000.00	15300000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_3190264_2_742	0.00	0.00	29332300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324_3372915_1_726	0.00	0.00	0.00	0.00	0.00	0.00	21112800.00	17202000.00	10773000.00	12243000.00	15752000.00	15750000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaeus;Thiobacillus thiopaeus DSM 505
Ga0586324_3639461_2_703	0.00	727600.00	0.00	93886.51	192759.35	0.00	0.00	0.00	446953.71	200700.99	1439900.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_3639671_3_704	0.00	0.00	0.00	0.00	2018809.00	6709300.00	7866000.00	9028000.00	3175200.00	2002000.00	1707200.00	1515000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324_3936839_1_681	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1935900.00	0.00	0.00	3247500.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_4494296_3_644	0.00	0.00	0.00	37335000.00	0.00	0.00	0.00	0.00	5670000.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_5040590_238_615	0.00	2760800.00	10190000.00	0.00	0.00	19929400.00	11422800.00	2714500.00	4519800.00	6937700.00	0.00	1050000.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_5599400_3_590	0.00	157738.92	0.00	0.00	0.00	0.00	3223396.52	121704.15	389167.74	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_6546222_2_553	2610000.00	2638400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thioploca;Thioploca ingrica;Thioploca ingrica Lake Okotanpe
Ga0586324_6987753_1_537	0.00	2869600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfotignatibadium;Desulfatitalbadium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_7430166_185_523	552355.00	0.00	0.00	0.00	0.00	195490.74	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11180	sulfite reductase alpha subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0000003_178378_179448	0.00	0.00	0.00	0.00	0.00	0.00	0.00	52539300.00	1644300.00	60137000.00	6708636.36	6510000.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0015890_333_1406	0.00	5814000.00	0.00	1330000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5107500.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324_0017488_2749_3849	0.00	20604000.00	44871100.00	0.00	0.00	0.00	0.00	0.00	42606000.00	0.00	0.00	24900000.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0028146_2701_3840	0.00	0.00	1068095.45	0.00	0.00	1185692.11	24168000.00	0.00	0.00	0.00	0.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324_0028735_1192_2262	0.00	0.00	0.00	4978000.00	6447800.00	0.00	0.00	14272800.00	0.00	0.00	0.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0051016_465_1535	2670000.00	0.00	0.00	0.00	0.00	0.00	8322000.00	19520000.00	13446000.00	11935000.00	0.00	3505029.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfurellaceae;Desulfurella;Desulfurella multivorans;Desulfurella multivorans TTN
Ga0586324_0070982_3025_4038	0.00	0.00	4579250.58	0.00	0.00	0.00	22458000.00	8174000.00	0.00	8701000.00	7066400.00	2310000.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaeus;Thiobacillus thiopaeus DSM 505
Ga0586324_0163121_3_527	31000000.00	0.00	29557500.00	0.00	0.00	46846000.00	52440000.00	0.00	24138000.00	0.00	0.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfotignatibadium;Desulfatitalbadium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0179166_4421_2494	15100000.00	13390000.00	22632600.00	0.00	0.00	0.00	15640800.00	1842200.00	0.00	13706000.00	17160000.00	15600000.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 10923
Ga0586324_0187036_1979_2551	0.00	0.00	0.00	271418.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetobacterium;Candidatus Magnetobacterium casensis;Candidatus Magnetobacterium casensis MYR-1
Ga0586324_0268276_204_1346	0.00	0.00	2924267.04	4569500.00	0.00	1097812.19	1295448.12	2653500.00	466590.78	0.00	1944800.00	1620000.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324_0327527_980_1976	0.00	1319200.00	0.00	0.00	3543200.00	331186.13	832154.40	0.00	464697.00	0.00	0.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324_0381402_342_1415	3380000.00	931600.00	0.00	5434000.00	1349300.00	0.00	0.00	0.00	9558000.00	0.00	924000.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiolinaceae;Thiolinea;Thiolinea disciformis;Thiolinea disciformis DSM 14473
Ga0586324_0445522_279_1418	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	344481.66	0.00	0.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324_0453867_3_1106	0.00	0.00	0.00	0.00	130810000.00	9431960.93	0.00	0.00	0.00	0.00	3467200.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus DSM 2032
Ga0586324_0538190_68_1147	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	33792000.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0596412_480_1517	0.00	5453600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	28567000.00	0.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfosalsimonas;Desulfosalsimonas propionicica;Desulfosalsimonas propionicica DSM 17721
Ga0586324_0671027_1_525	26800000.00	0.00	0.00	0.00	42230000.00	0.00	0.00	23729000.00	0.00	0.00	0.00	0.00	KO:K11181	sulfite reductase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfob

Ga0586324_2186811_3_869	496231.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11959	urea transport system substrate-binding protein
Ga0586324_4659583_2_634	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	825000.00	KO:K11959	urea transport system substrate-binding protein
Ga0586324_1343858_29_721	0.00	2924000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K11963	urea transport system ATP-binding protein
Ga0586324_0000078_41484_43568	0.00	0.00	0.00	0.00	0.00	365435.60	0.00	0.00	0.00	0.00	0.00	0.00	KO:K12132	HAMP domain-containing protein
Ga0586324_1918243_3_920	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3142800.00	3572800.00	0.00	0.00	0.00	KO:K12132	hypothetical protein
Ga0586324_4716551_3_533	0.00	2257600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K12261	2-hydroxyacyl-CoA lyase 1
Ga0586324_0380764_1_692	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1260000.00	0.00	KO:K12282	MSHA biogenesis protein MshL
Ga0586324_0000003_54335_55699	0.00	0.00	0.00	0.00	2242535.04	16372400.00	5961600.00	32832800.00	31416000.00	33892500.00	0.00	KO:K12340	outer membrane protein
Ga0586324_0000004_142184_143491	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1362900.00	1372800.00	1942500.00	KO:K12340	outer membrane protein
Ga0586324_0023208_2962_4410	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6491100.00	0.00	0.00	KO:K12340	outer membrane protein
Ga0586324_0329478_222_1562	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1432500.00	KO:K12340	outer membrane protein
Ga0586324_0514585_1_1110	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	363114.00	KO:K12340	outer membrane protein
Ga0586324_0626403_148_1485	0.00	0.00	0.00	0.00	0.00	0.00	3068300.00	0.00	2387000.00	0.00	0.00	KO:K12340	outer membrane protein
Ga0586324_0671718_3_1277	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7222500.00	KO:K12340	outer membrane protein
Ga0586324_3287222_1_507	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2400000.00	KO:K12340	outer membrane protein
Ga0586324_4075130_3_671	0.00	0.00	0.00	0.00	4009700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K12340	outer membrane protein
Ga0586324_0110526_1307_3079	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2812028.75	KO:K12507	acyl-CoA synthetase
Ga0586324_0000011_3246_5447	0.00	0.00	0.00	0.00	0.00	89527.26	0.00	0.00	0.00	0.00	0.00	KO:K12541	ATP-binding cassette subfamily C protein LapB
Ga0586324_0000652_22780_24699	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19373600.00	8215791.12	40748400.00	25810400.00	48735651.00	KO:K12543	adhesin transport system outer membrane protein
Ga0586324_2331687_2_502	0.00	0.00	0.00	0.00	11124000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K12543	adhesin transport system outer membrane protein
Ga0586324_0221029_3_1010	205948.00	0.00	0.00	550053.80	0.00	0.00	0.00	239283.48	0.00	0.00	0.00	0.00	KO:K12574	ribonuclease J
Ga0586324_0253183_1_438	0.00	0.00	0.00	0.00	0.00	0.00	0.00	234721.90	0.00	0.00	0.00	0.00	KO:K12574	ribonuclease J
Ga0586324_1886349_42_926	0.00	0.00	0.00	98577.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K12574	ribonuclease J
Ga0586324_0065518_2378_3349	0.00	1183200.00	3148712.62	2489000.00	1503800.00	0.00	0.00	671000.00	1960200.00	0.00	0.00	0.00	KO:K12686	outer membrane lipase/esterase
Ga0586324_0835308_110_1312	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1162500.00	KO:K13015	UDP-N-acetyl-D-alucosamine dehydroxeanase
Ga0586324_0034865_2658_3533	5500000.00	0.00	7600500.00	5671500.00	0.00	0.00	0.00	0.00	0.00	0.00	4777500.00	KO:K13075	N-acyl homoserine lactone hydrolase
Ga0586324_0434970_525_1397	599554.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1812800.00	0.00	KO:K13075	N-acyl homoserine lactone hydrolase
Ga0586324_0000519_7515_7823	0.00	0.00	0.00	2755000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_0002885_7498_7887	0.00	7480000.00	0.00	0.00	7848600.00	13021600.00	0.00	902800.00	0.00	0.00	0.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_0258146_731_1093	0.00	0.00	0.00	0.00	0.00	0.00	0.00	132853.73	0.00	0.00	0.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_1060368_691_1020	1710000.00	0.00	0.00	0.00	0.00	3262093.42	0.00	3226900.00	0.00	0.00	0.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_1255818_440_805	0.00	1196800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_1639625_187_558	0.00	5222400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_2504379_260_580	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5332500.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_4003122_233_559	0.00	4569600.00	4808667.45	3743000.00	4006700.00	2497717.56	0.00	2110600.00	0.00	1301300.00	1513600.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_6631954_23_382	0.00	2985200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13195	cold-inducible RNA-binding protein
Ga0586324_0047409_2338_3483	0.00	0.00	0.00	0.00	0.00	340269.48	0.00	210310.02	0.00	0.00	0.00	KO:K13290	aspartate aminotransferase-like enzyme
Ga0586324_0443136_944_1732	0.00	0.00	0.00	1643500.00	0.00	258547.44	0.00	158214.87	0.00	0.00	0.00	KO:K13290	aspartate aminotransferase-like enzyme
Ga0586324_0105831_1829_2782	0.00	0.00	0.00	0.00	0.00	0.00	3220800.00	0.00	0.00	0.00	0.00	KO:K13444	sulfatase modifying factor 1
Ga0586324_3623233_2_703	0.00	1917600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13444	sulfatase modifying factor 1
Ga0586324_0013466_1_1764	6110000.00	5256400.00	0.00	3990000.00	0.00	0.00	0.00	5337500.00	931500.00	6290900.00	7031200.00	1777500.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_0317119_189_2003	0.00	795600.00	0.00	0.00	0.00	0.00	0.00	399032.72	0.00	0.00	0.00	0.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_0593164_1_576	0.00	0.00	0.00	0.00	2729500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_0834648_3_1268	0.00	78758.28	0.00	1140000.00	0.00	0.00	0.00	0.00	1206900.00	0.00	0.00	0.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_1255573_1_1101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8855000.00	0.00	0.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_1460358_1_1032	9180000.00	0.00	0.00	0.00	0.00	0.00	0.00	192756.51	0.00	0.00	0.00	0.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_1996757_1_903	0.00	0.00	0.00	2087361.91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_2346188_1_843	0.00	11628000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_4148549_2_646	0.00	0.00	0.00	0.00	0.00	0.00	2696200.00	0.00	0.00	0.00	0.00	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_7016145_1_537	0.00	609117.48	0.00	0.00	0.00	0.00	1552281.00	2793800.00	1296000.00	0.00	0.00	354678.75	KO:K13525	transitional endoplasmic reticulum ATPase
Ga0586324_1083327_3_1172	0.00	0.00	0.00	279655.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13542	uroporphyrinogen III methyltransferase/synthase
Ga0586324_0320210_3_1193	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	354812.25	KO:K13587	two-component system cell cycle sensor histidine kinase/response regulator CckA
Ga0586324_0599285_2_1447	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	645546.75	KO:K13587	two-component system cell cycle sensor histidine kinase/response regulator CckA
Ga0586324_1616880_2_988	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1355200.00	0.00	0.00	KO:K13598	two-component system nitrogen regulation sensor histidine kinase NtrY
Ga0586324_3018128_3_761	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	299314.40	0.00	0.00	KO:K13598	two-component system nitrogen reeulation sensor histidine kinase NtrY
Ga0586324_0000001_110890_112167	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1487200.00	0.00	KO:K13599	two-component system nitrogen regulation response regulator NtrX
Ga0586324_0045136_3_5027	0.00	0.00	0.00	3515000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13688	cyclic beta-1,2-glucan synthetase
Ga0586324_0003519_9788_11329	0.00	0.00	2341241.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13889	glutathione transport system substrate-binding protein
Ga0586324_1670554_365_976	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1043100.00	923400.00	0.00	0.00	0.00	KO:K13953	propanol-preferring alcohol dehydrogenase
Ga0586324_0136868_2_1009	23450000.00	12920000.00	0.00	10925000.00	38357200.00	27948800.00	36936000.00	2549800.00	0.00	0.00	0.00	0.00	KO:K13954	alcohol dehydroenase
Ga0586324_0881029_727_1281	0.00	0.00	0.00	0.00	0.00	23343600.00	20634000.00	0.00	0.00	9680000.00	0.00	0.00	KO:K13954	alcohol dehydrogenase
Ga0586324_3425811_2_721	0.00	3991600.00	0.00	13585000.00	0.00	7225400.00	11491200.00	10675000.00	12393000.00	2148300.00	0.00	2452500.00	KO:K13954	alcohol dehydrogenase
Ga0586324_7725075_2_307	0.00	0.00	0.00	4104000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13954	alcohol dehydrogenase
Ga0586324_0007287_3047_3502	0.00	7371200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_0009935_1401_1853	0.00	0.00	0.00	0.00	4707100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_0018138_1750_2175	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1198800.00	0.00	2552000.00	2197500.00	KO:K13993	HSP20 family protein
Ga0586324_0048515_91_534	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7725000.00	KO:K13993	HSP20 family protein
Ga0586324_0047972_1313_3777	0.00	0.00	8163500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_0190226_834_1175	9480000.00	7480000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_0215373_197_640	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1909600.00	982500.00	KO:K13993	HSP20 family protein
Ga0586324_0236188_1040_1486	0.00	0.00	0.00	0.00	739090.92	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_0266745_272_649	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6885000.00	KO:K13993	HSP20 family protein
Ga0586324_0521173_666_1064	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1612500.00	KO:K13993	HSP20 family protein
Ga0586324_0795214_783_1235	0.00	0.00	653226.38	0.00	0.00	0.00	0.00	2125324.18	0.00	717635.38	1566640.00	1117500.00	KO:K13993	HSP20 family protein
Ga0586324_0779124_834_1202	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2370000.00	KO:K13993	HSP20 family protein
Ga0586324_0878275_224_685	0.00	1965200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_1018637_816_1205	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1270500.00	783049.52	795000.00	KO:K13993	HSP20 family protein
Ga0586324_1317879_440_886	0.00	0.00	0.00	5491000.00	0.00	0.00	4971500.00	6180300.00	4173400.00	0.00	4327500.00	KO:K13993	HSP20 family protein
Ga0586324_1724519_527_961	0.00	3107600.00	0.00	0.00	0.00	0.00	0.00	1433700.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_1740885_379_876	0.00	12920000.00	20718400.00	8521500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_1739398_3_368	0.00	0.00	0.00	1719500.00	2533800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_2077913_263_685	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3033800.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_2155781_146_679	0.00	0.00	0.00	0.00	0.00	2730272.22	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_2249690_211_657	0.00	0.00	0.00	0.00	12772000.00	16141444.32	0.00	854000.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_2547406_136_597	0.00	2958000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_2812697_1_480	11000000.00	5616800.00	5406460.85	0.00	0.00	0.00	5422900.00	0.00	4566100.00	4628800.00	4230000.00	KO:K13993	HSP20 family protein
Ga0586324_3139821_2_415	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1434400.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_3475159_108_554	0.00	0.00	0.00	0.00	0.00	0.00	1073880.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_4378537_2_241	14600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K13993	HSP20 family protein
Ga0586324_6693943_3_416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1964200.00	0.00	0.00	0.00	KO:K14003	F420-nonreducing hydrogenase I large subunit
Ga0586324_0259178_840_2198	0.00	0.00	0.00	0.00	0.00	0.00	841800.00	0.00	0.00	0.00	0.00	KO:K14068	F420-nonreducing hydrogenase I large subunit
Ga0586324_0285324_1199_2017	104700000.00	138060400.00	105900300.00	53827000.00	55939300.00	94692297.08	48039600.00	38844800.00	27507600.00	17448200.00	10454400.00	5315170.50	KO:K14081	methanol corrinoid protein
Ga0586324_0346203_1_351	0.00	0.00	0.00	0.00	1548500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14081	methanol corrinoid protein
Ga0586324_0353579_41_916	14500000.00	8228000.00	19648700.00	0.00	0.00	18857500.00	5061600.00	3989400.00	0.00	0.00	0.00	0.00	KO:K14081	methanol corrinoid protein
Ga0586324_0426406_285_1067	0.00	0.00	2616542.50	0.00	8672600.00	3923634.37	0.00	3458700.00	4503600.00	0.00	0.00	0.00	KO:K14081	methanol corrinoid protein
Ga0586324_0605793_3_539	2110000.00	1849600.00	4393477.47	5320000.00	5150000.00	1262277.38	2530800.00	2818200.00	2867400.00	3942400.00	6230400.00	658878.75	KO:K14081	methanol corrinoid protein
Ga0586324_4852330_87_623	0.00	0.00	6924900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14081	methanol corrinoid protein
Ga0586324_5041498_1_579	0.00	0.00	0.00	0.00	0.00	0.00	9370800.00	0.00	0.00	0.00	0.00	0.00	KO:K14081	methanol corrinoid protein
Ga0586324_6494203_272_553	11400000.00	7480000.00	0.00	0.00	9712900.00	8654600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14081	methanol corrinoid protein
Ga0586324_0195973_779_2125	0.00	8772000.00	0.00	0.00	0.00	0.00	0.00	0.00	8296000.00	6893100.00	0.00	7215000.00	KO:K14126	F420-non-reducing hydrogenase large subunit
Ga0586324_1453580_628_1035	0.00	0.00	0.00	0.00	5529000.00	0.00	0.00	0.00	0.00	0.00	1636800.00	0.00	KO:K14126	F420-non-reducing hydrogenase large subunit
Ga0586324_6981726_1_537	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1628100.00	0.00	0.00	KO:K14126	F420-reducing hydrogenase large subunit
Ga0586324_0259144_1327_1807	5140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14127	F420-non-reducing hydrogenase iron-sulfur subunit
Ga0586324_0003570_11991_14207	0.00	0.00	0.00	0.00	9342100.00	0.00	0.00	7625000.00	0.00	0.00	0.00	4095000.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0008881_8268_10481	8910000.00	0.00	0.00	0.00	0.00	15006600.00	19174800.00	8174000.00	21465000.00	0.00	8976000.00	5962500.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0031713_3_1217	4431000.00	0.00	866532.44	0.00	0.00	1390198.72	385671.12	11346000.00	32481000.00	18095000.00	15400000.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0053197_1161_3392	1630000.00	0.00	0.00	5522421.96	1757500.00	5809200.00	0.00	18855600.00	464755.95	4819500.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0063474_1858_4074	0.00	0.00	0.00	0.00	3258500.00	3563800.00	4724300.00	0.00	3672200.00	3296700.00	2148300.00	2085600.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0072078_286_2499	23490000.00	38093600.00	51175562.74	39520000.00	32651000.00	21776061.38	37164000.00	28487000.00	37980000.00	32501700.00	41254400.00	46117500.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0252085_1567_2226	0.00	0.00	0.00	0.00	0.00	1861878.39	0.00	0.00	0.00	648451.65	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0294731_964_2070	0.00	442975.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0389801_647_1828	0.00	1251200.00	0.00	0.00	0.00	1017861.45	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0392540_220_1824	0.00	0.00	0.00	0.00	18905000.00	10506000.00	0.00	0.00	2940300.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0439861_3_1706	143208.00	0.00	0.00	0.00	1947500.00	2704815.02	38628100.00	43456359.96	1016726.65	4221962.19	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0535760_1415_1591	0.00	0.00	0.00	0.00	0.00	0.00	8535500.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0849373_3_1424	3350000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0697252_1_1419	1120000.00	18421200.00	350808.12	28234000.00	4542300.00	1779878.04	14400163.08	27504900.00	21938722.83	3237486.56	25185600.00	21952500.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0718780_1_401	0.00	0.00	0.00	0.00	5263300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0917986_3_1259	0.00	40256000.00	39241100.00	1719500.00	12998600.00	65584400.00	53352000.00	2086200.00	0.00	0.00	0.00	19537500.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0921343_1_1259	66570000.00	28356000.00	18579000.00	36100000.00	39531400.00	10459842.37	28932607.20	17220300.00	24493362.39	23716000.00	16077600.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0979259_3_1226	4400000.00	8432000.00	6305600.00	911050.00	10506000.00	15880000.00	7045200.00	7076000.00	6091200.00	0.00	4056800.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_1028914_3_611	0.00	0.00	0.00	0.00	0.00	2795364.34	4218000.00	0.00	0.00	839300.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_1361676_3_1064	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1255500.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_1514031_288_1016	0.00	0.00	0.00	0.00	2564700.00	0.00	0.00	9028000.00	18306000.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_1572901_3_956	0.00	0.00	0.00	0.00	0.00	2146508.28	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_1860850_1_930	0.00	0.00	0.00	168614.55	105828.38	0.00	1593720.00	224171.34	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_2247774_3_860	0.00	0.00	11091100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_3578320_1_708	1720000.00	0.00	0.00	0.00	2077500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_4104197_2_670	4850000.00	3971200.00	890429.38	4911500.00	25853000.00	1636334.75	24852000.00	2263100.00	34942581.09	885500.00	1372800.00	772500.00	KO:K14138	acetyl-CoA synthase
Ga0586324_4127401_1_666	0.00	0.00	0.00	0.00	2641000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_4838020_2_625	0.00	0.00	0.00	0.00	2077500.00	0.00	0.00	3830800.00	0.00	0.00	2376000.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_5188758_1_606	0.00	897600.00	0.00	0.00	2099500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_5743070_3_581	1530000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_5796893_1_443	980986.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_6206620_1_564	0.00	4440400.00	0.00	12445000.00	6921600.00	0.00	0.00	0.00	3458700.00	2762100.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_6675125_3_548	7180000.00	5222400.00	0.00	0.00	0.00	10838100.00	8458800.00	9028000.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_7009754_2_535	0.00	0.00	0.00	0.00	0.00	3067055.26	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_7450588_1_522	0.00	8024000.00	0.00	9690000.00	9867400.00	0.00	0.00	0.00	7564000.00	6269400.00	0.00	0.00	KO:K14138	acetyl-CoA synthase
Ga0586324_0000001_19104_21206	0.00	0.00	0.00	0.00	0.00	0.00	40036800.00	17202000.00	10020829.14	31824100.00	10120000.00	6075000.00	K

Ga0586324_0000075_48573_50588	0.00	0.00	0.00	0.00	0.00	0.00	5836800.00	7039400.00	7500600.00	9702000.00	0.00	0.00	KO:K14393	cation/acetate symporter
Ga0586324_1839099_2_937	1410000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14447	(2R)-ethylmalonyl-CoA mutase
Ga0586324_0050460_2519_3973	1870000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14534	4-hydroxybutyryl-CoA dehydratase/vinylacetyl-CoA-Delta-isomerase
Ga0586324_0071715_1_1410	1090000.00	0.00	0.00	1643500.00	20600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14534	4-hydroxybutyryl-CoA dehydratase/vinylacetyl-CoA-Delta-isomerase
Ga0586324_0120464_670_2166	0.00	0.00	0.00	0.00	0.00	1534162.83	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14534	4-hydroxybutyryl-CoA dehydratase/vinylacetyl-CoA-Delta-isomerase
Ga0586324_0199858_1_1482	0.00	0.00	0.00	0.00	0.00	0.00	0.00	393090.10	0.00	579485.06	0.00	0.00	KO:K14534	4-hydroxybutyryl-CoA dehydratase/vinylacetyl-CoA-Delta-isomerase
Ga0586324_4110838_1_669	865886.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14534	4-hydroxybutyryl-CoA dehydratase/vinylacetyl-CoA-Delta-isomerase
Ga0586324_0025359_642_2858	0.00	3549600.00	7994600.00	0.00	0.00	8734000.00	0.00	5471700.00	4981500.00	6352500.00	5764000.00	5355000.00	KO:K14647	minor extracellular serine protease Vpr
Ga0586324_0647837_3_1463	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1932700.00	0.00	0.00	KO:K14647	minor extracellular serine protease Vpr
Ga0586324_5972388_3_572	0.00	0.00	0.00	3410500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14647	minor extracellular serine protease Vpr
Ga0586324_0000192_4583_5668	0.00	0.00	0.00	0.00	0.00	0.00	0.00	841800.00	0.00	0.00	0.00	0.00	KO:K14652	3,4-dihydroxy 2-butanone 4-phosphate synthase/GTP cyclohydrolase II
Ga0586324_0620536_1192_1491	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2138400.00	0.00	KO:K14742	tRNA threonylcarbamoyladenosine biosynthesis protein TsaB
Ga0586324_0317933_1363_2001	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5350400.00	0.00	KO:K14981	two-component system response regulator Chvl
Ga0586324_0420574_1212_1769	0.00	0.00	0.00	0.00	0.00	8892800.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K14981	two-component system response regulator Chvl
Ga0586324_0059579_744_2648	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2308500.00	0.00	0.00	0.00	KO:K15022	formate dehydrogenase beta subunit
Ga0586324_3564581_3_710	0.00	0.00	0.00	0.00	0.00	0.00	3898800.00	0.00	0.00	0.00	0.00	0.00	KO:K15022	formate dehydrogenase beta subunit
Ga0586324_0000241_17021_17923	2800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase
Ga0586324_0013713_2766_3656	38000000.00	4562800.00	4269887.71	0.00	0.00	0.00	3442800.00	0.00	2843100.00	14707000.00	30448000.00	0.00	KO:K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase
Ga0586324_0091922_436_1326	11680000.00	3094000.00	0.00	0.00	8476900.00	100838000.00	66120000.00	0.00	9153000.00	0.00	0.00	0.00	KO:K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase
Ga0586324_0168839_873_1751	0.00	0.00	0.00	0.00	0.00	14569900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase
Ga0586324_0380864_1123_1848	277641.00	0.00	0.00	0.00	68907000.00	0.00	0.00	0.00	45323000.00	44307000.00	0.00	0.00	KO:K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase
Ga0586324_0525890_43_933	0.00	0.00	0.00	11419000.00	0.00	0.00	0.00	0.00	2316600.00	0.00	0.00	0.00	KO:K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase
Ga0586324_1117361_25_903	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9416000.00	0.00	KO:K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase
Ga0586324_2672514_1_546	0.00	0.00	7656800.00	0.00	0.00	6391700.00	5380800.00	4812900.00	0.00	0.00	0.00	0.00	KO:K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase
Ga0586324_1163959_3_995	0.00	0.00	2697169.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15230	ATP-citrate lyase alpha-subunit
Ga0586324_1468077_1_1029	4600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15230	ATP-citrate lyase alpha-subunit
Ga0586324_0135044_1759_2973	0.00	0.00	0.00	0.00	0.00	0.00	2093621.40	0.00	0.00	0.00	997500.00	0.00	KO:K15515	sulfoacetaldehyde dehydrogenase
Ga0586324_0003545_6777_7781	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1082400.00	0.00	0.00	KO:K15553	sulfonate transport system substrate-binding protein
Ga0586324_0575113_1_1107	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1140000.00	0.00	KO:K15553	sulfonate transport system substrate-binding protein
Ga0586324_0575118_1_832	0.00	558212.68	0.00	0.00	0.00	0.00	3055200.00	1116300.00	907200.00	1809500.00	1364000.00	1702500.00	KO:K15553	sulfonate transport system substrate-binding protein
Ga0586324_0000004_18266_19660	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2208200.00	0.00	0.00	0.00	3187500.00	KO:K15576	nitrate/nitrite transport system substrate-binding protein
Ga0586324_0019358_1822_3687	0.00	0.00	64745000.00	28595000.00	2430800.00	0.00	0.00	1850596.20	0.00	4187700.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_0059665_2559_4217	0.00	0.00	0.00	0.00	0.00	5597700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_0049724_1146_2999	0.00	0.00	5060688.77	2270500.00	5871000.00	0.00	6292800.00	3818600.00	1879200.00	0.00	1108800.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_0080424_2295_3806	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	515624.94	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_0135862_1624_2934	0.00	3270800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_0168878_1012_2676	6790000.00	14232400.00	0.00	6032500.00	6705300.00	0.00	8595600.00	10296800.00	5111100.00	10853409.49	16984000.00	6217500.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_0239191_1_1656	3560000.00	0.00	0.00	0.00	2029100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_0350424_3_1229	6460000.00	2516000.00	0.00	0.00	4140600.00	0.00	2021767.20	0.00	0.00	1831951.89	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_1121999_3_965	0.00	248508.04	0.00	0.00	0.00	0.00	0.00	0.00	4430700.00	5628700.00	0.00	5542500.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_1327023_3_1076	1250000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_1381225_1_1056	10300000.00	6038400.00	0.00	0.00	0.00	2596622.17	3420000.00	12130000.00	1539000.00	0.00	0.00	16950000.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_2000255_1_900	897474.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_2949084_9_767	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7725500.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_3447989_1_703	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1332100.00	0.00	4589132.50	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_4144102_3_647	0.00	12580000.00	0.00	4028000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_5788662_1_579	6670000.00	0.00	8501300.00	7229500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_6933049_3_539	0.00	6643600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_7495251_3_521	0.00	0.00	9233200.00	988000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_7550333_3_521	0.00	4984400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15580	oligopeptide transport system substrate-binding protein
Ga0586324_1655780_3_980	0.00	0.00	0.00	0.00	3648000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15633	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
Ga0586324_1966797_1_651	1410000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8850000.00	KO:K15635	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
Ga0586324_0083219_2243_3511	1490000.00	3298000.00	0.00	1653000.00	1957000.00	6629900.00	0.00	1823900.00	4122900.00	8446900.00	5156800.00	6420000.00	KO:K15770	arabinogalactan oligomer/maltooligosaccharide transport system substrate-binding protein
Ga0586324_0136239_1696_2961	2240000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15770	arabinogalactan oligomer/maltooligosaccharide transport system substrate-binding protein
Ga0586324_0560066_393_1559	1940000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1147300.00	0.00	0.00	KO:K15770	arabinogalactan oligomer/maltooligosaccharide transport system substrate-binding protein
Ga0586324_0805642_24_1334	0.00	4678400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15770	arabinogalactan oligomer/maltooligosaccharide transport system substrate-binding protein
Ga0586324_2214455_3_866	4280000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15770	arabinogalactan oligomer/maltooligosaccharide transport system substrate-binding protein
Ga0586324_3371951_3_725	0.00	0.00	0.00	0.00	18128000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15770	arabinogalactan oligomer/maltooligosaccharide transport system substrate-binding protein
Ga0586324_0000123_34440_35822	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2571800.00	0.00	0.00	KO:K15778	phosphomannomutase/phosphoglucomutase
Ga0586324_0001357_4563_5936	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1031800.00	0.00	0.00	KO:K15778	phosphomannomutase/phosphoglucomutase
Ga0586324_0611666_709_1500	0.00	0.00	7487900.00	1158000.00	2286600.00	0.00	0.00	872300.00	0.00	0.00	3435000.00	0.00	KO:K15778	phosphomannomutase/phosphoglucomutase
Ga0586324_1061337_456_1184	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2648800.00	1082400.00	0.00	KO:K15778	phosphomannomutase/phosphoglucomutase
Ga0586324_0013864_5664_7262	3070000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4884000.00	0.00	KO:K15864	nitrite reductase (NO-forming)/hydroxylamine reductase
Ga0586324_0027612_1_1539	8790000.00	9057600.00	0.00	2261000.00	0.00	0.00	0.00	5105700.00	5605200.00	0.00	0.00	0.00	KO:K15864	nitrite reductase (NO-forming)/hydroxylamine reductase
Ga0586324_0168653_1042_2682	0.00	0.00	14187600.00	0.00	0.00	6352000.00	0.00	2342400.00	0.00	4835600.00	0.00	4792500.00	KO:K15864	nitrite reductase (NO-forming)/hydroxylamine reductase
Ga0586324_0870388_2_1288	0.00	5372000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15864	nitrite reductase (NO-forming)/hydroxylamine reductase
Ga0586324_0962956_2_835	0.00	4753200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15864	nitrite reductase (NO-forming)/hydroxylamine reductase
Ga0586324_1347244_1_789	6140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15864	nitrite reductase (NO-forming)/hydroxylamine reductase
Ga0586324_1623591_1_987	0.00	0.00	0.00	0.00	0.00	0.00	11126400.00	11041000.00	6650100.00	0.00	0.00	0.00	KO:K15864	nitrite reductase (NO-forming)/hydroxylamine reductase
Ga0586324_3190517_1_741	0.00	0.00	4350374.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15864	nitrite reductase (NO-forming)/hydroxylamine reductase
Ga0586324_0010664_1365_4309	77320000.00	49483600.00	45434100.00	10070000.00	11433000.00	24693400.00	24168000.00	0.00	14580000.00	15092000.00	27984000.00	21427500.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_0030240_4799_5728	0.00	0.00	0.00	0.00	0.00	0.00	3670800.00	0.00	0.00	0.00	0.00	0.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_0187049_1409_2407	0.00	6670800.00	0.00	0.00	0.00	0.00	0.00	732000.00	2664900.00	0.00	0.00	0.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_0375032_1_558	0.00	1692284.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_1214846_2_475	8720000.00	0.00	14581700.00	0.00	0.00	13339200.00	11445600.00	0.00	0.00	0.00	0.00	0.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_1833263_2_808	40900000.00	9180000.00	35131200.00	2935500.00	0.00	0.00	0.00	1067500.00	0.00	2833600.00	0.00	12525000.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_2146638_2_877	12149099.00	3128888.08	0.00	1691000.00	0.00	0.00	0.00	1372500.00	1142100.00	1786400.00	2788000.00	438200.25	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_2809471_2_784	0.00	7622800.00	0.00	0.00	5726800.00	0.00	3648000.00	4196800.00	0.00	0.00	0.00	1665000.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_3276020_2_406	1550000.00	2726800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_6003170_1_534	0.00	635245.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15986	manganese-dependent inorganic pyrophosphatase
Ga0586324_0000939_14722_16767	0.00	0.00	0.00	0.00	3120900.00	0.00	0.00	57480300.00	3685500.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_0065565_1414_3468	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18144000.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_0124297_1_938	0.00	0.00	0.00	0.00	0.00	0.00	0.00	103700000.00	79137000.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_0104842_1_2061	0.00	12444000.00	0.00	0.00	0.00	0.00	1663196.50	0.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_0187438_3_2033	0.00	0.00	0.00	0.00	0.00	0.00	7045200.00	0.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_0226948_525_2333	0.00	0.00	0.00	1216000.00	17819000.00	0.00	5358000.00	0.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_0231778_253_2313	0.00	0.00	0.00	0.00	0.00	0.00	291840000.00	0.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_0368554_536_1876	0.00	0.00	0.00	0.00	0.00	0.00	74100000.00	24217000.00	19602000.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_1040422_544_1194	0.00	0.00	0.00	49495000.00	0.00	0.00	0.00	786900.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_1045194_129_1190	0.00	9248000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_1257060_455_1099	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5898700.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_2735081_3_689	0.00	0.00	0.00	0.00	0.00	0.00	10191600.00	0.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_2828287_1_581	0.00	0.00	0.00	0.00	0.00	0.00	6156000.00	0.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_5533072_285_590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3782700.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_6996178_1_504	0.00	0.00	0.00	0.00	0.00	4274500.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_7399756_1_525	0.00	0.00	0.00	4911500.00	8178200.00	0.00	0.00	12106800.00	0.00	0.00	0.00	1927500.00	KO:K15987	K(+)-stimulated pyrophosphate-energized sodium pump
Ga0586324_0000244_38796_39410	7880000.00	0.00	0.00	0.00	0.00	0.00	0.00	11058000.00	2714500.00	27912600.00	1586200.00	35472800.00	42375000.00	KO:K16079
Ga0586324_0002577_1398_2234	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1270500.00	KO:K16079
Ga0586324_0003003_11032_11772	0.00	0.00	0.00	0.00	0.00	10322000.00	0.00	0.00	11773000.00	0.00	0.00	0.00	0.00	KO:K16079
Ga0586324_0006272_11928_12482	32200000.00	30872000.00	0.00	0.00	4864000.00	34814000.00	0.00	0.00	19276000.00	22275000.00	24486000.00	18392000.00	18225000.00	KO:K16079
Ga0586324_0022259_2310_3026	6630000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16079
Ga0586324_0061464_2705_3613	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9768000.00	0.00	0.00	KO:K16079
Ga0586324_0099334_2426_3193	0.00	0.00	0.00	0.00	4680267.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16079
Ga0586324_0148851_1949_2719	0.00	0.00	0.00	2517500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16079
Ga0586324_0192008_318_1112	3070000.00	3733200.00	0.00	4702500.00	3811000.00	0.00	0.00	3178100.00	3636900.00	0.00	0.00	0.00	0.00	KO:K16079
Ga0586324_0278907_946_1617	814372.00	0.00	0.00	14725000.00	0.00	0.00	0.00	10738000.00	0.00	0.00	0.00	6202500.00	0.00	KO:K16079
Ga0586324_0329348_604_1251	0.00	0.00	0.00	0.00	0.00	0.00	9918000.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16079
Ga0586324_0384432_890_1603	0.00	0.00	0.00	1130500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16079
Ga0586324_5575844_21_590	0.00	0.00	0.00	0.00	0.00	0.00	15139200.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16079
Ga0586324_6846245_1_543	0.00	140372.40	0.00	8483500.00	0.00	0.00	831657.36	0.00	5459400.00	0.00	1566400.00	1365000.00	0.00	KO:K16079
Ga0586324_0396875_676_1725	0.00	0.00	2363873.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16167
Ga0586324_0027042_5028_6192	0.00	0.00	0.00	0.00	11021000.00	0.00	0.00	0.00	515424.87	0.00	0.00	0.00	0.00	KO:K16173
Ga0586324_0230104_3_350	0.00	225654.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16173
Ga0586324_0513750_3_992	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	470673.18	0.00	0.00	0.00	0.00	KO:K16173
Ga0586324_0567595_1034_1552	0.00	225641.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16173
Ga0586324_0601234_917_1462	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	233697.15	0.00	0.00	0.00	0.00	KO:K16173
Ga0586324_0167625_923_1561	0.00	0.00	0.00	0.00	4387800.00	0.00	0.00	0.00	765450.00	0.00	0.00	0.00	0.00	KO:K16179
Ga0586324_0502047_1_1368	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	132396.12	0.00	0.00	0.00	0.00	KO:K16692
Ga0586324_1305675_1_1083	0.00	0.00	0.00	0.00	0.00	0.00	280836.44	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16885
Ga0586324_0000070_39790_41085	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22484000.00	28952000.00	25882500.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_0035720_3907_5175	0.00	0.00	0.00	2118500.00	0.00	0.00	6247200.00	4337100.00	0.00	0.00	0.00	0.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_0109371_3_1262	0.00	1666000.00	3086985.30	4056500.00	4542300.00	3837560.00	5677200.00	2964600.00	2088800.00	2225300.00	2059200.00	0.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_0179143_1131_2417	0.00	0.00	0.00	0.00	0.00	0.00	9484800.00	1634800.00	1757700.00	7499800.00	14264800.00	18517500.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_0388698_1_741	0.00	0.00	0.00	2337000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_0557942_675_1562	0.00	0.00	0.00	4883000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_0896937_1_1182	0.00	5304000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3713600.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_2885863_1_774	1840000.00	0.00	0.00	3163500.00	0.00	1842913.70	0.00	0.00	0.00	0.00	0.00	0.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_3408630_3_752	0.00	0.00	0.00	0.00	0.00	3847874.86	0.00	0.00	0.00	0.00	0.00	0.00	41685885	quinone-modifying oxidoreductase subunit QmoA
Ga0586324_3615294_3_704

Ga0586324_0055559_2432_4540	0.00	0.00	0.00	3667000.00	0.00	0.00	0.00	0.00	4473700.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Spirochaetes;Spirochaetia;Spirochetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_0122357_866_3085	0.00	3522400.00	0.00	1406000.00	10083700.00	9131000.00	0.00	0.00	5734800.00	0.00	1865600.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_0159580_2_1669	4170000.00	0.00	7882000.00	0.00	0.00	6828400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Spirochaetes;Spirochaetia;Spirochetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_0319884_1_1986	0.00	0.00	0.00	0.00	0.00	2251490.22	3556800.00	780800.00	1134000.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0355433_1_699	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2182500.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_0368236_147_1877	0.00	0.00	0.00	5130000.00	4284800.00	0.00	0.00	2891400.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_0372832_2_1495	0.00	0.00	0.00	3258500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0421817_3_1733	0.00	0.00	0.00	382356.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_0643275_1_1341	0.00	4182000.00	6868600.00	26505000.00	12051000.00	8257600.00	0.00	0.00	3750300.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0766622_1_723	0.00	0.00	0.00	0.00	0.00	0.00	841800.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofundulus;Desulfofundulus australicus;Desulfofundulus australicus DSM 11792
Ga0586324_0816961_3_1328	0.00	0.00	0.00	1814500.00	0.00	1482620.32	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Spirochaetes;Spirochaetia;Spirochetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_0848156_1_1305	0.00	0.00	0.00	3353500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Spirochaetes;Spirochaetia;Spirochetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_0913840_45_1262	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6991600.00	0.00	4605000.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0975510_65_1228	0.00	0.00	0.00	2137500.00	0.00	0.00	0.00	2948400.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus elongatus;Desulfobulbus elongatus DSM 2908
Ga0586324_1124266_3_1154	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9944000.00	4972500.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324_1500001_3_1019	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1478400.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1506275_343_1020	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6941700.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_1815953_2_940	0.00	0.00	0.00	20653000.00	6643500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1957032_3_911	2090000.00	0.00	0.00	2223000.00	1843700.00	0.00	2409500.00	1255500.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2064329_3_890	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Spirochaetes;Spirochaetia;Spirochetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_2126129_3_881	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1020600.00	1054900.00	0.00	907500.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_2170353_2_874	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	871309.12	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_2184226_2_838	0.00	1720400.00	0.00	0.00	0.00	0.00	0.00	0.00	1078000.00	0.00	634423.50	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Gammaproteobacteria;Thiocystales;Thiotrichaceae;Achromatium;uncultured Achromatium sp.;Achromatium sp. CelB
Ga0586324_2631318_2_805	0.00	0.00	0.00	5860700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Spirochaetes;Spirochaetia;Spirochetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_3275622_44_733	0.00	4630800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_4065758_2_670	0.00	4018800.00	0.00	0.00	0.00	0.00	0.00	8906000.00	2025000.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_4652899_2_634	0.00	3787600.00	9233200.00	3876000.00	5984300.00	4883100.00	6224400.00	2928000.00	3645000.00	0.00	3105000.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_4663063_2_634	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1970300.00	0.00	0.00	0.00	0.00	KO:K16886	quinone-modifying oxidoreductase subunit QmoB	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2592783_1_810	0.00	0.00	0.00	0.00	0.00	2235078.24	0.00	0.00	0.00	0.00	0.00	0.00	KO:K17080	prophilin 1	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0329813_1_2292	0.00	0.00	0.00	0.00	70761000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K17202	ethrtitol transport system substrate-binding protein	Bacteria;Chlorobi;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_3826561_3_650	0.00	6752400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K17213	inositol transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Azospirillaceae;Azospirillum;Azospirillum sp. TSH100;Azospirillum sp. TSH100
Ga0586324_0000423_19925_21193	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4396700.00	11431200.00	3187500.00	0.00	KO:K17218	sulfide:quinone oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324_0003206_1730_2998	0.00	0.00	0.00	0.00	0.00	0.00	16409000.00	0.00	0.00	0.00	7455000.00	0.00	KO:K17218	sulfide:quinone oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaus;Thiobacillus thiopaus DSM 505
Ga0586324_0022884_3208_4341	0.00	1625200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3465000.00	2631200.00	0.00	KO:K17218	sulfide:quinone oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Ferrovales;Ferrovaceae;Ferrovum;unclassified Ferrovum;Ferrovum sp. Zalaut-31
Ga0586324_0109810_1744_3012	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13847000.00	13041000.00	0.00	0.00	0.00	KO:K17218	sulfide:quinone oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324_5895249_113_577	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2482500.00	0.00	KO:K17218	sulfide:quinone oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter sp. PAE-UM;Curvibacter sp. PAE-UM
Ga0586324_8181678_2_502	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3067500.00	0.00	KO:K17218	sulfide:quinone oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Chitinimonas;Chitinimonas koreensis;Chitinimonas koreensis DSM 17726
Ga0586324_0000037_45798_46628	0.00	0.00	0.00	0.00	0.00	85044000.00	34949300.00	271269000.00	426410800.00	447145600.00	428017500.00	0.00	KO:K17222	sulfur-oxidizing protein SoxA	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324_0004144_4156_4998	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1093500.00	0.00	0.00	847500.00	0.00	KO:K17222	sulfur-oxidizing protein SoxA	Bacteria;Proteobacteria;Gammaproteobacteria;Bradyrhizobiaceae;Afipia;Afipia sp. 1N1;Afipia sp. 1N1
Ga0586324_0015713_1918_2763	0.00	0.00	0.00	0.00	0.00	0.00	25571200.00	67246200.00	13113100.00	15224000.00	0.00	0.00	KO:K17222	sulfur-oxidizing protein SoxA	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaus;Thiobacillus thiopaus DSM 505
Ga0586324_0043326_2379_3224	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7291900.00	0.00	4680000.00	0.00	KO:K17222	sulfur-oxidizing protein SoxA	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_0408771_771_1601	0.00	0.00	0.00	0.00	0.00	1386240000.00	139690000.00	1343000000.00	1108800000.00	1328800000.00	101250000.00	0.00	KO:K17222	sulfur-oxidizing protein SoxA	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfurifrerula;Sulfurifrerula multiseriata;Sulfurifrerula multiseriata TTN
Ga0586324_1930433_138_917	0.00	0.00	0.00	0.00	0.00	0.00	4880000.00	5532300.00	1609300.00	0.00	0.00	0.00	KO:K17222	sulfur-oxidizing protein SoxA	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaus;Thiobacillus thiopaus DSM 505
Ga0586324_0000037_44492_44857	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5682600.00	0.00	0.00	0.00	KO:K17222	sulfur-oxidizing protein SoxA	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324_0015713_497_952	0.00	0.00	0.00	0.00	0.00	17464800.00	21655000.00	17901000.00	0.00	13200000.00	0.00	0.00	KO:K17223	sulfur-oxidizing protein SoxX	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaus;Thiobacillus thiopaus DSM 505
Ga0586324_0002047_46777_46486	0.00	0.00	0.00	0.00	0.00	0.00	6136600.00	8594100.00	30661400.00	21736000.00	13522500.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324_0015713_2913_4655	0.00	0.00	0.00	0.00	0.00	0.00	2793800.00	0.00	0.00	11935000.00	20504000.00	15300000.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaus;Thiobacillus thiopaus DSM 505
Ga0586324_0043326_480_2222	0.00	0.00	0.00	0.00	0.00	0.00	23161700.00	25020900.00	5043500.00	3634400.00	4005000.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaus;Thiobacillus thiopaus DSM 505
Ga0586324_0262093_1802_3886	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8470000.00	0.00	0.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_0099464_2_1759	0.00	0.00	0.00	4454844.47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Firmicutes;Bacilli;Lactobacillales;Carnobacteriaceae;Alkalibacterium;Alkalibacterium outridalecola;Alkalibacterium outridalecola DSM 19182
Ga0586324_0117721_1977_3173	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3763700.00	3539700.00	0.00	4155000.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriflexus;Sulfuriflexus autotrophica;Sulfuriflexus autotrophica DSM 100309
Ga0586324_0697254_184_1419	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3110790.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriflexus;Sulfuriflexus autotrophica;Sulfuriflexus autotrophica DSM 100309
Ga0586324_0936315_2_1249	9180000.00	4923200.00	0.00	3781000.00	4748300.00	5637400.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_1287660_1_1088	3040000.00	6800000.00	0.00	3106500.00	2636800.00	0.00	0.00	1628100.00	10626000.00	7629600.00	0.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiogranum;Thiogranum longum;Thiogranum longum DSM 19610
Ga0586324_1612763_2_988	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4434700.00	0.00	0.00	0.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_3241436_2_571	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1584000.00	0.00	KO:K17224	sulfur-oxidizing protein SoxB	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_0045066_210_680	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11638800.00	1482300.00	15392300.00	47288201.84	19890000.00	KO:K17226	sulfur-oxidizing protein SoxY	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriflexus;Sulfuriflexus autotrophica;Sulfuriflexus autotrophica DSM 100309
Ga0586324_1259963_98_571	0.00	0.00	0.00	0.00	2420628.10	0.00	0.00	0.00	0.00	2841300.00	0.00	0.00	KO:K17226	sulfur-oxidizing protein SoxY	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa marina;Thiocapsa marina 5811, DSM 5653
Ga0586324_0000037_45401_45715	0.00	0.00	0.00	0.00	0.00	0.00	6133200.00	6222000.00	18630000.00	0.00	2481600.00	4132500.00	KO:K17227	sulfur-oxidizing protein SoxZ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Anmwoodia;Anmwoodia aquaesulis;Anmwoodia aquaesulis DSM 4255
Ga0586324_0524969_1001_1315	0.00	0.00	0.00	0.00	0.00	0.00	3078000.00	0.00	5880600.00	0.00	1170400.00	2092500.00	KO:K17227	sulfur-oxidizing protein SoxZ	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurifrerula;unclassified Sulfurifrerula;Sulfurifrerula sp. AH1 re-analysis
Ga0586324_0000002_52602_53903	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7299600.00	7515200.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Thiohalobacteraceae;Thiohalobacter;Thiohalobacter thiocyanaticus;Thiohalobacter thiocyanaticus JP2, DSM 5205
Ga0586324_0000011_47276_48637	0.00	0.00	0.00	0.00	0.00	10054800.00	18531800.00	15754500.00	78917300.00	80115200.00	51375000.00	41729000.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_0001373_3254_4573	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3888500.00	0.00	0.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiohalospira;Thiohalospira halophila;Thiohalospira halophila HL3
Ga0586324_0009452_6633_7997	3150000.00	3515600.00	0.00	0.00	0.00	4674000.00	0.00	0.00	10044000.00	13444200.00	0.00	13747500.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_0004299_3841_5199	0.00	1645600.00	0.00	0.00	0.00	0.00	0.00	1903200.00	5921100.00	5020400.00	0.00	7440000.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_0048721_3044_4411	0.00	0.00	0.00	0.00	0.00	0.00	2107508.88	5160600.00	0.00	3703700.00	2173600.00	2918680.50	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_0491732_2_970	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4706100.00	0.00	0.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiohalomonas;Thiohalomonas denitrificans;Thiohalomonas denitrificans HLD2
Ga0586324_0572497_192_1484	0.00	614701.64	0.00	13184000.00	0.00	3534000.00	902800.00	5629500.00	4181100.00	0.00	2520000.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_1179157_2_1132	10400000.00	1013200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_1532353_1_1010	0.00	1570800.00	4833248.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_1573693_1_697	0.00	0.00	0.00	0.00	0.00	0.00	945500.00	1206900.00	900900.00	0.00	0.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_3183976_1_603	31400000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa roseopersicina;Thiocapsa roseopersicina DSM 217
Ga0586324_5213702_2_607	0.00	0.00	0.00	0.00	0.00	11012400.00	11407000.00	10854000.00	0.00	12672000.00	9525000.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Magnetococcales;Magnetococcaceae;Magnetococcus;Magnetococcus marinus;Magnetococcus marinus MC-1
Ga0586324_5497243_2_592	0.00	7276000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7440000.00	0.00	KO:K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_0003813_798_2120	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17446000.00	0.00	0.00	12450000.00	0.00	KO:K17315	glucose/mannose transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0006948_8201_9622	0.00	0.00	0.00	2622000.00	0.00	3169200.00	0

Ga0586324_5757852_251_583	0.00	0.00	0.00	642406.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21071	E-phosphofructokinase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_0000025_45736_46770	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1320300.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324_0000819_19128_20105	0.00	0.00	0.00	0.00	0.00	0.00	432960.31	382954.23	0.00	0.00	0.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0006747_2973_4010	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3680600.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_0007732_2934_3959	2730000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_0008404_5067_6074	1100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;unclassified Hyphomicrobiales;Rhizobiales;Rhizobiales bacterium YIM 77505;Rhizobiales bacterium YIM 77505
Ga0586324_0009654_4421_5380	0.00	1985600.00	0.00	0.00	0.00	0.00	1860500.00	0.00	0.00	2156000.00	1695000.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Pelobacter;Pelobacter selenigenes;Pelobacter selenigenes DSM 18267
Ga0586324_0018383_603_1649	0.00	1373600.00	0.00	0.00	0.00	0.00	0.00	1247400.00	1493800.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Tistlia;Tistlia consotensis;Tistlia consotensis USBA 355
Ga0586324_0027822_168_1211	19900000.00	25840000.00	37383200.00	0.00	0.00	9528000.00	0.00	0.00	11761200.00	6514200.00	0.00	6750000.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0040515_3661_4710	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2932200.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter daltoni;Geobacter daltoni FRC-32
Ga0586324_0029812_1_1044	5420000.00	0.00	9627300.00	0.00	0.00	0.00	1701900.00	0.00	0.00	3220800.00	4545000.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas jejuensis;Polaromonas jejuensis NBRC 106434
Ga0586324_0115607_435_1460	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12012000.00	9944000.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Azonexus;Azonexus hydrophilus;Azonexus hydrophilus ZS02
Ga0586324_0116108_92_1087	0.00	1054000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Firmicutes;Clostridia;Eubacteriales;Desulfallaceae;Desulfoscipio;Desulfoscipio geothermicus;Desulfallas geothermicus DSM 3669
Ga0586324_0163265_1495_2487	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	230999.25	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Euryarchaeota;unclassified Atribacteria;unclassified Atribacteria;unclassified Atribacteria;unclassified Atribacteria;Atribacteria bacterium JGI 0000079-L04;Atribacteria bacterium JGI 0000079-L04 (contamination screened)
Ga0586324_0208045_1459_2430	0.00	2033200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Acutiococcaceae;Acuticoccus;Acuticoccus kandelijae;Acuticoccus kandelijae J103
Ga0586324_0283010_704_1732	0.00	3454400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 9736;Geobacter sp. DSM 9736
Ga0586324_0328231_1_537	0.00	0.00	0.00	0.00	536299.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_0341830_781_1788	0.00	0.00	0.00	0.00	1959520.54	0.00	0.00	0.00	0.00	1566400.00	0.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Thermotogae;Thermotogae;Kosmotogales;Kosmotogaceae;Kosmotoga;Kosmotoga pacifica;Kosmotoga pacifica SLHLJ1
Ga0586324_0350809_677_1732	5490000.00	5297200.00	0.00	4113500.00	1050600.00	0.00	1895131.44	0.00	1692900.00	9471000.00	7788000.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0402675_454_1488	1800000.00	7820000.00	0.00	0.00	2585300.00	0.00	0.00	0.00	2292300.00	0.00	29216000.00	1762500.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0422039_758_1765	3480000.00	3794400.00	2178826.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_1411352_46_1047	0.00	1094800.00	5742600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_1422360_3_1043	0.00	1659200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_1484076_176_1024	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	825000.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Propionivibrio;Propionivibrio pelophilus;Propionivibrio pelophilus DSM 12018
Ga0586324_1718969_3_428	0.00	1591200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_1836158_1_693	0.00	0.00	0.00	0.00	602119.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_2033040_2_181	0.00	0.00	6981200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_2043117_240_896	0.00	0.00	0.00	0.00	0.00	4168500.00	0.00	0.00	0.00	0.00	0.00	1207500.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_2221236_3_671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2068000.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_2275573_44_826	970571.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1012500.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Paracoccus;Paracoccus indiens;Paracoccus indiens DSM 12121
Ga0586324_2639656_1_762	0.00	0.00	1507657.70	0.00	0.00	916093.38	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Pseudoceanicola;Pseudoceanicola batsensis;Pseudoceanicola batsensis HTCC2597
Ga0586324_2884979_1_773	0.00	4930000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21495	tripartite ATP-independent transport DctP family solute receptor	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_3960362_1_678	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3634400.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_4225322_2_661	0.00	0.00	3358328.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter daltoni;Geobacter daltoni FRC-32
Ga0586324_4396908_2_649	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2610000.00	0.00	KO:K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Maenetospirillum;Maenetospirillum moscoviense;Maenetospirillum moscoviense BB-1
Ga0586324_0024968_2860_4005	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3766400.00	0.00	0.00	KO:K21430	glucose/arabinose dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Caulobacter;Caulobacter sp. OK245;Tardiphaga sp. OK245;Tardiphaga sp. OK245
Ga0586324_0000652_11010_13133	0.00	0.00	0.00	0.00	0.00	0.00	220612800.00	93488600.00	97159500.00	585230800.00	322264800.00	559680000.00	KO:K21449	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas jejuensis;Polaromonas jejuensis NBRC 106434
Ga0586324_0000676_28385_30187	27700000.00	33864000.00	10502059.61	20615000.00	32537700.00	0.00	0.00	11468000.00	14733900.00	10792942.16	13851200.00	3660000.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324_0002518_15696_18209	621340000.00	913770069.24	1324201924.92	1050650.00	906503000.00	291314741.16	243733000.00	152835500.00	160357700.00	304935400.00	236337885.52	351945000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanosarcinaceae;Methanococcoides;Methanococcoides burtonii;Methanococcoides burtonii DSM 6242
Ga0586324_0014171_2_8365	2740000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21449	Ca2+-binding RTX toxin-like protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Chroococcales;Chroococcaceae;Geminocystis;Geminocystis sp. NIES-3709;Geminocystis sp. NIES-3709
Ga0586324_0019129_1_1884	80390000.00	58969600.00	166085000.00	43605000.00	96099000.00	53584308.79	115596000.00	47580000.00	36612000.00	50589000.00	51392000.00	84825000.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0025527_2041_4698	0.00	7412000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GK2F2, DSM 4140
Ga0586324_0029787_408_3920	1840000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GK2F2, DSM 4140
Ga0586324_0031362_1_1965	15600000.00	20586670.88	12780100.00	13300000.00	0.00	0.00	0.00	594750.00	7055100.00	2333100.00	1469600.00	3150000.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GK2F2, DSM 4140
Ga0586324_0033523_4565_5815	0.00	1727200.00	3120337.42	0.00	0.00	269417.01	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21449	ElWxxDGT repeat protein	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophaeraceae;Flavisolibacter;Flavisolibacter ginsenositerrae;Flavisolibacter ginsenositerrae DSM 18136
Ga0586324_0035499_2708_4498	1860000.00	40913895.24	66828100.00	8141500.00	13596000.00	10163200.00	0.00	0.00	9558000.00	15253700.00	12021943.12	22514790.75	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324_0058422_1_1430	64600000.00	62689200.00	25503900.00	5462500.00	0.00	17261845.84	0.00	28029500.00	6212700.00	43551200.00	49772800.00	43687500.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0059539_284_3385	28000000.00	0.00	0.00	0.00	6427200.00	6232900.00	9576000.00	2543700.00	0.00	7584500.00	5940000.00	6577500.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0081761_1778_3730	0.00	15170800.00	16890000.00	1377500.00	2348400.00	0.00	5654400.00	0.00	658025.37	3133900.00	0.00	0.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324_0105012_2_2152	7450000.00	15245600.00	0.00	0.00	3625600.00	0.00	0.00	0.00	0.00	0.00	3731200.00	1380000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GK2F2, DSM 4140
Ga0586324_0143442_928_2889	5920000.00	3181108.76	23420800.00	4607500.00	3439170.00	37476800.00	9781200.00	3028862.28	26568000.00	28020300.00	23259838.80	26775000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0144796_3_2375	50700000.00	46484800.00	0.00	14535000.00	4027300.00	3208696.92	0.00	0.00	9963000.00	13997000.00	13024000.00	13260000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis liminatans;Methanofollis liminatans GK2F2, DSM 4140
Ga0586324_0218664_2_1198	13700000.00	11900000.00	0.00	11970000.00	0.00	0.00	0.00	0.00	0.00	15939000.00	13710400.00	8700000.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0269586_206_2158	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1515000.00	KO:K21449	hypothetical protein	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas sp. GP;Dehalogenimonas sp. GP
Ga0586324_0277913_1_902	28900000.00	24616000.00	34511000.00	23465000.00	24720000.00	22073200.00	11628000.00	11102000.00	8910000.00	27566000.00	27633000.00	21225000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324_0318397_125_1288	8600000.00	9805600.00	12323991.18	4446000.00	4264200.00	0.00	0.00	762500.00	63722700.00	33251405.11	40075200.00	8745000.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0346649_3_1001	0.00	4440400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3928705.55	1108800.00	KO:K21449	PGF-CTERM protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0463827_3_1583	0.00	158907.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	146027.42	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0516223_3_1616	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2917500.00	KO:K21449	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter dinghuensis;Edaphobacter dinghuensis EB95
Ga0586324_0541910_1_1583	0.00	50870800.00	0.00	0.00	0.00	0.00	0.00	14945000.00	0.00	566793.15	0.00	4852500.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0594544_3_1520	7630000.00	7419781.24	14581700.00	4579000.00	3769800.00	5438800.00	0.00	3355000.00	2438100.00	2702700.00	2349600.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324_0653594_2_1459	0.00	1108400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0839148_2_1309	0.00	5508000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4889500.00	6001600.00	KO:K21449	Ca2+-binding RTX toxin-like protein	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Sporomusaceae;Sporomusa;Sporomusa ovata;Sporomusa ovata DSM 2662
Ga0586324_1205374_3_1121	46870000.00	0.00	0.00	0.00	51706000.00	0.00	0.00	28487000.00	0.00	0.00	36729000.00	31152000.00	26625000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_1233459_3_1109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19950000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis ethanolicus;Methanofollis ethanolicus JCM 15103
Ga0586324_1235181_1_1110	0.00	349622.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324_1281273_2_1090	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3493600.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula boonei;Methanoregula boonei 6A8
Ga0586324_1329291_3_1073	0.00	6840800.00	0.00	0.00	8631400.00	0.00	0.00	2049600.00	2008800.00	0.00	1628000.00	722982.75	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_1518839_1_1014	5960941.00	938400.00	0.00	1083000.00	1411100.00	0.00	0.00	805200.00	511965.36	0.00	0.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_1727135_1_960	3540000.00	401411.48	0.00	0.00	1936400.00	0.00	0.00	0.00	963900.00	0.00	0.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324_1731774_1_960	3650000.00	12240000.00	6193000.00	2641000.00	12960000.00	0.00	1642580.40	1067500.00	10188000.00	35550900.00	5352877.20	21367500.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_1808577_2_943	0.00	2903600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1185000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_1934036_1_915	0.00	2563600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	25025000.00	10648000.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_2565376_1_813	0.00	1366800.00	0.00	0.00	2885979.59	0.00	0.00	0.00	0.00	0.00	2142588.80	1905000.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_2569870_3_812	0.00	0.00	0.00	0.00	1393847.15	0.00	0.00	0.00	0.00	0.00	1355200.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanospirillum;Methanospirillum hungatei;Methanospirillum hungatei JF-1
Ga0586324_2577579_1_810	0.00	0.00	6249300.00	0.00	0.00	4446400.00	4674000.00	0.00	0.00	0.00	0.00	0.00	KO:K21449	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_2685695_2_799	623503.00	0.00	3477583.44	1396500.00	0.00	0.00	0.00	0.00	4635400.00	10736000.00	5835000.00	2124449.75	KO:K21449

Ga0586324_0148439_64_2844	0.00	0.00	0.00	0.00	1194800.00	534207.17	0.00	17751000.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0149519_59_2833	0.00	431894.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0183553_3_1919	0.00	2101200.00	5104310.01	0.00	0.00	4247900.00	0.00	2726700.00	0.00	2594900.00	3388000.00	3862500.00	KO:K21573	hypothetical protein
Ga0586324_0193365_2_2425	0.00	0.00	0.00	11400000.00	0.00	0.00	0.00	9699000.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0263775_3_2180	567823.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0303717_3_2045	0.00	924800.00	0.00	433076.50	1030000.00	0.00	0.00	497300.06	0.00	35820400.00	976800.00	1035000.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0312915_3_2015	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1897100.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0332722_2_1552	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1812800.00	1327500.00	KO:K21573	hypothetical protein
Ga0586324_0335483_1_1956	19780000.00	12172000.00	3456966.38	50169500.00	59379500.00	42876000.00	46056000.00	0.00	0.00	22456810.17	75306000.00	43208000.00	47475000.00	KO:K21573
Ga0586324_0361129_2_1891	96600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0388538_2_1831	9090000.00	3121200.00	19367200.00	1064000.00	0.00	0.00	0.00	1274900.00	7401034.48	8008000.00	7612000.00	5137500.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0439102_3_1736	0.00	2985200.00	3112342.82	0.00	0.00	4605200.00	6429600.00	2616900.00	3879900.00	7022400.00	1399200.00	2662500.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0488716_2_1483	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	296803.50	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0505509_2_1630	1150000.00	666797.12	390703.98	650365.25	0.00	1035864.31	817348.08	0.00	0.00	0.00	1316700.00	1082400.00	1222500.00	KO:K21573
Ga0586324_0571340_2_1546	9660000.00	10948000.00	5323142.48	5291500.00	3584400.00	3862520.19	0.00	1653100.00	6269400.00	7430500.00	9750400.00	21292500.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0601043_3_1514	0.00	0.00	0.00	805421.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1860000.00	KO:K21573	hypothetical protein
Ga0586324_0720555_181_1398	0.00	1611600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-linked SusC/RagA family outer membrane protein
Ga0586324_0780848_525_1352	0.00	748000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_0813014_3_1106	0.00	0.00	0.00	0.00	4274500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_0895798_3_1274	0.00	0.00	0.00	4094500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_0957835_1_1236	0.00	0.00	17959700.00	0.00	0.00	0.00	0.00	0.00	678623.67	0.00	0.00	7950000.00	KO:K21573	hypothetical protein
Ga0586324_1133100_2_1150	0.00	0.00	0.00	1653000.00	1678900.00	0.00	0.00	0.00	0.00	67672000.00	92250000.00	92500000.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_1138020_3_1148	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1031800.00	651065.36	598620.00	1127500.00	KO:K21573
Ga0586324_1151592_3_1142	0.00	2189600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	outer membrane receptor protein involved in Fe transport
Ga0586324_1242431_2_1105	5150000.00	2638400.00	5030298.03	4237000.00	12432100.00	12624600.00	5403600.00	3666100.00	1733400.00	2263800.00	2164800.00	1942500.00	KO:K21573	hypothetical protein
Ga0586324_1247230_3_1103	1440000.00	2890000.00	0.00	5434000.00	0.00	0.00	0.00	2928000.00	2656800.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_1263573_3_722	0.00	0.00	0.00	0.00	0.00	0.00	745961.28	1122400.00	2997000.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_1276920_3_1094	264020.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_1326501_2_1075	3080000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_1329594_2_286	580459.00	550462.72	0.00	1016500.00	1174200.00	0.00	0.00	2275300.00	6235066.53	0.00	0.00	1252500.00	KO:K21573	hypothetical protein
Ga0586324_1350901_1_1068	0.00	0.00	0.00	0.00	3934600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_1372640_2_1060	0.00	7616000.00	0.00	9500000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	outer membrane receptor for ferrienterochelin and colicin
Ga0586324_1452202_3_1034	1250000.00	10744000.00	5544953.22	3192000.00	1534700.00	925000.00	9462000.00	2738000.00	10287000.00	4904900.00	6318400.00	8700000.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_1538271_266_1009	0.00	0.00	0.00	2242000.00	0.00	0.00	0.00	113803.43	7468200.00	0.00	0.00	2085000.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_1600171_2_994	0.00	0.00	0.00	1776500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_1752904_97_954	0.00	216462.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_1859721_1_930	0.00	662997.96	0.00	0.00	1483200.00	0.00	0.00	951600.00	0.00	900900.00	6424000.00	772500.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_1884188_2_925	18700000.00	13736000.00	0.00	0.00	1380200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_2242612_1_861	0.00	0.00	0.00	0.00	0.00	0.00	0.00	27145000.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_2278366_2_856	0.00	0.00	0.00	0.00	0.00	4009700.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_2378974_306_839	2910000.00	2509200.00	0.00	0.00	6313900.00	3629294.60	0.00	2684000.00	2762100.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_2424493_58_834	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1567500.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_2619419_2_805	0.00	0.00	0.00	0.00	0.00	0.00	1221883.92	0.00	0.00	970200.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_2645814_3_803	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	155894.22	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_2885823_1_798	0.00	0.00	0.00	0.00	0.00	0.00	0.00	126784.23	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_2715099_1_795	959878.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_2773839_3_788	0.00	0.00	0.00	342994.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_2828714_56_781	735257.00	1149200.00	0.00	0.00	6293300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_2920878_144_773	1100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	outer membrane receptor protein involved in Fe transport
Ga0586324_2918769_1_771	0.00	0.00	4265181.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_3083463_1_752	0.00	0.00	0.00	696306.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_3117094_3_749	0.00	0.00	0.00	0.00	5438400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_3174560_3_503	0.00	0.00	2790346.23	1216000.00	1442000.00	890284.41	895540.68	817400.00	1028700.00	1840300.00	2578400.00	1830000.00	KO:K21573	hypothetical protein
Ga0586324_3241194_369_737	0.00	0.00	0.00	3429500.00	1452300.00	1937157.53	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_3323093_2_710	6550000.00	15436000.00	0.00	0.00	0.00	25249200.00	6384000.00	5923100.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_3444396_2_718	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1771000.00	0.00	KO:K21573	hypothetical protein
Ga0586324_3582599_3_707	4410000.00	3998400.00	0.00	440113.15	604558.50	0.00	0.00	0.00	249719.36	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_3676512_2_700	0.00	0.00	0.00	0.00	0.00	0.00	0.00	123576600.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_3762489_3_692	8330000.00	6555200.00	0.00	0.00	3048800.00	0.00	4788000.00	4038200.00	907200.00	5798100.00	7189600.00	6180000.00	KO:K21573	hypothetical protein
Ga0586324_3863937_252_686	1350000.00	0.00	8568600.00	0.00	0.00	0.00	84132000.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_3980669_3_677	0.00	0.00	0.00	6317500.00	3697700.00	8773700.00	5221200.00	2530000.29	2494800.00	4050200.00	6230400.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_4028446_2_673	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1263600.00	0.00	0.00	0.00	KO:K21573	outer membrane receptor protein involved in Fe transport
Ga0586324_4304586_1_342	1810000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_4599927_3_638	12800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_4789698_2_628	0.00	1203600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_4949045_1_618	3670000.00	3624400.00	0.00	2869000.00	1339000.00	0.00	0.00	0.00	1749600.00	2548700.00	897600.00	2940000.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_5916719_2_574	1130000.00	1455200.00	0.00	1168500.00	1648000.00	0.00	0.00	0.00	802726.20	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_6717847_2_532	0.00	1387200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	453233.51	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_7757229_1_513	0.00	0.00	0.00	0.00	1854000.00	0.00	0.00	417160.09	0.00	2949100.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_8009471_1_507	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	588591.36	0.00	0.00	0.00	KO:K21573	hypothetical protein
Ga0586324_8274931_1_501	1190000.00	0.00	0.00	6684700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21573	TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_0203970_1219_2382	0.00	0.00	0.00	7562000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21619	hypothetical protein
Ga0586324_0094179_1246_2583	1560000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K21677	squalene-associated FAD-dependent desaturase
Ga0586324_1959000_323_910	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4593300.00	0.00	0.00	0.00	0.00	KO:K21960	DNA-binding transcriptional LysR family regulator
Ga0586324_6803415_199_543	1430000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22010	AmiR/NasT family two-component response reaulator
Ga0586324_0008867_4171_5667	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2781600.00	0.00	0.00	0.00	0.00	KO:K22169	proton-translocating NADH-quinone oxidoreductase chain N
Ga0586324_0024598_6491_6739	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1006500.00	0.00	0.00	0.00	KO:K22231	threonine dehydrogenase-like Zn-dependent dehydrogenase
Ga0586324_0000126_2018_6964	0.00	2556800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22349	PsbP/CotA-like multicopper oxidase with cupredoxin domain
Ga0586324_0002261_14138_15784	0.00	0.00	0.00	0.00	0.00	2890965.91	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	thermosome
Ga0586324_0010156_8147_9793	2330000.00	3882800.00	0.00	2251500.00	45824700.00	0.00	0.00	7661600.00	8569800.00	5713400.00	0.00	2460000.00	KO:K22447	thermosome
Ga0586324_0024431_2863_4506	0.00	224729.12	5007157.56	0.00	0.00	6669600.00	638146.92	591371.12	478846.89	0.00	9504000.00	0.00	KO:K22447	thermosome
Ga0586324_0028874_4290_5930	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1804000.00	0.00	KO:K22447	thermosome
Ga0586324_0097960_106_1755	0.00	0.00	0.00	0.00	623373.51	0.00	6801654.96	0.00	102796.29	0.00	0.00	930000.00	KO:K22447	thermosome
Ga0586324_0091267_2098_3585	1400000.00	3236800.00	0.00	4180000.00	7786800.00	0.00	13702800.00	0.00	7954200.00	0.00	4936800.00	5160000.00	KO:K22447	thermosome
Ga0586324_0115263_2_586	0.00	1904000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_0140914_646_2322	0.00	0.00	0.00	0.00	0.00	0.00	1097190.72	0.00	0.00	0.00	0.00	0.00	KO:K22447	thermosome
Ga0586324_0220638_723_2381	6590000.00	3305480.00	220536.11	0.00	5119100.00	3314715.77	1321084.44	1407482.28	785332.26	0.00	0.00	1200000.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_0229908_757_2322	0.00	7072000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	thermosome
Ga0586324_0255809_2_1588	0.00	0.00	0.00	0.00	0.00	0.00	2872800.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	thermosome
Ga0586324_0276332_1392_2132	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	33187000.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_0289604_20_1678	0.00	5997600.00	0.00	278678.70	0.00	0.00	0.00	0.00	0.00	1370600.00	0.00	0.00	KO:K22447	thermosome
Ga0586324_0290543_325_1974	0.00	0.00	0.00	1824000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	thermosome
Ga0586324_0307556_45_1720	0.00	863600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	thermosome
Ga0586324_0383934_1_552	0.00	0.00	3442542.32	0.00	694507.37	3659486.45	0.00	1134600.00	2300400.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_0447106_1_1017	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1458000.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_0539427_3_1514	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	20768000.00	0.00	KO:K22447	thermosome
Ga0586324_0615246_147_1499	0.00	0.00	0.00	4638838.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	thermosome
Ga0586324_0769596_3_812	4080000.00	0.00	0.00	0.00	0.00	0.00	0.00	3416000.00	3288600.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_0948820_3_527	8150000.00	0.00	0.00	9500000.00	9084600.00	0.00	0.00	4582800.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_1322215_1_1152	0.00	0.00	1702039.32	0.00	0.00	0.00	1466254.32	0.00	0.00	0.00	1057500.00	0.00	KO:K22447	thermosome
Ga0586324_1166234_2_1135	0.00	0.00	4710164.97	0.00	0.00	0.00	0.00	4873900.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_1298294_1_1086	6570000.00	31756000.00	0.00	10925000.00	19982000.00	18659000.00	8253600.00	7320000.00	5532300.00	11627000.00	9680000.00	7372500.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_1313300_1_774	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3318400.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_1339443_2_1057	3940000.00	0.00	0.00	0.00	0.00	0.00	0.00	1488400.00	0.00	0.00	0.00	1425000.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_1682390_3_971	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2976800.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_2852108_1_777	0.00	0.00	0.00	0.00	0.00	1461739.40	1703120.00	16524000.00	13013000.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_3309779_1_732	27300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_3363105_1_726	0.00	0.00	0.00	0.00	0.00	8257600.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_4000403_16_675	0.00	0.00	0.00	0.00	0.00	2278700.00	3693600.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_4319057_1_654	0.00	0.00	0.00	0.00	5215500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_4600698_3_638	0.00	0.00	0.00	0.00	0.00	0.00	5244000.00	10553000.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_4974467_1_618	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1978900.00	0.00	0.00	3045000.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_5249717_1_603	1560000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_5362442_2_598	0.00	0.00	0.00	0.00	0.00	5835900.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_6040384_1_570	907863.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_6684852_1_546	0.00	0.00	0.00	0.00	6458100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_6957484_3_539	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1062600.00	208126.16	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_7542085_1_519	0.00	0.00	0.00	0.00	0.00	13061300.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_7778650_3_512	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5093500.00	0.00	0.00	0.00	0.00	KO:K22447	chaperonin GroEL (HSP60 family)
Ga0586324_0474663_149_997	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1421300.00	0.00	0.00	0.00	0.00	KO:K22468	polyphosphate kinase 2
Ga0586324_4063764_37_672	0.00	0.00	0.00	0.00	2513200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22468	polyphosphate kinase 2
Ga0586324_0001475_11189_13255	0.00	623929.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22516	formate dehydrogenase alpha subunit
Ga0586324_0018309_1_759	2140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22516	predicted molibopterin-dependent oxidoreductase YjgC
Ga0586324_0098128_1584_3461	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9152000.00	0.00	KO:K22516	formate dehydrogenase alpha subunit
Ga0586324_0331340_1_768	0.00	1278400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22516	predicted molibopterin-dependent oxidoreductase YjgC
Ga0586324_0641545_1_1470	960230.00	700400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1365000.00	KO:K22516	predicted molibopterin-dependent oxidoreductase YjgC
Ga0586324_1592866_2_994	4170000.00	2346000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22516	predicted molibopterin-dependent oxidoreductase YjgC
Ga0586324_1968642_45_908	1530000.00	748000.00	0.00	0.00	0.00	1558717.28	0.00	0.00	0.00	0.00	0.00	0.00	KO:K22516	predicted molibopterin-dependent oxidoreductase YjgC
Ga0586324_2861521_3_776	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1976400.00	0.00	0.00	0.00	0.00	KO:K22516	predicted molibopterin-dependent oxidoreductase YjgC
Ga0586324_3277311_2_733	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15147000.00	0.00	0.00	0.00	KO:K22516	predicted molibopterin-dependent oxidoreductase YjgC
Ga0586324_6776635_1_543	9860000.00	8568000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3757500.00	KO:K22516	predicted molibopterin-dependent oxidoreductase YjgC
Ga0586324_0348708_2_313	0.00	0.00	0.00	2527000.00	2832500.00	0.00	0.00	0.00	411582.87	0.00	0.00	0.00	KO:K22684	hypothetical protein
Ga0586324_1662523_1_828	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100809.00	KO:K22684	hypothetical protein
Ga0586324_4437739

Ga0586324 0575289 952 1269	0.00	0.00	0.00	2299000.00	0.00	0.00	0.00	805200.00	1077300.00	0.00	0.00	0.00	KO:K23077	Tuf,DsrC/DsvC family sulfur relay protein
Ga0586324 0630249 144 461	553659.00	19584000.00	0.00	0.00	0.00	0.00	0.00	324252.48	522564.43	227819.79	0.00	0.00	80508.00	KO:K23077
Ga0586324 0770903 123 440	0.00	9656000.00	10978500.00	2584000.00	2811900.00	21755600.00	19995600.00	19154000.00	22680000.00	17325000.00	20592000.00	14325000.00	KO:K23077
Ga0586324 1139818 797 1147	22200000.00	1224000.00	0.00	10545000.00	0.00	0.00	26676000.00	16409000.00	16119000.00	14861000.00	5790400.00	14625000.00	KO:K23077
Ga0586324 3372719 43 360	0.00	0.00	0.00	3629000.00	0.00	0.00	0.00	0.00	4706100.00	0.00	0.00	0.00	KO:K23077
Ga0586324 6108798 65 382	218670.00	587536.32	0.00	988000.00	0.00	0.00	2667600.00	526135.37	223732.53	0.00	0.00	840000.00	KO:K23077
Ga0586324 0100146 1 1878	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	327538.89	0.00	0.00	0.00	KO:K23269
Ga0586324 0028555 1941 4424	0.00	0.00	0.00	0.00	946967.58	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23302
Ga0586324 3150718 3 746	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1357500.00	KO:K23356
Ga0586324 0017284 6656 7687	0.00	0.00	0.00	0.00	0.00	0.00	0.00	69540000.00	1236500.00	862400.00	0.00	0.00	KO:K23508
Ga0586324 0000031 2 1234	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1745500.00	0.00	0.00	0.00	KO:K23508
Ga0586324 0083255 1532 2590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1193500.00	0.00	KO:K23508
Ga0586324 0122508 3 944	0.00	0.00	0.00	0.00	15965000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23508
Ga0586324 0126217 1245 2276	38700000.00	46110800.00	46785300.00	2422500.00	0.00	0.00	0.00	2446100.00	2502900.00	0.00	22176000.00	0.00	KO:K23508
Ga0586324 0309029 355 1347	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	453087.27	0.00	0.00	0.00	KO:K23508
Ga0586324 0882461 81 1214	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3502400.00	0.00	KO:K23508
Ga0586324 1760665 3 842	2990000.00	4270400.00	0.00	1691000.00	0.00	0.00	534302.04	2430046.43	0.00	0.00	0.00	0.00	KO:K23508
Ga0586324 1856941 146 931	2310000.00	10336000.00	0.00	0.00	0.00	0.00	0.00	488015.25	0.00	0.00	0.00	0.00	KO:K23508
Ga0586324 2471015 1 825	0.00	1428000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23508
Ga0586324 2920810 1 624	0.00	0.00	10528100.00	1168500.00	0.00	1184334.22	16142400.00	673000.00	0.00	0.00	0.00	23100000.00	KO:K23508
Ga0586324 4884351 3 563	0.00	8098800.00	0.00	0.00	0.00	0.00	1113096.00	0.00	0.00	0.00	0.00	0.00	KO:K23508
Ga0586324 5166098 3 608	38000000.00	7276000.00	0.00	7125000.00	9156700.00	2429640.00	0.00	8784000.00	0.00	0.00	0.00	0.00	KO:K23508
Ga0586324 5510705 2 592	0.00	1774800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1852500.00	KO:K23508
Ga0586324 6029324 3 572	8710000.00	9248000.00	0.00	0.00	0.00	0.00	0.00	6032900.00	0.00	0.00	0.00	0.00	KO:K23508
Ga0586324 6453867 3 554	1590000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23508
Ga0586324 7698985 3 518	0.00	351234.96	0.00	393859.51	369466.15	0.00	0.00	364457.92	750937.23	0.00	0.00	0.00	KO:K23508
Ga0586324 0520671 20 1609	0.00	1951600.00	5128625.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23545
Ga0586324 5403159 3 596	2950000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23545
Ga0586324 0000970 23294 25180	7940000.00	1632000.00	0.00	148912.50	0.00	0.00	0.00	0.00	4033800.00	4712400.00	0.00	2962500.00	KO:K23995
Ga0586324 0004617 3968 5809	81970000.00	33688026.88	116355339.49	4396015.75	51217229.98	52404000.00	12077271.04	30811100.00	33768900.00	61677000.00	43806400.00	84307500.00	KO:K23995
Ga0586324 0015996 2105 4030	0.00	0.00	0.00	0.00	0.00	5716800.00	0.00	0.00	14337000.00	13629000.00	2472800.00	0.00	KO:K23995
Ga0586324 0023874 3647 5452	0.00	0.00	0.00	0.00	0.00	1052502.58	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0035136 1453 3249	3510000.00	7140000.00	0.00	5273052.37	0.00	2272650.32	0.00	2220400.00	0.00	0.00	8393000.00	0.00	KO:K23995
Ga0586324 0066014 1141 2961	0.00	3978000.00	4427910.55	0.00	0.00	2106160.43	2348400.00	2604700.00	3790800.00	3780700.00	4831200.00	4072500.00	KO:K23995
Ga0586324 0092928 964 2805	14550000.00	8812800.00	0.00	5944338.10	0.00	0.00	0.00	2635200.00	2106000.00	3984333.43	3940948.00	7116369.00	KO:K23995
Ga0586324 0100545 400 2220	0.00	0.00	0.00	706737.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0104842 1590 3353	0.00	5732400.00	0.00	0.00	0.00	0.00	0.00	499874.87	0.00	3041500.00	0.00	2722500.00	KO:K23995
Ga0586324 0177367 1810 2616	0.00	0.00	0.00	0.00	0.00	3519238.26	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0222319 3 1508	0.00	0.00	0.00	3595870.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0230246 1 1434	31300000.00	9513200.00	12160800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0247183 264 2084	0.00	11689200.00	32993303.21	13984000.00	9527500.00	13299500.00	3283200.00	4038200.00	4722300.00	14984200.00	9741600.00	4914394.50	KO:K23995
Ga0586324 0254780 1317 2213	0.00	0.00	0.00	0.00	0.00	3484052.15	0.00	0.00	0.00	2772000.00	0.00	0.00	KO:K23995
Ga0586324 0294134 2 1000	16500000.00	11968000.00	9345800.00	0.00	0.00	4947600.00	3788100.00	5572800.00	5028100.00	1284800.00	5542500.00	0.00	KO:K23995
Ga0586324 0301899 2 1597	0.00	2495600.00	2516942.17	5006500.00	0.00	3065495.05	0.00	1903200.00	12935700.00	0.00	0.00	3465000.00	KO:K23995
Ga0586324 0320822 515 1993	48201.88	0.00	0.00	1567500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0233245 1 1449	13190000.00	34748000.00	27755900.00	0.00	0.00	0.00	3716400.00	0.00	0.00	1632400.00	7128000.00	1507500.00	KO:K23995
Ga0586324 0340939 65 1942	18900000.00	0.00	0.00	0.00	11639000.00	0.00	0.00	0.00	1328400.00	0.00	0.00	6450000.00	KO:K23995
Ga0586324 0365898 2 613	0.00	0.00	29107100.00	486001.95	0.00	2231400.00	0.00	0.00	0.00	10934000.00	11616000.00	1792500.00	KO:K23995
Ga0586324 0374591 17 1861	14300000.00	10880000.00	0.00	0.00	0.00	0.00	0.00	860100.00	0.00	0.00	0.00	3667500.00	KO:K23995
Ga0586324 0443931 3 905	0.00	0.00	0.00	0.00	0.00	0.00	0.00	485679.56	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0540198 365 1583	0.00	3270800.00	0.00	2916500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0739858 108 1382	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2767500.00	KO:K23995
Ga0586324 1023369 3 1046	0.00	0.00	0.00	0.00	0.00	0.00	8094000.00	12566000.00	0.00	14168000.00	4769600.00	18600000.00	KO:K23995
Ga0586324 1160425 1 1041	0.00	0.00	0.00	28975000.00	0.00	22906900.00	16621200.00	20923000.00	22275000.00	36806000.00	33792000.00	32625000.00	KO:K23995
Ga0586324 1249251 6 1107	0.00	0.00	0.00	7838700.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 1408073 3 1049	2850000.00	3692400.00	5284284.22	2147000.00	0.00	6342527.58	0.00	1860500.00	3418200.00	6999300.00	8676800.00	6705000.00	KO:K23995
Ga0586324 1583581 1 996	6960000.00	0.00	17340400.00	0.00	11639000.00	16316700.00	6680400.00	6283000.00	0.00	0.00	9064000.00	6607500.00	KO:K23995
Ga0586324 2060581 73 891	13800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 2172787 251 871	60700000.00	112308800.00	57426000.00	0.00	0.00	0.00	9074400.00	35014000.00	29079000.00	31339000.00	0.00	37800000.00	KO:K23995
Ga0586324 2219072 3 863	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2587200.00	1657500.00	KO:K23995
Ga0586324 2247724 22 861	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1152800.00	13350000.00	2132500.00	KO:K23995
Ga0586324 2299633 2 853	0.00	0.00	0.00	0.00	2420500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 2756972 1 789	75628.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 2962098 1 765	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10912000.00	0.00	0.00	KO:K23995
Ga0586324 3229186 1 765	401997.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 3020901 1 411	0.00	0.00	0.00	0.00	590061.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 3027420 2 511	29070000.00	47940000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7368900.00	34056000.00	0.00	KO:K23995
Ga0586324 3162723 3 686	79910000.00	1918800.00	91114625.10	2565000.00	2801600.00	0.00	3625200.00	4038200.00	3936600.00	4019400.00	5244000.00	5640000.00	KO:K23995
Ga0586324 3270709 1 561	0.00	0.00	0.00	0.00	0.00	0.00	0.00	640500.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 3480127 3 716	70900000.00	70040000.00	85576000.00	0.00	3677100.00	6868100.00	20770800.00	17690000.00	13527000.00	9625000.00	17072000.00	11625000.00	KO:K23995
Ga0586324 3849179 227	9440000.00	9792000.00	9796200.00	0.00	8641700.00	10123500.00	0.00	6832000.00	15309000.00	13860000.00	12232000.00	9300000.00	KO:K23995
Ga0586324 5422384 3 596	0.00	2801600.00	1412775.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 5446189 3 596	0.00	0.00	0.00	2247214.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 6098200 1 567	6430000.00	1781600.00	20268000.00	710600.00	0.00	6572239.72	0.00	1144700.00	3134700.00	0.00	2508000.00	5287500.00	KO:K23995
Ga0586324 7039868 1 534	1540000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 7084956 2 535	7880000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 7699039 3 515	98921.00	0.00	17171500.00	0.00	0.00	0.00	1748734.32	1457900.00	3153793.98	1971200.00	4910400.00	2257500.00	KO:K23995
Ga0586324 8189017 2 502	0.00	0.00	94584000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23995
Ga0586324 0089292 1837 3423	0.00	0.00	0.00	0.00	9640800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23997
Ga0586324 0614558 1 1341	17800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K23997
Ga0586324 0154022 2 1771	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1098000.00	0.00	0.00	0.00	0.00	KO:K24119
Ga0586324 1765093 2 475	0.00	0.00	0.00	0.00	0.00	0.00	2302800.00	0.00	0.00	2325400.00	0.00	0.00	KO:K24119
Ga0586324 1805259 200 763	0.00	5807200.00	0.00	0.00	2029100.00	0.00	553073.28	0.00	0.00	5921300.00	17512000.00	4507500.00	KO:K24119
Ga0586324 0645579 987 1460	0.00	0.00	0.00	3410500.00	2039400.00	0.00	0.00	0.00	0.00	4435200.00	4250400.00	5137500.00	KO:K24129
Ga0586324 4324050 7 654	0.00	5650800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K24129
Ga0586324 0125028 1434 1916	0.00	3746800.00	0.00	0.00	3466254.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	KO:K24138
Ga0586324 0000001 103210 104415	0.00	0.00	0.00	0.00	0.00	0.00	8558300.00	6504300.00	2407020.00	8116697.00	2495250.00	0.00
Ga0586324 0000002 111816 112457	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2622400.00	1792500.00	0.00
Ga0586324 0000002 189616 190569	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4087500.00	0.00
Ga0586324 0000002 56313 58445	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	888800.00	226435.25	0.00
Ga0586324 0000003 12721 13170	0.00	0.00	0.00	0.00	0.00	0.00	2488800.00	0.00	3026100.00	1760000.00	7935000.00	0.00
Ga0586324 0000003 172392 174353	6360000.00	0.00	0.00	0.00	0.00	38554800.00	38545900.00	26065800.00	79387000.00	71535200.00	70807500.00	0.00
Ga0586324 0000004 122259 122657	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1098000.00	0.00	0.00	1208900.00	0.00
Ga0586324 0000004 123664 124560	0.00	0.00	0.00	0.00	0.00	0.00	5313100.00	7767900.00	17109400.00	16579200.00	10155000.00	0.00
Ga0586324 0000005 158962 159300	0.00	0.00	0.00	0.00	0.00	0.00	5874300.00	0.00	0.00	0.00	0.00	0.00
Ga0586324 0000005 36313 37335	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5667200.00	1760000.00	3447500.00
Ga0586324 0000007 112166 113494	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	515973.92	1027500.00
Ga0586324 0000007 33285 34436	0.00	2298400.00	2657528.90	0.00	1483200.00	2793911.32	47492400.00	27138289.39	25879500.00	69238400.00	52368800.00	40395000.00
Ga0586324 0000007 78078 78644	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13125000.00
Ga0586324 0000007 83821 84792	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2517900.00	6556000.00	1395000.00
Ga0586324 0000011 31458 32867	0.00	0.00	0.00	0.00	0.00	0.00	28609000.00	27864000.00	62447000.00	544759.60	50925000.00
Ga0586324 0000011 6456 8294	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9639000.00	7153300.00	12716000.00	21082500.00
Ga0586324 0000013 45844 46875	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1047200.00	0.00	1245000.00
Ga0586324 0000013 61899 62333	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2910600.00	0.00	0.00
Ga0586324 0000013 71030 74239	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1085700.00	0.00	0.00
Ga0586324 0000018 16215 17159	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9416000.00	3930000.00
Ga0586324 0000018 42136 42597	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1260000.00
Ga0586324 0000032 29918 30175	0.00	0.00	568630.00	648284.75	1205100.00	840222.71	0.00	0.00	0.00	0.00	0.00
Ga0586324 0000033 62152 62676	0.00	0.00	0.00	0.00	0.00	0.00	2235843.24	9638000.00	0.00	7092800.00	4665000.00
Ga0586324 0000033 65074 65499	0.00	0.00	0.00	0.00	0.00	0.00	2986800.00	3806400.00	0.00	10010000.00	10560000.00
Ga0586324 0000035 53685 55538	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2257500.00
Ga0586324 0000037 32177 33070	0.00	0.00	0.00	0.00	0.00	0.00	0.00	59927.86	0.00	0.00	0.00
Ga0586324 0000037 34663 35172	0.00	0.00	0.00	0.00	0.00	0.00	2530800.00	0.00	0.00	2587200.00	0.00
Ga0586324 0000037 68802 69647	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4596900.00	3361600.00
Ga0586324 0000041 23064 24878	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5165600.00
Ga0586324 0000046 30538 35268	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1817200.00	0.00
Ga0586324 0000070 43313 44773	0.00	0.00	0.00	0.00	0.00	0.00	1348100.00	1733400.00	0.00	5272100.00	4845000.00
Ga0586324 0000080 6188 7249	6790000.00	7877857.80	12386000.00	6631000.00	14450900.00	7026900.00	14865600.00	24766000.00	25312500.00	8670200.00	11422400.00	1642500.00
Ga0586324 0000092 30838 31752	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1355200.00
Ga0586324 0001003 24180 25175	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3063400.00	0.00
Ga0586324 0000105 22067 23551	813917.00	1224000.00	2257005.07	3306000.00	3812777.78	1278812.43	0.00	1049200.00	2260165.68	0.00	0.00
Ga0586324 0000147 1184 2944	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	980100.00	0.00	0.00
Ga0586324 0000151 2249 3661	0.00	0.00	0.00	0.00	0.00	0.00	2918400.00	2696200.00	0.00	0.00	0.00
Ga0586324 0000169 6878 8317	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ga0586324 0000181 14108 17032	8340000.00	12056400.00	0.00	3695500.00	0.00	7580377.55	1233258.84	2458300.00	0.00	2589554.66	4954400.00
Ga0586324 0000181 17052 20468	3920000.00	10764400.00	0.00	0.00	3069400.00	15125700.00	0.00	0.00	788164.83	0.00	0.00
Ga0586324 0000181 20552 21601	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ga0586324 0000192 5334 8912	0.00	1135600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3819200.00	0.00
Ga0586324 0000211 21187 24735	0.00	945200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ga0586324 0000217 1659 4838	78410000.00	54196000.00	98919100.00	42655000.00	63508962.61	35412400.00	46489200.00	32811900.00	26090100.00	84469000.00	81699200.00
Ga0586324 0000219 3914 4954	27700000.00	904400.00	29670100.00	16150000.00	0.00	0.00	1551872.88	13908000.00	11907000.00	8778000.00	1972100.00
Ga0586324 0000244 83 667	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2488800.00	972000.00	15631000.00	1795200.00
Ga0586324 0000270 22082 24850	0.00	0.00	0.00	0.00	0.00	0.00	769205.88	0.00	545424.03	0.00	0.00
Ga0586324 0000291 28342 31605	193059.00	0.00	0.00	3106500.00	2482300.00	3216990.25	0.00	0.00	0.00	0.00	3344000.00
Ga0586324 0000309 16191 18146	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	680502.87	0.00	0.00
Ga0586324 0000329 2673 5540	8740000.00	1176400.00	10162256.97	3220500.00	2492600.00	0.00	860608.28	1579900.00	1215000.00	0.00	2129600.00
Ga0586324 0000337 27529 29658	19880000.00	19584000.00	30739800.00	29849000.00	47235800.00	36682800.00	41427600.00	15433000.00	13713300.00	23461900.00	11844800.00
Ga0586324 0000361 12533 14101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2513200.00	0.00	0.00	1205600.00
Ga0586324 0000363 631 1803	352370000.00	108052000.00	18090967.39	307230000.00	341156600.00	47946972.31	352885904.00	74295402.01	170518328.55	81364744.23	112340800.00	158557500.00

Ga0586324 0000291 28342 31605	hypothetical protein
Ga0586324 0000309 16191 18146	hypothetical protein
Ga0586324 0000329 2673 5540	hypothetical protein
Ga0586324 0000337 27529 29658	outer membrane protein OmpA-like peptidoglycan-associated protein
Ga0586324 0000361 12533 14101	uncharacterized protein (PEP-CTERM system associated)
Ga0586324 0000363 631 1803	predicted porin

Ga0586324_0000365_20454_23741	0.00	1137255.80	5855200.00	1396500.00	1102100.00	0.00	0.00	933300.00	328626.72	962400.80	888800.00	381415.50	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0000365_636_4013	13590000.00	13933200.00	12723800.00	16055000.00	12586600.00	10574916.79	13292400.00	12718500.00	8221500.00	10017700.00	7708800.00	10425000.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidipila;Acidipila rosea;Acidipila rosea DSM 103428
Ga0586324_0000423_24008_25159	936392.00	37196000.00	25765646.25	2346500.00	5489900.00	17150400.00	174672537.36	356270802.56	115077997.62	291837700.00	364362276.08	453452394.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324_0000429_10739_12514	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1231200.00	0.00	0.00	0.00	MSHA type pilus biogenesis protein MshL	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0000431_19186_19905	0.00	0.00	0.00	0.00	463150.83	0.00	0.00	0.00	1101600.00	0.00	950400.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0000434_6653_9970	3950000.00	23881600.00	12632239.39	32110000.00	1359600.00	15789678.53	5859600.00	6703900.00	11372400.00	11357500.00	11070400.00	8647500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0000470_22417_22821	12400000.00	10030000.00	0.00	10260000.00	4964600.00	0.00	8399400.00	15231700.00	6131700.00	5574800.00	7040000.00	5730000.00	hypothetical protein	
Ga0586324_0000475_15100_16647	0.00	1360000.00	0.00	0.00	0.00	0.00	0.00	1750700.00	0.00	5428500.00	4822400.00	4012500.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfurivirellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324_0000491_6575_8887	677390.00	1813961.20	1444911.35	1320500.00	0.00	336977.57	0.00	0.00	0.00	0.00	0.00	423196.50	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0000518_28887_28231	1320000.00	0.00	0.00	1586500.00	0.00	0.00	0.00	0.00	0.00	0.00	841600.00	1492500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0000524_30320_31144	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2170800.00	5667200.00	7330400.00	1267500.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0000537_19185_20219	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1297500.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0000542_20285_21433	0.00	2128400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9317000.00	0.00	10125000.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0000542_21592_24315	0.00	0.00	2231326.64	0.00	0.00	6066799.56	8930400.00	6658200.00	14483700.00	17107200.00	10260000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0000543_15169_16437	0.00	10812000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 9736;Geobacter sp. DSM 9736
Ga0586324_0000576_17339_18628	0.00	0.00	0.00	0.00	0.00	0.00	567964.29	447932.43	491637.30	530063.60	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324_0000620_19859_23254	0.00	0.00	0.00	8787500.00	9609900.00	0.00	0.00	0.00	6081100.00	0.00	0.00	4777500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0000630_16007_16582	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3672900.00	4716800.00	1057500.00	polyisoprenoid-binding protein Ycel	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0000652_28176_30539	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1812800.00	1237500.00	Ca2+-binding RTX toxin-like protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Annwoodia;Annwoodia aquaesulis;Annwoodia aquaesulis DSM 4255
Ga0586324_0000679_1574_3100	0.00	931600.00	0.00	0.00	0.00	942755.90	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0000686_24489_27053	10800000.00	0.00	0.00	6156000.00	0.00	0.00	0.00	0.00	3353400.00	0.00	4760800.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324_0000732_5275_7188	3340000.00	2869600.00	0.00	5120500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	transketolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas lenta;Methylomonas lenta R-45370
Ga0586324_0000741_23484_25919	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2835000.00	formate dehydrogenase-N alpha subunit	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0000753_5636_6421	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1940400.00	0.00	0.00	short-subunit dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Propionivibrio;Propionivibrio pelophilus;Propionivibrio pelophilus DSM 12018
Ga0586324_0000755_13164_14306	0.00	4107200.00	0.00	0.00	1740700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	alkylation resonse protein AidB-like acyl-CoA dehydroxenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0000764_15803_16765	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6081100.00	0.00	1216600.00	0.00	single-stranded DNA-specific DHH superfamily exonuclease	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0000820_8658_10310	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3672900.00	4716800.00	1057500.00	PAS domain S-box-containing protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Sunxiuqinia;Sunxiuqinia dokdonensis;Sunxiuqinia dokdonensis SK
Ga0586324_0000830_13202_14503	12510000.00	25792400.00	10758839.92	16843500.00	41210300.00	18976600.00	41746800.00	16085700.00	34036200.00	9163000.00	24904000.00	18345000.00	hypothetical protein	
Ga0586324_0000943_10690_11634	0.00	0.00	0.00	0.00	0.00	0.00	1580119.80	0.00	0.00	0.00	0.00	0.00	DNA-binding transcriptional LysR family regulator	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0000975_8167_8664	0.00	2033200.00	0.00	0.00	19364000.00	0.00	5016000.00	2958500.00	38556000.00	0.00	25960000.00	0.00	rubrerythrin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0001021_11236_11571	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2909700.00	0.00	0.00	0.00	0.00	TusE/DsrC/DsvC family sulfur relay protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0001021_6706_8664	0.00	1142400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4807500.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase/Pyruvate/2-oxoacid:ferr	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0001096_10846_12051	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	451151.25	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0001135_4367_6148	0.00	0.00	1634850.66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	alkylation response protein AidB-like acyl-CoA dehydrogenase	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0001224_14088_15227	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1628000.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. Ai1a-2;Bradyrhizobium sp. Ai1a-2
Ga0586324_0001245_5092_6296	0.00	0.00	306400.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Bacteroidetes;Saprospirae;Saprospirales;Rhodospirillaceae;Auxipiria;Auxipiria sp. CCB-QB1;Auxipiria sp. CCB-QB1
Ga0586324_0001289_8270_12913	0.00	3529200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Limnochordia;Limnochordales;Limnochordaceae;Limnochorda;Limnochorda pilosa;Limnochorda pilosa HC45
Ga0586324_0001308_640_3012	0.00	0.00	0.00	1520000.00	0.00	1285561.43	0.00	0.00	0.00	1286071.02	1963500.00	704679.36	type IV pilus secretin PilQ/predicted competence protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-A06;Aminicenantes bacterium SCGC AAA255-A06 (contamination screened)
Ga0586324_0001371_9826_10515	0.00	0.00	0.00	0.00	0.00	0.00	1515324.48	2635200.00	0.00	0.00	0.00	1297500.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0001379_20967_22925	0.00	0.00	0.00	0.00	0.00	0.00	20907600.00	7869000.00	6625800.00	0.00	10190400.00	3705000.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase/Pyruvate/2-oxoacid:ferr	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0001505_3_3302	17410000.00	12947200.00	7262700.00	19218500.00	24987800.00	15087103.66	10465200.00	11980400.00	10278900.00	12469938.25	11888800.00	13455000.00	TonB-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Gaetbulibacter;Gaetbulibacter saemankumensis;Gaetbulibacter saemankumensis DSM 17032
Ga0586324_0001544_8982_9975	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1142100.00	0.00	0.00	0.00	CBS domain-containing protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0001554_11968_13557	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1832600.00	0.00	0.00	glutamate synthase domain-containing protein 2	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanolacinia;Methanolacinia petroleara;Methanolacinia petroleara DSM 11571
Ga0586324_0001628_11598_13982	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	319044.75	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0001715_4625_8344	0.00	999181.12	0.00	1558800.00	3697700.00	0.00	0.00	0.00	10335600.00	3210901.54	19527200.00	7005000.00	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. Root122;Nocardioides sp. Root122
Ga0586324_0001815_16787_17242	0.00	0.00	0.00	0.00	0.00	0.00	6748800.00	10187000.00	8262000.00	2949200.00	13900000.00	1065000.00	lipid-binding SYLF domain-containing protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Alkobacter;Alkobacter soli;Alkobacter soli SHI
Ga0586324_0001823_15552_15887	0.00	0.00	0.00	0.00	0.00	0.00	10921200.00	5703500.00	12393000.00	0.00	0.00	0.00	Elab/RqcD/DUF883 family membrane-anchored ribosome-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0001878_15789_17378	0.00	8976000.00	0.00	0.00	0.00	0.00	0.00	0.00	8343000.00	0.00	3872000.00	0.00	glutamate synthase domain-containing protein 2	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanosaeta harundinacea;Methanothrix harundinacea 6Ac
Ga0586324_0001918_1909_4815	6580000.00	2067200.00	0.00	8711500.00	8858000.00	8495800.00	0.00	0.00	8505000.00	1647800.00	22264000.00	13072500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotomaculum;Desulfotomaculum aerobicum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0002013_11662_12585	0.00	0.00	0.00	990778.66	0.00	0.00	597921.70	3237600.00	1573800.00	0.00	0.00	1815000.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0002022_40_4395	0.00	0.00	3971953.74	5310500.00	0.00	0.00	928404.35	5882400.00	2732800.00	6342300.00	0.00	1695000.00	hypothetical protein	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;unclassified Rhodothermaceae;Rhodothermaceae bacterium RA;Halothermothrix malaysiensis RA
Ga0586324_0002099_8926_12357	9180000.00	5419600.00	0.00	4199934.40	0.00	16480000.00	892342.46	0.00	3824700.00	5208300.00	5289900.00	3317600.00	3975000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium allauci PMMR2
Ga0586324_0002096_10428_11738	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6546.26	0.00	0.00	predicted dehydrogenase	Bacteria;Planctomycetes;Phycisphaerae;Sedimentisphaerales;Anaerohalosphaeraceae;Anaerohalosphaera;Anaerohalosphaera lusitana;Phycisphaerae bacterium ST-NAGAB-01
Ga0586324_0002126_3622_6714	0.00	0.00	12611200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7717600.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;unclassified Spongiibacteraceae;marine gamma proteobacterium HTCC2143;Marine gamma proteobacterium sp. HTCC2143
Ga0586324_0002126_9140_12235	4130000.00	1638800.00	2301482.67	2327500.00	1163900.00	2964113.16	0.00	0.00	0.00	2156000.00	2420025.66	155394.75	outer membrane receptor protein involved in Fe transport	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Spongiibacteraceae;unclassified Spongiibacteraceae;marine gamma proteobacterium HTCC2143;Marine gamma proteobacterium sp. HTCC2143
Ga0586324_0002173_3821_5230	4330000.00	0.00	0.00	0.00	0.00	0.00	8846400.00	0.00	0.00	0.00	7541600.00	0.00	glutamine synthetase type I	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0002189_4626_6137	3540000.00	3366000.00	2392834.45	2973500.00	4181800.00	0.00	0.00	6905200.00	8108100.00	8824200.00	8729600.00	6120000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0002270_3_18908	0.00	3806432.60	1692299.18	1358500.00	834797.71	272884.70	0.00	504557.84	352980.99	0.00	1056000.00	3105681.00	hypothetical protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Nostocales;Nostocaceae;Nostoc;Nostoc sp. PCC 7524;Nostoc sp. PCC 7524
Ga0586324_0002278_4027_5478	3650000.00	10492400.00	25560200.00	48618232.65	2904337.35	20523411.25	0.00	0.00	0.00	5428325.98	0.00	17864800.50	hypothetical protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Prominofilum;Candidatus Prominofilum breve;Candidatus Prominofilum breve Cfx-K
Ga0586324_0002303_218_1558	5260000.00	1672800.00	856700.21	3534000.00	320307.34	1173841.66	2736000.00	2177700.00	2551500.00	2109800.00	1636800.00	1650000.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0002309_206_4396	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3328800.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Kribbellaceae;Kribbella;Kribbella montcalmii;Kribbella montcalmii NEAU-SW521
Ga0586324_0002364_17741_18613	1100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium;Flavobacterium sp. A45;Flavobacterium sp. A45
Ga0586324_0002415_3_482	109000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	formyltetrahydrofolate synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_0002443_5377_18369	1200000.00	0.00	0.00	0.00	631159.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Youngiibacter;Youngiibacter fragilis;Youngiibacter fragilis 232.1
Ga0586324_0002444_4757_7189	0.00	1394000.00	0.00	0.00	0.00	0.00	3709655.34	0.00	0.00	0.00	6635200.00	0.00	type IV pilus secretin PilQ/predicted competence protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-K07;Aminicenantes bacterium SCGC AAA252-K07 (contamination screened)
Ga0586324_0002517_8902_12627	0.00	508987.48	0.00	1463000.00	26151700.00	2191400.00	0.00	14823000.00	0.00	0.00	0.00	256828.25	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. Root122;Nocardioides sp. Root122
Ga0586324_0002541_12112_15198	28650000.00	24244785.28	3411932.01	14592000.00	16459400.00	13425503.83	11272484.16	12297600.00	11080800.00	15631000.00	15655200.00	10462500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0002581_778_3943	7956177.00	4088000.00	6699700.00	0.00	567811.25	1342744.19	8846400.00	8228900.00	1020535.20	0.00	4848000.00	7650000.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0002581_17259_17771	8420000.00	0.00	0.00	0.00	0.00	0.00	0.00	2763300.00	3110400.00	0.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0002626_202_1494	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1903500.00	10626000.00	3528800.00	1312500.00	hypothetical protein	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetoovum;Candidatus Magnetoovum chiemensis;Candidatus Magnetoovum chiemensis CS-04
Ga0586324_0002664_1413_4940	3546370.00	5453600.00	0.00	5966000.00	5520800.00	5161000.00	0.00	0.00	3183300.00	1824900.00	3335200.00	2197500.00	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Caloramanas;Caloramanas aeorrhamnus;Caloramanas aeorrhamnus HS1214
Ga0586324_0002696_2864_3589	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4666500.00	4957200.00	0.00	0.00	1575000.00	flavorubredoxin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_0002712_183_3170	5730000.00	16061600.00	1139776.61	5880500.00	10227900.00	11855178.27	0.00	1348100.00	4416417.27	3873100.00	4030400.00	6854229.75	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-N07;Aminicenantes bacterium SCGC AAA252-N07 (contamination screened)
Ga0586324_0002748_1510_3384	0.00	4311200.00	0.00	0.00	0.00	0.00	0.00	2913800.00	5994000.00	8693300.00	5288000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324_0002755_756_2033	10000000.00	8500000.00	11428900.00	4664500.00	4974900.00	11711500.00	8618400.00	9089000.00	9315000.00	3072300.00	2974400.00	6705000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter anodireducens;Geobacter anodireducens SD-1
Ga0586324_0002758_2997_3617	0.00	0.00	0.00	0.00	0.00	0.00	508440.00	1592100.00	5313600.00	0.00	0.00	4275000.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Acetobacteroides;Acetobacteroides hydrogenigenes;Acetobacteroides hydrogenigenes DSM 24657
Ga0586324_0002766_11209_14610	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1845000.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0002793_14337_15797	0.00	0.00	12892700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Prominofilum;Candidatus Prominofilum breve;Candidatus Prominofilum breve Cfx-K
Ga0586324_0002943_6433_6660	0.00	0.00	0.00	0.00	3505500.00	2235100.00	6431400.00	0.00	1884900.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0002994_8995_10023	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	996300.00	0.00	2631200.00	0.00	TRAP-type

Ga0586324_0006265_6134_6814	8810000.00	1992400.00	2449770.64	0.00	0.00	10838100.00	1610507.64	713700.00	790541.37	0.00	0.00	1365000.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptostreptococcaceae;Sporacetigenium mesophilum;Sporacetigenium mesophilum DSM 16796
Ga0586324_0006300_1360_4665	3960000.00	1169600.00	0.00	0.00	0.00	7007867.82	1021709.04	1537200.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium;Flavobacterium notoginsengisoli;Flavobacterium notoginsengisoli S00128
Ga0586324_0006460_10446_11003	0.00	2794800.00	6699700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0006477_9306_9827	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3537600.00	0.00	uncharacterized protein (DUF302 family)	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324_0006581_6861_8783	0.00	0.00	0.00	0.00	1936400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Zetaproteobacteria;unclassified Zetaproteobacteria;unclassified Zetaproteobacteria;unclassified Zetaproteobacteria;unclassified Zetaproteobacteria;Unclassified zetaproteobacterium sp. KV
Ga0586324_0006694_1_588	22500000.00	29300800.00	70375000.00	0.00	30797000.00	27353300.00	17008800.00	16714000.00	22437000.00	39963000.00	37136000.00	33900000.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuirhabdus;Sulfuirhabdus autotrophica;Sulfuirhabdus autotrophica DSM 100309
Ga0586324_0006694_2688_5267	0.00	3712800.00	0.00	0.00	0.00	1681874.62	3328800.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiogranum;Thiogranum longum;Thiogranum longum DSM 19610
Ga0586324_0006769_6305_9643	18820000.00	17040800.00	13910829.20	26144000.00	24359500.00	20742833.15	13292400.00	11809600.00	15398100.00	17579100.00	17036800.00	14235000.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-N07;Aminicenantes bacterium SCGC AAA252-N07 (contamination screened)
Ga0586324_0006808_3133_6237	0.00	0.00	2715692.43	3268000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;unclassified Chitinophagaceae;Chitinophagaceae bacterium;Chitinophagaceae sp. OA5944
Ga0586324_0006808_9560_11080	14900000.00	13192000.00	18973100.00	26790000.00	25750000.00	6749000.00	4947600.00	62220000.00	12936097.71	11704000.00	7761600.00	35475000.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanosaeta harundinacea;Methanothrix harundinacea 6Ac
Ga0586324_0006897_5865_9974	1220000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Bryobacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0006955_7049_8248	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6087800.00	3693600.00	3668537.18	1628000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thiopaurus DSM 505
Ga0586324_0007242_541_4620	26332029.00	16979600.00	30394609.50	26372000.00	24771500.00	26202000.00	0.00	8893800.00	8991000.00	9963800.00	17512000.00	12508731.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0007443_6044_11257	2060000.00	1060800.00	0.00	0.00	0.00	24415500.00	0.00	5996300.00	7452000.00	0.00	0.00	14775000.00	PKD repeat protein;TIgP/CotA-like multicopper oxidase with cupredoxin domain	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324_0007494_7255_8847	0.00	958800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Rhodopseudomonas;Rhodopseudomonas palustris;Rhodopseudomonas palustris 7850. DSM 127
Ga0586324_0007536_9285_10085	0.00	0.00	0.00	0.00	0.00	5161000.00	0.00	4111400.00	0.00	0.00	0.00	0.00	enoyl-CoA hydratase/carnithine racemase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21,Smithella sp. F21
Ga0586324_0007575_1989_9734	0.00	2461600.00	0.00	710547.75	1380200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Balneolia;Balneolales;Balneolaceae;Gracilimonas;Gracilimonas mengyeensis DSM 21985
Ga0586324_0007617_6088_9705	9470000.00	5984000.00	15898489.44	19693500.00	0.00	12111918.17	1757574.48	0.00	492995.97	3749900.00	1962400.00	8655000.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0007623_8657_10624	2610000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase/Pyruvate/2-oxoacid:ferr	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0007763_9990_11060	96410000.00	129914000.00	1139450.07	57669487.80	740577000.00	3156959.88	94392000.00	72211800.00	15946775.60	40053476.54	73664800.00	8527500.00	uredicted porin	Bacteria;Acidobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skb26
Ga0586324_0007801_7031_8065	6190000.00	8908000.00	6981200.00	5168000.00	0.00	0.00	0.00	0.00	0.00	4173400.00	3115200.00	5010000.00	hypothetical protein	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Candidatus Nitrospira inopinata;Candidatus Nitrospira inopinata ENR4
Ga0586324_0007825_9691_10887	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	256275.09	0.00	0.00	1896031.50	DNA-binding beta-propeller fold protein YncE	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Immirania;Immirania thermothiophila;Immirania thermothiophila DSM 100275
Ga0586324_0007884_8826_9149	2970000.00	0.00	0.00	0.00	0.00	0.00	0.00	3214700.00	0.00	0.00	1504800.00	0.00	transcriptional regulator with XRE family HTH domain	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria protobacterium L13;beta proteobacterium L13
Ga0586324_0007889_7006_9561	0.00	1162800.00	0.00	0.00	0.00	0.00	1155647.15	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0007921_363_4004	0.00	629130.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Balneolaeota;Balneolia;Balneolales;Balneolaceae;Gracilimonas;Gracilimonas tropica;Gracilimonas tropica DSM 19535
Ga0586324_0007959_2226_4229	2290000.00	0.00	0.00	0.00	0.00	0.00	0.00	1213900.00	1263600.00	0.00	28668800.00	715947.75	ABC-type transport system substrate-binding protein	Bacteria;Chlorobi;Ancalomicrobia;Ancalomicrobiales;Ancalomicraceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324_0007994_3903_5003	8950000.00	11424000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7650000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. LTSP885;Bradyrhizobium sp. LTSP885
Ga0586324_0008126_5651_8932	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15997500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_0008226_3061_4953	2960000.00	6140400.00	1229687.71	3277500.00	6262400.00	0.00	0.00	646600.00	4471200.00	2695000.00	0.00	990000.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Eubacteriales Family XI. Incertae Sedis;Acidaminobacter;Acidaminobacter hydrogenoformans;Acidaminobacter hydrogenoformans DSM 2784
Ga0586324_0008231_2552_2866	0.00	0.00	0.00	0.00	5108800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	sugar (pentulose or hexulose) kinase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Deuftaricola;Deuftaricola sp. WP8;Burkholderiales sp. WP8;Burkholderiales sp. WP8
Ga0586324_0008387_6422_8893	0.00	0.00	0.00	0.00	1596500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	type IV pilus secretin PilQ/predicted competence protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-K07;Aminicenantes bacterium SCGC AAA252-K07 (contamination screened)
Ga0586324_0008773_1_608	0.00	3488400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Bacteroidetes;Bacteroidia;Porphyromonadales;Porphyromonadaceae;Microbacter;Microbacter marguliseae;Microbacter marguliseae DSM 27471
Ga0586324_0008898_1_10791	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	157896.00	hypothetical protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Nostocales;Nostocaceae;Nostoc;Nostoc sp. PCC 7524;Nostoc sp. PCC 7524
Ga0586324_0009038_3948_4610	0.00	0.00	0.00	2014000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Aliflexiaceae;Aliflexia;Aliflexia marina;Aliflexia marina DSM 2698
Ga0586324_0009076_4828_6243	0.00	0.00	0.00	0.00	0.00	0.00	2986800.00	1055300.00	0.00	0.00	0.00	2340000.00	glutamine synthetase type I	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Ruaroibacter;Ruaroibacter aromaticivorans;Ruaroibacter aromaticivorans PG1-Cab
Ga0586324_0009115_3012_4133	0.00	0.00	0.00	0.00	0.00	23026000.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0009115_4198_8118	5140000.00	5752800.00	6354772.42	3448500.00	4954300.00	5002200.00	1344082.80	6893000.00	5346000.00	5698000.00	7312800.00	5010000.00	hypothetical protein	Bacteria;Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;Marinimicrobia bacterium JGI 0000059-D20;Marinimicrobia bacterium JGI 0000059-D20 (contamination screened)
Ga0586324_0009115_8197_10617	8280000.00	11634800.00	0.00	11580500.00	11556600.00	5768799.06	1448969.64	9747800.00	7848900.00	22484000.00	13754400.00	15337500.00	hypothetical protein	Bacteria;Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;Marinimicrobia bacterium SCGC AAA257-N23;Marinimicrobia bacterium SCGC AAA257-N23 (contamination screened)
Ga0586324_0009134_7979_10024	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1417500.00	0.00	0.00	0.00	alkyl sulfatase B0351-like metallo-beta-lactamase superfamily hydrolase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia sp. WP8;Burkholderia sp. WP8;Burkholderia sp. WP8
Ga0586324_0009137_61_6249	6890000.00	0.00	0.00	4911500.00	0.00	0.00	0.00	2372900.00	0.00	0.00	5693600.00	0.00	uncharacterized repeat protein (TIGR01451 family)	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Cellulomonadaceae;Cellulomonas;Cellulomonas sp. KRMCY2;Cellulomonas sp. KRMCY2
Ga0586324_0009386_2_3211	0.00	656281.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	DNA-directed RNA polymerase beta' subunit	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio sp. N1;Thermodesulfovibrio sp. N1
Ga0586324_0009412_4878_6146	7630000.00	11050000.00	0.00	0.00	0.00	1401410.00	4058400.00	1451800.00	1825740.00	0.00	0.00	7500000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Laribacter;Laribacter hongkongensis;Laribacter hongkongensis HLH9
Ga0586324_0009413_3602_4123	4590000.00	8160000.00	8895400.00	18895500.00	23102900.00	22721092.09	13383600.00	11400900.00	8667000.00	0.00	0.00	0.00	uncharacterized membrane protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanoculleus;Methanoculleus thermophilus;Methanoculleus thermophilus DSM 2373
Ga0586324_0009414_4066_4740	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8601000.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0009578_1958_3229	0.00	1496000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10857000.00	0.00	0.00	hypothetical protein	
Ga0586324_0009598_6294_7604	0.00	0.00	0.00	0.00	0.00	0.00	0.00	308439.18	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomonadales;Hyphomonadaceae;Hyphomonas;Hyphomonas oceanitis;Hyphomonas oceanitis SCHB9
Ga0586324_0009663_9145_9996	0.00	1462000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	glyoxylase-like metal-dependent hydrolase (beta-lactamase superfamily II)	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Sporobacter;Sporobacter termitidis;Sporobacter termitidis DSM 10068
Ga0586324_0009727_3523_6897	1390000.00	1353200.00	5555498.21	4265500.00	6590735.16	8535500.00	0.00	7747000.00	2219400.00	954331.84	3199978.32	8820000.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidipila;Acidipila rosea;Acidipila rosea 103428
Ga0586324_0009852_1464_4643	39770000.00	27251647.36	8601919.36	21753000.00	0.00	4287500.00	0.00	2019100.00	8675000.00	8404998.91	10218000.00	10710000.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanospirillaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris 7850. DSM 127
Ga0586324_0009912_6735_10136	156287.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2100000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96. DSM 24297
Ga0586324_0009914_8347_10230	2260000.00	4216000.00	0.00	556743.70	2544100.00	2589811.10	0.00	342320.41	1812170.88	3257100.00	1258400.00	420608.25	hypothetical protein	
Ga0586324_0009916_1491_2981	4560000.00	4175200.00	4138950.80	3524500.00	4017000.00	3683691.54	0.00	2452200.00	2025000.00	3703700.00	3174800.00	2482500.00	hypothetical protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daveensis;Thermanaerothrix daveensis GNS-1
Ga0586324_0010330_4361_5446	0.00	10744000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	glyoxylase-like metal-dependent hydrolase (beta-lactamase superfamily II)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Azospirillaceae;Skermanella;Skermanella aerolata;Skermanella aerolata KACC 11604
Ga0586324_0010422_4741_7902	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9600000.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-D06;Aminicenantes bacterium SCGC AAA252-D06 (contamination screened)
Ga0586324_0010815_3544_6528	0.00	1706800.00	0.00	0.00	1565600.00	0.00	0.00	0.00	0.00	6360200.00	11176000.00	3540000.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA255-E10 (contamination screened)
Ga0586324_0010840_8516_9841	0.00	0.00	0.00	0.00	5304500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methylologella;Methylologella halotolerans;Methylologella halotolerans VKM B-2706
Ga0586324_0010969_4423_5859	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1183400.00	0.00	6814500.00	5693600.00	0.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Vitreoscilla;Vitreoscilla massiliensis;Vitreoscilla massiliensis SN6
Ga0586324_0011052_4826_7567	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1196800.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0011197_2431_3573	13440000.00	11689200.00	0.00	9205500.00	19570000.00	25481278.26	482562000.00	11291100.00	339633000.00	52976000.00	54621600.00	42075000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaurus;Thiobacillus thiopaurus DSM 505
Ga0586324_0011240_4940_6322	0.00	0.00	0.00	0.00	0.00	1225700.00	0.00	0.00	54567.06	999712.82	0.00	0.00	114553.50	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0011240_6951_8432	38420000.00	20400000.00	0.00	0.00	5434000.00	2657400.00	0.00	16666800.00	4653800.00	14317200.00	5035800.00	3520000.00	12150000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0011286_2842_7263	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4242700.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0011356_4026_5270	9450000.00	4671600.00	0.00	1833500.00	5005800.00	2460224.88	8413200.00	4971500.00	5046300.00	3642100.00	3484800.00	2820000.00	hypothetical protein	
Ga0586324_0011422_2114_5107	0.00	0.00	0.00	0.00	0.00	0.00	603636.84	0.00	1004400.00	640060.96	776673.92	185211.00	outer membrane receptor protein involved in Fe transport	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_0011505_7233_8135	0.00	0.00	0.00	0.00	2636800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptostreptococcaceae;Dethiobacter;Dethiobacter alkaliphilus;Dethiobacter alkaliphilus AHT1
Ga0586324_0011667_5513_6070	0.00	0.00	0.00	7001500.00	0.00	6868100.00	0.00	0.00	1863000.00	0.00	0.00	0.00	phasin family protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Paucibacter;Paucibacter sp. KCTC 42545;Paucibacter sp. KCTC 42545
Ga0586324_0011695_4595_7915	0.00	4195600.00	0.00	7467000.00	0.00	0.00	0.00	0.00	0.00	0.00	4963200.00	3637500.00	uncharacterized repeat protein (TIGR01451 family)	Bacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Humibacillus;Humibacillus santhopaliidus;Humibacillus santhopaliidus SLBN-155
Ga0586324_0011751_13_438	0.00	1870000.00	0.00	5082500.00	6046100.00	0.00	2302800.00	4753900.00	3977100.00	0.00	0.00	0.00	rubrerythrin	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Candidatus Nitrospira nitrificans;Candidatus Nitrospira nitrificans COMA2
Ga0586324_0012010_6951_8129	0.00	897600.00	0.00	0.00	0.00	6921600.00	0.00	0.00	1652400.00	0.00	0.00	2025000.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. YR216;Variovorax sp. YR216
Ga0586324_0012254_789_5090	43260000.00	58350800.00	27530700.00	32167000.00	36441400.00	40347173.52	20013267.04	21441500.00	17876700.00	33949300.00	34971200.00	31297500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0012267_3349_7344	0.00	0.00	0.00	0.00	0.00	893024.42	0.00	0.00	603912.51	0.00	0.00	0.00	hypothetical protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Chroococcales;Microcystaceae;Microcystis;Microcystis aeruginosa;Microcystis aeruginosa PCC 7806
Ga0586324_0012331_395_1750	10390000.00	7956000.00	7713100.00	8113000.00	7292400.00	7756379.56	13087200.00	6161000.00	10538100.00	12304600.00	13807200.00	15405000.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0012870_1488_8417	0.00	2318800.00	1788037.33	0.00	0.00	730261.65	3784800.00	683200.00	1166400.00	0.00	0.00	1417500.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_0012922_7744_9015	3830000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum OWC-G53F
Ga0586324_0012993_7805_9064	36200000.00	5181600.00	0.00	0.00	0.00	0.00	0.00	0.00	3126600.00	0.00	0.00	4882500.00	uredicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax koniaci;Acidovorax koniaci S00067
Ga0586324_0013020_372_3521	2850000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TonB-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Fulvivirgaceae;Ohtaekwangia;Ohtaekwangia kribbensis;Ohtaekwangia kribbensis DSM 25221
Ga0586324_0013101_1521_3026	20950000.00	16367000.00	12276687.92	14582500.00	20909000.00	12580861.51	19020999.48	16244300.00	16540000.00	15569400.00	15200248.80	13614717.75	hypothetical protein	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Schleiferiaceae;Schleiferia;Schleiferia thermophila;Schleiferia thermophila Yellowstone
Ga0586324_0013203_943_3516	0.00	5521600.00	10471800.00	4436500.00	2049700.00	3700333.78	11719200.00	4148000.00	4754700.00	7238000.00	623284.64	5962500.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_0013213_7270_8994	0.00	1604800.00	0.00	0.00	0.00	0.00	0.00	0.00	1198800.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Ideonella;Ideonella sp. A 288;Ideonella sp. A 288
Ga0586324_0013231_5069_6484	0.00	7004000.00	89517000.00	75525000.00	122261000.00	129025000.00	179664000.00	62281000.00	118503000.00	115654000.00	129976000.00	78000000.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22

Ga0586324_0021502_2_1714	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	472449.67	0.00	1147500.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter metallireducens RCH3
Ga0586324_0021508_321_1382	2370000.00	0.00	0.00	0.00	0.00	0.00	0.00	1344600.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0021655_2374_3504	69200000.00	178432000.00	55699552.19	127175927.15	143262700.00	190795321.75	46192800.00	142740000.00	134427600.00	110464200.00	96008000.00	145977432.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0021726_2665_4053	6880000.00	0.00	0.00	1525865.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1522500.00	0.00	glucose/arabinose dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS401
Ga0586324_0021868_5645_7129	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1169738.01	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0021876_1316_2569	0.00	0.00	0.00	0.00	465260.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324_0021909_913_5412	1130000.00	0.00	0.00	0.00	0.00	0.00	366422.12	0.00	0.00	0.00	0.00	0.00	0.00	heterodisulfide reductase subunit A-like polyferredoxin	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter curvatus;Desulfobacter curvatus DSM 3379
Ga0586324_0022034_517_1797	0.00	0.00	0.00	0.00	0.00	0.00	291879.45	0.00	0.00	450589.94	227520.75	0.00	0.00	sugar lactone lactonase YvrE	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Leptothrix;Leptothrix cholodnii;Leptothrix cholodnii SP-6
Ga0586324_0022044_4845_7106	0.00	0.00	0.00	0.00	0.00	0.00	326350.00	0.00	1994300.00	2288000.00	2685000.00	0.00	0.00	subtilisin family serine protease	Bacteria;Actinobacteria;Actinomycetia;Kineosporiales;Kineosporiaceae;Kineosporia;Kineosporia sp. A 224;Kineosporia sp. A 224 A 224
Ga0586324_0022155_3546_4643	13170000.00	5412800.00	0.00	0.00	0.00	0.00	0.00	5459400.00	0.00	0.00	0.00	0.00	0.00	kenurenine formamidase	Bacteria;Proteobacteria;Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;alpha proteobacterium BAL199;Nisaea sp BAL199
Ga0586324_0022415_1748_5260	0.00	0.00	0.00	3087500.00	5160300.00	0.00	0.00	0.00	0.00	2279200.00	2684000.00	1155000.00	0.00	2_2'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Dictyoglomi;Dictyoglomia;Dictyoglomales;Dictyoglomaceae;Dictyoglomus;Dictyoglomus thermophilum;Dictyoglomus thermophilum H-6-12, ATCC 35947
Ga0586324_0022451_4045_6513	0.00	0.00	796470.47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	Bacteria;Chloroflexi;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0022499_1831_5391	1940000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2648800.00	2167500.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0022604_5760_6515	0.00	0.00	0.00	95902.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0022634_6152_6688	0.00	0.00	0.00	0.00	0.00	0.00	0.00	354780.00	0.00	0.00	0.00	0.00	0.00	invasion protein IalB	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Kiloniellaceae;Elioraea;Elioraea tepidiphila;Elioraea tepidiphila DSM 17972
Ga0586324_0022670_5438_5746	0.00	0.00	0.00	0.00	4486100.00	0.00	6527000.00	0.00	0.00	0.00	0.00	2332500.00	0.00	chromosome segregation ATPase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_0022884_4352_4969	0.00	0.00	0.00	0.00	0.00	0.00	3775900.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized protein YgiD (DUF1641 family)	Bacteria;Proteobacteria;Betaproteobacteria;Ferrovaniales;Ferrovaceae;Ferrovum;Ferrovum myxofaciens;Ferrovum myxofaciens P3G
Ga0586324_0022884_5143_6906	14460000.00	13906000.00	15595100.00	0.00	0.00	4748667.86	5784266.52	19025900.00	8407800.00	32540200.00	20134400.00	14430000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium neotropicale;Bradyrhizobium neotropicale BR 10247
Ga0586324_0022996_3859_5166	30620000.00	27948000.00	43351000.00	33373500.00	43466000.00	38775879.28	12882000.00	41717900.00	24445800.00	20713000.00	21630400.00	14227500.00	0.00	hypothetical protein	
Ga0586324_0023006_4207_5454	17200000.00	13001600.00	0.00	0.00	22866000.00	190163300.00	0.00	9150000.00	13309000.00	12166000.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0023456_3_1310	0.00	3250400.00	0.00	0.00	0.00	146818.26	3727675.17	2416800.00	9333000.00	0.00	8932000.00	12672000.00	2272500.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta cellobiosiphila;Spirochaeta cellobiosiphila DSM 17781
Ga0586324_0023464_4819_6000	17400000.00	12920000.00	35919400.00	25032500.00	12051000.00	0.00	18194400.00	9028000.00	10926900.00	12628000.00	13288000.00	14040000.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_0023467_1395_6887	18200000.00	8989000.00	0.00	24415000.00	25368900.00	7588829.68	1535564.04	8521700.00	6763500.00	5474700.00	4954400.00	8857500.00	0.00	uncharacterized repeat protein (TIGR01451 family)	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Kribbellaceae;Kribbella;Kribbella antibiotica;Kribbella antibiotica JCM 13523
Ga0586324_0023837_2941_3822	9670000.00	7820000.00	0.00	0.00	17527500.00	14317000.00	18211759.65	0.00	12444000.00	0.00	2541000.00	11360800.00	2587500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Kiloniellaceae;Elioraea;Elioraea tepidiphila;Elioraea tepidiphila DSM 17972
Ga0586324_0024049_299_3874	0.00	0.00	0.00	0.00	4486100.00	0.00	6527000.00	0.00	0.00	0.00	0.00	2332500.00	0.00	asparate/methionine/tyrosine aminotransferase/ohosphoenolovruvate carboxylase	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Micrococcaceae;Micrococcus;Micrococcus luteus;Micrococcus luteus modasa
Ga0586324_0024377_1760_5101	42265.00	754561.32	0.00	0.00	0.00	0.00	3775900.00	0.00	85839.81	0.00	0.00	0.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Proteobacteria;Alphaproteobacteria;Acidiphilium;Acidiphilium rosea;Acidiphilium rosea DSM 10348
Ga0586324_0024787_2734_6072	8650000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0024943_2_1927	0.00	0.00	0.00	0.00	2204200.00	2730022.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0024975_3742_6693	0.00	2611200.00	0.00	62937500.00	0.00	199404.76	0.00	0.00	1300715.01	415621.36	0.00	499847.25	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0025111_1244_1675	8340000.00	10404000.00	0.00	6981200.00	4683500.00	0.00	29616200.00	0.00	0.00	4111800.00	0.00	0.00	0.00	nucleotide-binding universal stress UsoA family protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0025540_3648_4586	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1297500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0025573_2834_3958	44240000.00	26506400.00	2784265.83	0.00	0.00	3888908.78	0.00	8289900.00	11097000.00	17671500.00	68886400.00	29670000.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_0025726_311_4308	10069770.00	15184400.00	7769400.00	0.00	1545000.00	7047341.53	9154569.36	7100400.00	7111800.00	7584500.00	4470400.00	2047500.00	0.00	2_2'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillales;Fusmicrobia;Evosmicrobia;Evosmicrobia;Bacillus;Bacillus cellulolyticus;Bacillus cellulolyticus N-4, DSM 2522
Ga0586324_0025747_4437_6593	0.00	1054000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324_0025821_2611_3909	0.00	2936467.12	2812111.81	969000.00	3460800.00	0.00	0.00	1303305.87	1896520.23	2094400.00	4871942.24	1380000.00	0.00	hypothetical protein	Bacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324_0025828_4188_5327	0.00	0.00	0.00	1567500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HAS
Ga0586324_0026342_2961_4055	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1108800.00	0.00	0.00	regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0026398_2_553	0.00	5222400.00	0.00	0.00	6509600.00	7582700.00	4696800.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0026424_36_2960	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	315000.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album MarS9-16, JCM 16511
Ga0586324_0026483_1174_3912	0.00	2679200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1297500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_0027370_4062_6404	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1590000.00	0.00	OmcA/MtrC family decaheme c-type cytochrome	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324_0027544_1431_3806	0.00	1285200.00	0.00	3990000.00	1493500.00	0.00	0.00	1453800.00	1142100.00	3449600.00	1566400.00	6075000.00	0.00	type IV pilus secretin PilQ/predicted competence protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-K07;Aminicenantes bacterium SCGC AAA252-K07 (contamination screened)
Ga0586324_0027645_1_1182	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2939200.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0027689_169_6369	1550000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1762500.00	0.00	hypothetical protein	
Ga0586324_0027862_3590_6352	0.00	0.00	0.00	1558000.00	16140100.00	9091300.00	8527200.00	12261000.00	14158800.00	8008000.00	11176000.00	8265000.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0027963_4529_6044	1250000.00	6936000.00	413648.49	0.00	0.00	0.00	0.00	0.00	0.00	1401400.00	0.00	975000.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Saccharicrinis;Saccharicrinis fermentans;Saccharicrinis fermentans DSM 9555
Ga0586324_0028166_352_3459	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1213900.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-A06;Aminicenantes bacterium SCGC AAA255-A06 (contamination screened)
Ga0586324_0028653_4108_5142	0.00	0.00	0.00	690254.80	0.00	0.00	0.00	0.00	0.00	2009700.00	2340800.00	1665000.00	0.00	pyruvate/2-oxoacid ferredoxin oxidoreductase beta subunit	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Moorella;Moorella thermoautotrophica;Moorella thermoautotrophica JW701/3
Ga0586324_0028896_36_2387	0.00	0.00	0.00	1149500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0029060_3771_6221	2660000.00	2040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized repeat protein (TIGR01451 family)	Bacteria;Firmicutes;Clostridia;Halanaerobiales;unclassified Halanaerobiales;Anaerobacter;Anaerobacter fermentans;Anaerobacter fermentans DY22613
Ga0586324_0029102_5068_6219	0.00	0.00	0.00	0.00	0.00	4058400.00	0.00	2000700.00	0.00	0.00	0.00	0.00	0.00	crotonobetaityl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_0029235_5976_6206	39600000.00	34748000.00	70375000.00	23940000.00	31003000.00	58750000.00	0.00	15147000.00	15323000.00	13990000.00	19050000.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0029392_2662_5253	0.00	1108400.00	0.00	9139000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11512500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiogranum;Thiogranum longum;Thiogranum longum DSM 19610
Ga0586324_0029427_2888_4132	84800000.00	63172000.00	24428558.74	28215000.00	51088000.00	19858547.41	52440000.00	46360000.00	36053100.00	326795700.00	181700000.00	319095000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Legionella;Legionella cherrii;Legionella cherrii ORW
Ga0586324_0029649_5408_6166	364719.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	alpha-tubulin suppressor-like RCC1 family protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfobulbaceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324_0029905_1990_2730	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2664900.00	3041500.00	2340800.00	0.00	0.00	0.00	biopolymer transport protein ExbB/TolQ	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae;Acidobacteriaceae bacterium URHE0068;Acidobacteriaceae bacterium URHE0068
Ga0586324_0029992_447_2147	1490000.00	0.00	0.00	457811.65	0.00	0.00	0.00	0.00	0.00	9394000.00	6397600.00	5835000.00	0.00	hypothetical protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Chroococcales;Microcystaceae;Microcystis;Microcystis aeruginosa;Microcystis aeruginosa CHAOHU 1326
Ga0586324_0030041_3167_5146	144732.00	0.00	0.00	2489000.00	782917.42	0.00	1611177.96	2305800.00	1271700.00	0.00	0.00	0.00	0.00	ABC-type transport system substrate-binding protein	Bacteria;Chloroflexi;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0030050_2968_6126	22232140.00	2475200.00	3184271.70	1225500.00	988032.65	5900900.81	513389.88	598823.58	656737.47	3072300.00	1504800.00	2700000.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidisarcina;Acidisarcina polymorpha;Acidisarcina polymorpha SBC82
Ga0586324_0030083_422_4954	1290000.00	3542800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1065000.00	0.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sophorae;Paenibacillus sophorae S27
Ga0586324_0030236_3032_6109	315653.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0030270_4092_5900	0.00	3284400.00	0.00	0.00	10815000.00	0.00	12198000.00	8296000.00	0.00	0.00	0.00	2407500.00	0.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album MarS9-16, JCM 16511
Ga0586324_0030410_1003_5457	184534.00	6954296.76	6193000.00	488195.50	543390.92	18301700.00	0.00	0.00	3888000.00	0.00	11113615.92	0.00	0.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sophorae;Paenibacillus sophorae S27
Ga0586324_0030502_5331_6083	7850000.00	3957600.00	0.00	0.00	0.00	9647100.00	8914800.00	1714100.00	1215000.00	13706000.00	4241600.00	15450000.00	0.00	hypothetical protein	
Ga0586324_0030703_1937_3079	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3950100.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_0030709_3_3290	14150000.00	1638800.00	0.00	0.00	0.00	2343963.43	2019733.44	2116700.00	0.00	2787400.00	1786400.00	0.00	0.00	uncharacterized repeat protein (TIGR01451 family)	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified Myxococcales;Minicystis;Minicystis rosea;Minicystis rosea DSM 24000
Ga0586324_0031100_3_1964	1200000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0031205_3660_5375	0.00	1101600.00	0.00	0.00	10269100.00	0.00	1293498.72	1293498.72	5935300.00	0.00	2209900.00	1934000.00	2505000.00	tetratricopeptide (TPR) repeat protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Saccharicrinis;Saccharicrinis fermentans;Saccharicrinis fermentans DSM 9555
Ga0586324_0031316_1685_3109	5180000.00	8663200.00	14703189.77	14627994.55	27459800.00	17297182.81	29457660.00	14670500.00	20177100.00	16901500.00	5940000.00	15532500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter metallireducens;Geobacter metallireducens GS-15
Ga0586324_0031445_3_5294	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6699000.00	703532.72	4275000.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Cellulomonadaceae;Cellulomonas;Cellulomonas sp. KRMCY2;Cellulomonas sp. KRMCY2
Ga0586324_0031491_4593_5990	85912819.00	67347200.00	17899441.69	6094149.10	112290600.00	172337700.00	64638000.00	6134958.45	6541521.70	113028300.00	38605600.00	253027500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus DSM 10141
Ga0586324_0031701_3_5972	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	496785.52	0.00	0.00	GAF domain-containing protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. OAE829;Bradyrhizobium sp. OAE829 (Illumina draft)
Ga0586324_0031775_3_3590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3172000.00	0.00	0.00	0.00	0.00	0.00	glutamate synthase domain-containing protein 2/glutamate synthase domain-containing protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Chroococcales;Geminocystaceae;Cyanobacterium;Cyanobacterium aponinum;Cyanobacterium aponinum PCC 10605
Ga0586324_0031929_1954_5085	0.00	0.00	1214706.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	photosystem II stability/assembly factor-like uncharacterized protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0032060_4631_5938	0.00	0.00	0.00	0.00	0.00	0.00	1500600.00	0.00	0.00	2610300.00	583113.52	4492500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thioparus;Thiobacillus thioparus DSM 505
Ga0586324_0032066_4435_4671	0.00	8840000.00	9627300.00	0.00	0.00	0.00	15363900.00	0.00	0.00	7338100.00	8157600.00	5947500.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0032077_3693_5249	0.00	0.00	0.00	0.00	0.00	0.00	2044505.64	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Fulviviragaceae;Ohtaekwangia;Ohtaekwangia koreensis;Ohtaekwangia koreensis DSM 25262
Ga0586324_0032077_500_3670	2140000.00	3597200.00	9598553.22	4503000.00	12751400.00	26151600.85	11468400.00	9760000.00	4301100.00	2664200.00	7339200.00	3772500.00	0.00	TonB-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Fulviviragaceae;Chryseolinea;Chryseolinea flava;Chryseolinea flava SDU1-6
Ga0586324_0032510_4768_5898	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	488976.75	0.00	hypothetical protein	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;unclassified Rhodothermaceae;Rhodothermaceae bacterium RA;Halothermothamnus malaysiensis RA

Ga0586324_0045173_1262_4975	49100000.00	9404400.00	2205499.58	1083000.00	1411100.00	0.00	0.00	383369.75	5645700.00	22530200.00	2552000.00	27912854.25	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Acidobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Intrasporangium;Intrasporangium oryzae;Intrasporangium oryzae NRRL B-24470
Ga0586324_0045345_3419_5014	0.00	10200000.00	0.00	9443000.00	0.00	0.00	0.00	0.00	0.00	0.00	8738400.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidisarcina;Acidisarcina polymorpha;Acidisarcina polymorpha SBC82
Ga0586324_0045456_283_2805	0.00	788800.00	690609.58	0.00	907655.57	0.00	0.00	0.00	0.00	0.00	0.00	1297500.00	hypothetical protein	Bacteria;Proteobacteria;Oligoflexia;Bacteriovoracales;Bacteriovoracaceae;Bacteriovorax;Bacteriovorax sp. DB6_IX;Bacteriovorax sp. DB6_IX
Ga0586324_0046036_1485_4556	6143511.00	17217600.00	10266896.15	8768500.00	10176400.00	6669600.00	3556800.00	3239100.00	4552200.00	5197500.00	7233600.00	16132500.00	outer membrane receptor protein involved in Fe transport	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album MarS9-16, JCM 16511
Ga0586324_0046036_2_1420	0.00	0.00	0.00	0.00	0.00	0.00	0.00	322578.37	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0046204_1707_4967	0.00	0.00	0.00	0.00	563410.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0046671_1877_4678	0.00	3094000.00	6981200.00	4085000.00	6973100.00	5200700.00	9758400.00	5368000.00	4832900.00	6652800.00	6397600.00	5182500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0047029_3972_4511	0.00	0.00	0.00	1358500.00	0.00	0.00	0.00	493050.80	1093500.00	1686300.00	0.00	729176.25	hypothetical protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Leuliniea;Leuliniea saccharolytica;Leuliniea saccharolytica DSM 16555
Ga0586324_0047121_4197_4919	1190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	nucleoid-associated protein YgaU	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0047138_387_2354	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4797100.00	0.00	18675000.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase/Pyruvate/2-oxoacid ferr	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0047545_3_2142	450465.00	357969.00	971721.11	586150.00	6344800.00	870267.67	1538605.56	2982900.00	1692900.00	1932700.00	3379200.00	3637500.00	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Dermabacteraceae;Dermabacter;Dermabacter hodgkinii sp. Y123;Dermabacter hodgkinii sp. Y123
Ga0586324_0047604_3_2105	530030.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0047748_1104_2624	0.00	0.00	0.00	0.00	4233300.00	0.00	0.00	2482700.00	3029400.00	0.00	0.00	1402500.00	acyl-CoA hydrolase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0047828_2044_3390	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	379071.75	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micromonosporales;Micromonosporaceae;Micromonospora;Micromonospora echinospora ATCC 15837
Ga0586324_0047906_1_1938	0.00	8092000.00	0.00	0.00	0.00	0.00	0.00	359402.24	2988900.00	0.00	0.00	2497500.00	hypothetical protein	
Ga0586324_0047997_2836_4176	1550000.00	7330400.00	3552051.45	14231000.00	4356900.00	4406700.00	5677200.00	6002400.00	12798000.00	2294600.00	3150400.00	8190000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Pigmentiphaga;Pigmentiphaga kullae;Pigmentiphaga kullae DSM 13608
Ga0586324_0048155_134_3583	7910000.00	8044400.00	1417977.43	1987457.00	2791300.00	10079753.53	5090834.16	4965400.00	4673700.00	3434200.00	0.00	3697500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium allauci;Acidobacterium allauci PMM82
Ga0586324_0048211_82_1383	0.00	6086000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	YVTN family beta-propeller protein	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sapporoensis;Candidatus Brocadia sapporoensis 40
Ga0586324_0048534_1079_4405	0.00	1237600.00	0.00	5871000.00	0.00	0.00	0.00	0.00	0.00	0.00	836498.96	765000.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0048561_1380_4832	12570000.00	7820000.00	0.00	14839000.00	11433000.00	9105341.89	0.00	5825500.00	5880600.00	8393000.00	10120000.00	6660000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium;unclassified Acidobacterium;Acidobacterium sp. strain C40
Ga0586324_0048631_3432_4844	16700000.00	0.00	5586012.81	1985500.00	2379300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Saccharicrinis;Saccharicrinis fermentans;Saccharicrinis fermentans DSM 9555
Ga0586324_0048799_479_3190	0.00	1475600.00	0.00	0.00	0.00	0.00	0.00	1814400.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0048918_3566_4828	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2302500.00	predicted ribosome quality control (RQC) complex YloA/Tae2 family protein	Archaea;Candidatus Thermoplasmatota;Thermoplasmata;Methanomassiliicoccales;Methanomassiliicoccaceae;Methanomassiliicoccus;Methanomassiliicoccus luminyensis;Methanomassiliicoccus luminyensis B10
Ga0586324_0048934_209_1399	0.00	3706000.00	0.00	0.00	0.00	0.00	0.00	4628400.00	3830800.00	923400.00	8932000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter postgatei;Desulfobacter postgatei 2ac9
Ga0586324_0049121_1294_2622	2370000.00	0.00	3879024.96	2593500.00	0.00	1235229.77	0.00	5734000.00	1526364.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0049539_2199_3209	0.00	7820000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta lutea;Spirochaeta lutea JC230
Ga0586324_0049606_3264_4799	0.00	1856400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0049708_651_3590	0.00	1496000.00	0.00	0.00	0.00	3510944.93	0.00	0.00	0.00	0.00	0.00	0.00	outer membrane receptor for ferrienterochelin and colicin	Bacteria;Acidobacteria;Holophagae;Holophagales;Holophagaceae;Geothrix;Geothrix fermentans;Geothrix fermentans DSM 14018
Ga0586324_0050390_3_2897	0.00	0.00	0.00	1833500.00	0.00	0.00	0.00	0.00	0.00	1196800.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324_0050395_3990_4763	0.00	1088000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized coiled-coil DUF342 family protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0050501_1042_2631	0.00	8636000.00	0.00	10260000.00	11021000.00	7423900.00	5745600.00	4642100.00	0.00	0.00	4752000.00	4852500.00	glutamate synthase domain-containing protein 2	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Family III. Incertae Sedis;Caldicellulosiruptor;Caldicellulosiruptor saccharolyticus;Caldicellulosiruptor saccharolyticus DSM 8903
Ga0586324_0050544_2812_4344	2190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia sp. Y123;Burkholderia sp. Y123
Ga0586324_0050751_2887_4539	7770000.00	9894000.00	19142000.00	14725000.00	17716000.00	19413300.00	7683600.00	10553000.00	11988000.00	28721000.00	20706400.00	27660703.50	ABC-type oligopeptide transport system substrate-binding subunit	Bacteria;Proteobacteria;Betaproteobacteria;Gallionellales;Gallionellaceae;Gallella;Gallella occulta;Gallella occulta F2-223
Ga0586324_0051039_630_3815	856932.00	1808800.00	3787841.48	0.00	0.00	0.00	0.00	0.00	0.00	1601600.00	897600.00	802500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0051059_3_1988	0.00	796806.32	0.00	0.00	6206911.84	0.00	0.00	0.00	0.00	172403.64	0.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0051133_3_1140	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2165500.00	0.00	0.00	0.00	0.00	PAS domain S-box-containing protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324_0051458_1610_3097	1520000.00	10132000.00	0.00	1805000.00	0.00	0.00	0.00	2098400.00	22194000.00	15092000.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiobaca;Thiobaca trueperi;Thiobaca trueperi DSM 13587
Ga0586324_0052077_2670_4688	0.00	0.00	6136700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	dienelactone hydrolase	Bacteria;Acidobacteria;Holophagae;Holophagales;Holophagaceae;Geothrix;Geothrix fermentans;Geothrix fermentans DSM 14018
Ga0586324_0052435_2475_4670	0.00	1156000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	M6 family metalloprotease-like protein	Bacteria;Actinomycetia;Corynebacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. URHA0032;Nocardioides sp. URHA0032
Ga0586324_0052727_1802_2806	0.00	0.00	0.00	0.00	0.00	0.00	0.00	475570.44	0.00	0.00	0.00	0.00	basic membrane lipoprotein Med (substrate-binding protein (PBP1-ABC) superfamily)	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324_0052923_3_4442	8540000.00	1808800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	PKD repeat protein;FtsP/CotA-like multicopper oxidase with cupredoxin domain	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324_0053118_1941_4280	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1654400.00	0.00	DmcA/MtrC family decaheme c-type cytochrome	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfuromonas;Desulfuromonas soudanensis;Candidatus Desulfuromonas soudanensis WTL
Ga0586324_0053273_386_2056	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2986800.00	0.00	2063600.00	0.00	2242500.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Ideonella;Ideonella sp. A 288;Ideonella sp. A 288
Ga0586324_0053815_1075_2190	53090000.00	37542800.00	54676195.40	2023500.00	42693500.00	23586240.45	34004262.00	8716900.00	29970000.00	64298538.15	46184025.36	75810000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter delicatus;Curvibacter delicatus NBRC 14919
Ga0586324_0054028_362_2959	3720000.00	4012000.00	6136700.00	4427000.00	0.00	0.00	0.00	2110600.00	1611900.00	3349500.00	0.00	4290000.00	hypothetical protein	
Ga0586324_0054082_1129_2277	0.00	0.00	1903953.40	0.00	0.00	0.00	16621200.00	0.00	0.00	3080000.00	8870400.00	3150000.00	PAST-type mannitol/Chloroamoratic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Leptothrix;Leptothrix cholodnii;Leptothrix cholodnii SP-6
Ga0586324_0054502_1195_1527	1150000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter superfactus;Methyloceanibacter superfactus R-67175
Ga0586324_0054896_303_3815	20870000.00	7677200.00	7814936.81	0.00	0.00	0.00	0.00	0.00	0.00	8439748.24	0.00	9450000.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324_0054918_1307_3148	944794.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324_0055162_2084_2800	2560000.00	2101200.00	1881478.44	0.00	0.00	1580032.21	2277991.32	1262700.00	3280500.00	1578500.00	1460800.00	2265000.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_0055598_3_704	0.00	1672800.00	0.00	0.00	0.00	0.00	0.00	511891.26	0.00	0.00	0.00	1132500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0055923_3_2489	0.00	1210000.00	6756000.00	1434500.00	0.00	0.00	0.00	0.00	5744200.00	7374400.00	4675200.00	4675200.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0056218_429_914	0.00	11152000.00	0.00	0.00	0.00	0.00	0.00	4532300.00	0.00	0.00	3766400.00	0.00	ruberythrin	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0056675_3025_4134	0.00	0.00	0.00	0.00	0.00	0.00	0.00	402286.46	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroamoratic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324_0057259_9_764	0.00	59675.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	reductase of protease activity HRC (stomatin/prohibitin superfamily)	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;Dehalococcoidia Dehalococcoides;Dehalococcoides mccartyi;Dehalococcoides mccartyi strain Kalamazoo;Dehalococcoides mccartyi;Dehalococcoides sp. NSZ-14
Ga0586324_0057287_1654_4476	10660000.00	6961926.36	0.00	15618000.00	12174110.75	5240400.00	3283200.00	13755500.00	14434967.07	3780700.00	9301600.00	4230324.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0057358_1151_3748	0.00	1482400.00	2574677.82	4807000.00	2976700.00	2841043.16	0.00	2721600.00	0.00	0.00	1276000.00	3487500.00	glycolate oxidase subunit GlcD	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_0058286_2720_3268	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1276000.00	chlosomal sulphur interface protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiopaterus DSM 505
Ga0586324_0058706_1_2337	936552.00	6487200.00	0.00	1197000.00	2842800.00	0.00	0.00	0.00	3869213.67	1663200.00	0.00	3030000.00	hypothetical protein	Bacteria;Chloroflexi;Caldilineae;Caldilinchales;Caldilinchaceae;Caldilinthrix;Caldilinthrix abyssi;Caldilinthrix abyssi LF13, DSM 13497
Ga0586324_0058706_2392_4422	0.00	5188400.00	0.00	0.00	8332700.00	0.00	5973600.00	0.00	0.00	0.00	6089600.00	7185000.00	hypothetical protein	
Ga0586324_0058739_1_1710	14963159.00	8241600.00	8290647.92	10222000.00	11371200.00	24572259.42	31538800.00	29408100.00	5921100.00	4173400.00	4963200.00	6052500.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Flexithrix;Flexithrix dorotheae;Flexithrix dorotheae DSM 6795
Ga0586324_0058739_1740_3296	3600000.00	4432448.08	0.00	0.00	2080600.00	2053732.61	4468800.00	3782000.00	3118500.00	624127.35	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Dyadobacter;Dyadobacter fermentans;Dyadobacter fermentans NS114, DSM 18053
Ga0586324_0058864_3687_4418	0.00	37672000.00	83324000.00	0.00	7354200.00	0.00	4081200.00	30134000.00	26487000.00	53669000.00	10208000.00	46275000.00	ubiquitin	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0058874_589_1935	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5370300.00	0.00	0.00	ABC-type glycerol-3-phosphate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Stellaceae;Stella;Stella humosa;Stella humosa DSM 5900
Ga0586324_0059356_1446_2591	0.00	0.00	0.00	0.00	0.00	16515200.00	0.00	0.00	0.00	9801000.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Acidithiobacillales;Acidithiobacillaceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324_0060200_1866_2405	0.00	0.00	3805452.12	0.00	0.00	0.00	2713200.00	0.00	0.00	0.00	0.00	0.00	phasin family protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. CF059;Methylibium sp. CF059
Ga0586324_0060369_1798_2841	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3687200.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp13;Nitrosospira sp. Nsp13
Ga0586324_0060592_1629_3026	1320000.00	6623200.00	0.00	0.00	1060900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324_0060583_3763_4356	0.00	4902800.00	0.00	6593000.00	3296000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	glutamate synthase domain-containing protein 2	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0060696_656_2350	0.00	0.00	0.00	0.00	10124900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	outer membrane protein OmsA-like peptidoglycan-associated protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0060810_204_779	74797.71	4380000.00	0.00	0.00	4511400.00	0.00	0.00	1405100.00	0.00	1493800.00	3634400.00	0.00	ruberythrin	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanosaeta harundinacea;Methanothrix harundinacea 6Ac
Ga0586324_0061010_1_3486	2460000.00	10125200.00	4836451.50	0.00	3061957.22	519152.93	0.00	0.00	0.00	720824.72	0.00	982500.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus durus;Paenibacillus durus ATCC 35681
Ga0586324_0061682_285_3326	0.00	2040000.00	0.00	563464.95	5459000.00	4287600.00	6740165.64	3202500.00	2689200.00	3164700.00	0.00	6405000.00	hypothetical protein	Bacteria;Acidobacteria;Holophagae;Holophagales;Holophagaceae;Geothrix;Geothrix fermentans;Geothrix fermentans DSM 14018
Ga0586324_0061949_1_1542	0.00	0.00	0.00	3277200.00	0.00	0.00	1893275.52	671000.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia;Ralstonia solanacearum;Ralstonia solanacearum PSI07
Ga0586324_0062088_1447_4308	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5718600.00	0.00	0.00	0.00	0.00	diauanylate cyclase (GGDEF)-like protein/PAS domain S-box-containing protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-B84
Ga0586324_0063155_3069_4271	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1482300.00	0.00	0.00	0.00	0.00	cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfohalovibrio;Desulfohalovibrio alkaliotolerans;Desulfovibrio alkaliotolerans DSM 16529
Ga0586324_0063376_2042_3037	0.00	0.00	0.00	0.00	0.00	0.00	3853200.00	0.00	0.00	2864400.00	3634400.00	3172500.00	tripartite ATP-independent transporter DctP family solute receptor	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Sporomusaceae;Anaerosporomusa;Anaerosporomusa subterranea;Anaerosporomusa subterranea RU4
Ga0586324_0063616_1578_2948	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1208900.00	1267200.00	907500.00	hypothetical protein	
Ga0586324_0064760_3_3122	0.00	0.00	4610300.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0065262_1613_3040	0.00	13804000.00	0.00	5415000.00	0.00	0.00	0.00	22814000.00	907200.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_0065262_3040_4209	0.00	13532000.00	27755900.00	0.00	0.00	2751210.00	0.00	1334200.00	0.00	0.00	0.00	6502500.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfoloma;Desulfoloma caldarium;Desulfoloma caldarium DSM 23027
Ga0586324_0065262_76_504	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4867800.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;

Ga0586324_0081967_2945_3706	0.00	0.00	0.00	0.00	0.00	3730843.23	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sinica;Candidatus Brocadia sinica JPN1
Ga0586324_0082082_387_3716	0.00	0.00	0.00	0.00	2276300.00	0.00	0.00	1415200.00	0.00	0.00	3704800.00	3427500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0082340_525_3626	0.00	0.00	0.00	221714.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobacculia;Thermoanaerobaculales;Thermoanaerobacculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0082472_1_3267	5710000.00	0.00	0.00	5690500.00	5860700.00	0.00	0.00	0.00	0.00	2402400.00	5702400.00	5790000.00	hypothetical protein	Bacteria;Planctomycetes;Planctomycetia;Planctomycetales;Planctomycetaceae;Planctomyces;Planctomyces sp. SH-PL62;Planctomyces sp. SH-PL62
Ga0586324_0082667_1234_3045	0.00	0.00	0.00	0.00	1987900.00	0.00	1735716.12	0.00	117450000.00	0.00	0.00	0.00	formiltetrahydrofolate synthetase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfallas;Desulfallas thermosaovorans;Desulfallas thermosaovorans DSM 6562
Ga0586324_0082969_2490_3680	0.00	0.00	0.00	0.00	0.00	12566000.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0083766_1602_2849	0.00	0.00	0.00	0.00	0.00	0.00	69631200.00	22838400.00	18249300.00	20104700.00	11193600.00	20505000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Aromatoleum;Aromatoleum toluclasticum;Aromatoleum toluclasticum ATCC 700605
Ga0586324_0083793_1401_3050	0.00	0.00	0.00	5377000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	thiamine pyrophosphate-dependent acetolactate synthase large subunit-like protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Aquabacter;Aquabacter spiritensis;Aquabacter spiritensis DSM 9035
Ga0586324_0084272_1_345	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7854000.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides ginsengisegetis;Nocardioides ginsengisegetis DSM 21349
Ga0586324_0084349_1751_2110	35500000.00	38012000.00	0.00	22135000.00	12051000.00	5478600.00	8960400.00	16043000.00	0.00	48125000.00	53592000.00	16575000.00	hypothetical protein	
Ga0586324_0084810_386_3649	0.00	526184.00	0.00	0.00	1529500.00	8198800.00	0.00	0.00	0.00	831600.00	497042.48	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0085723_2432_3691	0.00	0.00	0.00	0.00	0.00	0.00	0.00	429992.05	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-D06;Aminicenantes bacterium SCGC AAA252-D06 (contamination screened)
Ga0586324_0086302_1929_3386	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	777700.00	0.00	0.00	FAD/FMN-containing dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_0086838_1825_3360	417720.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	487520.00	0.00	glycosyltarabinose dehydrogenase	Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Sphingobacteriaceae;Solitalea;Solitalea koreensis;Solitalea koreensis DSM 21342
Ga0586324_0087128_1042_2967	0.00	0.00	3504967.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodosporillales;Rhodosporillaceae;Maenetospirillum;Maenetospirillum maeneticum;Maenetospirillum maeneticum AMB-1
Ga0586324_0087478_271_3189	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1886500.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0088093_2281_3645	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1260000.00	predicted deacylase	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Marinobacter;Marinobacter lipolyticus SM19
Ga0586324_0088241_701_2422	0.00	0.00	11766700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocapsa;Thiocapsa roseopersicina DSM 217
Ga0586324_0088823_2_2737	4350000.00	4406400.00	8670200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2310000.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Micrococcaceae;Arthrobacter;Arthrobacter psychrochitiniphilus;Arthrobacter psychrochitiniphilus DSM 23143
Ga0586324_0088791_2_2473	0.00	10628400.00	0.00	9289500.00	3714500.00	13245800.00	3699825.62	5426400.00	0.00	834300.00	0.00	2993000.00	TonB-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Fexlihtvir;Flexlihtvir dorothae;Flexlihtvir dorothae DSM 6795
Ga0586324_0089812_1864_3444	1150000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	formylglycine-generating enzyme required for sulfatase activity	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So ce0747
Ga0586324_0090033_2100_2579	58100000.00	0.00	54106371.84	81481500.00	9661400.00	11347534.37	13338000.00	2110600.00	0.00	0.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0090146_2510_3604	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted CXXCH cytochrome family protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Intrasporangium;Intrasporangium calvum 7KIF; DSM 43043
Ga0586324_0090756_2405_3592	0.00	26180000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	25756500.00	19008000.00	0.00	formiltetrahydrofolate synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0090920_1742_2719	0.00	0.00	0.00	0.00	0.00	0.00	0.00	923400.00	0.00	0.00	0.00	1312500.00	alvoxylase-like metal-deoendent hydrolase (beta-lactamase superfamily II)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodosporillales;Azospirillaceae;Skermanella;Skermanella aerolata;Skermanella aerolata KACC 11604
Ga0586324_0091051_3_1430	0.00	14892000.00	0.00	0.00	106090000.00	5796200.00	0.00	12566000.00	14254000.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_0091085_718_1854	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	219371.25	173786.31	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum;Desulfotignum balticum;Desulfotignum balticum DSM 7044
Ga0586324_0091828_2_3433	27990000.00	10404000.00	0.00	7296000.00	17242200.00	0.00	0.00	3153700.00	6042600.00	3826900.00	7788000.00	5842500.00	PtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thioploca;Thioploca ingrica;Thioploca ingrica Lake Okotanpe
Ga0586324_0091861_2534_2917	5020000.00	0.00	0.00	0.00	0.00	0.00	2918400.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis parvus OBBP
Ga0586324_0091992_2884_3570	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8085000.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	Bacteria;Actinobacteria;Actinomycetia;Corynebacteriales;Nocardioidaceae;Nocardioides;Nocardioides einsneiensis;Nocardioides einsneiensis DSM 21349
Ga0586324_0092138_3_2045	0.00	0.00	0.00	4370000.00	1184500.00	0.00	0.00	0.00	536104.98	0.00	0.00	0.00	beta-glucosidase-like glycosyl hydrolase	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia sp. Leaf177;Burkholderia sp. Leaf177
Ga0586324_0092762_2504_3556	0.00	1679600.00	0.00	4579000.00	0.00	0.00	0.00	4007700.00	0.00	0.00	0.00	4042500.00	hypothetical protein	
Ga0586324_0092816_2093_3229	7990000.00	0.00	0.00	0.00	66744000.00	0.00	0.00	0.00	93410.82	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum;Desulfotignum balticum;Desulfotignum balticum DSM 7044
Ga0586324_0092818_1340_3556	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2602600.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0093298_2296_2808	0.00	0.00	0.00	0.00	2626500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized membrane protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylococcus;Methylococcus capsulatus;Methylococcus capsulatus Bath
Ga0586324_0094423_1_2133	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	387095.94	0.00	0.00	DNA-directed RNA polymerase beta subunit	Bacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324_0095103_931_2139	0.00	0.00	0.00	0.00	0.00	0.00	2140598.52	1988600.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. M18;Geobacter sp. M18
Ga0586324_0095116_763_1785	0.00	0.00	0.00	0.00	0.00	0.00	0.00	435370.95	0.00	0.00	0.00	0.00	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. OAE819;Bradyrhizobium sp. OAE819
Ga0586324_0095441_2_436	0.00	0.00	0.00	0.00	0.00	0.00	0.00	40257000.00	0.00	0.00	0.00	0.00	predicted porin	
Ga0586324_0095441_834_2075	25460000.00	2441200.00	0.00	0.00	0.00	0.00	29412000.00	0.00	15835500.00	4920300.00	20988000.00	11925000.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Ectothiorhodosspira;Ectothiorhodosspira mobilis;Ectothiorhodosspira marismortui DSM 4180
Ga0586324_0095579_2345_2614	0.00	0.00	4039136.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	nucleoid DNA-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulforegula;Desulforegula conservatrix;Desulforegula conservatrix Mb1Pa
Ga0586324_0095595_600_1925	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	36825000.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium URHE0068;Acidobacteriaceae bacterium URHE0068
Ga0586324_0095730_2941_3501	0.00	1951600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta cellobiosiphila;Spirochaeta cellobiosiphila DSM 17781
Ga0586324_0095754_2843_3502	0.00	3202800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324_0095806_328_3069	0.00	0.00	3938156.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0095876_178_1542	0.00	0.00	0.00	0.00	739287.65	0.00	0.00	378144.49	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_0097990_2_1045	0.00	0.00	0.00	0.00	0.00	1375069.05	0.00	0.00	2138400.00	0.00	0.00	0.00	glutamine synthetase type I	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. CP059;Methylibium sp. CP059
Ga0586324_0098011_106_1020	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18287500.00	21568800.00	10200000.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfurivellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324_0098343_1480_3456	2130000.00	8629200.00	15144700.00	0.00	2472000.00	4883100.00	0.00	8192300.00	2632500.00	3580500.00	4083200.00	0.00	MrdB/PbdB family decaheme-associated outer membrane protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfurivellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_0098864_1266_1685	0.00	0.00	0.00	0.00	1524400.00	0.00	0.00	10553000.00	0.00	0.00	0.00	0.00	rubrerythrin	Bacteria;Acidobacteria;Holophagae;Holophagales;Holophagaceae;Geothrix;Geothrix fermentans;Geothrix fermentans DSM 14018
Ga0586324_0099651_1_2661	4070000.00	12811200.00	0.00	0.00	14214000.00	3325720.61	0.00	3879600.00	646158.87	8547000.00	0.00	10672500.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidipila;Acidipila rosea;Acidipila rosea DSM 103428
Ga0586324_0099601_1379_2815	0.00	0.00	0.00	0.00	0.00	0.00	2804400.00	0.00	0.00	0.00	0.00	0.00	DNA modification methylase	Bacteria;Firmicutes;Bacilli;Lactobacillales;Aerococcaceae;Aerococcus;Aerococcus sp. Group B;Aerococcus sp. Group B
Ga0586324_0099724_336_1196	0.00	1067600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized coiled-coil DUF342 family protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0100181_112_1083	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11704000.00	17749600.00	17887500.00	molybdenum ABC transporter molybdate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Ferrovales;Ferrovaceae;Ferrovum;unclassified Ferrovum;Ferrovum sp. ZuIaaF-31
Ga0586324_0100543_2_1615	2380000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0100718_603_1058	8470000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	rubrerythrin	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobales;Methanomicrobiaceae;Methanoculleus;Methanoculleus thermophilus;Methanoculleus thermophilus DSM 2373
Ga0586324_0100814_1755_3416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4618239.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. Root122;Nocardioides sp. Root122
Ga0586324_0101138_303_3410	13540000.00	19230400.00	12199478.10	5101500.00	4492693.14	392743.76	0.00	3031700.00	0.00	5774421.73	6476800.00	6060000.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0101160_1065_3410	3180000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter lichenicola;Edaphobacter lichenicola MBUP22
Ga0586324_0101251_374_1027	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3788100.00	0.00	0.00	0.00	cuvB biogenesis system outer membrane secretion channel CuvG	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0101533_1489_2151	0.00	2271200.00	0.00	0.00	5572300.00	0.00	0.00	0.00	1854900.00	12936000.00	0.00	0.00	biopolymer transport protein ExbB/TolQ	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0102127_201_3395	0.00	4610400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	beta-glucosidase-like glycosyl hydrolase	Bacteria;Actinobacteria;Actinomycetia;Motilibacteriales;Motilibacteraceae;Motilibacter;Motilibacter rhizosphaerae;Motilibacter rhizosphaerae DSM 45622
Ga0586324_0102186_1786_2646	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	885500.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio sp. DMSS-1;Desulfovibrio sp. DMSS-1
Ga0586324_0102227_1245_2870	160870000.00	46066211.72	119243400.00	170191016.10	70318100.00	61523292.47	619543912.08	131522100.00	123306300.00	56933800.00	114848800.00	133965000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii CCBAU 43297
Ga0586324_0102520_1_861	0.00	0.00	0.00	0.00	0.00	4565500.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0102557_3_3275	0.00	0.00	0.00	1425000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Kribbellaceae;Kribbella;Kribbella catacumbae;Kribbella catacumbae DSM 19601
Ga0586324_0103547_1548_1940	0.00	0.00	42619100.00	47120000.00	38419000.00	40097000.00	0.00	0.00	0.00	0.00	0.00	20925000.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Sedimenticola;unclassified Sedimenticola;Sedimenticola thiotaurini SIP-G1
Ga0586324_0103547_240_1460	7590000.00	8928400.00	0.00	0.00	9291000.00	20826600.00	0.00	0.00	0.00	11005681.41	13297900.00	0.00	hypothetical protein	
Ga0586324_0103787_165_1697	47100000.00	18428000.00	0.00	3059000.00	3532900.00	0.00	0.00	6405000.00	6723000.00	7546000.00	10357600.00	11475000.00	hypothetical protein	
Ga0586324_0104162_2749_3264	0.00	52972000.00	0.00	0.00	164800000.00	0.00	0.00	0.00	42687000.00	0.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0104512_2393_3358	0.00	2040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	PtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Gammaproteobacteria;Hydrogenophagales;Hydrogenophagaceae;Hydrogenophaga;Hydrogenophaga sp. PAMC20947;Hydrogenophaga sp. PAMC20947
Ga0586324_0104609_268_999	1180000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroamortic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324_0105269_713_1291	0.00	0.00	0.00	0.00	0.00	0.00	7934400.00	4276100.00	3150900.00	2887500.00	4188800.00	3765000.00	lipid-binding SYLF domain-containing protein	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Leeuwenhoekiella;Leeuwenhoekiella aequorea;Leeuwenhoekiella aequorea LMG 22550
Ga0586324_0105777_14_1525	0.00	0.00	0.00	0.00	11124000.00	0.00	600757.20	0.00	0.00	0.00	0.00	0.00	crotonobetaine/CoA-carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfoscoma;Desulfoscoma caldarium;Desulfoscoma caldarium DSM 22027
Ga0586324_0106431_2_1381	0.00	418193.88	0.00	0.00	0.00	0.00	0.00	646600.00	0.00	0.00	0.00	0.00	acyl-CoA synthetase (AMP-forminal/AMP-acid ligase II	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0106547_1143_2231	0.00	6534800.00	563084.45	104779.30	1091800.00	758138.99	2074660.92	732000.00	899100.00	893200.00	430646.48	430861.50	TRAP-type mannitol/chloroamortic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium icense;Bradyrhizobium icense LMTR 13
Ga0586324_0106572_2_2101	0.00	112612.08	240134.70	0.00	0.00	718629.55	0.00	0.00	0.00	2025100.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0106683_291_866	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	112385.88	0.00	0.00	0.00	multimeric flavodoxin WrbA	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0107353_2730_3266	0.00	0.00	0.00	0.00	851977.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized membrane protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobales;Methanomicrobiaceae;Methanofollis;Methanofollis ethanolicus;Methanofollis ethanolicus JCM 15103
Ga0586324_0107408_1898_2449	0.00	0.00	0.00	16720000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	CBS domain-containing protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0108091_2_3394	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2405700.00	0.00	0.00	0.00	uncharacterized protein (TIGR03437 family)	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Spirosomaceae;Spirosoma;Spirosoma spitsbergense DSM 19989
Ga0586324_0108141_1425_2837	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7176400.00	3977600.00	0.00	cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0108504_1133_3298	1050000.00	0.00	0.00	959500.00	0.00	984941.12	0.00	0.00	1122400.00	0.00	0.00	1455000.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0108616_3_1712	0.00	0.00	0.00	0.00	2482300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Adhaeribacter;Adhaeribacter aboris;Ad

Ga0586324_0132617_546_2759	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11176000.00	6120000.00		anaerobic selenocysteine-containing dehydrogenase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_0133258_1496_1834	0.00	0.00	0.00	0.00	0.00	0.00	12068800.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0133518_1170_2306	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	744393.75		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus sp. KH32C;Azoarcus sp. KH32C
Ga0586324_0133960_802_2985	0.00	0.00	0.00	1934552.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0134179_3_2642	27770000.00	18768000.00	4404754.36	8027500.00	15862000.00	6913766.91	5130000.00	11126400.00	6836400.00	14375900.00	4232800.00	12315000.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0134209_549_2159	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4520100.00	0.00	0.00	0.00	0.00	0.00		enterochelin esterase-like enzyme	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter soli;Solirubrobacter soli DSM 22325
Ga0586324_0134644_752_1162	0.00	560509.04	0.00	0.00	0.00	0.00	0.00	0.00	641879.64	0.00	0.00	0.00	0.00		nucleotide-binding universal stress UspA family protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0134891_1_1491	38700000.00	35462000.00	34286700.00	29022500.00	26831500.00	25288900.00	11992800.00	11834000.00	9639000.00	26873000.00	0.00	15450000.00	0.00		hypothetical protein	Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;Thermosulfurimonas;Thermosulfurimonas dismutans;Thermosulfurimonas dismutans S95
Ga0586324_0136033_1_2961	0.00	0.00	4121300.75	0.00	0.00	0.00	0.00	0.00	0.00	2926000.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_0136111_845_2962	2690000.00	1339600.00	0.00	1016500.00	1349300.00	0.00	0.00	3867400.00	2470500.00	0.00	0.00	3450000.00	0.00		hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0136349_1313_2959	0.00	0.00	774671.11	0.00	0.00	648582.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00		ELWxDGT repeat protein	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Flavisolibacter;Flavisolibacter ginsengiterrae;Flavisolibacter ginsengiterrae DSM 18136
Ga0586324_0136600_2_2956	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1611900.00	0.00	0.00	4127200.00	0.00		outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidipila;Acidipila rosea;Acidipila rosea DSM 103428
Ga0586324_0136951_1_1869	1310000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9416000.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0137335_1806_2948	5020000.00	6358000.00	3361363.35	6954000.00	0.00	6709900.00	6931200.00	3611200.00	2689200.00	9240000.00	9944000.00	9150000.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Pseudonocardiales;Pseudonocardiaceae;Amycolatopsis;Amycolatopsis sp. CA-126428;Amycolatopsis sp. CA-126428
Ga0586324_0137750_1706_2548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5544000.00	5702400.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Pandoraea;Pandoraea sp. B-6;Pandoraea sp. B-6
Ga0586324_0138105_884_2932	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2824800.00	0.00	0.00		PAS domain S-box-containing protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geothermobacter;Geothermobacter sp. HR-1;Geothermobacter sp. HR-1
Ga0586324_0138379_3_1247	0.00	3182400.00	0.00	5880500.00	0.00	0.00	0.00	0.00	0.00	3873100.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_0138992_499_1512	0.00	0.00	0.00	0.00	0.00	0.00	536196.14	0.00	0.00	25718000.00	0.00	0.00	0.00		ABC-type sugar transport system substrate-binding protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides ginsengisegetis;Nocardioides ginsengisegetis DSM 21349
Ga0586324_0140040_3_2021	2430000.00	2169200.00	3342930.73	2460500.00	2595600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0140839_2133_2915	8680000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10425000.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodovulum;Rhodovulum sp. PH10;Rhodovulum sp. PH10
Ga0586324_0141116_1747_2223	7410000.00	3155200.00	7262700.00	2099500.00	2894300.00	16968581.94	6384000.00	3971100.00	4487400.00	0.00	2340800.00	4552500.00	0.00		predicted Zn-dependent protease	
Ga0586324_0141433_151_1275	0.00	0.00	0.00	0.00	0.00	0.00	1294739.04	0.00	290243.25	2648800.00	0.00	0.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Bordetella;Bordetella flabilis;Bordetella flabilis AU10664
Ga0586324_0141847_2_2905	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2102100.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Pseudonocardiales;Pseudonocardiaceae;Amycolatopsis;Amycolatopsis sp. CA-126428;Amycolatopsis sp. CA-126428
Ga0586324_0142327_2_2899	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1085700.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Cellulomonadaceae;Cellulomonas;Cellulomonas sp. KRMCY2;Cellulomonas sp. KRMCY2
Ga0586324_0142372_645_2828	0.00	0.00	1336297.39	0.00	0.00	0.00	0.00	0.00	0.00	3819200.00	0.00	2475000.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS401
Ga0586324_0142456_3_1004	0.00	5426400.00	18691600.00	5871000.00	9352400.00	14530200.00	14227200.00	7680000.00	8580000.00	6036800.00	11172000.00	6105000.00	0.00		alkylation response protein AidB-like acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324_0143291_1458_2597	0.00	0.00	0.00	0.00	0.00	0.00	536196.14	0.00	0.00	0.00	0.00	0.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324_0144152_1_2100	22700000.00	166598.64	3899270.44	0.00	4727700.00	1561845.64	0.00	210129.14	0.00	0.00	692845.12	1608152.25	0.00		PtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sophorae;Paenibacillus sophorae S27
Ga0586324_0144219_1_2184	0.00	2672400.00	0.00	0.00	0.00	0.00	6201600.00	0.00	6083100.00	0.00	5913600.00	0.00	0.00		hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta africana;Spirochaeta africana Z-7692, DSM 8902
Ga0586324_0144368_863_2380	9670000.00	8092000.00	11364250.71	5035000.00	10289700.00	12711411.99	4696800.00	7460300.00	5872500.00	3318700.00	6564800.00	4575000.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina cyanea;Desulfosarcina cyanea DSM 28570
Ga0586324_0145683_1_2580	4960000.00	4270400.00	5315052.17	7619000.00	5077900.00	5161000.00	3328800.00	2238700.00	3102300.00	0.00	3960000.00	3727500.00	0.00		subtilisin family serine protease	Bacteria;Proteobacteria;Gammaproteobacteria;Nevskiales;Steroidobacteraceae;Povalibacter;Povalibacter uvarum;Povalbacter uvarum DSM 26723
Ga0586324_0145691_558_2867	0.00	1740800.00	2828816.02	0.00	0.00	0.00	3468767.65	0.00	0.00	0.00	0.00	0.00	0.00		glutamine synthetase type I	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Streptosporangiaceae;Nonomuraea;Nonomuraea longispora;Nonomuraea longispora KC201
Ga0586324_0145835_3_1146	2340000.00	5875200.00	0.00	490687.35	2739800.00	0.00	0.00	5459500.00	2251800.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-D06;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA252-D06 (contamination screened)
Ga0586324_0145836_1525_1863	0.00	0.00	3458897.47	0.00	0.00	484340.00	0.00	0.00	2057400.00	0.00	0.00	0.00	0.00		TusE/DsrC/DsvC family sulfur relay protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thioflavicoccus;Thioflavicoccus mobilis;Thioflavicoccus mobilis 8321
Ga0586324_0146181_1_507	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14775000.00	0.00		rubrerythrin	Bacteria;Deferribacteres;Deferribacteres;Deferribacteraceae;Calditerrivibrio;Calditerrivibrio nitroreducens;Calditerrivibrio nitroreducens Yu37-1. DSM 19672
Ga0586324_0146489_561_2861	0.00	1156000.00	0.00	0.00	0.00	0.00	0.00	0.00	531191.52	0.00	0.00	0.00	0.00		Dme/A/MtrC family decaheme c-type cytochrome	Bacteria;Acidobacteria;Holophagae;Holophagales;Holophagaceae;Geothrix;Geothrix fermentans;Geothrix fermentans DSM 14018
Ga0586324_0146720_2039_2860	0.00	0.00	0.00	0.00	0.00	0.00	4788000.00	0.00	0.00	0.00	0.00	327981.75	0.00		hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0146720_3_1991	0.00	0.00	0.00	0.00	0.00	0.00	935727.96	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_0146806_1_2568	0.00	0.00	4384328.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0146915_2421_2780	4010000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		quercetin dioxygenase-like cupin family protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Shimia;Shimia sp. SK013;Shimia sp. SK013
Ga0586324_0147449_1295_2710	0.00	14416000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		glutamine synthetase type I	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium GJ-E10;Burkholderiales bacterium GJ-E10
Ga0586324_0148124_554_2521	869278.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		uncharacterized membrane protein YqiK	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiorhodovibrio;Thiorhodovibrio litoralis;Lamprocystis litoralis DSM 27648
Ga0586324_0148280_2_2668	3400000.00	2856000.00	0.00	3828500.00	4120000.00	6537633.23	4400400.00	6228100.00	3337200.00	2464000.00	6362400.00	7654036.50	0.00		TonB-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Hymenobacteraceae;Adhaeribacter;Adhaeribacter pallidiroseus;Adhaeribacter pallidiroseus HMF7616
Ga0586324_0148299_3_2012	0.00	0.00	0.00	0.00	0.00	0.00	1450887.12	0.00	0.00	0.00	0.00	1179200.00	2415000.00		MtrB/PioB family decaheme-associated outer membrane protein	Bacteria;Proteobacteria;Gammaproteobacteria;Rhodocyclales;Rhodocyclaceae;Niveibacterium;Niveibacterium umoris;Niveibacterium umoris DSM 106739
Ga0586324_0148552_2_2842	0.00	0.00	0.00	829693.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		PtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sophorae;Paenibacillus sophorae S27
Ga0586324_0148899_173_2839	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	200869.68	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_0149277_478_2835	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1987500.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae;Acidobacteriaceae bacterium KBS 146;Acidobacteriaceae sp. KBS 146
Ga0586324_0149500_2_2833	0.00	306382.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		PtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Acidobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Terribacter;Terribacter sp. 28;Terribacter sp. 28
Ga0586324_0149742_503_796	0.00	0.00	0.00	2935500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		gas vesicle protein	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Lederbergia;Lederbergia lentus;Bacillus lentus NBRC 15444
Ga0586324_0149799_998_2830	642826.00	0.00	0.00	919591.45	0.00	0.00	575973.60	538664.77	0.00	0.00	0.00	862500.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0150197_423_2828	0.00	6800000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1663200.00	0.00	0.00	0.00		2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Acidobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides soli;Nocardioides soli DSM 105498
Ga0586324_0151145_492_989	0.00	0.00	0.00	5291500.00	5943100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		rubrerythrin	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Jettenia;Candidatus Jettenia caeni;Planctomycetaceae bacterium KSU-1
Ga0586324_0151594_515_1522	0.00	0.00	4331812.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11250000.00	0.00		ABC-type sugar transport system substrate-binding protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides ginsengisegetis;Nocardioides ginsengisegetis DSM 21349
Ga0586324_0151875_3_2273	9630000.00	4970800.00	0.00	3657500.00	7848600.00	1155285.88	0.00	5093500.00	7630200.00	15554000.00	12645600.00	3225000.00	0.00		hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_0151941_1_360	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11178000.00	0.00	18832000.00	12375000.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Azospirillum;Azospirillum sp. B506;Azospirillum sp. B506
Ga0586324_0152667_1_2580	1996861.00	4970800.00	0.00	4778500.00	2472000.00	4724300.00	0.00	771437.11	378661.23	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-D06;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA252-D06 (contamination screened)
Ga0586324_0153306_452_2800	737820.00	748000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax paradoxus;Variovorax paradoxus HD84
Ga0586324_0153762_721_2796	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1660000.00	1270500.00	0.00	3120000.00	0.00		MtrB/PioB family decaheme-associated outer membrane protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_0154561_381_2534	95430000.00	99511200.00	63229637.08	29516500.00	38728000.00	17841529.36	16324800.00	118479762.59	70583400.00	20393195.13	9829600.00	22267500.00	0.00		5-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0154948_1787_2215	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1348100.00	0.00	0.00	637732.50	0.00		hypothetical protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Merismopediaceae;Aphanocapsa;Aphanocapsa montana;Aphanocapsa montana BDHKU210001
Ga0586324_0155123_3_1877	6120000.00	0.00	0.00	0.00	5348500.00	8590200.00	6510800.00	0.00	0.00	0.00	5561600.00	8925000.00	0.00		TonB-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Fulvivirgaceae;Ohtaekwangia;Ohtaekwangia koreensis;Ohtaekwangia koreensis DSM 25262
Ga0586324_0155568_1120_2781	0.00	0.00	0.00	0.00	0.00	0.00	29576500.00	0.00	0.00	0.00	0.00	0.00	0.00		ELWxDGT repeat protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Chroococcidiopsidales;Chroococcidiopsidaceae;Chroococcidiopsis;Chroococcidiopsis;Chroococcidiopsis sp. PCC 6712;Chroococcidiopsis sp. PCC 6712
Ga0586324_0155642_637_1203	2040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0155787_211_720	5440000.00	1768000.00	0.00	0.00	11319700.00	2494183.66	6999600.00	7246800.00	10189800.00	3118500.00	2147200.00	0.00	0.00		tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0155882_1241_2644	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7884800.00	0.00	0.00		cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_0155936_1341_2624	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1610400.00	0.00	0.00		hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Halalkalibacillus;Halalkalibacillus halophilus;Halalkalibacillus halophilus DSM 18494
Ga0586324_0156239_1_528	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1101100.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalkalivibrio;Thioalkalivibrio thiocyanodentrificans;Thioalkalivibrio thiocyanodentrificans ARhD 1
Ga0586324_0159027_2_2754	3650000.00	1761200.00	0.00	0.00	1369900.00	2856228.41	2713200.00	0.00	0.00	1524600.00	848004.08	0.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Chryseobacterium;Chryseobacterium koreense;Chryseobacterium koreense CCUG 49689
Ga0586324_0159904_722_2137	3700000.00	0.00	0.00	0.00	889344.23	6384573.85	4005002.40	3135400.00	6115500.00	0.00	0.00	1230000.00	0.00		hypothetical protein	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio islandicus;Thermodesulfovibrio islandicus DSM 12570
Ga0586324_0160572_1771_2742	697021.00	1217200.00	0.00	0.00	1266900.00	4168500.00	3784800.00	0.00	392769.81	1824900.00	870611.28	485268.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Coxiellaceae;Rickettsiella;Rickettsiella aryli;Rickettsiella aryli
Ga0586324_0163136_368_1645	0.00	0.00	0.00	0.00	18128000.00	20445500.00	0.00	0.00	0.00	120689800.00	159491200.00	5632500.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Ferrovales;Ferrovaceae;Ferrovum;Ferrovum myxofaciens;Ferrovum myxofaciens JA12
Ga0586324_0163521_1_873	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	38577000.00	41888000.00	0.00	0.00		hypothetical protein	
Ga0586324_0163640_542_988	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1126400.00	0.00	0.00		nucleotide-binding universal stress UspA family protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324_0163738_117_1454	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3556300.00	0.00	0.00	0.00	0.00	0.00		ABC-type glycerol-3-phosphate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;unclassified Alphaproteobacteria;unclassified Alphaproteobacteria;Phreatobacter;Phreatobacter stygius;Phreatobacter stygius KCTC 52518
Ga0586324_0164308_2_2710	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1549400.00	0.00	0.00	0.00	2002500.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0164788_1_2709	0.00	0.00	0.00	0.00	0.00	0.00	2039106.60	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Hymenobacteraceae;Hymenobacter;Hymenobacter sp. 1B;Hymenobacter artigasensis 1B
Ga0586324_0165161_1907_2704	10410000.00	7548000.00	8951700.00	0.00	7781200.00	0.00	556320.00	5086800.00	5174400.00	0.00	5280000.00	0.00	0.00		hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanocorpusculaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_0166102_1621_2541	0.00	1958400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;unclassified Chromatiales;Thiohalobacter;Thiohalobacter thiocyanaticus;Thiohalobacter thiocyanaticus FOKN1
Ga0586324_0166726_1_855	5610000.00	0.00	0.00	0.00	0.00	6344800.00	0.00	0.00	3165900.00	0.00	0.00	0.00	0.00		uncharacterized surface protein with fasciclin (FAS1) repeats	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina lacustris;Methanosarcina lacustris Z-7289
Ga0586324_0166767_1_1269	6110000.00	3440800.00	0.

Ga0586324_0213623_3_1358	0.00	0.00	19479800.00	15580000.00	0.00	40896692.98	52234800.00	5514400.00	0.00	5828900.00	5209600.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii WSM2783
Ga0586324_0214395_563_1408	0.00	0.00	0.00	0.00	0.00	0.00	674699.88	1244400.00	0.00	0.00	0.00	0.00	0.00	chromosome segregation ATPase	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0216499_2_1066	0.00	7344000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1917300.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter curvatus;Desulfobacter curvatus DSM 3379
Ga0586324_0216595_876_2216	3590000.00	6847600.00	0.00	2584000.00	0.00	0.00	1480235.28	0.00	0.00	1757700.00	3372600.00	2226400.00	2077500.00	ABC-type glycerol-3-phosphate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324_0217059_935_2311	0.00	0.00	0.00	0.00	1308100.00	0.00	0.00	633892.23	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Nitrosoirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio islandicus;Thermodesulfovibrio islandicus DSM 12570
Ga0586324_0217126_598_1059	229952.00	0.00	0.00	0.00	1452300.00	0.00	0.00	2122200.00	0.00	0.00	0.00	0.00	0.00	rubrerythrin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0217619_698_2380	0.00	6235600.00	19648700.00	7999000.00	11330000.00	17190100.00	4879200.00	5758400.00	8343000.00	9009000.00	8685600.00	7875000.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Pedobacter;Pedobacter psychrotolerans;Pedobacter psychrotolerans DSM 103236
Ga0586324_0218114_3_2339	0.00	2529600.00	0.00	0.00	0.00	0.00	2209586.76	2159400.00	3563842.86	0.00	4012800.00	1912500.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium;unclassified Acidobacterium;Acidobacterium strain C40
Ga0586324_0218207_118_1449	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1035000.00	0.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Humibacillus;Humibacillus xanthopallidus;Humibacillus xanthopallidus DSM 21776
Ga0586324_0219075_1368_2033	0.00	0.00	0.00	1016500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0219647_1_558	0.00	17952000.00	0.00	0.00	15347000.00	0.00	0.00	16897000.00	10611000.00	29621900.00	27711200.00	29175000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus necator;Cupriavidus necator H16
Ga0586324_0220031_1176_2264	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	425706.84	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium UKL13-2;Betaproteobacteria bacterium UKL13-2
Ga0586324_0220603_1037_2340	2340000.00	0.00	0.00	0.00	0.00	2736000.00	0.00	0.00	0.00	1663200.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. A1a-2;Bradyrhizobium sp. A1a-2
Ga0586324_0220656_946_2364	0.00	0.00	0.00	988000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	type IV pilus secretin PilQ/predicted competence protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_0220679_685_2184	0.00	0.00	0.00	0.00	0.00	0.00	0.00	193047.31	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0221336_1_1044	0.00	0.00	0.00	0.00	936552.76	0.00	0.00	503395.18	0.00	0.00	0.00	1245000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_0221460_3_2360	1970000.00	0.00	0.00	3420000.00	2276300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Ca2+-binding RTX toxin-like protein	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Rhodopirellula;Rhodopirellula baltica SWK14
Ga0586324_0221543_85_2031	15540000.00	11206400.00	14525400.00	4645500.00	4655600.00	3813181.03	18308400.00	3300100.00	5372287.74	0.00	19351200.00	18480000.00	25182800.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Leptonema;Leptonema illini 3055, DSM 21528
Ga0586324_0221833_3_1247	883710000.00	46464400.00	19879670.75	851314.00	37986400.00	2743977.54	191034733.92	17482600.00	2167357.50	50935500.00	1786400.00	3735000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophilei;Bradyrhizobium erythrophilei GAS138
Ga0586324_0221858_916_1887	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4941000.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324_0222323_1_2358	6380000.00	6528000.00	10359200.00	0.00	0.00	16991600.00	7615200.00	9455000.00	5418900.00	0.00	0.00	4200000.00	0.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0222340_321_2357	1370000.00	1638800.00	0.00	1653000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0224289_571_2349	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17933300.00	22704000.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas sp. GP;Sphingomonas sp. GP
Ga0586324_0225538_2_1603	99100000.00	11832000.00	0.00	17480000.00	38213000.00	27265090.57	5745600.00	14762000.00	10044000.00	3264800.00	0.00	13950000.00	0.00	TonB-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Sunxiuqinia;Sunxiuqinia elliptica;Sunxiuqinia elliptica 114D
Ga0586324_0225626_2_1693	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1245000.00	0.00	predicted porin	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophilei;Bradyrhizobium erythrophilei GAS401
Ga0586324_0226452_1328_1825	0.00	3087200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	rubrerythrin	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio inopinatus;Desulfovibrio inopinatus DSM 10711
Ga0586324_0227644_3_2330	0.00	1645600.00	0.00	0.00	1871500.00	0.00	0.00	0.00	0.00	3110800.00	0.00	0.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0228501_3_2327	3550000.00	3298000.00	8445000.00	4075500.00	0.00	3172816.06	3762000.00	2128900.00	0.00	4265800.00	3863200.00	1620000.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0228527_1384_2328	0.00	12172000.00	0.00	0.00	15485000.00	11845000.00	0.00	0.00	11651000.00	0.00	6029100.00	4479200.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_0228612_1275_1952	0.00	0.00	0.00	0.00	5823500.00	0.00	0.00	5084400.00	3397700.00	2883600.00	2887500.00	0.00	0.00	biopolymer transport protein ExbB/TolQ	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0228619_1565_2044	11000000.00	7888000.00	16158100.00	12929310.00	16377000.00	19330708.52	6156000.00	6161000.00	4625100.00	10395000.00	4576000.00	3442500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0229010_1042_2100	0.00	0.00	0.00	1558000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	transcriptional regulator with GAF, ATPase, and Fis domain	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0229504_1_360	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	636950.79	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0232875_198_1973	22600000.00	17884000.00	17959700.00	3743000.00	32754000.00	30172670.93	19790400.00	18605000.00	28026000.00	7007000.00	22932800.00	15975000.00	0.00	formyltetrahydrofolate synthetase	Bacteria;Chloroflexi;Dehalococcoidia;unclassified Dehalococcoidia;unclassified Dehalococcoidia;Dehalogenimonas;Dehalogenimonas sp. GP;Dehalogenimonas sp. GP
Ga0586324_0233789_511_2088	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5471700.00	0.00	0.00	0.00	0.00	0.00	glutamate synthase domain-containing protein 2	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0234781_1199_2086	0.00	285056.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0235137_1143_2132	0.00	0.00	176434.07	0.00	266678.33	0.00	0.00	1851234.82	0.00	0.00	0.00	1215000.00	0.00	RND family efflux transporter MFP subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia massiliensis;Afipia massiliensis DSM 17498
Ga0586324_0236504_1_2292	0.00	3808000.00	1275673.55	1121000.00	707093.97	768842.11	0.00	382911.03	2438729.37	4435200.00	0.00	3045000.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-D03;Aminicenantes bacterium SCGC AAA252-D03
Ga0586324_0237303_942_1562	0.00	0.00	0.00	0.00	0.00	0.00	0.00	646600.00	842400.00	0.00	0.00	2055000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;unclassified Hyphomicrobiales;Rhizobiales sp. GAS191;Rhizobiales sp. GAS191
Ga0586324_0238168_997_1752	0.00	0.00	0.00	687267.05	792977.43	0.00	0.00	0.00	1069200.00	1031800.00	1478400.00	0.00	0.00	reaulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sulfurreducens;Geobacter sulfurreducens PCA
Ga0586324_0238224_2_2284	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	631058.12	0.00	0.00	0.00	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Firmicutes;Clostridia;Halanaerobiales;unclassified Halanaerobiales;Anaerobacter;Anaerobacter fermentans;Anaerobacter fermentans DY22613
Ga0586324_0238419_290_2281	0.00	5582800.00	0.00	0.00	2513200.00	0.00	0.00	0.00	0.00	0.00	3572400.00	1732500.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Terracidiphilus;Terracidiphilus gabretensis;Acidobacteriaceae bacterium SS5
Ga0586324_0238739_1450_1866	0.00	0.00	32259900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	523455.75	0.00	rubrerythrin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324_0239771_3_560	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12749900.00	0.00	0.00	0.00	0.00	formyltetrahydrofolate synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0239839_95_1990	2760000.00	2495600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5346271.17	0.00	0.00	0.00	hydrolase protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0240123_3_1118	0.00	0.00	0.00	0.00	0.00	1851234.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/Chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Rivbacter;Rivbacter subsaxonicus;Rivbacter subsaxonicus DSM 19570
Ga0586324_0240626_3_2273	1910000.00	1264800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	468711.75	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324_0241003_1664_2170	39200000.00	25432000.00	0.00	6726000.00	0.00	63123000.00	0.00	26535000.00	31347000.00	0.00	0.00	15825000.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0242092_358_2202	0.00	678118.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_0243056_968_1390	0.00	0.00	0.00	0.00	0.00	0.00	0.00	782236.08	0.00	0.00	0.00	0.00	0.00	rhodanese-related sulfurtransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0244248_2_2257	4620000.00	1530000.00	6339943.00	3695500.00	0.00	0.00	3146400.00	0.00	0.00	2017400.00	1663200.00	1282500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0244517_276_827	0.00	1271600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0245479_3_1154	11400000.00	4732800.00	13680900.00	0.00	15553000.00	12068800.00	0.00	8540000.00	10287000.00	11627000.00	12056000.00	11550000.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324_0245549_1_2253	0.00	0.00	0.00	0.00	7632300.00	0.00	0.00	0.00	2551500.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;Roseiflexus;Roseiflexus castenholzii;Roseiflexus castenholzii HLDB, DSM 13941
Ga0586324_0245575_1_2250	0.00	0.00	1039129.10	0.00	0.00	0.00	0.00	0.00	1325300.00	0.00	0.00	0.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacterales;Succinatibacteraceae;Succinatibacter;Succinatibacter sp. CG3;Marine gamma proteobacterium HTCC2143;Marine gamma proteobacterium sp. HTCC2143
Ga0586324_0246032_1055_2092	9390000.00	4633261.24	0.00	111150000.00	149375033.12	17547400.00	107388000.00	134119292.73	154629000.00	30122400.00	65876800.00	37067826.75	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Sufurifiltus;Sufurifiltus calidifontis;Sufurifiltus calidifontis DSM 103923
Ga0586324_0246476_928_2247	0.00	0.00	0.00	0.00	0.00	1651516.03	0.00	0.00	0.00	0.00	0.00	523455.75	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0246766_3_1172	0.00	0.00	0.00	0.00	0.00	6788700.00	0.00	4684800.00	1093500.00	0.00	3414400.00	626761.50	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Pseudohaliea;Pseudohaliea rubra;Pseudohaliea rubra DSM 19751
Ga0586324_0247189_209_994	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1624700.00	0.00	2145000.00	0.00	uncharacterized protein (TIGR02001 family)	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;Halothiobacillus;Halothiobacillus neapolitanus;Halothiobacillus neapolitanus c2, ATCC 23641
Ga0586324_0247490_1260_2243	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1136117.35	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-B84
Ga0586324_0248711_187_1533	0.00	0.00	0.00	0.00	0.00	0.00	6247200.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type glycerol-3-phosphate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0088;Rhodospirillales bacterium URHD0088
Ga0586324_0250766_1238_2230	36300000.00	104584000.00	226100800.00	174980500.00	199614000.00	94089000.00	39900000.00	194407000.00	130653000.00	113729000.00	82280000.00	186300000.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Quisquiliibacterium;Quisquiliibacterium transilvanicum;Quisquiliibacterium transilvanicum DSM 29781
Ga0586324_0252062_2_2179	0.00	0.00	0.00	0.00	2242000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0252154_207_791	1380000.00	0.00	0.00	0.00	12445000.00	0.00	0.00	0.00	7808000.00	8262000.00	0.00	0.00	0.00	opacity protein-like surface antigen	
Ga0586324_0252590_94_609	1650000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0252895_667_2220	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4374000.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cyclobacteriaceae;Algoriphagus;Algoriphagus mannitolivorans;Algoriphagus mannitolivorans DSM 15301
Ga0586324_0254111_586_2217	8190000.00	4807600.00	0.00	12920000.00	67795319.74	0.00	0.00	3745400.00	10206000.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-D06;Aminicenantes bacterium SCGC AAA252-D06 (contamination screened)
Ga0586324_0254255_1148_2215	72900000.00	56372000.00	0.00	20900000.00	0.00	0.00	0.00	57962000.00	72276000.00	44408000.00	73629000.00	24178000.00	4582500.00	crotonobetaityl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Ferroglobus;Ferroglobus placidus;Ferroglobus placidus AEDII12DO, DSM 10642
Ga0586324_0255123_663_2213	0.00	0.00	1062116.39	0.00	0.00	1332137.47	0.00	707600.00	668546.46	0.00	0.00	0.00	0.00	NADPH-dependent 2,4-dienoyl-CoA reductase/sulfur reductase-like enzyme	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Oscillatoriales;Microcoleaceae;Planktothrix;Planktothrix serta;Planktothrix serta PCC 8927
Ga0586324_0255425_91_2211	0.00	4406400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Candidimonas;Candidimonas bauzanensis;Candidimonas bauzanensis CGMCC 1.10190
Ga0586324_0255914_1_1443	0.00	1115200.00	960348.51	1672000.00	0.00	542621.76	689300.00	842400.00	893200.00	1337600.00	855000.00	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Micrococcaceae;Sinomonas;Sinomonas mesophila;Sinomonas mesophila MPKL 26
Ga0586324_0256352_1_1119	0.00	1203600.00	0.00	0.00	0.00	0.00	0.00	1433500.00	1247400.00	2748900.00	2842400.00	2242500.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Candidimonas;Candidimonas bauzanensis;Candidimonas bauzanensis CGMCC 1.10190
Ga0586324_0259919_2_2194	0.00	0.00	3806138.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0260591_985_2190	0.00	0.00	0.00	0.00	0.00	1161721.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_0261629_936_2114	38130000.00	15572000.00	44308100.00	12331000.00	161699700.00	138751500.00	156567600.00	98881000.00	115028100.00	20790000.00	12883200.00	57405000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter postgatei;Desulfobacter postgatei 2ac9
Ga0586324_0263436_3_1979	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4568400.00	0.00	0.00	0.00	0.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase/Pyruvate/2-oxoacid:ferr	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_0263697_2_1951	0.00	2699600.00	0.00	3439000.00	3944900.00	2565826.88	0.00	3074400.00	2041200.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sophorae;Paenibacillus sophorae 527
Ga0

Ga0586324 0302558 1 2049	4080000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 0302583 1061 2047	1810000.00	5222400.00	4437881.28	2726500.00	4552600.00	4066431.30	6498000.00	10656700.00	8326800.00	2537164.63	3467200.00	1972500.00	hypothetical protein	
Ga0586324 0304858 1468 2040	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5996300.00	6407100.00	11319000.00	10560000.00	7132500.00	glutamine synthetase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324 0305298 2 808	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9779000.00	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Jiangellales;Jiangellaceae;Jiangella;Jiangella aurantiaca;Jiangella aurantiaca 8K307
Ga0586324 0307745 581 1195	0.00	11893200.00	11991900.00	3059000.00	18776900.00	5280100.00	11673600.00	11919400.00	0.00	23223200.00	20988000.00	11212500.00	hypothetical protein	
Ga0586324 0308321 676 1446	0.00	270478.84	0.00	0.00	0.00	361924.65	0.00	0.00	0.00	0.00	0.00	0.00	regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 0311341 71 2020	0.00	897600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	816200.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas sp. Nm141;Nitrosomonas sp. Nm141
Ga0586324 0312272 2 2017	3740000.00	2573432.80	3352569.29	0.00	1957000.00	5838933.08	1075327.80	269895.72	477456.12	2202200.00	3634400.00	322188.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0312585 962 1717	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3385800.00	0.00	0.00	0.00	regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Niastella;Niastella sp. CF465;Niastella sp. CF465
Ga0586324 0312836 1648 2016	0.00	0.00	0.00	0.00	0.00	5756500.00	7888800.00	0.00	0.00	0.00	0.00	0.00	methanogenic corrinoid protein MtbC1	Bacteria;Firmicutes;Clostridia;Halanaerobiales;Halobacteroidaceae;Selenihalanaerobacter;Selenihalanaerobacter shriftii;Selenihalanaerobacter shriftii ATCC BAA-73
Ga0586324 0313955 195 821	0.00	0.00	0.00	0.00	0.00	0.00	5130000.00	0.00	0.00	0.00	0.00	0.00	methanogenic corrinoid protein MtbC1	Bacteria;Firmicutes;Clostridia;Halanaerobiales;Halobacteroidaceae;Selenihalanaerobacter;Selenihalanaerobacter shriftii;Selenihalanaerobacter shriftii ATCC BAA-73
Ga0586324 0317618 490 2004	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2336300.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methyloceanibacter;Methyloceanibacter methanicus;Methyloceanibacter methanicus R-67174
Ga0586324 0318678 185 1201	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	703810.03	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Thioalkalispiraceae;Thiohalophilus;Thiohalophilus thiocyanatoxydans;Thiohalophilus thiocyanatoxydans DSM 16326
Ga0586324 0318780 1515 2000	22430000.00	26316000.00	0.00	17290000.00	0.00	0.00	0.00	17873000.00	4050000.00	0.00	22176000.00	16800000.00	hypothetical protein	
Ga0586324 0318996 3 2000	16620000.00	1156000.00	0.00	0.00	0.00	3403893.88	0.00	2812100.00	0.00	5751900.00	0.00	729431.25	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0319524 3 578	0.00	0.00	0.00	0.00	5489900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	polyhydroxyalkanoate synthesis repressor PhaR	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. URHD0069;Bradyrhizobium sp. URHD0069
Ga0586324 0319665 483 1574	0.00	0.00	0.00	4487693.60	0.00	0.00	0.00	9333000.00	10854000.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324 0320264 1024 1995	0.00	5453600.00	0.00	3353500.00	0.00	12545200.00	0.00	4782400.00	8982900.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324 0321156 684 1994	62000000.00	63920000.00	124986000.00	75810000.00	81370000.00	84561000.00	77064000.00	48495000.00	41310000.00	71764000.00	75407200.00	84660000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfofaba;Desulfofaba hansenii;Desulfofaba hansenii DSM 12642
Ga0586324 0321852 2 601	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2541000.00	3036000.00	0.00	hypothetical protein	
Ga0586324 0322396 633 1133	0.00	11492000.00	0.00	0.00	13390000.00	1426615.53	0.00	0.00	3377700.00	0.00	0.00	0.00	rubrerythrin	Bacteria;Chlorobi;Chlorobia;Chlorobiales;Chlorobiaceae;Chlorobium;Chlorobium phaeobacteroides;Chlorobium phaeobacteroides BS1
Ga0586324 0322845 57 1139	625750.00	0.00	0.00	0.00	0.00	0.00	1027919.76	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 0323183 1091 1987	0.00	720800.00	243658.52	0.00	0.00	1412795.96	1466382.00	1140700.00	1790100.00	1470700.00	1144000.00	628708.50	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS499
Ga0586324 0323387 256 1719	0.00	1142400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1522400.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Nitrosococcus;Nitrosococcus halophilus;Nitrosococcus halophilus Nc4
Ga0586324 0325293 1252 1875	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2979900.00	3713600.00	0.00	opacity protein-like surface antigen	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Rhodocyclus;Rhodocyclus tenuis;Rhodocyclus tenuis DSM 109
Ga0586324 0326165 3 1979	0.00	8726537.92	0.00	15960000.00	0.00	8932500.00	0.00	0.00	0.00	0.00	0.00	6600000.00	hypothetical protein	
Ga0586324 0328677 267 1973	0.00	0.00	0.00	0.00	0.00	7066600.00	0.00	0.00	0.00	0.00	0.00	0.00	Zn-dependent protease with chaperone function	Bacteria;Planctomycetes;Planctomycetia;Gemmatales;Gemmataceae;Gemmata;Gemmata massiliana;Gemmata massiliana IIL30
Ga0586324 0328691 1214 1972	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1370600.00	0.00	0.00	MFS family permease	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324 0329116 907 1200	0.00	0.00	0.00	0.00	3357800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0329536 2 754	35000000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 0329564 2 1567	0.00	0.00	0.00	0.00	0.00	2525035.13	2850000.00	0.00	0.00	1755600.00	0.00	3697500.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Dyadobacter;Dyadobacter psychrophilus;Dyadobacter psychrophilus DSM 22270
Ga0586324 0331667 1 1890	36260000.00	53168520.00	0.00	28595000.00	26347400.00	0.00	0.00	24314600.00	32173200.00	44128700.00	21692000.00	2490000.00	transketolase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas lenta;Methylomonas lenta R-45370
Ga0586324 0331992 1 936	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1427400.00	1806300.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. Ai1a-2;Bradyrhizobium sp. Ai1a-2
Ga0586324 0332560 1173 1877	0.00	0.00	9289500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted membrane protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;unclassified Eubacteriales;Natranaerovirga;Natranaerovirga pectinivora;Natranaerovirga pectinivora DSM 24629
Ga0586324 0333072 750 1961	0.00	2250800.00	0.00	3334500.00	9651100.00	0.00	3716400.00	2031300.00	2478600.00	3757600.00	3528800.00	2557500.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermodesulfitimonas;Thermodesulfitimonas autotrophica;Thermodesulfitimonas autotrophica DSM 102936
Ga0586324 0333352 3 1082	0.00	0.00	0.00	0.00	0.00	0.00	1074007.68	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 0333962 672 1958	0.00	0.00	0.00	0.00	0.00	0.00	4833600.00	9625800.00	7565400.00	36652000.00	33492800.00	23887500.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0334128 641 1912	2601453.00	85775795.00	28994500.00	18430000.00	143695300.00	41288000.00	22070400.00	102785000.00	89262000.00	88396000.00	36080000.00	72375000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythrobacter;Erythrobacter neustonensis;Erythrobacter neustonensis DSM 9434
Ga0586324 0334753 1302 1958	106000000.00	85408000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10857000.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Quisquiliibacterium;Quisquiliibacterium transsilvanicum;Quisquiliibacterium transsilvanicum DSM 29781
Ga0586324 0335176 173 1957	0.00	0.00	0.00	0.00	0.00	0.00	3625200.00	0.00	0.00	0.00	0.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 0335724 1 954	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1654400.00	0.00	hypothetical protein	
Ga0586324 0335741 77 979	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1909600.00	0.00	gliding motility-associated protein GldL	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Crocinitomicaceae;Brumimicrobium;Brumimicrobium sp. C305;Brumimicrobium sp. C305
Ga0586324 0335965 745 1953	0.00	343537.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Thermanaerothrix;Thermanaerothrix daxensis;Thermanaerothrix daxensis GNS-1
Ga0586324 0336812 222 1952	0.00	1196800.00	0.00	0.00	2204200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Streptomycetales;Streptomycetaceae;Kitasatospora;Kitasatospora cineracea;Kitasatospora cineracea DSM 44780
Ga0586324 0337200 3 1952	0.00	0.00	0.00	0.00	1874600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Haloarculaceae;Natronomonas;Natronomonas moolapensis;Natronomonas moolapensis 8.8.11, DSM 18674
Ga0586324 0337362 545 1744	0.00	0.00	0.00	0.00	0.00	0.00	12973200.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thioflavicoccus;Thioflavicoccus mobilis;Thioflavicoccus mobilis 8321
Ga0586324 0338714 797 1948	0.00	0.00	0.00	0.00	0.00	0.00	1797932.76	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. URHD0069;Bradyrhizobium sp. URHD0069
Ga0586324 0339013 188 1945	26360000.00	45478400.00	2729880.03	36537000.00	63551000.00	2754786.97	20428800.00	57279000.00	38750400.00	32147500.00	27588000.00	37899185.25	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 0339423 206 1237	3850000.00	21467600.00	18128600.00	7609500.00	14821700.00	25765300.00	22321200.00	18702600.00	17544600.00	23315600.00	17661600.00	12997500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium sp. CF059;Methylibium sp. CF059
Ga0586324 0339689 114 1454	0.00	2135200.00	0.00	6327000.00	2719200.00	0.00	0.00	0.00	3361500.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0340171 3 401	0.00	0.00	0.00	0.00	2956100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324 0340732 1631 1942	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2478600.00	0.00	1830400.00	0.00	phasin family protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Aromatoleum;Aromatoleum aromaticum;Aromatoleum aromaticum EbN1
Ga0586324 0341052 739 1926	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	606827.25	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus basilensis;Cupriavidus basilensis 4G11
Ga0586324 0341413 1313 1939	0.00	0.00	0.00	0.00	0.00	9051600.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Janthinobacterium;Janthinobacterium sp. CG3;Janthinobacterium sp. CG3
Ga0586324 0341514 63 1940	0.00	992800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Chitinophaga;Chitinophaga terrae (ex Kim and Jung 2007);Chitinophaga terrae DSM 23920
Ga0586324 0343559 1 1935	558482.00	2774400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. PSR-1;Anaeromyxobacter sp. PSR-1
Ga0586324 0343707 1 1935	0.00	4005200.00	0.00	0.00	5283900.00	0.00	0.00	0.00	4511700.00	5921300.00	0.00	0.00	CO/xanthine dehydrogenase Mo-binding subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 0344736 49 1011	0.00	0.00	0.00	0.00	0.00	0.00	0.00	263920.77	0.00	0.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Oscillochloridaceae;Oscillochloris;Oscillochloris trichoides;Oscillochloris trichoides DG6
Ga0586324 0345379 368 1930	0.00	0.00	0.00	0.00	3326900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324 0346591 69 1928	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1634800.00	0.00	0.00	0.00	0.00	multidrug efflux pump subunit AcrB	Bacteria;Thermodesulfobacteria;Thermodesulfobacteria;Thermodesulfobacteriales;Thermodesulfobacteriaceae;Thermosulfuriphilus;Thermosulfuriphilus ammonigenes;Thermosulfuriphilus ammonigenes DSM 102941
Ga0586324 0346999 1 1926	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	230896.17	0.00	0.00	0.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0347370 3 1250	0.00	0.00	68123000.00	0.00	0.00	81782000.00	30552000.00	0.00	42525000.00	0.00	0.00	19200000.00	predicted porin	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324 0347786 605 1924	5370000.00	5875200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	putative cell wall-binding protein	Bacteria;Actinobacteria;Actinomycetia;Acidothermales;Acidothermaceae;Acidothermus;Acidothermus cellulolyticus;Acidothermus cellulolyticus 11B
Ga0586324 0350138 1 1917	0.00	0.00	2924824.41	0.00	0.00	0.00	2553600.00	0.00	0.00	0.00	0.00	2085000.00	alkyl sulfatase BDS1-like metallo-beta-lactamase superfamily hydrolase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Rhodopseudomonas;Rhodopseudomonas palustris;Rhodopseudomonas palustris 7850, DSM 127
Ga0586324 0350256 3 983	39100000.00	31397211.60	75723500.00	63460000.00	18952000.00	37159200.00	52827600.00	64782000.00	46008000.00	4835600.00	0.00	11100000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythrobacter;Erythrobacter neustonensis;Erythrobacter neustonensis DSM 9434
Ga0586324 0350405 557 1918	2080000.00	1842800.00	0.00	959500.00	0.00	0.00	3556800.00	1665300.00	1522800.00	0.00	0.00	2062500.00	hypothetical protein	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio islandicus;Thermodesulfovibrio islandicus DSM 12570
Ga0586324 0351704 356 1915	5050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	916300.00	464229.92	885000.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas koyamae;Methylomonas koyamae R-45383
Ga0586324 0352375 892 1914	0.00	0.00	0.00	0.00	0.00	16237300.00	0.00	10492000.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 0352663 1193 1912	0.00	1285200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	enoyl-CoA hydratase/carnithine racemase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfarculus;Desulfarculus baarsii;Desulfarculus baarsii 2st14, DSM 2075
Ga0586324 0353095 186 1910	0.00	0.00	0.00	0.00	0.00	2536464.76	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Noviherbaspirillum;Noviherbaspirillum autotrophicum;Noviherbaspirillum autotrophicum TSA66
Ga0586324 0353681 166 1425	0.00	5610000.00	0.00	3838000.00	11124000.00	0.00	0.00	3794200.00	0.00	1278200.00	1707200.00	2965164.00	hypothetical protein	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetoovum;Candidatus Magnetoovum chiemensis;Candidatus Magnetoovum chiemensis CS-04
Ga0586324 0353806 1 324	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2016900.00	0.00	0.00	0.00	dipeptidyl aminopeptidase/acylaminoacyl peptidase	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Flavisolibacter;Flavisolibacter ginsengiterrae;Flavisolibacter ginsengiterrae DSM 18136
Ga0586324 0353885 2 691	0.00	0.00	0.00	9880000.00	589626.59	0.00	6224400.00	0.00	6220800.00	0.00	0.00	0.00	alkylation response protein AidB-like acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0355536 2 1906	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3599000.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324 0356765 36 1532	4330000.00	6738800.00	0.00	0.00	0.00	0.00	0.00	3001200.00	1757700.00	0.00	2684000.00	1245000.00	hypothetical protein	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira marina;Nitrospira marina Nb-295
Ga0586324 0357651 1 1233	0.00	0.00	0.00	0.00	45011000.00	39183900.00	28500000.00	28609000.00	0.00	0.00	2587200.00	32250000.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Legionella;Legionella drancourtii;Legionella drancourtii LLAP12
Ga0586324 0358338 261 1532	7970000.00	4188800.00	47292000.00	34675000.00	74160000.00	81742300.00	37392000.00	38606900.00	71093700.00	50427300.00	83248000.00	33225000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter dehalogenans;Anaeromyxobacter dehalogenans 2CP-C
Ga0586324 0358511 3 1748	0.00	4052800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	432580.61	0.00	2625000.00	outer membrane receptor protein involved in Fe transport	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Hydrobacter;Hydrobacter penzbergensis;Hydrobacter penzbergensis DSM 25353
Ga0586324 0363619 1168 1659	0.00	2495600.00	0.00	6289000.00	4717400.00	0.00	0.00	3983300.00	0.00	0.00	0.00	0.00	uncharacterized surface protein with fasciclin (FAS1) repeats	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cyclobacteriaceae;Algoriphagus;Algoriphagus mannitolivorans;Algoriphagus mannitolivorans DSM 15301
Ga0586324 0363986 2 862	27300000.00	13124000.00	0.00	46455000.00	53354000.00	42479000.00	58368000.00	44286000.00	37746000.00	0.00	0.00	24525000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rubrivivax;Rubrivivax benzoatilyticus;Rubrivivax benzoatilyticus JA2
Ga0586324 0364021 3 1886	0.00	0.00	0.00	0.00	8549000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0365186 244 1884	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1214400.00	0.00	putative PEP-CTERM system TPR-repeat lipoprotein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 0366095 1 1329	0.00	0.00	0.00	452078.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324 0367678 578 1078	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	546847.84	0.00	1860000.00	2-oxoacid:acceptor oxidoreductase delta subunit (pyruvate/2-ketoisovalerate family)	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324 0367877 3 977	0.00	1475600.00	8107200.00	0.00	2121800.00	3663202.37	4537200.00	1116300.00	3349597.86	8470000.00	3590400.00	3720000.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Lamprocystis;Lamprocystis purpurea;Lamprocystis purpurea DSM 4197
Ga0586324 0368378 3 1874	16400000.00	22236000.00	10190300.00	16340000.00	16068000.00	11354200.00	68400000.00	8601000.00	6674400.00	7638400.00	6177600.00	4845000.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Actinobacteria;Actinomycetia;Micromonosporales;Micromonosporaceae;Micromonospora;Micromonospora humi;Micromonospora humi DSM 45647
Ga0586324 0368767 801 1451	0.00	0.00	0.00	5434000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Granulicella;Granulicella sp. GAS466;Granulicella sp. GAS466
Ga0586324 0369096 349 1875	0.00	4454000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Delftia;Delftia sp. HK171;Delftia sp. HK171 (v2)
Ga0586324 0369100 1 300	0.00	0.00	533003.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 0369460 952 1413	0.00	0.00	0.00	19855000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	nucleotide-binding universal stress UspA family protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 0369526 960 1520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2728000.00	0.00	phasin family protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 0369753 1033 1872	0.00	0.00	0.00	467750.55	0.00	0.00	0.00	0.00	882900.00	0.00	0.00	0.00	OmcA/MtrC family decaheme c-type cytochrome	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax ferrireducens;Rhodoferax ferrireducens T118
Ga0586324 0370213 1046 1870	5820000.00	0.00	9739900.00	9785000.00	8188500.00	12902500.00	6292800.00	0.00	4997700.00	6953100.00	8280800.00	0.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324 0370479 2 1870	0.00	2862800.00	3538038.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1117600.00	0.00	hypothetical protein	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Lacunisphaera;Lacunisphaera limnophila;Opitutaceae bacterium IG16b
Ga0586324 0371984 200 1588	0.00	0.00	0.00	4626500.00	1771600.00	1067401.99	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 0373321 192 869	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1372500.00	1053000.00	0.00	0.00	0.00	biopolymer transport protein ExbB/TolQ	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-P13;Aminicenantes bacterium SCGC AAA252-P13 (contamination screened)
Ga0586324 0375376 3 677	0.00	0.00	0.00	1539000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3-hydroxyisobutyrate dehydrogenase-like beta-hydroxyacid dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Rhodoplanes;Rhodoplanes sp. Z2-YC6860;Rhodoplanes sp. Z2-YC6860
Ga0586324 0375864 205 546	0.00	1761200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	RNA recognition motif-containing protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Sunxiuqinia;Sunxiuqinia dokdonensis;Sunxiuqinia dokdonensis SK
Ga0586324 0377614 110 1855	3700000.00	0.00	0.00	2945000.00	0.00	0.00	0.00	2183800.00	2122200.00	4643100.00	0.00	0.00	hypothetical protein	Bacteria;Balneolaeota;Balneolia;Balneolales;Balneolaceae;Gracilimonas;Gracilimonas mengyeensis;Gracilimonas mengyeensis DSM 21985
Ga0586324 0377691 2 1855	0.00	4644400.00	4826610.26	2337000.00	2626500.00	623671.12	3739200.00	3184200.00	3280500.00	4812500.00	3572800.00	4087500.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 0378165 3 1853	1430000.00	279949.88	0.00	0.00	0.00	0.00	797842.68	0.00	2850636.24	0.00	493402.80	832500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0378185 3 1853	0.00	2556971.36	0.00	0.00	2080600.00	0.00	3169200.00	1939800.00	0.00	1678600.00	1320000.00	3420000.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-O03;Aminicenantes bacterium SCGC AAA252-O03 (contamination screened)
Ga0586324 0378948 1 1722	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6899200.00	1732500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium URHE0068;Acidobacteriaceae bacterium URHE0068
Ga0586324 0381737 368 1612	0.00	5800400.00	0.00	0.00	8888900.00	0.00	0.00	0.00	10871981.19	0.00	11352000.00	1507500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Quisquiliibacterium;Quisquiliibacterium transsilvanicum;Quisquiliibacterium transsilvanicum DSM 29781
Ga0586324 0382262 135 1370	0.00	0.00	0.00	0.00	0.00	0.00	0.00	860100.00	0.00	0.00	0.00	817500.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS165
Ga0586324 0382325 249 1844	0.00	4909600.00	0.00	0.00	0.00	0.00	0.00	0.00	13608000.00	0.00	15136000.00	0.00	ABC-type transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Oscillochloridaceae;Oscillochloris;Oscillochloris trichoides;Oscillochloris trichoides DG6
Ga0586324 0383543 28 495	3770000.00	6358000.00	0.00	0.00	0.00	0.00	3739200.00	3251300.00	2940300.00	8547000.00	6916800.00	10125000.00	hypothetical protein	
Ga0586324 0384837 490 1839	5210000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Terrabacter;Terrabacter sp. 28;Terrabacter sp. 28
Ga0586324 0389241 1 525	5520000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized protein (DUF1015 family)	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324 0392444 318 1670	0.00	0.00	0.00	4740500.00	0.00	0.00	0.00	2226500.00	0.00	5043500.00	1786400.00	2197500.00	predicted CXXCH cytochrome family protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Intrasporangium;Intrasporangium calvum;Intrasporangium calvum 7KIP, DSM 43043
Ga0586324 0394323 195 1061	0.00	5807200.00	0.00	0.00	0.00	0.00	7136400.00	0.00	0.00	0.00	0.00	0.00	uncharacterized surface protein with fasciclin (FAS1) repeats/plastocyanin	Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Deinococcaceae;Deinococcus;Deinococcus puniceus;Deinococcus puniceus DY1
Ga0586324 0395179 264 1334	298668.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	excisionase family DNA binding protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 0397200 3 458	2850000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfofustis;Desulfofustis glycolicus;Desulfofustis glycolicus DSM 9705
Ga0586324 0399994 3 638	2100000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1777500.00	hypothetical protein	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia sinica;Candidatus Brocadia sinica JPN1
Ga0586324 0401694 158 1804	0.00	0.00	0.00	0.00	1431700.00	1233431.36	0.00	866200.00	1204408.44	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sp. 453mf;Paenibacillus sp. 453MF
Ga0586324 0402153 1 696	0.00	0.00	0.00	0.00	0.00	0.00	2024272.92	0.00	0.00	2086700.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 0403311 183 1802	0.00	7004000.00	7882000.00	0.00	5397200.00	0.00	0.00	16775000.00	17496000.00	17787000.00	14960000.00	517476.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Terriglobus;Terriglobus saanensis;Terriglobus saanensis SP1PR4, DSM 23119
Ga0586324 0406334 720 1796	8840000.00	20264000.00	5014365.13	38836000.00	7343900.00	8995067.20	8436000.00	2513200.00	3134700.00	4643100.00	3150400.00	29550000.00	hypothetical protein	
Ga0586324 0408798 91 1449	0.00	0.00	0.00	0.00	2173300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Ferroglobus;Ferroglobus placidus;Ferroglobus placidus AEDII12DO, DSM 10642
Ga0586324 0409773 3 1286	0.00	0.00	25144272.49	0.00	21012000.00	25805000.00	0.00	2269200.00	0.00	2741200.00	9328000.00	3592500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Halodesulfovibrio;Halodesulfovibrio aestuarii;Halodesulfovibrio aestuarii aestuarii ATCC 29578
Ga0586324 0410126 3 1790	2620000.00	5956800.00	7431600.00	0.00	0.00	12704000.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0410548 3 542	0.00	0.00	0.00	0.00	0.00	0.00	1875081.12	0.00	1733400.00	571811.24	0.00	922500.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324 0410550 1 1095	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	654957.90	0.00	0.00	0.00	hypothetical protein	Bacteria;Balneolaeota;Balneolia;Balneolales;Balneolaceae;Aliifodinibius;Aliifodinibius sediminis;Aliifodinibius sediminis DSM 21194
Ga0586324 0412931 452 1492	0.00	5644000.00	0.00	8170000.00	0.00	0.00	8892000.00	5886500.00	5386500.00	0.00	0.00	4417500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI 001;Burkholderiales sp. JOSHI 001
Ga0586324 0413577 1140 1760	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1749600.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 0415975 379 1776	7340000.00	4488000.00	0.00	0.00	0.00	11314500.00	0.00	9516000.00	0.00	0.00	0.00	6465000.00	hypothetical protein	Bacteria;Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;Verrucomicrobia bacterium LW23;Verrucomicrobia bacterium LW23
Ga0586324 0416886 3 1052	0.00	0.00	0.00	0.00	6313900.00	0.00	0.00	1634800.00	0.00	0.00	2666400.00	2115000.00	hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 0417258 220 1140	76600000.00	40800000.00	15201000.00	10355000.00	10207300.00	1224983.20	0.00	2427800.00	8829000.00	0.00	3414400.00	1965000.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum miyakonense;Methylovulum miyakonense HT12
Ga0586324 0417845 889 1773	0.00	0.00	0.00	0.00	0.00	0.00	1914570.72	0.00	1814400.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324 0418092 3 1772	0.00	890800.00	0.00	0.00	0.00	1055075.14	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 0418393 3 1013	0.00	1190000.00	0.00	761882.90	1874600.00	1629073.62	1131249.36	1177300.00	1644300.00	3542000.00	0.00	1905000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324 0419448 3 1772	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	501364.50	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324 0420644 1 1770	1860000.00	1101600.00	0.00	0.00	0.00	0.00	0.00	695400.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas;Sphingomonas sp. R1S6C;Sphingomonas sp. R1S6C
Ga0586324 0421182 1361 1768	0.00	4998000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324 0421320 1242 1514	0.00	0.00	0.00	0.00	3718300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 0430070 183 1751	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3697500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 89;Acidobacteriaceae bacterium KBS 89, DSM 24296
Ga0586324 0433357 1 1746	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	29484000.00	0.00	0.00	0.00	pyruvate/2-oxoacid:ferredoxin oxidoreductase alpha subunit/Pyruvate/2-oxoacid:ferredoxin oxic	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 0435825 122 1087	0.00	0.00	0.00	0.00	0.00	0.00	6315600.00	0.00	0.00	0.00	0.00	0.00	VWFA-related protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium ailaaui;Acidobacterium ailaaui PMMR2
Ga0586324 0436050 1 1515	3600000.00	9785200.00	5855200.00	7410000.00	7642600.00	4843400.00	2827200.00	9656300.00	9963000.00	6175400.00	7761600.00	3255000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758

Ga0586324_0436056_152_961	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	48587000.00	25608000.00	24900000.00	cytochrome c553	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0436530_2_847	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	156459.38	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. Root122;Nocardioides sp. Root122
Ga0586324_0436831_479_1445	0.00	1319200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type glycerol-3-phosphate transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella sp. OAS946;Reyranella sp. OAS946
Ga0586324_0438706_502_1641	1520000.00	6154000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. OAE819;Bradyrhizobium sp. OAE819
Ga0586324_0440108_423_914	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2117500.00	2534400.00	0.00	nucleotide-binding universal stress UsoA family protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_0443053_1_1728	1420000.00	2203200.00	0.00	1320500.00	3986100.00	0.00	0.00	2604700.00	0.00	0.00	0.00	1395000.00	hypothetical protein	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus terrae;Opitutus terrae PB90-1
Ga0586324_0443863_1_1728	0.00	3386400.00	0.00	0.00	0.00	5928000.00	1464000.00	4147200.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0445288_2_1186	4560000.00	4386000.00	0.00	3458000.00	2914900.00	0.00	0.00	1701000.00	3542000.00	2930400.00	0.00	0.00	predicted peptidase	Bacteria;Actinobacteria;Actinomycetia;Streptomycetales;Streptomycetaceae;Streptomyces;Streptomyces sp. PRh5;Streptomyces sp. PRh5
Ga0586324_0446604_1_576	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5235000.00	radical SAM superfamily enzyme YgiQ (UPF0313 family)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfarculus;Desulfarculus;Dethiosulfatarculus;Dethiosulfatarculus sandiegensis;Dethiosulfatarculus sandiegensis SPR
Ga0586324_0446753_1028_1723	0.00	0.00	0.00	0.00	1091800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0446899_2_1723	0.00	2216800.00	0.00	3040000.00	3450500.00	0.00	4468800.00	628300.00	2956500.00	2310000.00	0.00	2482500.00	PKD repeat protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Micrococcaceae;Leifsonia;Leifsonia sp. Leaf325;Leifsonia sp. Leaf325
Ga0586324_0447788_1193_1648	0.00	924800.00	505531.21	1149500.00	2774701.55	0.00	226247.14	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0450067_3_1667	837188.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1860000.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0451313_578_1714	52500000.00	12920000.00	47348300.00	6669000.00	74160000.00	10957200.00	20064000.00	29585000.00	25920000.00	36290100.00	136840000.00	28500000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324_0455379_3_1709	0.00	0.00	0.00	0.00	0.00	1938646.28	0.00	2714500.00	0.00	1332100.00	3009600.00	2265000.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324_0456890_1_1704	0.00	0.00	0.00	0.00	0.00	4525800.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0457635_1_1530	0.00	0.00	0.00	1026000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii USDA 76
Ga0586324_0459983_895_1701	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	291331.08	0.00	0.00	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Pseudorhodoplanes;Pseudorhodoplanes sinuspersici;Pseudorhodoplanes sinuspersici RIPI110
Ga0586324_0460731_3_773	0.00	0.00	4964916.84	8046500.00	0.00	5716800.00	0.00	4166300.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0461948_127_1698	0.00	629312.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0462240_3_1697	0.00	0.00	2436979.28	0.00	0.00	0.00	0.00	0.00	0.00	962500.00	0.00	0.00	uncharacterized repeat protein (TIGR01451 family)	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;intrasporangiaceae;Humibacillus;Humibacillus xanthopallidus;Humibacillus xanthopallidus SLBN-155
Ga0586324_0462454_842_1696	5220000.00	2189600.00	2611593.73	23180000.00	16583000.00	1743663.70	0.00	17202000.00	13777000.00	592525.01	18128000.00	12675000.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0462920_3_1208	41010000.00	46022400.00	11203700.00	35519611.75	23576700.00	0.00	8846400.00	3834119.98	35302231.62	56125300.00	59118400.00	100809164.25	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Gallionella;Gallionella;Gallionella capsiferriformans;Gallionella capsiferriformans ES-2
Ga0586324_0463858_985_1695	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2562000.00	0.00	0.00	0.00	0.00	uncharacterized protein YqfA (UPF0365 family)	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta isovalerica;Spirochaeta isovalerica DSM 2461
Ga0586324_0465592_481_912	29500000.00	1421200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	nucleotide-binding universal stress UsoA family protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0466835_2_1690	0.00	0.00	893233.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;unclassified Rhodothermaceae;Rhodothermaceae bacterium RA;Halothermobacillus malaysiensis RA
Ga0586324_0467224_1_1392	1490000.00	0.00	4770270.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted ATP-dependent protease	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_0468321_1_1686	0.00	1156000.00	984478.69	0.00	1452300.00	1135717.75	238939.44	945500.00	931500.00	993300.00	932800.00	483494.25	hypothetical protein	Bacteria;Rhodothermaeota;Rhodothermia;Rhodothermales;Rubricoccaceae;Rubricoccus;Rubricoccus marinus;Rubricoccus marinus SG-29
Ga0586324_0468560_492_1541	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	325862.25	LDH2 family malate/lactate/ureidoglycolate dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324_0470825_441_1682	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3599200.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Sulfuritalea;Sulfuritalea;Sulfuritalea hydrogenivorans;Sulfuritalea hydrogenivorans DSM 100309
Ga0586324_0475905_3_1676	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	891000.00	0.00	0.00	ABC-type bacteriocin/lantibiotic exporter with double-glycine peptidase domain	Bacteria;Actinobacteria;Actinomycetia;Streptomycetales;Streptomycetaceae;Kitasatospora;Kitasatospora sp. MBT63;Kitasatospora sp. MBT63
Ga0586324_0476544_236_1675	0.00	1822400.00	0.00	0.00	1606800.00	905755.50	0.00	0.00	1012500.00	4211900.00	3801600.00	2932500.00	hypothetical protein	Bacteria;Chlorobi;Ancalorobinae;Ancalorobinales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0477008_720_1673	0.00	0.00	0.00	5263000.00	0.00	0.00	0.00	1067500.00	0.00	0.00	0.00	0.00	uncharacterized 2Fe-2S/4Fe-4S cluster protein (DUF4445 family)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfomonile;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_0477957_17_859	0.00	3651600.00	0.00	4113500.00	10403000.00	0.00	10123200.00	0.00	16848000.00	0.00	0.00	16200000.00	cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1. DSM 6799
Ga0586324_0478838_2_1669	600331.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_0479015_524_1669	0.00	3617600.00	8332400.00	1577000.00	2348400.00	3216132.73	5768400.00	3812500.00	4252500.00	3080000.00	2191200.00	5190000.00	ABC-type transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_0480922_200_622	0.00	26044000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0481767_121_1665	0.00	0.00	0.00	0.00	769793.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	methyl-accepting chemotaxis protein	Bacteria;Caldiseriza;unclassified Caldiseriza;unclassified Caldiseriza;unclassified Caldiseriza;unclassified Caldiseriza;Caldiseriza bacterium JGI 0000059-M03;Caldiseriza bacterium JGI 0000059-M03 (contamination screened)
Ga0586324_0482689_776_1663	0.00	2176000.00	0.00	500688.00	0.00	156157.68	0.00	207031.56	1152000.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_0483823_3_929	0.00	0.00	1158811.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Comeetbacteraceae;Candidatus Comeetbacter;Candidatus Comeetbacter dentrificans;Candidatus Comeetbacter dentrificans Run A D11
Ga0586324_0484262_538_1092	0.00	0.00	0.00	3040000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	L-amino acid N-acyltransferase YncA	Bacteria;Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;unclassified Candidatus Calescamantes;Candidatus Calescamantes bacterium SCGC AAA471-M6;Candidatus Calescamantes bacterium SCGC AAA471-M6 (contamination screened)
Ga0586324_0484747_644_1660	0.00	0.00	0.00	0.00	0.00	1566776.38	0.00	0.00	0.00	0.00	0.00	0.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;intrasporangiaceae;Humibacillus;Humibacillus xanthopallidus;Humibacillus xanthopallidus DSM 21776
Ga0586324_0485533_1_661	0.00	0.00	0.00	0.00	0.00	0.00	580476.00	0.00	0.00	0.00	0.00	0.00	N-methylhydantoinase A/oxoprolinase/acetone carboxylase beta subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324_0487306_1_656	0.00	0.00	1419413.08	0.00	6386000.00	3503703.65	3100800.00	3800300.00	3183300.00	1593900.00	3273600.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0488071_776_1657	0.00	434576.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides;Bacteroides ovatus;Bacteroides ovatus CL02T12C04
Ga0586324_0489048_91_1656	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22725000.00	cytochrome c peroxidase	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_0489420_1_1653	11939339.00	0.00	0.00	4189500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Tom-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteraceae;Flavobacterium;Flavobacterium weaverense;Flavobacterium weaverense DSM 19727
Ga0586324_0490050_300_1652	728800.00	6976800.00	3038370.25	12065000.00	12916200.00	3529330.00	0.00	23411800.00	21287599.47	0.00	650900.80	183702.00	Flp pilus assembly protein TadD	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinifilaceae;Ancylomarina;Ancylomarina subtilis;Ancylomarina subtilis DSM 28825
Ga0586324_0492625_213_1649	1150000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	outer membrane protein assembly factor BamB	Bacteria;Planctomycetes;Planctomycetia;Gemmatales;Gemmataceae;Gemmata;Gemmata obscuriglobus;Gemmata obscuriglobus UC 2246
Ga0586324_0493847_2_1648	0.00	0.00	0.00	0.00	722470.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0496316_1_1644	0.00	653694.20	0.00	0.00	648396.33	0.00	0.00	1049200.00	818100.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E05;Aminicenantes bacterium SCGC AAA255-E05 (contamination screened)
Ga0586324_0496888_1_642	0.00	6310400.00	12160800.00	6621500.00	9723200.00	0.00	6247200.00	4892200.00	4387100.00	7700000.00	8976000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96. DSM 24297
Ga0586324_0500324_1_638	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3041500.00	1416800.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylotenticola;Methylotenticola oryzae;Methylotenticola oryzae 73a
Ga0586324_0501285_2_1198	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1992600.00	0.00	0.00	0.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Paludibacteraceae;Paludibacter;Paludibacter propionicigenes;Paludibacter propionicigenes WB4. DSM 17365
Ga0586324_0501574_177_1637	0.00	0.00	0.00	0.00	0.00	945647.78	0.00	0.00	0.00	0.00	0.00	0.00	heterodisulfide reductase subunit A-like oxiferrredoxin	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyriavorans;Desulfatirhabdium butyriavorans DSM 18734
Ga0586324_0501577_832_1611	0.00	884000.00	0.00	0.00	0.00	7940000.00	0.00	1543300.00	1101600.00	2525600.00	0.00	0.00	CBS domain-containing protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0501784_3_1637	0.00	952000.00	0.00	1729000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	20025000.00	outer membrane receptor protein involved in Fe transport	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_0501861_2_1636	0.00	754800.00	0.00	1909000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter metallireducens;Geobacter metallireducens RCH3
Ga0586324_0502058_1_1635	0.00	7820000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium capsulatum;Acidobacterium capsulatum ATCC 51196
Ga0586324_0502402_1_252	0.00	1863200.00	2919470.28	0.00	1699500.00	1583736.22	1676249.16	1598200.00	1871100.00	3688300.00	4030400.00	5422500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;unclassified Hyphomicrobium;Hyphomicrobium sp. VS
Ga0586324_0502436_2_1297	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	939600.00	0.00	0.00	0.00	ABC-type transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Oxalobacter;Oxalobacter formigenes;Oxalobacter formigenes OXCC13
Ga0586324_0507971_1_1578	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4852500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium valentinum;Bradyrhizobium valentinum LmjM6
Ga0586324_0510685_3_1625	521674.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	201213.75	hypothetical protein	Bacteria;Chloroflexi;Ardenticatenia;Ardenticatenales;Ardenticateraceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Chx-K
Ga0586324_0511939_311_1621	0.00	1319200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter modestus;Edaphobacter modestus DSM 18101
Ga0586324_0513090_2_409	9240000.00	10744000.00	10415500.00	11020000.00	22866000.00	5081600.00	12357600.00	17366700.00	11340000.00	27412000.00	27632000.00	2387500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324_0513275_1201_1539	0.00	0.00	0.00	0.00	0.00	8654600.00	0.00	0.00	0.00	0.00	0.00	0.00	nitrogen regulatory protein PII	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;unclassified Rhodospirillales;unclassified Rhodospirillales;Rhodospirillales bacterium URHD0017;Rhodospirillales bacterium URHD0017
Ga0586324_0514206_746_1618	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2875500.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Thauera;Thauera chlorobenzoica;Thauera chlorobenzoica 3CB-1
Ga0586324_0517271_688_1452	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	182001.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfocurvibacter;Desulfocurvibacter africanus;Desulfovibrio africanus DSM 2603
Ga0586324_0517395_347_967	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1765800.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0518064_1_1613	0.00	0.00	0.00	1771600.00	0.00	0.00	0.00	599196.90	374117.13	1370600.00	1311200.00	587360.25	hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_0521023_2_1609	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1894200.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sophorae;Paenibacillus sophorae S27
Ga0586324_0521281_3_1484	0.00	0.00	0.00	0.00	0.00	877687.60	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Jiangellales;Jiangellaceae;Jiangella;Jiangella rhizosphaerae;Jiangella rhizosphaerae NEAU-YY265
Ga0586324_0525804_3_1055	0.00	0.00	0.00	3743000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfoluna;Desulfoluna acetoxidans;Desulfoluna acetoxidans ASRB2. DSM 11109
Ga0586324_0526838_1_1062	0.00	0.00	0.00	1244500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type transport system substrate-binding protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus fonticola;Paenibacillus fonticola DSM 21315
Ga0586324_0527464_3_1601	0.00	1217200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteraceae;Flavobacterium;Flavobacterium fluvii;Flavobacterium fluvii DSM 19978
Ga0586324_0528358_1339_1599	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	289497.12	0.00	0.00	osmotically-inducible protein OsmY	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Steroliibacteraceae;Steroliibacterium;Steroliibacterium dentrificans;Steroliibacterium dentrificans Chol
Ga0586324_0528865_1_822	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	625263.10	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Collimonas;Collimonas sp. OK607;Collimonas sp. OK607
Ga0586324_0530916_853_1596	2180000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	signal transduction protein with GAF and PtsI domain	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfoluna;Desulfoluna acetoxidans;Desulfoluna acetoxidans ASRB2. DSM 11109
Ga0586324_0531432_263_1414	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3231900.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax antarcticus;Rhodoferax antarcticus DSM 24876
Ga0586324_0533600_43_1593	0.00	0.00	0.00	1320500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TonB-dependent SusC/RagA subfamily outer membrane receptor	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Paludibacteraceae;Paludibacter;Paludibacter propionicigenes;Paludibacter propionicigenes WB4. DSM 17365
Ga0586324_0534969_2_1084	0.00	0.00	28206300.00	22990000.00	0.00	22572000.00	0.00	16038000.00	23793000.00	18832000.00	17775000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfoluna;Desulfoluna acetoxidans;Desulfoluna acetoxidans ASRB2. DSM 11109
Ga0586324_0536776_1_831	0.00	3080400.00	10021400.00	4759500.00	6581700.00	6788700.00	4149600.00	3965000.00	4017600.00	4981900.00	4796000.00	4717500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta prote

Ga0586324_0623202_291_1031	7170000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0623578_1_1170	0.00	12512000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	arylsulfatase A-like enzyme	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter modestus;Edaphobacter modestus DSM 18101
Ga0586324_0624186_2_1489	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	854700.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus sophorae;Paenibacillus sophorae S27
Ga0586324_0625040_3_1487	0.00	2876400.00	0.00	3885500.00	3399000.00	0.00	0.00	2232600.00	0.00	9463300.00	0.00	10620000.00	Ca2+ binding RTX toxin-like protein	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Aquaspirillum;Aquaspirillum serpens;Aquaspirillum serpens DSM 68
Ga0586324_0626027_780_1448	0.00	0.00	0.00	2954500.00	0.00	0.00	0.00	0.00	0.00	1540000.00	0.00	2010000.00	corrinoid protein of di/trimethylamine methyltransferase	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Alkalispirochaeta;Alkalispirochaeta odontotermitis;Alkalispirochaeta odontotermitis JC202
Ga0586324_0627586_9_1352	0.00	0.00	0.00	0.00	0.00	2170537.95	0.00	0.00	0.00	0.00	0.00	0.00	long-subunit fatty acid transport protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum;Desulfotignum phosphitoxidans;Desulfotignum phosphitoxidans FiPS-3, DSM 13687
Ga0586324_0628742_32_1483	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1207500.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Hymenobacteraceae;Hymenobacter;Hymenobacter sp. YR204;Hymenobacter sp. YR204
Ga0586324_0629515_2_1483	0.00	359179.40	0.00	0.00	1843700.00	0.00	0.00	1561600.00	899100.00	2733500.00	0.00	1830000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Granulicella;Granulicella aggregans;Granulicella aggregans MBLP14
Ga0586324_0630029_3_1481	0.00	0.00	0.00	2875910.97	2033000.00	10238200.00	0.00	3602400.00	0.00	5467500.00	0.00	2261600.00	2850000.00	hypothetical protein
Ga0586324_0631260_36_1481	0.00	0.00	0.00	0.00	0.00	0.00	4525800.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted molibdopterin-dependent oxidoreductase YieC
Ga0586324_0631499_1_99	17000000.00	897600.00	24659400.00	0.00	0.00	0.00	0.00	921100.00	14985000.00	0.00	5112800.00	0.00	translation elongation factor EF-Tu-like GTPase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Brucellaceae;Brucella;Brucella ovis
Ga0586324_0631655_1_1482	7220000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	glucose/arabinose dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Brucellaceae;Brucella;Brucella ovis
Ga0586324_0631789_1_702	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7875000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylosinus;Methylosinus trichosporium;Methylosinus trichosporium OB3b
Ga0586324_0634904_2_1288	6050000.00	0.00	0.00	9880000.00	0.00	0.00	0.00	0.00	0.00	21868000.00	11704000.00	1725000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia caffeinilytica;Paraburkholderia caffeinilytica CF1
Ga0586324_0637655_1_1278	0.00	1747600.00	0.00	3486500.00	2739800.00	0.00	1307874.12	2324100.00	1782000.00	0.00	0.00	0.00	NodT family efflux transporter outer membrane factor (OMF) lipoprotein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;Methylocystis;Methylocystis parvus;Methylocystis parvus OBBP
Ga0586324_0638644_251_1474	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1701700.00	0.00	0.00	hypothetical protein	
Ga0586324_0640389_3_1472	0.00	58647.72	1036865.84	0.00	2904600.00	0.00	0.00	2858971.79	2389500.00	4159300.00	831154.72	0.00	hypothetical protein	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Calditrix;Calditrix abysssi;Calditrix abysssi LF13, DSM 13497
Ga0586324_0640602_841_1275	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	816324.08	0.00	cytoskeletal protein CcmA (bactofilin family)	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0640650_3_1472	0.00	0.00	0.00	2945000.00	0.00	0.00	0.00	0.00	1631870.55	0.00	0.00	0.00	hypothetical protein	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira lenta;Nitrospira lenta N. lenta BS10
Ga0586324_0641639_508_1470	0.00	0.00	0.00	0.00	0.00	8416400.00	0.00	0.00	0.00	0.00	10824000.00	0.00	alkyl sulfatase BDS1-like metallo-beta-lactamase superfamily hydrolase	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina mazei;Methanosarcina mazei S-6
Ga0586324_0641859_287_1414	20300000.00	8173600.00	6530800.00	0.00	2482300.00	5637400.00	51938400.00	50782500.00	7558217.73	35512400.00	29190601.44	1845000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum;Desulfotignum balticum;Desulfotignum balticum DSM 7044
Ga0586324_0644740_374_931	0.00	3454400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3405000.00	lipid-binding SYLF domain-containing protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter luteus;Methylobacter luteus IMV-B-3098
Ga0586324_0645937_823_1467	0.00	0.00	0.00	0.00	0.00	4962500.00	0.00	0.00	0.00	4265800.00	0.00	2767500.00	hypothetical protein	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0647176_397_1299	843312.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2137500.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Syntrophomonadaceae;Dethiobacter;Dethiobacter alkaliphilus;Dethiobacter alkaliphilus AHT1
Ga0586324_0647673_1_1464	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	990000.00	TonB-linked SusC/RagA family outer membrane protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cyclobacteriaceae;Lunatimonas;Lunatimonas lonarensis;Lunatimonas lonarensis AK24
Ga0586324_0648793_854_1462	0.00	7140000.00	0.00	0.00	0.00	0.00	0.00	1104100.00	0.00	0.00	0.00	0.00	transketolase N-terminal domain/subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas methanica;Methylomonas methanica MC09
Ga0586324_0649312_3_1013	0.00	391350.20	0.00	0.00	3677100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	type II secretory pathway component GspD/PulD (secretin)	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0652207_294_1460	0.00	384393.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type multidrug transport system fused ATPase/permease subunit	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Chitinophaga;Chitinophaga niabensis;Chitinophaga niabensis DSM 24787
Ga0586324_0654594_73_1428	21000000.00	16592000.00	40254500.00	0.00	0.00	40216100.00	12631200.00	0.00	0.00	0.00	0.00	11250000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0654702_1_1457	0.00	8568000.00	0.00	0.00	16150400.00	0.00	10237200.00	11584878.44	20355300.00	11195800.00	3212000.00	7192500.00	outer membrane receptor for ferrientero chelin and colicin	Bacteria;Proteobacteria;Gammaproteobacteria;Thermoanaerobacales;Thermoanaerobacalaceae;Moorella;Thermoanaerobacium;Thermoanaerobacium aouaticum;Thermoanaerobacium aouaticum MP-01
Ga0586324_0654815_217_1326	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	265678.16	1147500.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Azospirillaceae;Azospirillum;Azospirillum brasilense;Azospirillum brasilense MTCC 4039
Ga0586324_0656114_1_1350	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	823900.00	0.00	0.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_0662689_248_1450	699082.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Terriglobus;Terriglobus roseus;Terriglobus roseus ABS5.6
Ga0586324_0664301_1_480	510850.00	461017.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	156670.36	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Spirosoma;Spirosoma linguale;Spirosoma linguale DSM 74
Ga0586324_0666656_1_1446	0.00	0.00	0.00	0.00	2090900.00	0.00	0.00	1073600.00	0.00	1216600.00	1408000.00	1417500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aseroeatus;Bryobacter aseroeatus DSM 18758
Ga0586324_0667440_1_1446	0.00	1326000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0667647_118_990	0.00	53788000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1469600.00	0.00	HK97 family phage major capsid protein	
Ga0586324_0667693_1121_1444	0.00	7956000.00	0.00	0.00	11433000.00	0.00	0.00	12200000.00	26406000.00	0.00	11616000.00	4597500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_0667693_3_596	0.00	5239353.68	0.00	0.00	872084.64	0.00	0.00	2952400.00	0.00	327614.98	6899200.00	5644442.25	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium petroleiphilum;Methylibium petroleiphilum PM1
Ga0586324_0668343_966_1445	0.00	0.00	0.00	0.00	2822200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	reeulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculacae;Thermoanaerobaculum;Thermoanaerobaculum aouaticum;Thermoanaerobaculum aouaticum MP-01
Ga0586324_0671861_794_1441	0.00	6004400.00	44195500.00	45030000.00	50058000.00	22390800.00	69768000.00	15677000.00	20817000.00	11396000.00	5984000.00	3450000.00	hypothetical protein	Bacteria;Deferribacteres;Deferribacteres;Deferribacteriales;Deferribacteraceae;Deferribacter;Deferribacter desulfuricans;Deferribacter desulfuricans SSM1
Ga0586324_0672599_3_1442	24200000.00	9656000.00	0.00	0.00	13699000.00	0.00	0.00	0.00	20898000.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methylocean;Methylocean superfactus;Methylocean superfactus R-67175
Ga0586324_0672829_1_1116	0.00	2822000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1801800.00	1865600.00	0.00	hypothetical protein	
Ga0586324_0676300_2_1438	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2519100.00	1001000.00	4655200.00	0.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylotenticola;Methylotenticola oryzae;Methylotenticola oryzae 73a
Ga0586324_0677737_239_787	0.00	0.00	0.00	0.00	1442000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatalans;Desulfatalans anilini;Desulfatalans anilini DSM 4660
Ga0586324_0679426_461_1435	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	113567.25	cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfocurvibacter;Desulfobacter africanus;Desulfobacter africanus Walvis Bay
Ga0586324_0679987_1_726	0.00	0.00	0.00	2413000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Brucellaceae;Brucella;Brucella ovis
Ga0586324_0680719_2_1432	3700000.00	7330400.00	0.00	0.00	0.00	1772189.28	1091900.00	1790100.00	5443900.00	4004000.00	7560000.00	0.00	subtilisin family serine protease	Bacteria;Chlorflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_0682989_3_1430	1850000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus beijingensis;Paenibacillus beijingensis DSM 24997
Ga0586324_0685542_262_1380	6220000.00	6840800.00	14207198.03	12179000.00	4429000.00	0.00	20149185.12	42456000.00	24543000.00	14306600.00	8641600.00	26047500.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0686148_620_1429	0.00	0.00	47629800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	DNA-binding GntR family transcriptional regulator	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Methylibium;Methylibium petroleiphilum;Methylibium petroleiphilum PM1
Ga0586324_0686314_2_1429	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14168000.00	0.00	0.00	ABC-type transport system substrate-binding protein	Bacteria;Chlorflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_0686655_214_1428	2120000.00	2026400.00	2402304.11	0.00	0.00	1923500.73	0.00	1988600.00	1790100.00	3595900.00	4347200.00	2557500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;unclassified Acidobacteraceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_0688744_1_477	0.00	0.00	0.00	0.00	3326900.00	468372.66	0.00	707600.00	751275.00	0.00	0.00	0.00	peroxiredoxin	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0688937_238_1242	8710000.00	2754000.00	3117732.66	5253000.00	5253000.00	5041900.00	4378800.00	4378800.00	7500600.00	17710000.00	3062400.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia cepacia complex;Burkholderia cepacia complex GG4;Burkholderia cepacia GG4 chromosome II
Ga0586324_0690399_2_883	0.00	1822400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	215801.52	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;unclassified Rhodothermaceae;Rhodothermaceae bacterium RA;Halothermothamnus malaysiensis RA
Ga0586324_0692256_402_1424	39050000.00	25160000.00	30514600.00	3363000.00	0.00	50498400.00	59721127.56	27267000.00	31266000.00	17332700.00	27174400.00	19950000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Quisquilibacterium;Quisquilibacterium transsilvanicum;Quisquilibacterium transsilvanicum DSM 29781
Ga0586324_0693875_748_1152	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1955800.00	0.00	0.00	predicted flap endonuclease-1-like 5' DNA nuclease	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Roseospirillum;Roseospirillum parvum;Roseospirillum parvum 930I
Ga0586324_0694573_2_631	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3819200.00	0.00	hypothetical protein	
Ga0586324_0695138_1_1419	0.00	0.00	0.00	0.00	4398100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Brucellaceae;Brucella;Brucella ovis
Ga0586324_0696161_151_1146	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16533000.00	0.00	0.00	0.00	0.00	tripartite ATP-independent transporter DctP family solute receptor	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Sporomusaceae;Anaeropropora;Anaeropropora hongkongensis;DSM 15969
Ga0586324_0696509_1_224	10400000.00	9044000.00	0.00	0.00	0.00	19570000.00	18500200.00	11787600.00	13603000.00	10773000.00	0.00	3696000.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0701924_2_1096	0.00	0.00	0.00	0.00	0.00	934811.93	0.00	0.00	0.00	0.00	2725800.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Janthinobacterium;Janthinobacterium sp. CG3;Janthinobacterium sp. CG3
Ga0586324_0702425_268_1413	0.00	9384000.00	0.00	0.00	0.00	0.00	33880800.00	13298000.00	13298000.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Methylocean;Methylocean superfactus;Methylocean superfactus R-67175
Ga0586324_0705170_291_1412	28050000.00	25071600.00	10373128.62	2567850.00	33538498.47	10083800.00	192432000.00	31219800.00	32634900.00	17748500.00	123200000.00	15787500.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Thiotrichales;Thiothrix;Thiothrix nivea;Thiothrix eikelboria;Thiothrix eikelboria D-3
Ga0586324_0705441_354_1034	0.00	0.00	0.00	0.00	0.00	0.00	0.00	171426.47	0.00	0.00	0.00	0.00	putative intracellular protease/amidase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. NpAV;Nitrosospira sp. NpAV
Ga0586324_0706703_711_1409	1190000.00	3134800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Quisquilibacterium;Quisquilibacterium transsilvanicum;Quisquilibacterium transsilvanicum DSM 29781
Ga0586324_0710811_144_1407	0.00	523323.24	0.00	0.00	0.00	0.00	0.00	0.00	2316600.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta isovalerica;Spirochaeta isovalerica DSM 2461
Ga0586324_0711829_115_996	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9450000.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas;Pseudoxanthomonas spadix;Pseudoxanthomonas spadix BD-a59
Ga0586324_0712841_1_1404	7640000.00	4549200.00	1946758.29	2251500.00	2997300.00	8972200.00	7774800.00	2934100.00	2583900.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0713593_419_1306	0.00	0.00	0.00	0.00	0.00	564133.03	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_0714763_496_1341	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2802800.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas;Pseudomonas abietaniphila;Pseudomonas abietaniphila LMG 20220
Ga0586324_0716829_3_1400	0.00	2264400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0718031_3_701	1160000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	850500.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Thiotrichales;Gemmamonas;Gemmamonas phototrophica;Gemmamonas phototrophica AP64
Ga0586324_0719362_580_852	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1223100.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium;Phenylobacterium sp. Root77;Phenylobacterium sp. Root77
Ga0586324_0720194_313_1044	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2825900.00	2622400.00	1845000.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurihabdus;Sulfurihabdus autotrophica;Sulfurihabdus autotrophica DSM 100309
Ga0586324_0721328_666_1397	0.00	0.00	0.00	0.00	0.00	6828400.00	0.00	0.00	0.00	0.00	0.00	0.00	RND family efflux transporter MFP subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfoprunum;Desulfoprunum benzoelyticum;Desulfoprunum benzoelyticum DSM 28570
Ga0586324_0724213_688_1395	0.00	0.00	0.00	0.00	0.00	1697232.57	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia;Ralstonia solanacearum;Ralstonia solanacearum PSI07
Ga0586324_0726582_1_1392	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2109800.00	0.00	0.00	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase family)	Bacteria;Firmicutes;Clostridia;Halanaerobiales;unclassified Halanaerobiales;Anoxybacter;Anoxybacter fermentans;Anoxybacter fermentans DY22613
Ga0586324_0728827_1_857	3450000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	outer membrane receptor protein involved in Fe transport	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-N07;Aminicenantes bacterium SCGC AAA252-N07 (contamination screened)
Ga0586324_0731099_286_771	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1944000.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira sp. NO1;Nitrospira sp. NO1
Ga0586324_0731822_1_1389	0.00	0.00	0.00	0.00	0.00	0.00	0.00	695400.00	0.00	0.00	0.00	0.00	heterodisulfide reductase subunit A-like polyferredoxin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0732096_268_1389	115260000.00	14557440.00	45833216.33	2527000.00	10434930.00	7146000.00	100502400.00	20569800.00	50827500.00	125710200.00	79299528.00	3675000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Aquaspirillum;Aquaspirillum sp. LM1;Aquaspirillum sp. LM1
Ga0586324_0732414_3_1388	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11664000.00	0.00	0.00	0.00	alkylation response protein AidB-like acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum;Desulfotignum phosphitoxidans;Desulfotignum phosphitoxidans DSM 22410
Ga0586324_0733230_497_1096	0.00	0.00	4553352.58	3401000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	shasin family arsenite	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Paucibacter;Paucibacter oligotrophus;Paucibacter oligotrophus S00239
Ga0586324_0734409_2_1228	0.00	9248000.00	17058900.00	11115000.00	11433000.00	13339200.00	13885200.00	8967000.00	8667000.00	28721000.00	20064

Ga0586324_0832278_182_1264	24220000.00	0.00	0.00	5681000.00	33568892.74	12428589.19	27382800.00	22185700.00	22477500.00	15700300.00	596264.24	4177500.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Aquincola;Aquincola tertiaricarbonis;Aquincola tertiaricarbonis MIMtkpLc11
Ga0586324_0837258_3_1310	6230000.00	897600.00	0.00	0.00	0.00	0.00	6641530.56	0.00	12789900.00	2186800.00	5517600.00	1650000.00		hypothetical protein	Bacteria;Atribacterota;unclassified Atribacterota;unclassified Atribacterota;unclassified Atribacterota;unclassified Atribacterota;Atribacteria bacterium SCGC AB-164-P05;Atribacteria bacterium SCGC AB-164-P05 (contamination screened)
Ga0586324_0838761_95_1177	0.00	0.00	0.00	0.00	0.00	1411898.74	0.00	0.00	0.00	0.00	0.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium JOSHI_001;Burkholderiales sp. JOSHI_001
Ga0586324_0842214_2_952	7520000.00	6772800.00	22873734.25	7742500.00	11999500.00	0.00	0.00	6380600.00	5386500.00	0.00	0.00	2632500.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Erythrobacter;Erythrobacter neustonensis;Erythrobacter neustonensis DSM 9434
Ga0586324_0843122_1_636	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1410000.00		hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_0844806_1_1284	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3015000.00		Ni,Fe-hydrogenase I large subunit	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfosporosinus;Desulfosporosinus sp. HMP52;Desulfosporosinus sp. HMP52
Ga0586324_0845207_38_1306	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2955000.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium labiatii;Bradyrhizobium labiatii GA5499
Ga0586324_0856097_3_875	24730000.00	33857200.00	0.00	35340000.00	8807205.55	0.00	6452400.00	61830758.39	8829000.00	69270000.80	68393600.00	54082500.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Duganella;Duganella sp. Leaf61;Duganella sp. Leaf61
Ga0586324_0856904_633_1211	0.00	0.00	0.00	0.00	0.00	0.00	28728000.00	0.00	0.00	0.00	0.00	0.00		rubrerythrin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_0859217_289_1296	0.00	0.00	0.00	0.00	811896.47	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324_0861778_3_1133	0.00	0.00	0.00	2769250.00	13184000.00	0.00	0.00	0.00	0.00	3226300.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Betaproteobacteria;unclassified Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiosphilus;Thiobacillus thiosphilus DSM 19892
Ga0586324_0864959_495_1292	0.00	0.00	0.00	1149500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Azospirillum;Azospirillum sp. TSA2s;Azospirillum sp. TSA2s
Ga0586324_0865959_336_1292	0.00	0.00	0.00	0.00	0.00	687099.81	0.00	1000400.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-D06;Aminicenantes bacterium SCGC AAA252-D06 (contamination screened)
Ga0586324_0867371_244_1290	11100000.00	2801600.00	0.00	13575500.00	3790400.00	0.00	0.00	0.00	0.00	12766660.00	4382400.00	3885000.00		hypothetical protein	
Ga0586324_0870941_126_695	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2656800.00	2094400.00	3581600.00	2932500.00	0.00		osmotically-inducible protein OsmY	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_0871187_531_1289	0.00	3039600.00	47161221.51	11685000.00	8899200.00	11195400.00	5266800.00	2141100.00	4179600.00	1955800.00	4153600.00	2812500.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus oleovorans;Desulfococcus oleovorans Hxd3
Ga0586324_0875604_1_360	0.00	3236800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azoneuraceae;Dechloromonas;Dechloromonas dentrificans;Dechloromonas dentrificans ATCC BAA-841
Ga0586324_0875963_129_1286	3350000.00	7208000.00	0.00	5728500.00	6725900.00	0.00	4582800.00	6063400.00	6147900.00	3241700.00	3766400.00	3607500.00		subtilisin family serine protease	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Woeseiaceae;unclassified Woeseiaceae;uncultured Woeseiaceae SAG 1868_B
Ga0586324_0880334_3_1232	0.00	1489200.00	0.00	1919000.00	0.00	0.00	0.00	0.00	2907900.00	0.00	1126400.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0881612_326_1282	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3483100.00	0.00	4727800.00	6740800.00	4425000.00		hypothetical protein	Bacteria;Acidobacteria;Betaproteobacteria;unclassified Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiosphilus;Thiobacillus thiosphilus DSM 19892
Ga0586324_0882006_850_1281	0.00	0.00	0.00	0.00	0.00	6590200.00	0.00	0.00	0.00	0.00	0.00	0.00		membrane protease subunit (stomatin/prohibitin family)	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Pelolinea;Pelolinea submarina;Pelolinea submarina DSM 23923
Ga0586324_0882864_722_1174	3050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0883910_2_1279	0.00	5671200.00	0.00	0.00	0.00	0.00	3214800.00	0.00	0.00	0.00	2455200.00	3330000.00		hypothetical protein	
Ga0586324_0884729_208_1281	1920000.00	1611600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	513137.24	0.00	0.00		arylsulfatase A-like enzyme	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. URHA0002;Bradyrhizobium sp. URHA0002
Ga0586324_0886746_1_1083	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7476300.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Thermoeutrtaceae;Thermopeutta;Thermopeutta terrifontis;Thermopeutta terrifontis R1
Ga0586324_0890948_1_1092	6330000.00	0.00	0.00	5491000.00	5623800.00	0.00	0.00	0.00	6561000.00	0.00	6520800.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Rugosibacter;Rugosibacter aromaticivorans;Rugosibacter aromaticivorans PG1-Ca6
Ga0586324_0893399_907_1275	0.00	3719600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0893500_2_1273	0.00	5440000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfofustis;Desulfofustis glycolicus;Desulfofustis glycolicus DSM 9705
Ga0586324_0894461_375_1274	0.00	0.00	2548571.51	0.00	4243600.00	0.00	0.00	1806400.00	0.00	0.00	2833600.00	0.00		membrane protease subunit (stomatin/prohibitin family)	Archaea;Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;Aigarchaeota archaeon JGI 0000106-J15;Aigarchaeota archaeon JGI 0000106-J15 (contamination screened)
Ga0586324_0896139_479_982	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7793525.64	4294000.00	0.00	0.00	0.00		ferritin-like metal-binding protein YciE	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Rhizobium;Rhizobium leguminosarum;Rhizobium leguminosarum ATCC 14479
Ga0586324_0896683_1_875	1970000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter modestus;Edaphobacter modestus DSM 18101
Ga0586324_0899242_2_889	372166.00	986000.00	189514.81	763190.10	739030.15	142106.55	488895.84	713700.00	601591.05	793100.00	775539.60	1080000.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_0900074_665_1270	0.00	1774800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Cytophaga;Cytophaga aurantiaca;Cytophaga aurantiaca DSM 3654
Ga0586324_0901930_48_1004	0.00	0.00	4430900.08	0.00	0.00	0.00	0.00	0.00	2891700.00	0.00	0.00	0.00		predicted flap endonuclease-1-like 5' DNA nuclease	Bacteria;Aquificae;Aquificae;Desulfurobacteriales;Desulfurobacteriaceae;Thermovibrio;Thermovibrio ammonificans;Thermovibrio ammonificans HB-1
Ga0586324_0903654_1_269	0.00	2420800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	629949.32	0.00	0.00		D-xylose ABC transporter substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Leviliniea;Leviliniea saccharolytica;Leviliniea saccharolytica DSM 16555
Ga0586324_0910832_959_1264	27800000.00	27540000.00	39353700.00	32870000.00	53560000.00	42876000.00	69084000.00	7076000.00	8100000.00	6575800.00	78584000.00	69300000.00		predicted porin	
Ga0586324_0912481_2_1264	0.00	0.00	0.00	2270500.00	1023153.59	0.00	0.00	0.00	1223100.00	650183.38	0.00	0.00		hypothetical protein	
Ga0586324_0913927_3_722	4170000.00	3481600.00	0.00	2175500.00	3285700.00	0.00	0.00	3702700.00	0.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium UKL13-2;Betaproteobacteria bacterium UKL13-2
Ga0586324_0914692_133_1260	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1670800.00	0.00		hypothetical protein	Bacteria;Rhodothermaeota;Rhodothermia;Rhodothermales;Rhodothermaceae;Rubrivirga;Rubrivirga marina;Rubrivirga marina SAORIC-28
Ga0586324_0915873_2_937	0.00	1203600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0916226_1_351	0.00	583516.16	0.00	0.00	0.00	0.00	0.00	0.00	996300.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0919283_2_526	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7241400.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_0926379_3_1256	0.00	2794800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium;Flavobacterium circumlabens;Flavobacterium circumlabens PS626
Ga0586324_0927304_1_2254	1470000.00	441278.52	287220.08	0.00	0.00	0.00	0.00	0.00	0.00	3013927.84	1848000.00	0.00		ABC-type xylose transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticateria;Ardenticatenales;Ardenticateraceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324_0929048_1_1254	0.00	0.00	1831126.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;DesulfoBulbus;Desulfobulbus laoticus;Desulfobulbus laoticus DSM 18378
Ga0586324_0931941_4_708	0.00	0.00	11034800.00	2346500.00	40994000.00	42876000.00	32604000.00	24766000.00	30537000.00	12936000.00	0.00	8100000.00		peptidoglycan hydrolase CwlO-like protein	Bacteria;Proteobacteria;Gammaproteobacteria;Ignatzschineria;Ignatzschineria ureiphila;Ignatzschineria ureiphila strain Mat5-16, JCM 16511
Ga0586324_0932511_285_1250	0.00	0.00	0.00	3809500.00	1606800.00	2533141.87	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0933126_3_1250	0.00	0.00	7600500.00	14725000.00	13802000.00	4605200.00	0.00	0.00	13527000.00	0.00	5376800.00	0.00		formyltetrahydrofolate synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_0933217_328_1251	41970000.00	30008400.00	37419068.73	55670000.00	70307800.00	34578700.00	24076800.00	53497000.00	25531200.00	16793700.00	30272000.00	14932500.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax sp. 2AP
Ga0586324_0934620_2_1249	0.00	0.00	0.00	0.00	1236000.00	0.00	0.00	388020.39	0.00	2594900.00	1346400.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_0935747_3_515	0.00	4508400.00	20155400.00	0.00	0.00	9686800.00	17578800.00	7991000.00	7476300.00	0.00	8272000.00	6952500.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium symbiodeficiens;Bradyrhizobium symbiodeficiens BSS1MIB
Ga0586324_0938334_3_887	0.00	0.00	0.00	0.00	0.00	0.00	1117464.48	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0939811_1_1248	0.00	3298000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus durus;Paenibacillus durus VPI 6563-1
Ga0586324_0940624_1_1245	0.00	1346400.00	0.00	0.00	0.00	328303.12	4058400.00	2470500.00	2114100.00	3826900.00	1645600.00	3000000.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiogranum;Thiogranum longum;Thiogranum longum DSM 19610
Ga0586324_0942165_2_973	4790000.00	2182800.00	2702624.15	4398500.00	3790400.00	0.00	9120000.00	6426063.80	7978400.00	4412100.00	3819200.00	7050000.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Fluviicoccus;Fluviicoccus keumensis;Fluviicoccus keumensis DSM 105135
Ga0586324_0942710_3_467	0.00	0.00	0.00	0.00	0.00	500987.88	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Siphonobacter;Siphonobacter sp. BAB-5405;Siphonobacter sp. BAB-5405
Ga0586324_0943400_3_1244	5710000.00	6052000.00	0.00	1330000.00	3285700.00	2363940.47	0.00	1384700.00	1838700.00	5728800.00	2244000.00	1672500.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_0945992_264_1244	776679.00	1774800.00	0.00	0.00	0.00	1761300.00	0.00	0.00	1213900.00	691265.34	1247400.00	994400.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Rhodocyclus;Rhodocyclus tenuis;Rhodocyclus tenuis DSM 109
Ga0586324_0948965_219_791	0.00	2033200.00	0.00	3743000.00	0.00	0.00	0.00	0.00	0.00	5678100.00	0.00	0.00		lipid-binding SYLF domain-containing protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Roseobacteraceae;Ruegeria;Ruegeria atlantica;Ruegeria atlantica CECT 4293
Ga0586324_0952320_966_1241	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1987500.00		hypothetical protein	
Ga0586324_0954743_291_623	5290000.00	0.00	0.00	0.00	0.00	0.00	12783400.00	9188400.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_0956657_669_1238	0.00	0.00	4257360.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		poly(hydroxyalkanoate) granule-associated protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP65;Rubrivivax sp. AAP65
Ga0586324_0957269_3_884	184078.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0957735_1_1236	0.00	870400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	885500.00	0.00	0.00		hypothetical protein	
Ga0586324_0960131_1_1194	0.00	809200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0966067_3_980	0.00	562771.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1695000.00		uncharacterized protein (DUF2252 family)	Bacteria;Actinobacteria;Actinomycetia;Streptomycetales;Streptomycetaceae;Streptomyces;Streptomyces sp. TLI_053;Streptomyces sp. TLI_053
Ga0586324_0969107_1054_1230	3710000.00	19176000.00	0.00	8151000.00	49543000.00	0.00	0.00	1708000.00	42201000.00	35776000.00	0.00	0.00		predicted porin	
Ga0586324_0969709_126_1229	0.00	4848400.00	0.00	0.00	2461700.00	0.00	0.00	0.00	0.00	0.00	0.00	1500000.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium zhanjiangense;Bradyrhizobium zhanjiangense CCBAU 51778
Ga0586324_0970199_2_1117	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3294000.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;unclassified Candidatus Marinimicrobia;Marinimicrobia bacterium SCGC AAA257-N23;Marinimicrobia bacterium SCGC AAA257-N23 (contamination screened)
Ga0586324_0971183_272_1228	0.00	0.00	0.00	0.00	0.00	0.00	1152261.84	1335900.00	1628100.00	3072300.00	0.00	3022500.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus sp. KH32C;Azoarcus sp. KH32C
Ga0586324_0977936_3_371	0.00	0.00	0.00	0.00	0.00	3469780.00	0.00	0.00	0.00	0.00	0.00	4290000.00		predicted 2n-dependent protease	
Ga0586324_0979697_3_1103	0.00	0.00	0.00	0.00	0.00	0.00	5152800.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter soli;Geobacter soli GS501
Ga0586324_0985984_3_1220	0.00	0.00	0.00	5434000.00	2987000.00	1854633.14	0.00	768600.00	332759.34	0.00	0.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Hymenobacteraceae;Pontibacter;Pontibacter sp. S10-8;Pontibacter sp. S10-8
Ga0586324_0988266_309_1220	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2068000.00	0.00		hypothetical protein	Bacteria;Nitrospirae;Nitrospiria;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira japonica;Nitrospira japonica NJ11
Ga0586324_0990923_1_995	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6150000.00		Fe-S oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_0991056_1_771	9630000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0994704_156_1217	12900000.00	4399600.00	13737200.00	0.00	0.00	10679300.00	5198400.00	4367600.00	3539700.00	7777000.00	9064000.00	6270000.00		hypothetical protein	
Ga0586324_0995456_178_735	0.00	2461600.00	0.00	1824000.00	5386900.00	0.00	0.00	0.00	0.00	0.00	2543200.00	2422500.00		phasin family protein	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Andreprevotia;Andreprevotia chitinilytica;Andreprevotia chitinilytica DSM 18519
Ga0586324_0995897_1_279	0.00	0.00	0.00	0.00	7381500.00	3131200.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324_0997304_137_1063	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11473000.00	12777600.00	3592500.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Rhodoferax;Rhodoferax sp. TH121;Rhodoferax sp. TH121
Ga0586324_1004304_684_1211	0.00	4569600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		CBS domain-containing protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_1004564_625_1212	0.00	0.00	0.00	0.00	343602.85	0.00	0.00	19818.05	0.00	0.00	0.00	33838.28		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324_1005885_25_1140	56850000.00	20723000.00	34969607.74	94751286.20	141681181.35	83647900.00	172026000.00	71026255.24	91794852.18	33067599.18	121501600.00	84810000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter delicatus;Curvibacter delicatus NBRC 14919
Ga0586324_1006231_414_1211	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5728800.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;beta proteobacterium AAP65;Rubrivivax sp. AAP65
Ga0586324_1008183_79_1146	0.00	0.00	0.00	4047000.00	3965500.00	2558712.64	1763716.80	2000800.00	2316600.00	0.00	0.00	0.00		sienal transduction protein with GAF and PtsI domain	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1008977_395_1210	19000000.00	18482400.00	9514700.00	15361500.00	16304900.00	12505500.00	14037383.16	18885600.00	53411400.00	15723400.00	13886400.00	10320000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. C04;Polaromonas sp. C04
Ga0586324_1009347_352_858	0.00	0.00	0.00	0.00	0.00	12386400.00	0.00	549600.00	0.00	0.00	0.00	0.00		tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1009697_343_1185	43300000.00	31892000.00	85688600.00	46569000.00	68495000.00	0.00	0.00	0.00	0.00	0.00	0.00	33900000.00		hypothetical protein	
Ga0586324_1011537_53_1207	0.00	0.00	1095513.55	0.00	0.00	0.00	0.00	544171.85	1717200.00	3003000.00

Ga0586324_1112253_421_1161	10100000.00	3284400.00	3118333.88	3952000.00	6674400.00	2162232.71	0.00	0.00	38151000.00	0.00	0.00	2925000.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_1112219_1_1161	0.00	1373600.00	0.00	1282500.00	1606800.00	0.00	848574.96	483997.79	718596.36	0.00	0.00	1057500.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_1113574_302_1159	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	772500.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micromonosporales;Micromonosporaceae;Micromonospora;Micromonospora rhizophaerae;Micromonospora rhizophaerae DSM 45431
Ga0586324_1113723_1_1158	3030000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia;Burkholderia sp. H160;Burkholderia sp. H160
Ga0586324_1113878_381_1160	0.00	0.00	0.00	515045.35	581950.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized protein YofA (UPF0365 family)	Bacteria;Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;unclassified Verrucomicrobia;Verrucomicrobia bacterium LW23;Verrucomicrobia bacterium LW23
Ga0586324_1114174_3_1160	0.00	707200.00	0.00	764819.35	843057.06	0.00	0.00	273291.59	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas sp. EUR3 1.2.1;Polaromonas sp. EUR3 1.2.1
Ga0586324_1114201_2_646	4260000.00	0.00	0.00	0.00	0.00	0.00	0.00	2531500.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Yoonia;Yoonia vestfoldensis;Loktanella vestfoldensis DSM 16212
Ga0586324_1114764_3_881	0.00	0.00	0.00	600179.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324_1115828_1_315	0.00	0.00	0.00	0.00	6736200.00	0.00	0.00	3574600.00	3750300.00	3773000.00	0.00	2670000.00	hypothetical protein	
Ga0586324_1115917_364_1158	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2917500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii USDA 76
Ga0586324_1117630_172_1158	6910000.00	7684000.00	0.00	8673500.00	9517200.00	7543000.00	13292400.00	7564000.00	5086800.00	6899200.00	6476800.00	0.00	uncharacterized protein (TIGR02001 family)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. YR681;Bradyrhizobium sp. YR681
Ga0586324_1119900_145_969	332519.00	1285200.00	12723800.00	227576.30	0.00	0.00	1527611.40	0.00	0.00	0.00	0.00	0.00	DNA-binding MurR/RpiR family transcriptional regulator	Bacteria;Chlorroflexi;Ktedonobacteria;Ktedonales;Ktedonobacteraceae;Dictyobacter;Dictyobacter aurantiacus
Ga0586324_1121337_3_1157	0.00	0.00	0.00	0.00	0.00	4525800.00	5084400.00	0.00	0.00	0.00	0.00	3900000.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Legionellales;Legionellaceae;Legionella;Legionella drancourtii;Legionella drancourtii LLAP12
Ga0586324_1124176_232_552	0.00	0.00	0.00	3583652.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylobacteriaceae;Microvirga;Microvirga flocculans;Microvirga flocculans ATCC BAA-817
Ga0586324_1124915_2_703	1360000.00	0.00	0.00	323584.25	155723.64	0.00	0.00	584893.01	0.00	0.00	0.00	511647.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylovulum;Methylovulum miyakonense;Methylovulum miyakonense HT12
Ga0586324_1125509_5_1153	0.00	0.00	0.00	0.00	0.00	0.00	6224400.00	0.00	0.00	2079000.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Pigmentiphaga;Pigmentiphaga kullae;Pigmentiphaga kullae DSM 13608
Ga0586324_1125515_3_1154	0.00	0.00	0.00	0.00	3388700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Kribbellaceae;Kribbella;Kribbella catacumbae;Kribbella catacumbae DSM 19601
Ga0586324_1127032_3_1154	1400000.00	0.00	0.00	9595000.00	8301800.00	0.00	0.00	1439600.00	0.00	2510200.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Paucibacter;Paucibacter toxinivorans;Paucibacter toxinivorans DSM 16998
Ga0586324_1130629_391_738	5850000.00	0.00	0.00	0.00	17819000.00	0.00	10488000.00	9943000.00	9234000.00	0.00	0.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_1131084_218_1153	1560000.00	20536000.00	17453000.00	24510000.00	10506000.00	16197600.00	23712000.00	7564000.00	0.00	1108800.00	0.00	0.00	cytochrome c oxeroidase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter soli;Geobacter soli GS501
Ga0586324_1133490_2_751	37110000.00	78349600.00	77074700.00	112005000.00	96717000.00	102426000.00	64820400.00	65379800.00	35073000.00	86193800.00	71720000.00	48300000.00	hypothetical protein	
Ga0586324_1135954_92_1150	0.00	0.00	0.00	0.00	2492600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oleiphilaceae;Oleiphilus;Oleiphilus messinensis;Oleiphilus messinensis ME102
Ga0586324_1136113_1_945	208988000.00	170578000.00	282435604.66	137237000.00	162626700.00	136758401.20	78454800.00	104767500.00	88160400.00	226537234.00	180400000.00	280005000.00	predicted porin	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324_1137507_2_673	8780000.00	7276000.00	0.00	12635000.00	0.00	11790900.00	22344000.00	20618000.00	17415000.00	27181000.00	24464000.00	15600000.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Thiomonas;Thiomonas sp. X19;Thiomonas sp. X19
Ga0586324_1137683_1_1149	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3264800.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundrilealudum;Methylobacter tundrilealudum SV96
Ga0586324_1138232_144_1070	7330000.00	2971600.00	0.00	0.00	0.00	0.00	0.00	2643300.00	2535300.00	0.00	0.00	1237500.00	CsA family cysteine protease	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_1139648_2_1147	0.00	0.00	0.00	0.00	0.00	1961195.88	0.00	0.00	3855600.00	0.00	0.00	0.00	ABC-type branched-subunit amino acid transport system substrate-binding protein	Bacteria;Chlorroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Flexilinea;Flexilinea flocculi;Flexilinea flocculi TC1
Ga0586324_1139912_673_1149	536293.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Spy/CpxP family protein refolding chaperone	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1140000_1_876	0.00	1115200.00	1678348.04	900740.60	0.00	0.00	0.00	0.00	776699.28	0.00	0.00	745059.00	hypothetical protein	
Ga0586324_1140521_3_1148	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1785000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS138
Ga0586324_1143221_134_631	0.00	16592000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ruberythrin	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_1144702_389_1144	0.00	8160000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter gracilis;Curvibacter gracilis ATCC BAA-807
Ga0586324_1145133_2_1144	0.00	0.00	0.00	0.00	3193000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-003;Aminicenantes bacterium SCGC AAA252-003 (contamination screened)
Ga0586324_1145994_2_1144	7370000.00	0.00	0.00	0.00	2492600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324_1154480_363_1142	7480000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	
Ga0586324_1158173_379_1065	0.00	0.00	0.00	0.00	6034400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	multimeric flavodoxin WrbA	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum hydrothermale;Desulfacinum hydrothermale DSM 13146
Ga0586324_1163174_105_1001	0.00	0.00	0.00	911688.40	1514100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	nucleotide-binding universal stress UspA family protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324_1165225_2_1138	2420000.00	8384400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4920300.00	0.00	4755000.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiorhodococcus;Thiorhodococcus drewsii;Thiorhodococcus drewsii AZ1
Ga0586324_1165554_2_841	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1927600.00	931500.00	0.00	0.00	UbiD family decarboxylase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_1166656_419_1135	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13969000.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324_1167824_1_513	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1087500.00	curli biogenesis system outer membrane secretion channel CsgG	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_1177332_3_1001	4590800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4966500.00	0.00	3247500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_1177365_1_1131	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1636200.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus;Candidatus;Candidatus;Candidatus;Candidatus;Candidatus;Candidatus abysii;Candidatus abysii LF13, DSM 13497
Ga0586324_1183064_2_1129	0.00	0.00	0.00	0.00	2523500.00	0.00	0.00	1830000.00	6212700.00	0.00	4778400.00	595422.75	predicted porin	Bacteria;Acidobacteria;Acidobacteria;Acidobacteria;Acidobacteraceae;unclassified Acidobacteraceae;Acidobacteraceae;Acidobacteraceae bacterium KBS 83;Acidobacteraceae bacterium KBS 83
Ga0586324_1186629_219_1127	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	866700.00	728704.90	1135200.00	1417500.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Salinisaphaerales;Salinisaphaeraceae;Abyssibacter;Abyssibacter profundi;Abyssibacter profundi OUC007
Ga0586324_1190357_3_1127	0.00	335438.60	0.00	3087500.00	3821300.00	10807491.30	8983200.00	1110200.00	0.00	0.00	0.00	5805000.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-006;Aminicenantes bacterium SCGC AAA252-006 (contamination screened)
Ga0586324_1191181_1_1125	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	924000.00	0.00	877500.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-F06;Aminicenantes bacterium SCGC AAA255-F06 (contamination screened)
Ga0586324_1191601_1_870	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6367900.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_1193179_299_1126	0.00	0.00	0.00	0.00	251401.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	alkylation response protein AidB-like acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini DSM 4660
Ga0586324_1195797_284_760	2320000.00	4372400.00	3714178.56	5728500.00	17201000.00	17626800.00	0.00	22936000.00	972000.00	23716000.00	0.00	1305000.00	predicted Zn-dependent protease	
Ga0586324_1200127_1_1122	8580000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5931200.00	0.00	ABC-type xylose transport system substrate-binding protein	Bacteria;Chlorroflexi;Ardenticatenia;Ardenticatenales;Ardenticatenaceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Chx-K
Ga0586324_1200675_228_686	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3634400.00	2887500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Alkalibacter;Alkalibacter soli;Alkalibacter soli SHB
Ga0586324_1200882_2_376	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1944000.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolibacteraceae;Draconiibacterium;Draconiibacterium sediminis;Draconiibacterium sediminis JN1:4CK-3
Ga0586324_1201805_1_657	0.00	2244000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfitobacterium;Desulfitobacterium chlororespirans;Desulfitobacterium chlororespirans DSM 11544
Ga0586324_1202791_2_946	10660000.00	33814000.00	8467520.00	4483000.00	0.00	4883100.00	7006440.00	4942830.00	5259300.00	6912290.00	6494000.00	2779500.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiorhodosira;Thiorhodosira sibirica;Thiorhodosira sibirica A12. ATCC 700588
Ga0586324_1204498_2_1120	0.00	0.00	0.00	1737716.39	3971000.00	3635900.00	0.00	0.00	0.00	0.00	950400.00	0.00	2′,3′-cyclic-nucleotide 2′-phosphodiesterase (5′-nucleotidase family)	Bacteria;Firmicutes;Clostridia;Eubacteriales;Thermohalobacteraceae;Caloranaerobacter;Caloranaerobacter sp. TR13;Caloranaerobacter sp. TR13
Ga0586324_1205440_469_1119	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2040000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Azoarcus;Azoarcus sp. CIB;Azoarcus sp. CIB
Ga0586324_1206772_1_1119	604554.00	2271200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-006;Aminicenantes bacterium SCGC AAA252-006 (contamination screened)
Ga0586324_1210763_532_1119	14500000.00	22644000.00	21731800.00	4769000.00	5459000.00	11711500.00	131556000.00	12890520.00	98658000.00	91476000.00	163856000.00	135180000.00	predicted porin	
Ga0586324_1212660_481_1116	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2407500.00	glutamate synthase domain-containing protein 2	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1213847_3_491	3570000.00	2869600.00	0.00	0.00	5273600.00	5677100.00	0.00	2799900.00	2154600.00	0.00	0.00	0.00	phasin family protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia sp. LRH80060;Dongia sp. LRH80060
Ga0586324_1215850_2_1117	0.00	809200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Frateuria;Frateuria sp. Soil773;Frateuria sp. Soil773
Ga0586324_1217132_2_1117	123860000.00	169694000.00	190121153.37	172710000.00	149586900.00	102981800.00	56886000.00	74395600.00	104166000.00	66628100.00	61679200.00	51105000.00	S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324_1218125_2_748	600990.00	0.00	4738635.88	0.00	6756800.00	7041477.84	3055200.00	0.00	0.00	0.00	0.00	0.00	PGI-CTERM protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methanosarcinales;Methanosaricinaceae;Methanosarcina;Methanosarcina vacuolata;Methanosarcina vacuolata Z-761
Ga0586324_1218556_2_757	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	693217.50	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Ferroglobus;Ferroglobus placidus;Ferroglobus placidus AEDII12DO; DSM 10642
Ga0586324_1218692_3_1115	0.00	0.00	0.00	1358500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Ignavibacteria;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mat9-16, JCM 16511
Ga0586324_1222452_3_353	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2310000.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Methylophilaceae;Methylobacillus;Methylobacillus;glycogenes;Methylobacillus glycogenes JCM 2850
Ga0586324_1224909_21_1112	5400000.00	5154400.00	0.00	12445000.00	11845000.00	0.00	0.00	6344000.00	6666300.00	7630700.00	5175000.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324_1227182_633_1112	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13054000.00	0.00	8393000.00	11528000.00	0.00	hypothetical protein	
Ga0586324_1228529_1_1092	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	624875.25	0.00	ABC-type transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_1229838_1_1110	0.00	0.00	0.00	0.00	6709300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	formyltetrahydrofolate synthetase	Bacteria;Firmicutes;Clostridia;Eubacteriales;Clostridiaceae;Desulfitispora;Desulfitispora thermophilia;Desulfitispora thermophilia DSM 16022
Ga0586324_1231789_1_1104	0.00	0.00	0.00	0.00	1266900.00	0.00	0.00	0.00	0.00	0.00	281033.28	0.00	methylmalonyl-CoA mutase cobalamin-binding domain/chain	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Pedobacter;Pedobacter indicus;Pedobacter indicus SM1810
Ga0586324_1234041_3_605	0.00	1802000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1237833_3_1109	1320000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2077500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;Algicola;Algicola sagamiensis;Algicola sagamiensis DSM 14643
Ga0586324_1238086_3_1109	0.00	0.00	0.00	0.00	26162000.00	22152600.00	31692000.00	3690500.00	20655000.00	17248000.00	15928000.00	7800000.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodosovilaceae;Indiocenaicola;Indiocenaicola profundi;Indiocenaicola profundi SCSIO 08040
Ga0586324_1238281_3_836	0.00	1074400.00	0.00	0.00	0.00	0.00	0.00	0.00	276729.55	359456.13	0.00	1795200.00	1080000.00	hypothetical protein
Ga0586324_1239554_2_1108	0.00	0.00	0.00	6222500.00	6540500.00	4962500.00	0.00	3007300.00	3045600.00	2895200.00	1381600.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324_1243763_315_1028	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	281033.28	0.00	hypothetical protein	
Ga0586324_1248437_2_1003	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5012700.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;unclassified Chromatiales;unclassified Chromatiales;unclassified Chromatiales;Chromatiales bacterium
Ga0586324_1254642_3_1100	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2648800.00	0.00	0.00	hypothetical protein	Bacteria;Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas;Gemmatimonas phototrophica;Gemmatimonas phototrophica AP64
Ga0586324_1255047_208_798	4610000.00	0.00	4124425.40	4750000.00	5150000.00	4049400.00	4924800.00	5471700.00	0.00	4335100.00	5473600.00	5017500.00	hypothetical protein	Bacteria;Bacteroidetes;Rhodothermaeota;Rhodothermales;Rhodothermaceae;Gracilimonas;Gracilimonas amylolytica;Gracilimonas amylolytica LA399
Ga0586324_1255245_97_1101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13937000.00	0.00	0.00	formyltetrahydrofolate synthetase	Bacteria;Chlorroflexi;Ktedonobacteria;Ktedonales;Ktedonobacteraceae;Dictyobacter;Dictyobacter aurantiacus
Ga0586324_1256193_3_1070	22700000.00	4644400.00	9176900.00	22952000.00	15141000.00	0.00	0.00	2013000.00	1830600.00	4535300.00	2376000.00	1762500.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochataceae;Spirochaeta;Spirochaeta cellobiosiphila;Spirochaeta cellobiosiphila DSM 17781
Ga0586324_1256217_3_1100	0.00	0.00	0.00	0.00	2802500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1258207_1_960	0.00	0.00	2333556.18	0.00	2276300.00	0.00	0.00	0.00	0.00	1328400.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	Bacteria;Chlorroflexi;Ktedonobacteria;Ktedonales;Ktedonobacteraceae;Dictyobacter;Dictyobacter aurantiacus
Ga0586324_1259791_3_1100	7400000.00	7276000.00	16527484.30	11115000.00	14121300.00	13995814.18	16210800.00	9406200.00	4762800.00	5859700.00	7304000.00	9375000.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;un

Ga0586324_1365278_2_1063	0.00	1672800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_1368067_1_1062	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	786929.58	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_1369658_526_1062	9240000.00	0.00	0.00	4769000.00	5654700.00	0.00	0.00	0.00	0.00	0.00	17512000.00	9000000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus sp. GA3-3;Cupriavidus sp. GA3-3
Ga0586324_1370041_1_720	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2159113.16	0.00	0.00	383344.08	298866.75	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas naphthalenivorans;Polaromonas naphthalenivorans CJ2
Ga0586324_1371469_473_1060	0.00	0.00	0.00	1054500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinifilaceae;Labilibaculum;Labilibaculum manganireducens;Labilibaculum manganireducens 59.10-2M
Ga0586324_1372194_171_905	0.00	0.00	0.00	7961000.00	0.00	0.00	4126800.00	0.00	0.00	0.00	0.00	1830000.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Dongia;Dongia sp. URHE0060;Dongia sp. URHE0060
Ga0586324_1379355_3_569	4540000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3467200.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_1381886_598_1056	0.00	9112000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1383702_48_1055	0.00	3202800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium japonicum;Bradyrhizobium japonicum 22
Ga0586324_1386765_3_1055	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1182600.00	0.00	0.00	0.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2. DSM 11109
Ga0586324_1394906_314_952	1600000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Pyruvate/2-oxoacid ferredoxin oxidoreductase gamma subunit	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermosediminibacter litoriparvensis;Thermosediminibacter litoriparvensis DSM 16647
Ga0586324_1396216_12_479	0.00	7004000.00	8613900.00	3382000.00	3357800.00	0.00	3876000.00	0.00	0.00	4627700.00	0.00	3307500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324_1397920_3_1037	0.00	0.00	0.00	0.00	0.00	0.00	3921600.00	0.00	0.00	7854000.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. F21;Smithella sp. F21
Ga0586324_1408358_3_425	1870000.00	0.00	0.00	0.00	0.00	0.00	0.00	144659.06	0.00	0.00	597605.36	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324_1412303_1_1047	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2640000.00	0.00	0.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Terriglobus;Terriglobus roseus;Terriglobus roseus ABS5.6
Ga0586324_1412895_509_1048	0.00	2944400.00	0.00	0.00	4315700.00	0.00	3275700.00	3442500.00	0.00	0.00	0.00	0.00	CBS domain-containing protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_1415173_3_1046	0.00	0.00	0.00	0.00	4521700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted ATP-dependent protease	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_1417493_601_1044	18200000.00	0.00	66997000.00	0.00	0.00	0.00	0.00	3190300.00	3167100.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum;Desulfotignum balticum;Desulfotignum balticum DSM 7044
Ga0586324_1417565_670_1044	3190000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1419469_1_1014	13360000.00	27446115.80	0.00	3885500.00	189108000.00	37079800.00	8415258.48	32696000.00	58142131.29	403816.49	577351.92	23610000.00	S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_1420025_199_585	0.00	0.00	216340.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_1420540_3_1043	2310000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1422659_2_940	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	490885.25	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium EN84
Ga0586324_1429645_92_1042	1760000.00	3094000.00	7600500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type C4-dicarboxylate transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_1437845_3_1040	0.00	0.00	0.00	0.00	0.00	0.00	388894.52	0.00	0.00	0.00	0.00	0.00	peroxiredoxin	Bacteria;Armatimonadetes;Armatimonadia;Armatimonadales;Armatimonadaceae;Armatimonas;Armatimonas rosea;Armatimonas rosea DSM 23562
Ga0586324_1438947_45_1040	852205.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	glucose/arabinose dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii WSM1741
Ga0586324_1439671_1_1038	5710000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5674900.00	0.00	4822500.00	hypothetical protein	
Ga0586324_1442646_1_810	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2347500.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas;Pseudomonas benzenivorans;Pseudomonas benzenivorans DSM 8628
Ga0586324_1443345_3_572	0.00	0.00	0.00	0.00	5768000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized membrane protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis ethanolicus;Methanofollis ethanolicus JCM 15103
Ga0586324_1443955_371_913	2090000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	phasin family protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Antarctobacter;Antarctobacter heliothamni;Antarctobacter heliothamni DSM 23236
Ga0586324_1444259_1_1038	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10648000.00	0.00	LysM repeat protein	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Odoribacteraceae;Butyricimonas;Butyricimonas synergistica;Butyricimonas synergistica DSM 23225
Ga0586324_1446617_95_1036	0.00	0.00	0.00	0.00	0.00	0.00	1933700.00	963900.00	0.00	0.00	0.00	915000.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylobacteriaceae;Microvirga;Microvirga ossetica;Microvirga ossetica VS/3m
Ga0586324_1447744_79_411	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1832600.00	0.00	0.00	0.00	phasin family protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylocystaceae;unclassified Hyphomicrobiales;Methylocearabacter;Methylocearabacter superfactus;Methylocearabacter superfactus R-67175
Ga0586324_1447800_1_1035	0.00	0.00	3527532.80	0.00	0.00	1562556.27	0.00	0.00	0.00	0.00	0.00	0.00	outer membrane receptor for ferrienterochelin and colicin	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Gallaecimonas;Gallaecimonas mangrovi;Gallaecimonas mangrovi HK-28
Ga0586324_1448126_3_1037	0.00	0.00	0.00	2147000.00	2080600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Cruaella;Cruaella takakiae;Cruaella takakiae DSM 26897
Ga0586324_1449500_1_1035	0.00	0.00	0.00	3638500.00	0.00	2740756.99	0.00	0.00	0.00	3003000.00	1874400.00	1695000.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Streptosporangiaceae;Thermoactinospora;Thermoactinospora rubra;Thermoactinospora rubra YIM 77501
Ga0586324_1452752_2_304	2690000.00	2366400.00	3687554.29	2394000.00	0.00	0.00	0.00	1182600.00	0.00	0.00	0.00	1702500.00	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. LVNP
Ga0586324_1458344_3_581	0.00	2019600.00	0.00	6555000.00	5541400.00	26360800.00	0.00	0.00	4098600.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Ferroglobus;Ferroglobus placidus;Ferroglobus placidus AEDII12DO, DSM 10642
Ga0586324_1458344_600_1034	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1755600.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Desulfosporosinus;Desulfosporosinus thermosuricus;Desulfosporosinus thermosuricus DSM 16036
Ga0586324_1458585_67_1032	0.00	0.00	0.00	0.00	0.00	1171200.00	0.00	0.00	0.00	0.00	0.00	0.00	PAS domain S-box-containine protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanosarcinaceae;Methanosarcinillum;Methanosarcinillum hunateiei;Methanosarcinillum hunateiei JF-1
Ga0586324_1465229_2_1030	0.00	0.00	0.00	0.00	0.00	1892066.27	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1465319_425_1030	0.00	5984000.00	0.00	2973500.00	2502900.00	0.00	0.00	1887300.00	0.00	0.00	1672500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Marinobacter;Marinobacter sp. Arc7-DN-1;Marinobacter sp. Arc7-DN-1
Ga0586324_1466044_1_1029	0.00	4270400.00	5362158.38	0.00	0.00	3191510.79	8299200.00	3367200.00	1798200.00	0.00	0.00	7755000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_1467393_602_1030	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8250000.00	phasin family protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas agitata;Dechloromonas agitata CKB
Ga0586324_1470069_1_1029	1410000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1372500.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporaniaceae;Intrasporanium;Intrasporanium flavum;Intrasporanium flavum MUSC 78
Ga0586324_1470453_2_1030	1390000.00	1652400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_1472446_235_1029	50700000.00	40936000.00	0.00	0.00	17098000.00	0.00	0.00	0.00	0.00	7569100.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS401
Ga0586324_1486583_294_851	1620000.00	2298400.00	2127779.68	0.00	0.00	2470872.42	0.00	0.00	0.00	0.00	0.00	0.00	lipid-binding SYLF domain-containing protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324_1489418_754_1023	2410000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	794824.65	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1491450_2_1024	0.00	0.00	0.00	0.00	11875000.00	15965000.00	0.00	0.00	0.00	0.00	0.00	0.00	formiltetrahydrofolate synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_1491555_172_1023	0.00	3026000.00	12104500.00	0.00	5912200.00	12267300.00	7318800.00	6161000.00	11866500.00	7045500.00	6117600.00	6900000.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_1492076_2_1024	0.00	0.00	0.00	0.00	1936400.00	0.00	0.00	1213900.00	0.00	1339000.00	269163.84	473940.75	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_1494830_160_639	1540000.00	1468800.00	0.00	3002000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	
Ga0586324_1497193_2_1021	0.00	2284800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Dysgonomonadaceae;Petrimonas;Petrimonas sulfuriphila;Petrimonas sulfuriphila DSM 16547
Ga0586324_1500156_72_1019	0.00	0.00	0.00	0.00	0.00	1719010.00	0.00	0.00	0.00	0.00	0.00	3285000.00	hypothetical protein	
Ga0586324_1503550_152_859	0.00	0.00	0.00	4370000.00	4418700.00	0.00	0.00	0.00	2705400.00	0.00	0.00	0.00	nucleoid-associated protein YgaU	Bacteria;Spirochaetes;Leptospirae;Leptospiraceae;Leptospira;Leptospira alstonii;Leptospira alstonii serovar Mankarso str. Mankarso;Leptospira alstonii serovar Mankarso str. Mankarso
Ga0586324_1505883_2_619	10400000.00	7888000.00	0.00	0.00	0.00	4168500.00	0.00	9150000.00	11421000.00	22561000.00	10824000.00	17025000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_1506729_1_840	0.00	0.00	0.00	0.00	0.00	0.00	3328800.00	7625000.00	0.00	0.00	0.00	0.00	transketolase C-terminal domain/subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324_1514654_1_1017	2090000.00	1904000.00	2199325.72	3952000.00	3841900.00	3368644.25	2713200.00	3416000.00	3450600.00	0.00	2508000.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Holophagae;Holophagales;Holophagaceae;Geothrix;Geothrix fermentans;Geothrix fermentans DSM 14018
Ga0586324_1514912_47_1015	0.00	0.00	0.00	409000.00	0.00	0.00	0.00	605408.53	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324_1517033_652_1014	2780000.00	0.00	0.00	0.00	4676200.00	0.00	3602400.00	4257800.00	2932200.00	3411000.00	2191200.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. Root404;Rhizobacter sp. Root404
Ga0586324_1518474_3_1016	0.00	5596400.00	0.00	3258500.00	3296000.00	0.00	0.00	0.00	0.00	9702000.00	2252800.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. Root122;Nocardioides sp. Root122
Ga0586324_1518624_3_632	39700000.00	75888000.00	35637900.00	11789500.00	10712000.00	22311400.00	0.00	27999000.00	27054000.00	127327200.00	110767514.00	91950000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus sp. GA3-3;Cupriavidus sp. GA3-3
Ga0586324_1523736_2_1015	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	817400.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Candidatus Aminicenantes bacterium SCGC AAA255-A06;Aminicenantes bacterium SCGC AAA255-A06 (contamination screened)
Ga0586324_1525566_1_813	2710000.00	4195600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2497500.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolibacteraceae;Marinihaea;Marinihaea anaerophila;Marinihaea anaerophila DSM 26910
Ga0586324_1528392_3_1013	2470000.00	2740400.00	3151899.20	3420000.00	0.00	0.00	0.00	1439600.00	143040.33	2833600.00	0.00	2002500.00	hypothetical protein	
Ga0586324_1531845_441_1010	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2708400.00	0.00	0.00	0.00	0.00	signal transduction histidine kinase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Azospirillaceae;Azospirillum;Azospirillum palustre;Azospirillum palustre B2
Ga0586324_1533858_63_1010	0.00	0.00	0.00	0.00	0.00	0.00	0.00	980100.00	0.00	0.00	318744.75	0.00	TonB-dependent SusC/RagA subfamily outer membrane receptor	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Arenibacter;Arenibacter nanhaiticus;Arenibacter nanhaiticus CGMCC 1.8863
Ga0586324_1534989_1_330	0.00	12512000.00	0.00	0.00	1545000.00	1435428.93	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Leptothrix;Leptothrix cholodnii;Leptothrix cholodnii SP-6
Ga0586324_1542277_3_1007	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2358400.00	2985000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1544993_101_1008	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1378300.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_1552963_1_966	0.00	3597200.00	2522121.77	0.00	9373000.00	6312300.00	10191600.00	5361900.00	6860700.00	4296600.00	4144800.00	3637500.00	hypothetical protein	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio islandicus;Thermodesulfovibrio islandicus DSM 12570
Ga0586324_1553958_3_1004	0.00	0.00	0.00	1406993.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Turneriella;Turneriella parva;Turneriella parva H, DSM 21527
Ga0586324_1556371_366_1004	0.00	1509600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae;Mannheimia;Mannheimia succiniciproducens;Mannheimia succiniciproducens MBEL55E
Ga0586324_1561089_1_1002	0.00	0.00	0.00	0.00	481119.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TonB-dependent SusC/RagA subfamily outer membrane receptor	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Fulviviraceae;Ohtaekwangia;Ohtaekwangia koreensis;Ohtaekwangia koreensis DSM 25262
Ga0586324_1566317_3_1001	0.00	0.00	0.00	4522000.00	543583.53	0.00	0.00	0.00	0.00	0.00	1724800.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Saprospiria;Saprospirales;Lewinellaceae;Lewinella;Lewinella cohaerens;Lewinella cohaerens DSM 23179
Ga0586324_1568044_3_662	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	502160.12	0.00	0.00	basic membrane lipoprotein Med (substrate-binding protein (PBP1-ABC) superfamily)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Thermaeromonas;Thermaeromonas dawensis;Thermaeromonas dawensis GNS-1
Ga0586324_1571972_295_738	2240000.00	0.00	0.00	3068500.00	1617100.00	0.00	0.00	829600.00	0.00	0.00	0.00	0.00	nucleotide-binding universal stress UspA family protein	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Rudaea;Rudaea cellulosilytica;Rudaea cellulosilytica DSM 22992
Ga0586324_1575508_3_998	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	575077.58	0.00	571025.25	ABC-type xylose transport system substrate-binding protein	Bacteria;Chloroflexi;Ardenticaterii;Ardenticatenales;Ardenticateraceae;Candidatus Promineofilum;Candidatus Promineofilum breve;Candidatus Promineofilum breve Cfx-K
Ga0586324_1576282_1_999	0.00	0.00	27024000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1579037_1_999	40800000.00	6800000.00	25053500.00	4417500.00	0.00	14530200.00	0.00	0.00	1344600.00	8778000.00	12038400.00	5527500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_1583275_268_996	0.00	0.00	0.00	0.00	0.00	0.00	3990000.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_1583351_175_996	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	497692.35	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Limibacillus;Limibacillus halophilus;Limibacillus halophilus CECT 8803
Ga0586324_1584565_1_996	0.00	0.00	0.00	0.00	0.00	0.00	153706.20	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_1586041_2_997	746948.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	FtsP/CotA-like multicopper oxidase with curedoxin domain	Bacteria;Chloroflexi;Ktedonobacteria;Ktedonobacterales;Dictyobacteraceae;Dictyobacter;Dictyobacter aurantiacus;Dictyobacter aurantiacus S27
Ga0586324_1586130_667_996	0.00	0.00	0.00	1757500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	Archaea;Euryarchaeota;Halobacteria;Haloferacales;Halorubra

Ga0586324_1740362_338_958	0.00	1768000.00	0.00	0.00	1483200.00	0.00	0.00	113043.98	0.00	0.00	0.00	183094.50		hypothetical protein
Ga0586324_1740907_3_749	0.00	6364800.00	0.00	0.00	1483200.00	13974400.00	56316000.00	8845000.00	12798000.00	7700000.00	8888000.00	12000000.00		predicted porin
Ga0586324_1744020_1_657	0.00	0.00	0.00	1463000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		CBS domain-containing protein
Ga0586324_1744428_3_956	0.00	0.00	0.00	0.00	0.00	1533170.33	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1757155_121_954	0.00	469425.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1762535_2_358	0.00	17612000.00	23983800.00	6479000.00	16480000.00	23621500.00	0.00	0.00	10773000.00	4758600.00	0.00	4477500.00		hypothetical protein
Ga0586324_1763957_315_782	0.00	0.00	0.00	4750000.00	3965500.00	0.00	0.00	0.00	0.00	0.00	0.00	2092500.00		hypothetical protein
Ga0586324_1772297_2_805	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2656500.00	0.00	0.00		TonB-dependent SusC/RagA subfamily outer membrane receptor
Ga0586324_1774388_3_950	3870000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1775024_114_950	224612.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1776467_2_949	1520000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1776896_83_949	0.00	0.00	0.00	0.00	0.00	3521874.34	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1777428_52_948	0.00	0.00	48305400.00	0.00	0.00	27432700.00	12608400.00	0.00	0.00	25872000.00	0.00	21375000.00		hypothetical protein
Ga0586324_1782301_1_810	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	21750000.00		arylsulfatase A-like enzyme
Ga0586324_1784481_2_949	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1064800.00	0.00		hypothetical protein
Ga0586324_1785065_1_948	16600000.00	0.00	0.00	42845000.00	0.00	0.00	0.00	26779000.00	0.00	36883000.00	29216000.00	20850000.00		hypothetical protein
Ga0586324_1787738_332_946	0.00	2781200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1789881_252_638	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3226900.00	0.00	0.00	0.00	0.00		uncharacterized spore protein YtfJ
Ga0586324_1790359_2_904	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3126200.00	2983200.00	0.00		hypothetical protein
Ga0586324_1794208_2_208	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	748941.39	0.00	0.00	3187500.00		RNA recognition motif-containing protein
Ga0586324_1794688_1_945	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	84750000.00		hypothetical protein
Ga0586324_1795535_3_944	1160000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1795759_552_923	0.00	0.00	684365.91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		transposase
Ga0586324_1796410_3_944	0.00	0.00	4028000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		ABC-type glutathione transport system ATPase component
Ga0586324_1800902_650_943	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3788100.00	0.00	0.00	0.00	0.00		TusE/DsrC/DsvC family sulfur relay protein
Ga0586324_1802464_653_943	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18711000.00	14225600.00	1230000.00		FAD/FMN-containing dehydrogenase
Ga0586324_1807967_2_943	0.00	0.00	0.00	0.00	18952000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		methyl-accepting chemotaxis protein
Ga0586324_1808817_527_943	0.00	0.00	0.00	0.00	0.00	4962500.00	0.00	0.00	0.00	0.00	4743200.00	3735000.00		polyhydroxyalkanoate synthesis repressor PhaR
Ga0586324_1809896_2_943	4050000.00	0.00	0.00	0.00	4140600.00	0.00	0.00	0.00	0.00	0.00	3986400.00	0.00		hypothetical protein
Ga0586324_1814081_2_940	0.00	0.00	17903400.00	15485000.00	0.00	60224900.00	17898000.00	14152000.00	18711000.00	0.00	0.00	16575000.00		crotonobetaine/L-carnitine CoA-transferase CaiB-like acyl-CoA transferase
Ga0586324_1816385_1_924	3300000.00	7208000.00	0.00	0.00	7014300.00	0.00	10921200.00	4764100.00	7776000.00	8085000.00	11176000.00	4905000.00		hypothetical protein
Ga0586324_1817786_134_940	22300000.00	32096000.00	31528000.00	41990000.00	75396000.00	47640000.00	24396000.00	34587000.00	19602000.00	0.00	16544000.00	8475000.00		predicted porin
Ga0586324_1820745_144_941	550927.00	8636000.00	0.00	0.00	0.00	0.00	16963200.00	15372000.00	14499000.00	13475000.00	17072000.00	2052675.50		predicted porin
Ga0586324_1836335_1_936	0.00	0.00	0.00	0.00	0.00	1175894.15	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1838472_2_937	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15015000.00	0.00	0.00		hypothetical protein
Ga0586324_1847052_1_933	620818.00	1584400.00	0.00	0.00	0.00	0.00	0.00	390296.91	1887300.00	1355200.00	447516.16	0.00		hypothetical protein
Ga0586324_1849890_181_933	0.00	0.00	0.00	0.00	0.00	0.00	2986800.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1852152_124_690	11900000.00	14592800.00	0.00	10450000.00	7529300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1857431_344_931	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1732400.00	0.00	0.00	0.00	0.00		phenylphosphate carboxylase alpha subunit
Ga0586324_1858939_72_932	0.00	0.00	0.00	0.00	0.00	15759000.00	0.00	0.00	0.00	0.00	0.00	0.00		probable F420-dependent oxidoreductase
Ga0586324_1871440_184_930	1620000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1872419_3_917	0.00	594038.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		nitrous oxide reductase accessory protein NosL
Ga0586324_1874174_1_927	6990000.00	5100000.00	0.00	0.00	38110000.00	6272600.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1874235_3_929	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	923400.00	0.00	0.00	0.00		DNA-directed RNA polymerase beta' subunit
Ga0586324_1874661_289_849	0.00	0.00	0.00	1805000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1875223_3_929	2650000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1877802_234_929	0.00	0.00	0.00	0.00	1895200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		TRAP-type mannitol/chloroamotic compound transport system substrate-binding protein
Ga0586324_1880991_503_883	0.00	6052000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1885560_3_926	422873.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1886540_134_925	0.00	1931200.00	0.00	1520000.00	1864300.00	0.00	0.00	0.00	1036800.00	3526600.00	0.00	0.00		hypothetical protein
Ga0586324_1895824_502_925	1440000.00	720800.00	0.00	0.00	0.00	0.00	0.00	0.00	1952100.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1896196_1_567	0.00	0.00	0.00	0.00	1400800.00	0.00	2016206.28	2135000.00	2219400.00	1563100.00	0.00	0.00		hypothetical protein
Ga0586324_1897111_1_924	0.00	0.00	0.00	0.00	0.00	0.00	2576400.00	1323700.00	0.00	2071300.00	1381600.00	3292500.00		hypothetical protein
Ga0586324_1898378_3_923	7670000.00	8024000.00	14919500.00	9091500.00	13081000.00	11155700.00	0.00	4367600.00	2972700.00	5351500.00	3924800.00	3360000.00		hypothetical protein
Ga0586324_1910812_227_922	4330000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		uncharacterized protein (TIGR02001 family)
Ga0586324_1911824_3_152	3610000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1913768_316_921	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	816966.48	0.00		hypothetical protein
Ga0586324_1916254_2_898	0.00	924800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1922734_3_917	0.00	843200.00	16188310.79	0.00	0.00	0.00	0.00	695400.00	0.00	0.00	679850.25	0.00		hypothetical protein
Ga0586324_1928159_1_918	0.00	2495600.00	4195093.16	0.00	0.00	0.00	0.00	1659200.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1930196_2_916	0.00	0.00	25166100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1932545_2_748	0.00	5093200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6555000.00		hypothetical protein
Ga0586324_1938506_239_631	4880000.00	2006000.00	0.00	0.00	6725900.00	0.00	0.00	2427800.00	2130300.00	0.00	0.00	1282500.00		hypothetical protein
Ga0586324_1938506_721_915	0.00	9112000.00	0.00	21375000.00	22454000.00	0.00	0.00	0.00	0.00	19789000.00	14960000.00	11625000.00		hypothetical protein
Ga0586324_1939160_193_915	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1812800.00	0.00		NADP(+)-dependent dehydroxenase (short-subunit alcohol dehydroenase family)
Ga0586324_1942008_288_731	1870000.00	0.00	0.00	0.00	0.00	0.00	2037143.52	0.00	0.00	3896200.00	0.00	0.00		uncharacterized membrane protein
Ga0586324_1943226_3_914	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	510390.75		succinate dehydrogenase/fumarate reductase flavoprotein subunit
Ga0586324_1948765_1_912	258564.00	0.00	1815686.26	2356000.00	0.00	2483159.57	0.00	0.00	0.00	0.00	0.00	1890000.00		hypothetical protein
Ga0586324_1953432_3_911	0.00	0.00	0.00	1672000.00	2111500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1968500_1_840	0.00	0.00	5798900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		arylsulfatase A-like enzyme
Ga0586324_1973313_2_907	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	667755.75	0.00		NADPH-dependent glutamate synthase beta subunit-like oxidoreductase
Ga0586324_1978044_1_906	6070000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1979020_1_906	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1799500.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1979588_117_908	0.00	0.00	9281500.00	8260600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		cytochrome c peroxidase
Ga0586324_1984204_3_542	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8910000.00	0.00	0.00		hypothetical protein
Ga0586324_1992160_2_904	0.00	0.00	0.00	1900000.00	0.00	0.00	0.00	0.00	0.00	1555200.00	0.00	0.00		hypothetical protein
Ga0586324_1992449_1_279	0.00	218491.48	0.00	0.00	1102100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_1995406_1_891	0.00	0.00	0.00	0.00	2914900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase
Ga0586324_2002716_2_523	0.00	0.00	0.00	0.00	0.00	0.00	12266400.00	0.00	7905600.00	0.00	0.00	0.00		DNA-binding Nar1/Fix1 family response regulator
Ga0586324_2007165_2_901	31000000.00	7820000.00	0.00	4389000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2008660_2_901	0.00	0.00	8050900.00	7999000.00	0.00	7860600.00	4947600.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2011212_1_900	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5337900.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2012904_1_417	0.00	3576800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		ABC-type sugar transport system substrate-binding protein
Ga0586324_2014401_3_899	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1162700.00	0.00	0.00		hypothetical protein
Ga0586324_2014498_1_900	576116.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2017405_494_901	0.00	2352800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12166000.00	13904000.00	0.00		hypothetical protein
Ga0586324_2023075_1_348	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2675200.00	0.00		uberoylTic
Ga0586324_2024497_1_900	0.00	628829.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6593400.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase
Ga0586324_2031541_329_898	0.00	0.00	0.00	0.00	2842800.00	0.00	0.00	0.00	0.00	0.00	3033800.00	0.00		hypothetical protein
Ga0586324_2035552_2_763	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4470000.00		hypothetical protein
Ga0586324_2037903_2_895	15456106.00	10206800.00	0.00	43158500.00	14626000.00	16852380.04	0.00	2165500.00	866700.00	658461.65	0.00	0.00		hypothetical protein
Ga0586324_2038310_1_897	0.00	0.00	0.00	0.00	0.00	0.00	8299200.00	12566000.00	0.00	17232600.00	23056000.00	3300000.00		NADPH-dependent glutamate synthase beta subunit-like oxidoreductase
Ga0586324_2039068_1_753	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	406926.52	0.00	0.00		predicted dehydrogenase
Ga0586324_2044649_584_895	8430000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin
Ga0586324_2054240_1_821	953475.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2054627_1_894	0.00	1203600.00	0.00	824532.51	4851300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2054845_412_681	0.00	1815600.00	0.00	0.00	0.00	6987200.00	0.00	0.00	0.00	1976400.00	0.00	945000.00		hypothetical protein
Ga0586324_2057925_3_893	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	154000000.00	0.00		predicted porin
Ga0586324_2059257_2_748	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2989000.00	3248100.00	0.00	0.00		opacity protein-like surface antigen
Ga0586324_2061808_2_892	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	722735.86	2411200.00		hypothetical protein
Ga0586324_2071498_1_402	0.00	0.00	0.00	950000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	950400.00		hypothetical protein
Ga0586324_2073414_1_888	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7381000.00	0.00	0.00	0.00	1125000.00		DNA-directed RNA polymerase beta subunit
Ga0586324_2074902_122_888	6790000.00	6670800.00	0.00	10355000.00	10815000.00	1478638.41	0.00	5148400.00	0.00	1247400.00	1064800.00	1612500.00		hypothetical protein
Ga0586324_2080404_605_889	0.00	0.00	0.00	0.00	0.00	1496400.19	0.00	7564000.00	0.00	2879800.00	0.00	0.00		predicted porin
Ga0586324_2081701_623_889	0.00	1727200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2062500.00		hypothetical protein
Ga0586324_2081730_2_889	0.00	0.00	0.00	0.00	1508600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		arylsulfatase A-like enzyme
Ga0586324_2086814_1_765	0.00	0.00	0.00	3999500.00	0.00	0.00	0.00	1165100.00	0.00	0.00	0.00	0.00		GAF domain-containing protein
Ga0586324_2088181_1_888	0.00	0.00	0.00	0.00	0.00	0.00	1077977.16	391812.15	0.00	1062600.00	1610400.00	1380000.00		hypothetical protein
Ga0586324_2089928_139_885	1140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin
Ga0586324_2090822_2_886	0.00	1482400.00	0.00	0.00	0.00	332343.39	0.00	0.00	0.00	0.00	0.00	0.00		outer membrane receptor protein involved in Fe transport
Ga0586324_2094769_229_816	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1226100.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2098736_3_884	0.00	2305200.00	0.00	3705000.00	0.00	0.00	4924800.00	0.00	0.00	0.00	0.00	1410000.00		ABC-type transport system substrate-binding protein
Ga0586324_2100579_1_885	0.00	0.00	0.00	0.00	0.00	4089100.00	0.00	0.00	0.00	0.00	0.00	0.00		ABC-type transport system substrate-binding protein
Ga0586324_2101278_340_885	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	930000.00		TRAP-type mannitol/chloroamotic compound transport system substrate-binding protein
Ga0586324_2101863_3_884	0.00	3168800.00	0.00	7258000.00	5325100.00	0.00	0.00	0.00	3196400.00	2031100.00	0.00	0.00		hypothetical protein
Ga0586324_2101954_384_884	0.00	0.00	0.00	0.00	0.00	1687022.16	0.00	0.00	0.00	611504.64	0.00	0.00		methanogenic corrinoid protein MtbC1
Ga0586324_2102491_1_693	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1101600.00	0.00	0.00		uncharacterized protein (TIGR02001 family)
Ga0586324_2104721_35_883	0.00	2488800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2106348_2_883	43800000.00	57395891.64	4842306.70	71673996.40	82220827.38	0.00	10123200.00	41785000.00	18111600.00	48664000.00	54594664.96	33959038.50		TRAP-type mannitol/chloroamotic compound transport system substrate-binding protein
Ga0586324_2107450_3_836	0.00	0.00	0.00	0.00	0.00	0.00	6589200.00	1037000.00	0.00	0.00	1654400.00	0.00		hypothetical protein
Ga0586324_2107649_1_882	7770000.00	4195600.00	5126745.56	0.00	0.00	4883100.00	0.00	1598200.00	0.00	6699000.00	5341600.00	5707500.00		hypothetical protein
Ga0586324_2108185_2_775	0.00	0.00	0.00	0.00	0.00	0.00	0.00	593093.85	0.00	0.00	0.00	0.00		transcriptional regulator with PAS, ATPase and Fis domain
Ga0586324_2113673_246_881	0.00	1598000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2115497_3_881	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1220000.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2116229_3_743	0.00	0.00	2546000.00	2235100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		uncharacterized membrane protein
Ga0586324_2117842_2_883	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3263500.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2118604_2_880	0.00	635808.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1108800.00	0.00	518082.00		hypothetical protein
Ga0586324_2121436_439_882	2100000.00	73607.28	480791.87	14630000.00	69319000.00	17190100.00	0.00	1891000.00	4657500.00	689717.49	7594400.00	6855000.00		hypothetical protein
Ga0586324_2128573_3_461	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	915300.00	0.00	0.00	0.00		nucleotide-binding universal stress UspA family protein
Ga0586324_2136697_3_767	0.00	0.00	0.00	2793000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		MoxR-like ATPase
Ga0586324_2140075_2_814	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7184100.00	0.00	0.00		NADPH-dependent glutamate synthase beta subunit-like oxidoreductase
Ga0586324_2141407_3_575	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	878400.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2145006_300_692	7430000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		CBS domain-containing protein
Ga0586324_2145052_3_878	942276.00	1319200.00	0.00	2888000.00	3213600.00	0.00	0.00	701500.00	0.00	0.00	0.00	1462500.00		hypothetical protein
Ga0586324_2145423_1_696	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4549600.00	0.00		Flp pilus assembly protein TadB
Ga0586324_2146840_2_877	4890000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3472500.00		hypothetical protein
Ga0586324_2149807_110_877	0.00	4426800.00	2230324.50	3980500.00	24853900.00	0.00	1291145.76	878400.00	0.00	0.00	0.00	0.00		hypothetical protein
Ga0586324_2149954_875	0.00	2278000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		ABC-type sugar transport system substrate-binding protein
Ga0586324_2154412_572_874	0.00	0.00	0.00	0.00	0.00	6629900.00	0.00	2952400.00	0.00	0.00	0.00	0.00		acyl-coenzyme A synthetase/AMP-(fatty) acid ligase

Ga0586324_1740362_338_958	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Quisquilibacterium;Quisquilibacterium transsilvanicum;Quisquilibacterium transsilvanicum DSM 29781
Ga0586324_1740907_3_749	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Quisquilibacterium;Quisquilibacterium transsilvanicum;Quisquilibacterium transsilvanicum DSM 29781
Ga0586324_1744020_1_657	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS242
Ga0586324_1744428_3_956	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolibacteraceae;Mariniphaga;Mariniphaga anaerophila;Mariniphaga anaerophila DSM 26910
Ga0586324_1757155_121_954	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Rhodopseudomonas;Rhodopseudomonas palustris;Rhodopseudomonas palustris BAL398
Ga0586324_1762535_2_358	hypothetical protein
Ga0586324_1763957_315_782	hypothetical protein
Ga0586324_1772297_2_805	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Lentimicrobiaceae;Lentimicrobium;Lentimicrobium saccharophilum;Bacteroidales bacterium TBC1
Ga0586324_1774388_3_950	hypothetical protein
Ga0586324_1775024_114_950	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae;Acidobacteriaceae bacterium URHE0068;Acidobacteriaceae bacterium URHE0068
Ga0586324_1776467_2_949

Ga0586324_2156704_3_875	0.00	0.00	0.00	3885500.00	0.00	0.00	0.00	2793800.00	2494800.00	0.00	0.00	0.00	cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfohalovibrio;Desulfohalovibrio alkaliotolerans;Desulfovibrio alkaliotolerans DSM 16529
Ga0586324_2165615_2_874	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1963500.00	0.00	0.00	signal transduction histidine kinase	Bacteria;Proteobacteria;Alphaproteobacteria;Maricaulales;Maricaulaceae;Euryhalocaulis;Euryhalocaulis caribicus;Euryhalocaulis caribicus JL2009
Ga0586324_2168727_3_848	6510000.00	7792800.00	10134000.00	4389000.00	0.00	3807305.43	14614800.00	18544000.00	13883400.00	15453900.00	19096000.00	15412500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans ATCC 25259
Ga0586324_2171270_3_872	18590000.00	12938827.84	17589285.41	15409000.00	17705700.00	12376244.74	7785292.56	3074400.00	7549200.00	19457900.00	14546400.00	17167500.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax sp. JS42;Acidovorax sp. JS42
Ga0586324_2175162_3_872	1380000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_2178557_76_864	3530000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized linocin/CFP29 family protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanonatronarchaeaceae;Methanosphaerula;Methanosphaerula palustris;Methanosphaerula palustris E1-9c, DSM 19958
Ga0586324_2179249_1_870	0.00	449834.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	731728.80	253566.00	hypothetical protein	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae;Ignavibacterium;Ignavibacterium album;Ignavibacterium album Mar9-16, JCM 16511
Ga0586324_2183609_1_870	0.00	348339.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium nitrativorans;Hyphomicrobium nitrativorans NL23
Ga0586324_2187337_37_870	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1402500.00	hypothetical protein	
Ga0586324_2191410_1_825	0.00	2536400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2191575_1_870	0.00	1754400.00	99096.45	3173000.00	3615300.00	0.00	911049.24	1634800.00	1571400.00	2440900.00	1856800.00	1215000.00	hypothetical protein	
Ga0586324_2197211_1_867	0.00	0.00	0.00	0.00	0.00	7741500.00	0.00	0.00	0.00	0.00	0.00	0.00	arylsulfatase A-like enzyme	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium neotropicale;Bradyrhizobium neotropicale BR 10247
Ga0586324_2201727_2_868	0.00	1305600.00	0.00	0.00	0.00	0.00	0.00	55197.02	0.00	2479400.00	0.00	1305000.00	hypothetical protein	
Ga0586324_2202265_416_868	0.00	0.00	50805258.89	0.00	0.00	0.00	0.00	0.00	0.00	700305.76	3622500.00	0.00	predicted ABP superfamily pyrophosphatase or phosphodiesterase	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Intrasporangium;Intrasporangium oryzae;Intrasporangium oryzae NRRL B-24470
Ga0586324_2203764_3_866	1980000.00	0.00	0.00	4294000.00	0.00	0.00	4058400.00	3641700.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_2207454_3_779	0.00	16592000.00	0.00	25745000.00	30900000.00	0.00	0.00	23119000.00	31185000.00	26180000.00	22000000.00	7725000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;unclassified Hyphomicrobiales;Nordella;Nordella sp. OAE833;Nordella sp. OAE833
Ga0586324_2209801_1_774	0.00	2332400.00	3805283.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	Bacteria;Chlorroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_2216085_3_866	0.00	0.00	0.00	0.00	0.00	11628000.00	0.00	0.00	0.00	0.00	0.00	0.00	ATPase subunit of ABC transporter with duplicated ATPase domains	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys sp. Root1462;Pseudolabrys sp. Root1462
Ga0586324_2222635_250_864	3120000.00	570391.48	0.00	463998.05	4851300.00	0.00	0.00	5673000.00	0.00	5705700.00	391903.60	305453.25	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_2222960_3_827	0.00	986000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1005000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium allaiseu;Acidobacterium allaiseu PMMR2
Ga0586324_2224652_1_864	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6098400.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Azospirillaceae;Azospirillum;Azospirillum baldanium;Azospirillum baldanium Sp245
Ga0586324_2225761_497_862	4950000.00	3767200.00	4117094.05	5339000.00	5047000.00	0.00	4833600.00	3489200.00	2956500.00	2533300.00	0.00	3307500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Caldimonas;Caldimonas taiwanensis;Caldimonas taiwanensis NBRC 104434
Ga0586324_2232517_1_861	685004.00	0.00	0.00	3458000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;Pseudohaliea;Pseudohaliea rubra;Pseudohaliea rubra DSM 19751
Ga0586324_2234628_469_861	0.00	9112000.00	10302900.00	11305000.00	0.00	11711500.00	0.00	0.00	0.00	0.00	0.00	7650000.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;unclassified Blastocatellia;unclassified Blastocatellia;Chloracidobacterium;Chloracidobacterium thermophilum B
Ga0586324_2245556_287_715	12000000.00	0.00	3277999.94	7058500.00	3677100.00	42479000.00	7569600.00	6893000.00	6172200.00	0.00	0.00	6922500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfarcinum;Desulfarcinum hydrothermale;Desulfarcinum hydrothermale DSM 13146
Ga0586324_2247443_326_859	0.00	0.00	0.00	11685000.00	13905000.00	10322000.00	8208000.00	7503000.00	6123600.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;unclassified Eubacteriales;unclassified Eubacteriales;Clostridiales bacterium PH28 bin88;Clostridiales bacterium PH28 bin88
Ga0586324_2250130_363_860	0.00	0.00	0.00	0.00	0.00	8456100.00	0.00	0.00	0.00	0.00	0.00	0.00	Pyruvate/2-oxoacid:ferredoxin oxidoreductase gamma subunit	Bacteria;Firmicutes;Clostridia;Thermoanaerobacteria;Thermoanaerobacteraceae;Thermanaeromonas;Thermanaeromonas toyohensis;Thermanaeromonas toyohensis ToBE, DSM 14490
Ga0586324_2252457_324_860	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7991000.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;unclassified Gammaproteobacteria;Codakia orbicularis gill symbiont;Codakia orbicularis gill symbiont
Ga0586324_2253379_1_786	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	513641.59	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Saccharicrinis;Saccharicrinis fermentans;Saccharicrinis fermentans DSM 9555
Ga0586324_2254475_398_859	2290000.00	795600.00	0.00	1311000.00	1339000.00	0.00	0.00	0.00	38833.35	121648.23	0.00	197721.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhodomicrobiaceae;Rhodomicrobium;Rhodomicrobium vannielii;Rhodomicrobium vannielii BP-6 RK 2
Ga0586324_2254945_1_858	703655.00	3291200.00	0.00	4085000.00	0.00	7143411.56	10351200.00	4019900.00	3240000.00	2517900.00	2085600.00	1942500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_2271121_3_857	3480000.00	8228000.00	14591192.18	4161000.00	5582600.00	11116000.00	0.00	0.00	0.00	0.00	0.00	2842500.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_2272996_338_775	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4769600.00	3135000.00	flavoredoxin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfarcinum;Desulfarcinum hydrothermale;Desulfarcinum hydrothermale DSM 13146
Ga0586324_2300210_3_851	0.00	4617200.00	0.00	0.00	4490800.00	0.00	0.00	8025600.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_2309659_1_849	12000000.00	3855600.00	0.00	6479000.00	0.00	0.00	6338400.00	0.00	0.00	0.00	0.00	0.00	ABC-type xylose transport system substrate-binding protein	Bacteria;Chlorroflexi;Anaerolineae;Anaerolinales;Anaerolineaceae;Pelolinea;Pelolinea submarina DSM 23923
Ga0586324_2312748_2_718	0.00	6759200.00	0.00	8550000.00	0.00	0.00	0.00	6588000.00	6423300.00	0.00	6290000.00	6337500.00	opacity protein-like surface antigen	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2314049_529_849	0.00	0.00	0.00	0.00	4006700.00	0.00	1709961.24	4422500.00	2057400.00	5266800.00	0.00	4597500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_2319744_2_847	3040000.00	0.00	0.00	0.00	0.00	4565500.00	0.00	8302100.00	4422600.00	1524600.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraniireducens;Geobacter uraniireducens Rf4
Ga0586324_2326094_1_762	0.00	0.00	0.00	0.00	0.00	2974355.76	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized protein YbaA (DUF1428 family)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Reyranellaceae;Reyranella;Reyranella massiliensis;Reyranella massiliensis 521, DSM 23428
Ga0586324_2326338_2_847	0.00	1489200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1147500.00	hypothetical protein	
Ga0586324_2329767_144_848	0.00	0.00	5203741.44	3553000.00	4933700.00	0.00	6589200.00	0.00	3701700.00	0.00	3423200.00	2797500.00	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;unclassified Rhodopila;Rhodopila sp. UYNP
Ga0586324_2342382_183_455	0.00	0.00	2032430.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4769600.00	3135000.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_2343064_1_846	18230000.00	26125600.00	54069540.38	0.00	3574100.00	14411100.00	10374000.00	0.00	13381200.00	7561400.00	0.00	9345000.00	S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanosaeta harundinacea;Methanothrix harundinacea 6Ac
Ga0586324_2344751_240_845	0.00	0.00	0.00	0.00	0.00	1122700.00	0.00	0.00	0.00	0.00	0.00	0.00	Ca2+ binding RTX toxin-like protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Chroococcales;Microcystaceae;Microcystis;Microcystis aeruginosa;Microcystis aeruginosa NIES-87
Ga0586324_2346311_118_843	0.00	0.00	0.00	3743000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	allotamate synthase domain-containing protein 2	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfarculales;Desulfarculaceae;Desulfocarbo;Desulfocarbo indianensis;Desulfocarbo indianensis SCBM
Ga0586324_2366441_1_840	0.00	0.00	0.00	150005.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Actinomycetota;Actinomycetia;Streptomycetales;Streptomycetaceae;Streptomyces;Streptomyces odonnelli;Streptomyces odonnelli NRRL B-24891
Ga0586324_2366627_321_842	11200000.00	0.00	0.00	0.00	0.00	0.00	23859700.00	0.00	0.00	0.00	0.00	0.00	adenylate kinase family enzyme	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_2367798_3_842	2930000.00	5752800.00	3431479.37	0.00	0.00	1534385.15	0.00	2720600.00	0.00	0.00	3511200.00	3105000.00	hypothetical protein	Archaea;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibriones;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio hydrogeniphilus;Thermodesulfovibrio hydrogeniphilus DSM 18151
Ga0586324_2369402_186_548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2407500.00	RNA recognition motif-containing protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2379708_1_840	0.00	22304000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiorhodococcus;Thiorhodococcus drewsii;Thiorhodococcus drewsii AZ1
Ga0586324_2379962_59_838	0.00	0.00	0.00	1368000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_2388315_1_683	0.00	0.00	0.00	693932.25	0.00	0.00	0.00	0.00	0.00	415647.54	0.00	0.00	nucleoid-associated protein YgaU	Bacteria;Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;latescibacteria bacterium SCGC AAA257-K07;latescibacteria bacterium SCGC AAA257-K07 (contamination screened)
Ga0586324_2388993_3_668	0.00	0.00	0.00	0.00	0.00	0.00	490200.00	0.00	0.00	0.00	0.00	0.00	opacity protein-like surface antigen	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2392586_495_836	83500000.00	32300000.00	68123000.00	47690000.00	51500000.00	56374000.00	25080000.00	25559000.00	22356000.00	30492000.00	30184000.00	32850000.00	phasin family protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run_B_J11
Ga0586324_2393178_2_838	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1387500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfomonile tiedjei DCB-1;Desulfomonile tiedjei DCB-1;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_2399817_3_680	0.00	0.00	2807371.35	0.00	0.00	0.00	0.00	0.00	1490400.00	0.00	1953600.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Leptothrix;Leptothrix cholodnii;Leptothrix cholodnii SP-6
Ga0586324_2401007_3_836	0.00	938400.00	0.00	0.00	3687400.00	0.00	0.00	0.00	1725300.00	0.00	0.00	0.00	nucleotide-binding universal stress UspA family protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_2402590_2_835	0.00	0.00	0.00	9975000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TonB-dependent SusC/RagA subfamily outer membrane receptor	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Spirosoma;Spirosoma radiotolerans;Spirosoma radiotolerans DGSA
Ga0586324_2408819_1_834	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1372500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium TAA 166;Acidobacteriaceae bacterium TAA 166
Ga0586324_2410994_289_834	4240000.00	7888000.00	5630000.00	5443500.00	5592900.00	0.00	0.00	6466000.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter sp. Leaf400;Ramlibacter sp. Leaf400
Ga0586324_2413928_3_833	0.00	0.00	0.00	852988.85	0.00	4089100.00	0.00	0.00	0.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2418108_64_276	3620000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted RNA binding protein with TRAM domain	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Candidatus Methanoperedenaceae;Candidatus Methanoperedens;Candidatus Methanoperedens nitroreducens;Candidatus Methanoperedens nitroreducens ANME-2d
Ga0586324_2420610_2_832	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	783915.57	0.00	0.00	0.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Humibacillus;Humibacillus xanthopallidus;Humibacillus xanthopallidus DSM 21776
Ga0586324_2421346_2_607	1050000.00	4637600.00	0.00	7296000.00	0.00	0.00	7204800.00	5050800.00	4398300.00	13552000.00	0.00	4387500.00	DNA-binding Nar1/Fnu family response regulator	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Blastopirellula;Blastopirellula marina;Blastopirellula marina DSM 3645
Ga0586324_2422625_276_833	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1935000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfosarcina;Desulfosarcina;Desulfosarcina benzoelyticum;Desulfosarcina benzoelyticum DSM 28570
Ga0586324_2425334_2_832	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2397300.00	0.00	0.00	0.00	0.00	opacity protein-like surface antigen	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_2425397_3_833	1140000.00	1142400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15169000.00	0.00	2647500.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_2432542_1_412	0.00	0.00	0.00	0.00	0.00	0.00	1945900.00	0.00	0.00	0.00	0.00	0.00	3-polyprenyl-4-hydroxybenzoate decarboxylase	Bacteria;Proteobacteria;Gammaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Desulfosarcina;Desulfosarcina variabilis;Desulfosarcina variabilis Montpellier
Ga0586324_2438590_221_718	0.00	0.00	0.00	0.00	2555500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	rubrerythrin	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_2447211_64_828	2360000.00	9180000.00	0.00	0.00	0.00	0.00	0.00	0.00	774700.00	0.00	0.00	627231.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Ectothiorhodosinus;Ectothiorhodosinus monoalicus;Ectothiorhodosinus monoalicus M9
Ga0586324_2451556_2_829	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10560000.00	0.00	0.00	hypothetical protein	
Ga0586324_2452343_1_828	0.00	0.00	0.00	0.00	0.00	8367600.00	0.00	2737800.00	0.00	6098400.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GAS165
Ga0586324_2464892_188_574	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7747000.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum 31/32
Ga0586324_2466647_2_826	1430000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiobaca;Thiobaca trueperi;Thiobaca trueperi DSM 13587
Ga0586324_2468616_3_827	0.00	454616.72	821749.17	0.00	0.00	1058540.95	1557700.56	1049200.00	0.00	2795100.00	3625600.00	1717500.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium JGI 0000014-B08;Aminicenantes bacterium JGI 0000014-B08 (contamination screened)
Ga0586324_2471117_1_825	4460000.00	2080800.00	3815935.18	5757000.00	3708000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;Pseudoalteromonas;Pseudoalteromonas sp. BS20495;Pseudoalteromonas sp. BS20495
Ga0586324_2474729_265_825	0.00	3610800.00	0.00	0.00	1102100.00	0.00	1930284.48	2037400.00	2308500.00	0.00	2103200.00	2722500.00	predicted ABP superfamily pyrophosphatase or phosphodiesterase	Bacteria;Chlorroflexi;Thermoflexia;Thermoflexales;Thermoflexaceae;Thermoflexus;Thermoflexus hugenholtzii;Thermoflexus hugenholtzii JA02
Ga0586324_2474981_2_826	0.00	0.00	0.00	0.00	2791300.00	0.00	0.00	1122400.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_2485340_3_824	0.00	4195600.00	0.00	5054000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter metallireducens;Geobacter metallireducens RCH3
Ga0586324_2486252_2_823	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1740000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 146;Acidobacteriaceae sp. KBS 146
Ga0586324_2487540_1_825	2910000.00	2108000.00	0.00	4522000.00	8806500.00	5558000.00	5791200.00	6405000.00	11599200.00	4027100.00	6624600.00	1905000.00	predicted porin	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacter;Rhodobacter sp. Root404;Rhodobacter sp. Root404
Ga0586324_2491040_3_683	25530000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanomicrobiaceae;Methanofollis;Methanofollis ethanolicus;Methanofollis ethanolicus JCM 15103
Ga0586324_2494074_1_822	0.00	0.00	0.00	0.00	0.00	5472000.00	0.00	0.00	0.00	5772800.00	0.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-B84
Ga0586324_2502886_2_823	2990000.00	2665175.00	4909748.47	0.00	3265100.00	3380097.70	0.00	1506700.00	0.00	9994600.00	0.00	2840364.75	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
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Ga0586324_2783756_1_453	0.00	3889600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_2788353_230_784	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2891700.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. BK119;Variovorax sp. BK119
Ga0586324_2792658_3_326	0.00	0.00	8163500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	methanogenic corrinoid protein MtbC1	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified Bacteroidales;unclassified Bacteroidales;Bacteroidales bacterium KHT7;Bacteroidales bacterium KHT7
Ga0586324_2798287_31_363	0.00	0.00	0.00	4674000.00	10186700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82_DSM 11109
Ga0586324_2805763_1_782	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1053000.00	0.00	0.00	0.00	NADPH-dependent glutamate synthase beta subunit-like oxidoreductase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiooxus;Thiobacillus thiooxus DSM 505
Ga0586324_2806687_108_782	0.00	0.00	0.00	0.00	0.00	5200700.00	0.00	0.00	0.00	0.00	0.00	0.00	formylglycine-generating enzyme required for sulfatase activity	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oceanospirillaceae;Marinobacterium;Marinobacterium stanieri;Marinobacterium stanieri S30
Ga0586324_2808636_3_443	0.00	972400.00	0.00	1168500.00	801109.28	0.00	0.00	744200.00	0.00	900900.00	0.00	385626.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324_2811270_54_614	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2533300.00	0.00	0.00	uncharacterized membrane protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina barkeri;Methanosarcina barkeri Fusaro, DSM 804
Ga0586324_2819406_3_782	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3862500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium neotropicale;Bradyrhizobium neotropicale BR 10247
Ga0586324_2834180_2_781	0.00	195330.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	rieculator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Chlorobiei;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_2843680_2_475	0.00	4467600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	rubrerythrin	Bacteria;Proteobacteria;Gammaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324_2845761_1_777	0.00	0.00	0.00	2451000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	L-serine deaminase	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_2848270_2_778	3660000.00	0.00	2279750.27	5500500.00	5840100.00	4803700.00	3237600.00	3092700.00	3523500.00	0.00	0.00	0.00	predicted molibopterin-dependent oxidoreductase YjgC	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_2860823_3_776	0.00	2849200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter uraninireducens;Geobacter uraninireducens R4
Ga0586324_2866194_1_777	0.00	80277.40	388231.29	0.00	0.00	0.00	0.00	1988600.00	0.00	0.00	2569600.00	1409894.25	hypothetical protein	
Ga0586324_2867014_3_692	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5281200.00	9086000.00	8703200.00	0.00	hypothetical protein	
Ga0586324_2868405_1_777	0.00	0.00	0.00	0.00	0.00	0.00	2063691.84	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_2869390_486_776	0.00	1550400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_2881119_1_774	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	217923.00	arylsulfatase A-like enzyme	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;Desulfovibrio magneticus;Desulfovibrio cf. magneticus FRC170
Ga0586324_2900651_1_771	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	654592.40	0.00	hvoothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Woeseiaceae;unclassified Woeseiaceae;unclassified Woeseiaceae;uncultured Woeseiaceae SAG 1868 8
Ga0586324_2905725_1_528	13400000.00	24388293.16	42956900.00	0.00	1266900.00	0.00	3556800.00	0.00	0.00	12628000.00	0.00	13875000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_2916236_130_609	10830000.00	7187600.00	25616500.00	11010500.00	35442300.00	11433600.00	55404000.00	0.00	2114100.00	4612300.00	0.00	2995000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82_DSM 11109
Ga0586324_2931864_2_760	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1710000.00	uncharacterized protein (DUF362 family)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324_2935187_2_769	0.00	754800.00	0.00	0.00	0.00	0.00	0.00	896700.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium;Acidobacterium allaiau;Acidobacterium allaiau PMMR2
Ga0586324_2936548_412_768	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	931700.00	0.00	0.00	hvoothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter lichenicola;Edaphobacter lichenicola MBUP22
Ga0586324_2942204_1_768	15400000.00	38624000.00	62221500.00	0.00	14172800.00	23661200.00	42864000.00	19880000.00	53784000.00	14784000.00	33096800.00	34425000.00	predicted porin	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuricellaceae;Sulfuricella;Sulfuricella denitificans;Sulfuricella denitificans sk8.26
Ga0586324_2942625_3_767	0.00	0.00	0.00	2185000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Pyruvate/2-oxoacid:ferredoxin oxidoreductase gamma subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82_DSM 11109
Ga0586324_2949218_1_768	0.00	0.00	0.00	0.00	0.00	0.00	1582176.36	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Leptospirales;Leptospiraceae;Leptonema;Leptonema illini;Leptonema illini 3055, DSM 21528
Ga0586324_2962898_2_640	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4788500.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Hyphomicrobiaceae;Hyphomicrobium;Hyphomicrobium facile;Hyphomicrobium facile facile DSM 1565
Ga0586324_2964674_163_765	0.00	0.00	0.00	3353500.00	3203300.00	0.00	0.00	0.00	0.00	0.00	3842300.00	1848000.00	3187500.00	predicted porin
Ga0586324_2969469_290_766	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1311500.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingobium;Sphingobium xanthum;Sphingobium xanthum DSM 100901
Ga0586324_2974987_1_369	0.00	0.00	0.00	0.00	0.00	9925000.00	0.00	0.00	0.00	0.00	0.00	2340000.00	Flp pilus assembly protein TadD	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82_DSM 11109
Ga0586324_2977018_2_763	0.00	4046000.00	0.00	5538500.00	0.00	2692315.05	3055200.00	1407800.00	6658200.00	5443900.00	5121600.00	4380000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324_2979412_1_765	0.00	0.00	0.00	0.00	2147000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Planctomycetes;Planctomycetia;Gemmatales;Gemmataceae;Gemmata;Gemmata massiliana;Gemmata massiliana IIL30
Ga0586324_2995727_81_761	3580000.00	0.00	7544200.00	6232000.00	8147300.00	7940000.00	7455600.00	7137000.00	6269400.00	2633400.00	3520000.00	2287500.00	predicted porin	
Ga0586324_2999479_3_761	0.00	1094800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA255-E10;Aminicenantes bacterium SCGC AAA255-E10 (contamination screened)
Ga0586324_3003954_3_761	0.00	3536000.00	0.00	0.00	3337200.00	0.00	2269254.36	2183800.00	874800.00	2202200.00	3511200.00	780000.00	MFS family permease	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. Fw109-5;Anaeromyxobacter sp. Fw109-5
Ga0586324_3004846_1_762	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22264000.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Desulfotomaculum;Desulfotomaculum thermocuniculi;Desulfotomaculum thermocuniculi DSM 16036
Ga0586324_3013475_2_760	0.00	0.00	0.00	0.00	1823100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2′,3′-cyclic-nucleotide 2′-phosphodiesterase (5′-nucleotidase family)	Bacteria;Thermotogae;Thermotogae;Petrotogales;Petrotogaceae;Marinitoga;Marinitoga piezophila;Marinitoga piezophila KA3
Ga0586324_3016226_2_760	0.00	0.00	0.00	0.00	0.00	0.00	0.00	707600.00	573166.53	0.00	0.00	0.00	hvoothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Pandoraea;Pandoraea thiooxydans;Pandoraea thiooxydans DSM 25325
Ga0586324_3016679_1_759	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1707200.00	0.00	iron-only hydrogenase group A	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324_3017385_1_759	0.00	0.00	0.00	0.00	0.00	0.00	1391933.16	0.00	0.00	0.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	
Ga0586324_3030626_2_757	3010000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11473000.00	2816000.00	9975000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium elkanii;Bradyrhizobium elkanii USDA 76
Ga0586324_3031177_1_759	0.00	0.00	0.00	2223000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_3033053_1_759	427944.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	serine phosphatase RsbU (regulator of sigma subunit)	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Maenetobacterium;Candidatus Maenetobacterium casensis;Candidatus Maenetobacterium casensis MYR-1
Ga0586324_3033599_3_758	2550000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4527600.00	4822400.00	0.00	hypothetical protein	
Ga0586324_3034432_2_757	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	802537.47	0.00	0.00	0.00	NADH:ubiquinone oxidoreductase subunit F (NADH-binding)	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Desulfofundulus;Desulfofundulus australicus;Desulfofundulus australicus DSM 11792
Ga0586324_3036154_38_757	6980000.00	0.00	12386000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_3041236_66_758	0.00	68680000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_3046798_326_676	0.00	1625200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	RNA recognition motif-containing protein	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira lenta;Nitrospira lenta N_lenta BS10
Ga0586324_3055055_2_628	0.00	204540.60	421598.61	0.00	0.00	0.00	0.00	0.00	0.00	3441900.00	0.00	0.00	long-subunit fatty acid transport protein	
Ga0586324_3059346_3_719	0.00	11471600.00	0.00	7533500.00	0.00	0.00	0.00	1226100.00	0.00	7145600.00	6292000.00	0.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_3060087_2_754	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	17787000.00	420803.68	0.00	hypothetical protein	Bacteria;Deferribacteres;Deferribacteres;Deferribacteraceae;Deferribacter;Deferribacter desulfuricans;Deferribacter desulfuricans SSM1
Ga0586324_3063347_1_756	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2094400.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Sulfuritortus;Sulfuritortus calidifontis;Sulfuritortus calidifontis DSM 103923
Ga0586324_3066749_1_756	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8800000.00	0.00	hvoothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas sp. Nm166;Nitrosomonas sp. Nm166
Ga0586324_3076159_2_316	4230000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_3077858_1_606	0.00	0.00	0.00	0.00	0.00	0.00	924191.16	1738500.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacterales;Bruguieriivoracaceae;Sodalis;Sodalis sp.;Sodalis ignotolerans 159R
Ga0586324_3078369_3_710	0.00	0.00	0.00	0.00	202919000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_3083489_3_752	0.00	0.00	0.00	0.00	0.00	0.00	0.00	673347.84	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;unclassified Chromatiales;Thiohalobacter;Thiohalobacter thiocyanaticus;Thiohalobacter thiocyanaticus FOKN1
Ga0586324_3084917_435_752	0.00	0.00	0.00	213180000.00	0.00	0.00	14751600.00	5020300.00	0.00	8316000.00	0.00	8625000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS478
Ga0586324_3086107_1_753	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1056000.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_3096435_532_753	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11878800.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS242
Ga0586324_3110341_120_749	4680000.00	8228000.00	5855200.00	1064000.00	3223900.00	0.00	4446000.00	2006900.00	5799600.00	7176400.00	7374400.00	2610000.00	hypothetical protein	
Ga0586324_3113641_1_749	0.00	0.00	0.00	0.00	0.00	2698401.06	0.00	2763300.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_3117983_2_748	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10187000.00	0.00	0.00	0.00	0.00	ABC-type nitrate/sulfonate/bicarbonate transport system substrate-binding protein	Bacteria;Actinobacteria;Actinomycetia;Corynebacteriales;Nocardiaceae;Rhodococcus;Rhodococcus rhodochrous;Rhodococcus rhodochrous 11Y
Ga0586324_3129392_3_527	0.00	0.00	0.00	0.00	921850.00	0.00	37255200.00	5258200.00	0.00	10857000.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82_DSM 11109
Ga0586324_3130442_3_749	0.00	0.00	0.00	0.00	2945800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_3140304_3_662	0.00	0.00	9008000.00	4227500.00	3749200.00	5637400.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus;Bacillus sp. AF506103;Bacillus sp. AF506103
Ga0586324_3142728_1_747	0.00	0.00	0.00	0.00	3182700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobacula;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324_3143676_1_747	0.00	0.00	0.00	0.00	0.00	2477625.39	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter arallaceus;Geobacter arallaceus ATCC BAA-1139
Ga0586324_3143683_1_567	27800000.00	26384000.00	52800000.00	36195000.00	61903000.00	12584000.00	32832000.00	41663000.00	18549000.00	0.00	42064000.00	35325000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Sharmanella;Sharmanella aerolata;Sharmanella aerolata KACC 11604
Ga0586324_3144979_3_746	0.00	0.00	7600500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1582500.00	arylsulfatase A-like enzyme	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Rhodopirellula;Rhodopirellula bahusiensis;Rhodopirellula bahusiensis SWK21
Ga0586324_3151576_110_745	3220000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	opacity protein-like surface antigen	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82_DSM 11109
Ga0586324_3168225_3_419	0.00	7391600.00	8107200.00	6887500.00	7261500.00	0.00	5061600.00	7076000.00	7411500.00	6575800.00	7321600.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Sulfuricellaceae;Sulfuricella;Sulfuricella denitificans;Sulfuricella denitificans sk8.26
Ga0586324_3168636_2_745	3540000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type uncharacterized transport system YnlBCD substrate-binding protein	Bacteria;Firmicutes;Bacilli;Bacillales;Paenibacillaceae;Paenibacillus;Paenibacillus naphthalenovorans;Paenibacillus naphthalenovorans PR-N1
Ga0586324_3177177_1_621	0.00	0.00	0.00	0.00	2296900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	tetratricopeptide (TPR) repeat protein	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Pedobacter;Pedobacter jinsengisoil;Pedobacter jinsengisoil T01R-27
Ga0586324_3179110_58_744	6620000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_3180045_1_579	0.00	11560000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_3180872_2_742	4160000.00	0.00	0.00	0.00	12669000.00	0.00	9188400.00	8967000.00	0.00	0.00	7488800.00	2092500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_3184817_1_744	0.00	573178.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Desulfotomiculus;Desulfotomiculus thermocuniculi;Desulfotomiculus thermocuniculi DSM 16036
Ga0586324_3187790_319_741	5490000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2842400.00	0.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Caldanaerobacteraceae;Caldanaerovirga acetigignens;Caldanaerovirga acetigignens DSM 18802
Ga0586324_3190524_1_741	0.00	0.00	0.00	0.00	0.00	0.00	0.00	725900.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Kofleriaceae;Haliangium;Haliangium sp. UPWRP_2;Haliangium sp. TSM_HC
Ga0586324_3194319_2_742	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3511200.00	0.00	0.00	hypothetical protein	
Ga0586324_3195143_2_742	0.00	610016.44	1196977.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324_3197384_3_743	2870000.00	0.00	0.00	4370000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	aldehyde:ferredoxin oxidoreductase	
Ga0586324_3202881_1_456	0.00	0.00	0.00	0.00	10917500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Bizionia;Bizionia paragorgiae;Bizionia paragorgiae DSM 23842
Ga0586324_3212627_1_741	0.00	0.00	4441298.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_3219854_149_739	2150000.00	2475200.00	11541500.00	2850000.00	2502900.00	2647886.78	1966862.52	2061800.00	5823900.00	0.00	1830400.00	2497500.00	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Rhodopila;Rhodopila globiformis;Rhodopila globiformis DSM 161
Ga0586324_3222710_2_547	0.00	4331600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Tangfeifania;Tangfeifania diversiorginum;Tangfeifania diversiorginum DSM 27063
Ga0586324_3223201_1_738	0.00	4598600.00	7310000.00	0.00	0.00	3100800.00	0.00	0.00	4382100.00	0.00	879120.00	4207500.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ
Ga0586324_3225345_3_572	0.00	1421200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1424500.00	2103200.00	0.00	PAS domain-containing protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus gentianae;Syntrophus gent

Ga0586324 3519527 2 712	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11250000.00		hypothetical protein	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter soli;Solirubrobacter soli DSM 22325
Ga0586324 3520287 2 712	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7532800.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodovulum;Rhodovulum sp. PH10;Rhodovulum sp. PH10
Ga0586324 3524173 3 371	0.00	5650800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Ferroglobus;Ferroglobus placidus;Ferroglobus placidus AEDII12DO, DSM 10642
Ga0586324 3528080 70 711	0.00	17000000.00	0.00	12635000.00	62521000.00	0.00	47424000.00	13481000.00	31023000.00	0.00	0.00	11700000.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium macuxiense;Bradyrhizobium macuxiense BR 10355
Ga0586324 3530595 100 711	0.00	0.00	5518723.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324 3533941 3 710	0.00	0.00	0.00	0.00	0.00	0.00	1568291.16	1152900.00	0.00	0.00	0.00	1102500.00		ABC-type branched-subunit amino acid transport system substrate-binding protein	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Streptosporangiaceae;Nonomuraea;Nonomuraea coxensis;Nonomuraea coxensis DSM 45129
Ga0586324 3546496 64 711	0.00	0.00	0.00	0.00	11536000.00	0.00	0.00	6527000.00	6982200.00	0.00	0.00	0.00		glutamate synthase domain-containing protein 2	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 3553212 1 711	0.00	22440000.00	0.00	25080000.00	36256000.00	0.00	0.00	14884000.00	24462000.00	20944000.00	16280000.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacter;Desulfobacter curvatus;Desulfobacter curvatus DSM 3379
Ga0586324 3553310 3 242	2620000.00	2216800.00	4610896.81	3144500.00	3326900.00	3278977.83	0.00	0.00	1522800.00	3765300.00	3264800.00	2242500.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 3554025 1 666	0.00	0.00	0.00	3410500.00	3306300.00	1482147.89	0.00	2513200.00	16524000.00	4750900.00	0.00	1492500.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia niastensis;Massilia niastensis DSM 21313
Ga0586324 3554292 1 705	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12090000.00		kynurenine formamidase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Acuticoccaceae;Acuticoccus;Acuticoccus kandeliae;Acuticoccus kandeliae J103
Ga0586324 3560638 296 709	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2086700.00	4919200.00	4275000.00		hypothetical protein	
Ga0586324 3564620 1 426	7070000.00	17000000.00	15144700.00	5386500.00	0.00	83767000.00	0.00	22570000.00	47547000.00	64834000.00	23496000.00	68175000.00		hypothetical protein	
Ga0586324 3567605 1 708	111170000.00	76309600.00	25111973.18	36860000.00	61495858.51	123744900.00	23871600.00	21594000.00	17455500.00	68737900.00	39582400.00	15120000.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324 3568790 1 708	2200000.00	0.00	8050900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium valentinum;Bradyrhizobium valentinum LmjM3
Ga0586324 3569559 1 708	0.00	5161200.00	7150100.00	8075000.00	8868300.00	4089100.00	8527200.00	15067000.00	13122000.00	11988900.00	11440000.00	10875000.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Altererythrobacter;Altererythrobacter epoxidivorans;Altererythrobacter epoxidivorans CGMCC 1.7731
Ga0586324 3600209 2 706	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	850500.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 3614667 2 706	0.00	3359200.00	3833022.23	5377000.00	7446900.00	5399200.00	0.00	5368000.00	4179600.00	6183100.00	6538400.00	6142500.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter dinghuensis;Edaphobacter dinghuensis EB95
Ga0586324 3622761 3 704	24900000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin	
Ga0586324 3638456 1 474	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	846961.28	0.00		EpsD family peptidyl-prolyl cis-trans isomerase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324 3638910 3 704	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3617300.00	0.00	0.00	0.00	0.00		Tfp pilus assembly protein PilF	
Ga0586324 3642467 3 704	5300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4957500.00		hypothetical protein	
Ga0586324 3650511 2 703	0.00	3940534.72	0.00	0.00	0.00	2754497.16	0.00	0.00	0.00	0.00	0.00	681587.25		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfobacterium;Desulfobacterium autotrophicum;Desulfobacterium autotrophicum HRM2, DSM 3382
Ga0586324 3652739 1 702	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	899100.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus sp. GAS368;Opitutus sp. GAS368
Ga0586324 3656447 3 653	20600000.00	0.00	5798900.00	10165000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6712500.00		predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas;Pseudomonas gingeri;Pseudomonas gingeri NCPPB 3146
Ga0586324 3657468 3 497	38400000.00	0.00	0.00	0.00	0.00	0.00	0.00	6093900.00	0.00	0.00	0.00	0.00		rubrerythrin	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Kuenenia;Candidatus Kuenenia stuttgartiensis;Candidatus Kuenenia stuttgartiensis MBR1
Ga0586324 3659984 52 702	173000000.00	0.00	0.00	0.00	0.00	0.00	90060000.00	0.00	59454000.00	0.00	0.00	30600000.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodovulum;Rhodovulum sp. PH10;Rhodovulum sp. PH10
Ga0586324 3674147 1 699	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1563300.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Erythrobacteraceae;Altererythrobacter;Altererythrobacter xiamenensis;Altererythrobacter xiamenensis CGMCC 1.12494
Ga0586324 3674156 1 699	0.00	1292000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		formyltetrahydrofolate synthetase	Bacteria;Firmicutes;Clostridia;Eubacteriales;unclassified Eubacteriales;unclassified Eubacteriales;Clostridiales bacterium PH28 bin88;Clostridiales bacterium PH28 bin88
Ga0586324 3690547 3 224	0.00	9044000.00	0.00	32870000.00	20909000.00	0.00	0.00	11407000.00	17091000.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Thauera;Thauera sp. 28;Thauera sp. 28
Ga0586324 3696922 1 699	0.00	0.00	0.00	0.00	1833400.00	0.00	0.00	1793400.00	0.00	924000.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Thermodesulforhabdus;Thermodesulforhabdus norvegica;Thermodesulforhabdus norvegica DSM 9990
Ga0586324 3709196 168 590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2992500.00		uncharacterized surface protein with fasciclin (FAS1) repeats	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Synechococcales;Merismopediaceae;Merismopedia;Merismopedia glauca;Merismopedia glauca CCAP 1448/3
Ga0586324 3722431 3 695	0.00	0.00	0.00	0.00	0.00	225879.11	0.00	0.00	0.00	0.00	0.00	0.00		TonB-dependent SusC/RagA subfamily outer membrane receptor	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Flexithrix;Flexithrix dorotheae;Flexithrix dorotheae DSM 6795
Ga0586324 3730128 488 697	0.00	4025600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 3731788 3 695	0.00	169371.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	660649.99	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Thermoanaerobaculia;Thermoanaerobaculales;Thermoanaerobaculaceae;Thermoanaerobaculum;Thermoanaerobaculum aquaticum;Thermoanaerobaculum aquaticum MP-01
Ga0586324 3743110 1 696	0.00	0.00	0.00	0.00	14523000.00	17348900.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324 3745399 2 694	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4268000.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324 3758571 2 694	0.00	1101600.00	0.00	0.00	0.00	0.00	0.00	0.00	655274.61	176837.43	0.00	0.00		predicted CXXCH cytochrome family protein	Bacteria;Firmicutes;Clostridia;Eubacteriales;Peptococcaceae;Thermincola;Thermincola ferriacetica;Thermincola ferriacetica Z-0001
Ga0586324 3763019 3 692	0.00	1074400.00	1585419.26	0.00	0.00	1745497.84	0.00	0.00	1344600.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Rhodothermaeota;Rhodothermia;Rhodothermales;Rubricoccaceae;Rubricoccus;Rubricoccus marinus;Rubricoccus marinus SG-29
Ga0586324 3796379 146 619	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11956000.00	0.00	0.00	0.00	0.00		predicted Zn-dependent protease	
Ga0586324 3798063 3 692	0.00	0.00	3857889.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3036000.00	3382500.00		parallel beta-helix repeat protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanohalophilus;Methanohalophilus mahii;Methanohalophilus mahii SLP, DSM 5219
Ga0586324 3800472 1 690	22400000.00	37400000.00	25109800.00	19665000.00	47380000.00	11195400.00	27998400.00	28853000.00	28188000.00	22022000.00	39424000.00	44895000.00		hypothetical protein	
Ga0586324 3802614 1 690	0.00	7276000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		ATP-dependent Clp protease ATP-binding subunit ClpA	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 3804726 2 691	0.00	1667731.28	0.00	1368000.00	1194800.00	0.00	0.00	1049200.00	0.00	2510200.00	0.00	1545000.00		hypothetical protein	
Ga0586324 3807355 2 691	0.00	0.00	0.00	1491500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		glyoxylase-like metal-dependent hydrolase (beta-lactamase superfamily II)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. Tv2a-2;Bradyrhizobium sp. TV2a.2
Ga0586324 3808139 222 689	8090000.00	7888000.00	11091100.00	14725000.00	0.00	12412030.32	18285600.00	8906000.00	3588300.00	8316000.00	7198400.00	2257500.00		hypothetical protein	
Ga0586324 3814894 1 690	0.00	1666000.00	0.00	0.00	0.00	4764000.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Rhodanobacteraceae;Ahniella;Ahniella affigens;Ahniella affigens D13
Ga0586324 3815812 2 379	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3599200.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Streptosporangiaceae;Sphaerisporangium;Sphaerisporangium album;Sphaerisporangium album CCTCC AA 208026
Ga0586324 3831585 2 688	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1750700.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio islandicus;Thermodesulfovibrio islandicus DSM 12570
Ga0586324 3842194 1 687	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2902500.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Intrasporangium;Intrasporangium chromatireducens;Intrasporangium chromatireducens Q5-1
Ga0586324 3843662 3 686	0.00	1203600.00	0.00	0.00	0.00	0.00	0.00	4855600.00	0.00	461099.10	0.00	0.00		hypothetical protein	
Ga0586324 3855478 170 685	0.00	542359.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		outer membrane receptor protein involved in Fe transport	
Ga0586324 3870956 147 416	0.00	0.00	0.00	0.00	1081500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		nucleoid DNA-binding protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulforegula;Desulforegula conservatrix;Desulforegula conservatrix Mb1Pa
Ga0586324 3876937 1 684	0.00	2250800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2684000.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Fulvivirgaceae;Ohtaekwangia;Ohtaekwangia koreensis;Ohtaekwangia koreensis DSM 25262
Ga0586324 3886312 3 683	8170000.00	4154800.00	0.00	13338000.00	0.00	5835900.00	10305600.00	4703100.00	4811400.00	0.00	3511200.00	3517500.00		hypothetical protein	Bacteria;Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;unclassified Nitrospirae;Nitrospirae bacterium HCH-1;Nitrospirae bacterium HCH-1
Ga0586324 3886919 232 684	2850000.00	1822400.00	2922127.64	6555000.00	0.00	0.00	0.00	1390800.00	1547100.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 3887468 3 683	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2867000.00	0.00	0.00	0.00	0.00		subtilisin family serine protease	Bacteria;Firmicutes;Limnochordia;Limnochordales;Limnochordaceae;Limnochorda;Limnochorda pilosa;Limnochorda pilosa HC45
Ga0586324 3891068 327 683	0.00	0.00	0.00	2394000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Kribbellaceae;Kribbella;Kribbella sp. VKM Ac-2568;Kribbella pushchinensis VKM Ac-2568
Ga0586324 3904508 225 683	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19712000.00	0.00	0.00		hypothetical protein	
Ga0586324 3909454 258 683	44900000.00	6460000.00	29895300.00	41705000.00	7941300.00	37437100.00	36571200.00	7503000.00	7395300.00	22792000.00	26065600.00	9030000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum;Herbaspirillum autotrophicum;Herbaspirillum autotrophicum IAM 14942
Ga0586324 3918447 3 683	6840000.00	3032800.00	0.00	0.00	0.00	0.00	0.00	1665300.00	1296000.00	1809500.00	2358400.00	2025000.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324 3919987 3 683	0.00	0.00	0.00	0.00	0.00	33030400.00	0.00	0.00	26892000.00	0.00	0.00	0.00		S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 3927666 1 588	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18873000.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 146;Acidobacteriaceae sp. KBS 146
Ga0586324 3930851 176 682	544576.00	493633.08	0.00	870946.70	13657800.00	7618207.68	722864.88	732000.00	980100.00	3542000.00	1416800.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Aquabacterium;Aquabacterium tepidiphilum;Aquabacterium tepidiphilum YIM 730274
Ga0586324 3931990 1 681	4550000.00	2978400.00	7319000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 3935348 1 681	0.00	11696000.00	0.00	4227500.00	23896000.00	0.00	11126400.00	4471300.00	11826000.00	8778000.00	7295200.00	10125000.00		predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiobaca;Thiobaca trueperi;Thiobaca trueperi DSM 13587
Ga0586324 3957913 3 680	0.00	0.00	0.00	0.00	0.00	0.00	310998.84	0.00	0.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiogranum;Thiogranum longum;Thiogranum longum DSM 19610
Ga0586324 3959299 1 678	0.00	4637600.00	0.00	0.00	0.00	0.00	0.00	0.00	1336500.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 3970132 3 677	0.00	5249600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta africana;Spirochaeta africana Z-7692, DSM 8902
Ga0586324 3972977 2 679	0.00	0.00	0.00	0.00	0.00	0.00	1822301.40	0.00	1984500.00	2356200.00	0.00	0.00		hypothetical protein	
Ga0586324 3977899 276 677	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3036000.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas sp. 11b;Methylomonas sp. 11b
Ga0586324 3982290 513 677	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1478400.00	0.00	0.00		hypothetical protein	
Ga0586324 3983887 227 676	0.00	12784000.00	3877431.67	0.00	47792000.00	11830600.00	39900000.00	0.00	10935000.00	0.00	0.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Noviherbaspirillum;Noviherbaspirillum massiliense;Noviherbaspirillum massiliense JC206
Ga0586324 3983937 209 676	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1793400.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium lacus;Methylosarcina lacus LW14
Ga0586324 3998242 358 675	0.00	4916400.00	0.00	0.00	0.00	0.00	0.00	2202100.00	0.00	3534300.00	0.00	2385000.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324 3998485 3 452	0.00	632578.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		membrane protease subunit (stomatin/prohibitin family)	Bacteria;Chloroflexi;Chloroflexia;Kallotenuales;Kallotenuaceae;Kallotenue;Kallotenue papyrolyticum;Kallotenue papyrolyticum JKG1
Ga0586324 4003741 1 675	0.00	0.00	0.00	0.00	0.00	1538041.52	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Candidatus Poribacteria;unclassified Candidatus Poribacteria;unclassified Candidatus Poribacteria;unclassified Candidatus Poribacteria;unclassified Candidatus Poribacteria;uncultured Poribacteria bacterium;Uncultured Poribacteria bacterium AGPOR5
Ga0586324 4004618 3 677	3920000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Chlorobi;Chlorobia;Chlorobiales;Chlorobiaceae;Chlorobaculum;Chlorobaculum limnaeum;Chlorobaculum limnaeum DSM 1677
Ga0586324 4008061 2 565	0.00	0.00	0.00	0.00	7240900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta lutea;Spirochaeta lutea JC230
Ga0586324 4011692 2 553	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	346502.31	0.00	0.00		NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Rhizobium;Rhizobium gallicum;Rhizobium gallicum IE4872
Ga0586324 4012610 2 676	1720000.00	2271200.00	0.00	2356000.00	2049700.00	0.00	1148730.12	1561600.00	882900.00	2802800.00	3291200.00	1042500.00		hypothetical protein	
Ga0586324 4016646 404 676	5600000.00	2516000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4022590 66 674	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	305875.68	0.00		predicted AlkP superfamily pyrophosphatase or phosphodiesterase	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. OAS665;Nocardioides sp. OAS665
Ga0586324 4025802 1 675	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2156000.00	2323200.00	2025000.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324 4030034 1 675	0.00	0.00	0.00	0.00	15656000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4032538 174 674	0.00	0.00	0.00	2232500.00	0.00	0.00	3511200.00	1610400.00	3410100.00	0.00	0.00	0.00		uncharacterized membrane protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 4032539 1 675	2360000.00	8024000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	109370800.00	8439024.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas denitrificans;Dechloromonas denitrificans ATCC BAA-841
Ga0586324 4051335 1 672	5660000.00	0.00	0.00	4256000.00	0.00	0.00	0.00	0.00	0.00	0.00	3828000.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 4052799 3 671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1327500.00		hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 4054075 3 671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1530000.00		DNA-binding transcriptional LysR family regulator	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Phyllobacteriaceae;Mesorhizobium;Mesorhizobium sp. M6A.T.Cr.TU.016.01.1.1;Mesorhizobium sp. M6A.T.Cr.TU.016.01.1.1
Ga0586324 4064928 3 383	1630000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		Tfp pilus assembly protein PilF	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4068171 3 671	0.00	2114800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified Oxalobacteraceae;Oxalobacteraceae bacterium;Oxalobacteraceae sp. OAS666
Ga0586324 4071999 3 671	0.00	0.00	0.00	0.00	0.00	5002200.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;Betaproteobacteria bacterium GR16-43;Betaproteobacteria bacterium GR16-43
Ga0586324 4082241 3 476	239277.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		rubrerythrin	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 4084643 237 671	0.00	1258000.00	0.00	2546000.00	0.00	3461379.48	0.00	1482300.00	2656800.00	1794100.00	1962400.00	0.00		hypothetical protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Chroococcales;Microcystaceae;Microcystis;Microcystis aeruginosa;Microcystis aeruginosa FACHB-524
Ga0586324 4086762 3 671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9944000.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Terriglobus;Terriglobus roseus;Terriglobus roseus AB35.6
Ga0586324 4088508 3 671	0.00	0.00	0.00	48383500.00	43507200.00	47441500.00	8960400.00	10797000.00	9234000.00	0.00	0.00	5392500.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatiglans;Desulfatiglans anilini;Desulfatiglans anilini DSM 4660
Ga0586324 4089212 2 670	0.00	0.00	2937536.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		glutamate synthase domain-containing protein 2	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacterales Family III. Incertae Sedis;Caldicellulosiruptor;Caldicellulosiruptor bescii;Caldicellulosiruptor bescii DSM 6725
Ga0586324 4091162 1 498	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4481400.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4095173 113 487	0.00	0.00	0.00	0.00	0.00	0.00	5928000.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloglobulus;Methyloglobulus morosus;Methyloglobulus morosus KoM1
Ga0586324 4095214 425 670	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	450369.04	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified Myxococcales;Minicystis;Minicystis rosea;Minicystis rosea DSM 24000
Ga0586324 4098118 2 412	0.00	2108000.00	0.00	8607000.00	5819500.00	0.00	0.00	4575000.00	4179600.00	2664200.00	870279.52	0.00		hypothetical protein	
Ga0586324 4105491 3 668	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6267800.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Piscirickettsiaceae;Cycloclasticus;Cycloclasticus sp. P1;Cycloclasticus sp. P1
Ga0586324 4111442 36 347	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2238700.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Acidimicrobiia;Acidimicrobiales;Ilumatobacteraceae;Ilumatobacter;Ilumatobacter nonamiensis;Ilumatobacter nonamiensis YM16-303
Ga0586324 4115170 3 668	24920000.00	0.00	0.00	16216500.00	23793000.00	27710600.00	31486800.00	22997000.00	7119900.00	0.00	6881600.00	0.00		hypothetical protein	
Ga0586324 4127448 3 668	0.00	0.00	0.00	0.00	0.00	0.00	204372.59	0.00	0.00	0.00	0.00	787500.00		hypothetical protein	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio yellowstonii;Thermodesulfovibrio yellowstonii DSM 11347
Ga0586324 4131977 2 448	0.00	0.00	0.00	5158500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4132496 1 666	0.00	1925618.56	0.00	0.00	291777.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00		transketolase C-terminal domain/subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylobacter;Methylobacter tundripaludum;Methylobacter tundripaludum SV96
Ga0586324 4138233 1 666	0.00	2679200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micromonosporales;Micromonosporaceae;Micromonospora;Micromonospora humi;Micromonospora humi DSM 45647
Ga0586324 4138309 1 666	0.00	0.00	218925.93	0.00	786970.47	684983.80	804796.68	608870.89	674840.97	484407.00	491656.00	191352.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS242
Ga0586324 4149026 2 667	0.00	0.00	11710400.00	0.00	0.00	0.00	0.00	0.00	6390900.00	0.00	0.00	0.00		PAS domain S-box-containing protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Desulfuromonadaceae;Pelobacter;Pelobacter propionicus;Pelobacter propionicus DSM 2379
Ga0586324 4151850 3 665	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	377288.45	0.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micromonosporales;Micromonosporaceae;Asanoa;Asanoa ferruginea;Asanoa ferruginea DSM 44099
Ga0586324 4152111 3 665	0.00	5528400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		glutamate synthase domain-containing protein 2	Bacteria;Firmicutes;Clostridia;Eubacteriales;Oscillospiraceae;Papillibacter;Papillibacter cinnamivorans;Papillibacter cinnamivorans DSM 12816
Ga0586324 4160434 329 664	0.00	0.00	0.00	0.00	0.00	3735067.31	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfococcus;Desulfococcus multivorans;Desulfococcus multivorans DSM 2059
Ga0586324 4169612 1 489	0.00	2108000.00	0.00	0.00	1545000.00	0.00	0.00	847900.00	1142100.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter pickeringii;Geobacter pickeringii G13
Ga0586324 4172811 2 334	0.00	0.00	0.00	2992500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 4174321 1 426	2730000.00	3862400.00	0.00	5491000.00	0.00	0.00	0.00	0.00	0.00	1509200.00	1504800.00	1155000.00		hypothetical protein	
Ga0586324 4174504 3 665	1330000.00	0.00	0.00	2660000.00	2801600.00	0.00	0.00	0.00	1717200.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4178147 3 665	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2737800.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Caballeronia;Caballeronia pedi;Caballeronia pedi LMG 29323
Ga0586324 4200877 1 663	1690000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 4202606 3 662	0.00	2155600.00	9064300.00	10545000.00	13802000.00	15205100.00	7660800.00	0.00	8343000.00	2625700.00	0.00	0.00		hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina vacuolata;Methanosarcina vacuolata Z-761
Ga0586324 4211374 3 662	0.00	918000.00	0.00	0.00	0.00	0.00	0.00	0.00	534918.33	0.00	0.00	2212500.00		hypothetical protein	
Ga0586324 4212198 3 305	0.00	0.00	0.00	0.00	0.00	0.00	0.00	939400.00	0.00	0.00	0.00	0.00		osmotically-inducible protein OsmY	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosomonas;Nitrosomonas eutropha;Nitrosomonas eutropha C91
Ga0586324 4214625 1 630	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1763300.00	0.00	2227500.00		opacity protein-like surface antigen	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum;Herbaspirillum hiltneri;Herbaspirillum hiltneri N3
Ga0586324 4222624 75 662	4050000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4224435 2 661	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22792000.00	1135200.00	0.00		hypothetical protein	
Ga0586324 4226202 3 662	1110000.00	0.00	0.00	0.00	0.00	22112900.00	0.00	0.00	0.00	416076.43	0.00	6210000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum;Herbaspirillum rhizosphaerae;Herbaspirillum rhizosphaerae UMS-37
Ga0586324 4227637 1 660	0.00	3420400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1687500.00		hypothetical protein	
Ga0586324 4235832 281 661	0.00	1645600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		phasin family protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas sp. SG708;Dechloromonas sp. SG708
Ga0586324 4235857 157 660	8830000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 2909;Geobacter sp. DSM 2909
Ga0586324 4241758 152 661	9303505.80	6324000.00	5366836.91	5899500.00	0.00	5677100.00	6292800.00	4941000.00	4714200.00	9471000.00	7972800.00	10425000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rubrivivax;Rubrivivax benzoatilyticus;Rubrivivax benzoatilyticus JA2
Ga0586324 4243396 133 660	0.00	190189200.00	243779000.00	194750000.00	218360000.00	214380000.00	282720000.00	126880000.00	105300000.00	174020000.00	191840000.00	169500000.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. OAE819;Bradyrhizobium sp. OAE819
Ga0586324 4247355 269 658	5490000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16362000.00	0.00	0.00	0.00		phasin family protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Contendobacter;Candidatus Contendobacter odensis;Candidatus Contendobacter odensis Run B J11
Ga0586324 4251737 396 659	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	403527.74	0.00	0.00		hypothetical protein	
Ga0586324 4254669 3 659	2410000.00	0.00	1849775.91	0.00	1864300.00	1405832.58	3328800.00	0.00	0.00	2456300.00	2798400.00	2287500.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia sp. P52-10;Afipia sp. P52-10
Ga0586324 4262153 1 660	3140000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin	
Ga0586324 4264875 3 659	0.00	0.00	2095480.37	0.00	0.00	0.00	0.00	628300.00	0.00	0.00	0.00	736863.00		acetyl-CoA acetyltransferase	Bacteria;Proteobacteria;Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;unclassified Deltaproteobacteria;delta proteobacterium NaphS2;delta proteobacterium NaphS2
Ga0586324 4268610 3 659	2700000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324 4284506 56 562	0.00	0.00	0.00	0.00	0.00	0.00	136800000.00	0.00	0.00	0.00	0.00	0.00		tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109

Ga0586324 4284924 71 658	7180000.00	0.00	9627300.00	0.00	0.00	6312300.00	0.00	0.00	4260600.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4288109 3 656	3800000.00	6446400.00	2831022.98	1862000.00	3213600.00	2405403.15	3625200.00	5752300.00	3564000.00	1324400.00	206976.88	1455000.00		S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4292377 1 657	0.00	0.00	1896375.42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 4319551 1 654	0.00	362927.56	373712.64	502355.25	398880.89	236574.68	234687.24	0.00	212261.31	0.00	358285.84	0.00		cytochrome c peroxidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfoglaeba;Desulfoglaeba alkanexedens;Desulfoglaeba alkanexedens ALDC
Ga0586324 4328507 2 655	0.00	0.00	1816829.15	0.00	5294200.00	0.00	0.00	0.00	2081700.00	1963500.00	0.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Intrasporangium;Intrasporangium oryzae;Intrasporangium oryzae NRRL B-24470
Ga0586324 4333406 1 654	1950000.00	4698800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		bacillopeptidase F (M6 metalloprotease family)	Bacteria;Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;unclassified Candidatus Cloacimonetes;Cloacimonetes bacterium SCGC AAA252-K16;Cloacimonetes bacterium SCGC AAA252-K16 (contamination screened)
Ga0586324 4336290 3 653	17500000.00	4943600.00	15932900.00	13048458.05	0.00	7979700.00	7090800.00	0.00	1449900.00	7184100.00	0.00	19867500.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Azonexus;Azonexus hydrophilus;Azonexus hydrophilus DSM 23864
Ga0586324 4338054 3 653	0.00	5854800.00	0.00	997500.00	11330000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Marinobacter;Marinobacter sp.;Marinobacter sp. MIT1353
Ga0586324 4343361 2 652	0.00	0.00	0.00	1548500.00	0.00	0.00	0.00	0.00	0.00	0.00	6943200.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-BB4
Ga0586324 4352577 2 652	90200000.00	62016000.00	197387800.00	34390000.00	16583000.00	125849000.00	0.00	0.00	10530000.00	3803800.00	3088800.00	14625000.00		hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4357828 3 653	0.00	0.00	0.00	0.00	10300000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		outer membrane receptor for ferrienterochelin and colicin	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324 4361707 14 652	5570000.00	2223600.00	5234092.77	0.00	0.00	0.00	3146400.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4361715 3 653	3850000.00	2309794.76	0.00	4332000.00	4130300.00	0.00	0.00	0.00	0.00	0.00	0.00	2617500.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;Bryobacter aggregatus DSM 18758
Ga0586324 4364312 3 587	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5218400.00	0.00		hypothetical protein	
Ga0586324 4381176 2 652	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3157000.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter metallireducens;Geobacter metallireducens GS-15
Ga0586324 4383295 1 282	0.00	13872000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		RNA recognition motif-containing protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Draconibacterium;Draconibacterium orientale;Draconibacterium orientale FH5
Ga0586324 4384000 8 652	0.00	0.00	637237.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. Ai1a-2;Bradyrhizobium sp. Ai1a-2
Ga0586324 4388607 178 468	1630000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		uncharacterized protein with GYD domain	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira;Nitrospira marina;Nitrospira marina Nb-295
Ga0586324 4392760 1 213	0.00	171126.08	0.00	0.00	0.00	0.00	0.00	0.00	826200.00	0.00	0.00	0.00		cystathionine beta-lyase/cystathionine gamma-synthase	
Ga0586324 4402229 1 651	0.00	1346400.00	0.00	0.00	1431700.00	0.00	0.00	994300.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4412595 2 649	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	52375.05		hypothetical protein	
Ga0586324 4412632 92 649	2640000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4414353 1 531	4750000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfotignum;Desulfotignum balticum;Desulfotignum balticum DSM 7044
Ga0586324 4414407 2 649	1294096.00	0.00	0.00	794442.25	114466.99	0.00	0.00	0.00	0.00	0.00	0.00	3772500.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Granulicella;Granulicella sp. GAS466;Granulicella sp. GAS466
Ga0586324 4429402 2 442	0.00	12172000.00	0.00	0.00	0.00	0.00	11559600.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 4430588 3 647	0.00	1074400.00	0.00	0.00	0.00	1616290.22	4248807.36	0.00	0.00	0.00	1029600.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Prolixibacter;Prolixibacter denitrificans;Prolixibacter denitrificans DSM 27267
Ga0586324 4437708 416 649	0.00	3631200.00	0.00	1415500.00	0.00	0.00	0.00	0.00	3458700.00	0.00	0.00	0.00		NAD(P)H-nitrite reductase large subunit	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324 4440395 2 646	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2049300.00	0.00	0.00	0.00		arylsulfatase A-like enzyme	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS138
Ga0586324 4448312 3 647	0.00	0.00	0.00	0.00	5603200.00	4128800.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter argillaceus;Geobacter argillaceus ATCC BAA-1139
Ga0586324 4451036 2 646	0.00	0.00	0.00	8350500.00	9043400.00	0.00	0.00	10553000.00	0.00	10857000.00	10032000.00	9975000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 4459780 217 645	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5111100.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4473295 1 282	0.00	2944400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	
Ga0586324 4477176 1 645	0.00	0.00	0.00	3667000.00	3975800.00	0.00	0.00	1366400.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4482022 1 645	14200000.00	8704000.00	13455700.00	15105000.00	15965000.00	13498000.00	5608800.00	8235000.00	6763500.00	11473000.00	10208000.00	11925000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Neisseriales;Chromobacteriaceae;Pseudogulbenkiania;Pseudogulbenkiania ferrooxidans;Pseudogulbenkiania ferrooxidans 2002
Ga0586324 4483073 3 644	0.00	0.00	0.00	0.00	2018800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 4500463 2 643	13200000.00	12770400.00	5407479.88	17160243.30	14317000.00	8568288.23	3214800.00	7015000.00	6204600.00	7007000.00	7128000.00	5760000.00		hypothetical protein	
Ga0586324 4511420 3 644	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	649553.52	0.00		EpsD family peptidyl-prolyl cis-trans isomerase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans RG
Ga0586324 4527108 3 641	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2780800.00	0.00		CheY-like chemotaxis protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Variovorax;Variovorax sp. OV329;Variovorax sp. OV329
Ga0586324 4530052 3 641	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5105100.00	0.00	0.00		ABC-type oligopeptide transport system substrate-binding subunit	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Rhizobiaceae;Rhizobium;Rhizobium flavum;Rhizobium flavum CCTCC AB 2013042
Ga0586324 4534538 3 641	0.00	7140000.00	0.00	0.00	0.00	30846900.00	0.00	0.00	0.00	0.00	0.00	0.00		S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix thermoacetophila;Methanothrix thermoacetophila PT
Ga0586324 4557333 1 642	0.00	0.00	0.00	2831000.00	4830700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4559319 20 499	0.00	0.00	0.00	0.00	0.00	4327300.00	0.00	0.00	0.00	0.00	0.00	0.00		tetratricopeptide (TPR) repeat protein	
Ga0586324 4565370 1 639	0.00	3434000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter modestus;Edaphobacter modestus DSM 18101
Ga0586324 4566916 3 641	0.00	0.00	10640700.00	0.00	0.00	0.00	33060000.00	0.00	11907000.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 4570116 1 468	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1188000.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 4581734 3 638	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	20064000.00	0.00		arylsulfatase A-like enzyme	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium japonicum;Bradyrhizobium japonicum SEMIA 5079
Ga0586324 4586705 109 639	0.00	0.00	3798696.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324 4605855 174 638	0.00	1332800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2687300.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Achromatium;uncultured Achromatium sp.;Achromatium sp. Cell8
Ga0586324 4612819 1 636	0.00	2631600.00	0.00	6479000.00	0.00	0.00	0.00	0.00	0.00	0.00	3440800.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thiorhodospira;Thiorhodospira sibirica;Thiorhodospira sibirica A12, ATCC 700588
Ga0586324 4618810 352 636	0.00	20060000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. Root404;Rhizobacter sp. Root404
Ga0586324 4622718 122 637	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	760693.68	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4626290 1 636	0.00	0.00	2003199.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		TonB-dependent receptor	Bacteria;Ignavibacteriae;Ignavibacteria;Ignavibacteriales;Melioribacteraceae;Melioribacter;Melioribacter roseus;Melioribacter roseus P3M
Ga0586324 4636875 1 624	0.00	497101.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4645488 2 637	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1790100.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Firmicutes;Bacilli;Bacillales;Thermoactinomycetaceae;Shimazuella;Shimazuella kribbensis;Shimazuella kribbensis DSM 45090
Ga0586324 4654546 3 635	0.00	1319200.00	0.00	0.00	2688300.00	740305.75	0.00	0.00	0.00	0.00	0.00	1567500.00		hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Flammeovirgaceae;Flexithrix;Flexithrix dorotheae;Flexithrix dorotheae DSM 6795
Ga0586324 4669613 3 296	4050000.00	2536400.00	2399680.53	2498500.00	2111500.00	1732623.13	2251821.48	1695800.00	1814400.00	0.00	0.00	596761.50		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Afipia;Afipia sp. P52-10;Afipia sp. P52-10
Ga0586324 4678068 2 634	1890000.00	1332800.00	0.00	0.00	1030000.00	0.00	0.00	2232600.00	1757700.00	0.00	1029600.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuriferula;Sulfuriferula thiophila;Sulfuriferula thiophila mst6
Ga0586324 4679736 1 216	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	324309.04	0.00		uncharacterized membrane protein YqjE	
Ga0586324 4680016 3 635	1490000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		ABC-type oligopeptide transport system ATPase subunit	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324 4694232 1 633	0.00	2815200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira multiformis;Nitrosospira multiformis Nl1
Ga0586324 4705894 2 631	0.00	538337.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So0157-25
Ga0586324 4710843 74 595	0.00	2828800.00	0.00	0.00	6365400.00	7384200.00	0.00	0.00	0.00	0.00	0.00	0.00		Flp pilus assembly protein TadD	
Ga0586324 4712126 2 631	0.00	1536800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Candidimonas;Candidimonas bauzanensis;Candidimonas bauzanensis CGMCC 1.10190
Ga0586324 4716483 2 631	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	549291.75		hypothetical protein	
Ga0586324 4717159 3 632	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5467500.00		hypothetical protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 4720353 3 632	352235.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4723372 330 632	0.00	657572.24	0.00	0.00	0.00	2012464.46	0.00	6893000.00	5459400.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;unclassified Oxalobacteraceae;Oxalobacteraceae bacterium IMCC9480;beta proteobacterium sp. IMCC9480
Ga0586324 4732531 1 630	0.00	212087.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurirhabdus;Sulfurirhabdus autotrophica;Sulfurirhabdus autotrophica DSM 100309
Ga0586324 4744838 3 629	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2625000.00		UbiD family decarboxylase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 4751609 2 631	0.00	4297600.00	12667500.00	0.00	0.00	8575200.00	8071200.00	3996753.55	0.00	124609100.00	112112000.00	46545000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;unclassified Burkholderiales;Burkholderiales bacterium GJ-E10;Burkholderiales bacterium GJ-E10
Ga0586324 4763592 31 630	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3080500.00	3969000.00	0.00	0.00	2310000.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Streptomycetales;Streptomycetaceae;Kitasatospora;Kitasatospora atroaurantiaca;Kitasatospora atroaurantiaca DSM 41649
Ga0586324 4796343 3 626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3458700.00	0.00	3106400.00	0.00		hypothetical protein	
Ga0586324 4797735 3 626	91816306.00	126242000.00	0.00	125732500.00	262165900.00	6946809.22	9507600.00	171397800.00	110459700.00	633428.95	1879254.96	57225000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas denitrificans;Dechloromonas denitrificans ATCC BAA-841
Ga0586324 4810397 2 625	0.00	1081200.00	0.00	3182500.00	2832500.00	0.00	0.00	70760000.00	1360800.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Saccharicrinis;Saccharicrinis fermentans;Saccharicrinis fermentans DSM 9555
Ga0586324 4812608 2 625	0.00	0.00	0.00	0.00	2214500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Geoglobus;Geoglobus ahangari;Geoglobus ahangari 234
Ga0586324 4825068 2 625	0.00	0.00	0.00	1102000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		tetratricopeptide (TPR) repeat protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Ideonella;Ideonella sp. A 288;Ideonella sp. A 288
Ga0586324 4825453 1 627	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19459000.00	0.00	17633000.00	0.00	0.00		hypothetical protein	
Ga0586324 4837861 2 625	0.00	0.00	0.00	0.00	0.00	0.00	0.00	707600.00	0.00	4373600.00	3203200.00	2092500.00		hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus thiophilus;Thiobacillus thiophilus DSM 19892
Ga0586324 4839887 3 626	0.00	0.00	0.00	0.00	2688300.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		ABC-type sugar transport system substrate-binding protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324 4845237 1 624	0.00	0.00	0.00	1206500.00	863427.37	0.00	747308.76	1598200.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 4850573 2 625	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7673600.00	0.00		hypothetical protein	Bacteria;Atribacterota;unclassified Atribacterota;unclassified Atribacterota;unclassified Atribacterota;unclassified Atribacterota;Atribacteria bacterium JGI 0000059-I14;Atribacteria bacterium JGI 0000059-I14 (contamination screened)
Ga0586324 4850698 3 623	0.00	0.00	0.00	0.00	8260600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;unclassified Gammaproteobacteria;Candidatus Competibacteraceae;Candidatus Competibacter;Candidatus Competibacter denitrificans;Candidatus Competibacter denitrificans Run A D11
Ga0586324 4851065 121 624	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4228200.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Sunxiuqinia;Sunxiuqinia dokdonensis;Sunxiuqinia dokdonensis SK
Ga0586324 4855055 125 625	0.00	1060800.00	0.00	0.00	1998200.00	0.00	0.00	0.00	730240.92	0.00	275113.52	0.00		hypothetical protein	
Ga0586324 4859779 1 624	1050000.00	2950921.20	1247557.33	0.00	675187.66	2355218.38	2652166.68	927200.00	2535300.00	0.00	0.00	1170000.00		S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 4864616 116 625	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	347023.60	0.00	0.00		hypothetical protein	
Ga0586324 4867658 146 622	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7327500.00		alkylation response protein AidB-like acyl-CoA dehydrogenase	Bacteria;Nitrospirae;Thermodesulfovibrionia;Thermodesulfovibrionales;Thermodesulfovibrionaceae;Thermodesulfovibrio;Thermodesulfovibrio hydrogeniphilus;Thermodesulfovibrio hydrogeniphilus DSM 18151
Ga0586324 4879808 164 622	2990000.00	0.00	0.00	790573.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		rubrerythrin	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Jettenia;Candidatus Jettenia caeni;Planctomycetaceae bacterium KSU-1
Ga0586324 4883289 135 623	1040000.00	0.00	0.00	0.00	0.00	0.00	0.00	701500.00	0.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Ectothiorhodospiraceae;Thioalkalivibrio;Thioalkalivibrio sp. ALJ24;Thioalkalivibrio sp. ALJ24
Ga0586324 4891251 17 622	0.00	263038.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		transketolase N-terminal domain/subunit	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas methanica;Methylomonas methanica MC09
Ga0586324 4905657 2 622	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1458000.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4907945 1 621	13120000.00	1373600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Treponemataceae;Treponema;Treponema caldarium;Treponema caldarium DSM 7334
Ga0586324 4930896 3 620	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	144136.96	227985.75		hypothetical protein	Bacteria;Actinobacteria;Thermoleophilia;Solirubrobacterales;Solirubrobacteraceae;Solirubrobacter;Solirubrobacter pauli;Solirubrobacter pauli DSM 14954
Ga0586324 4938958 3 620	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1689600.00	0.00		hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Sunxiuqinia;Sunxiuqinia elliptica;Sunxiuqinia elliptica CGMCC 1.9156
Ga0586324 4951546 3 620	0.00	0.00	0.00	0.00	0.00	0.00	20793600.00	0.00	0.00	0.00	0.00	0.00		protein-export membrane protein SecD	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Caldithrix;Caldithrix abyssi;Caldithrix abyssi LF13, DSM 13497
Ga0586324 4955744 3 620	2180000.00	822800.00	2358474.56	0.00	0.00	2022746.76	1748541.12	0.00	955800.00	893200.00	0.00	473068.50		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Limnohabitans;Limnohabitans sp. 63ED37-2;Limnohabitans sp. 63ED37-2
Ga0586324 4955800 407 619	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3183300.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 4957523 1 381	0.00	0.00	0.00	0.00	8435700.00	0.00	0.00	3879600.00	0.00	0.00	0.00	0.00		Tfp pilus assembly protein PilF	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 4961278 3 545	0.00	3685600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 4967588 126 617	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12993000.00	14742000.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. M18;Geobacter sp. M18
Ga0586324 4968752 12 617	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1496000.00	0.00		hypothetical protein	
Ga0586324 4986499 3 581	0.00	18020000.00	1365708.51	14155000.00	12679300.00	0.00	0.00	21708875.20	35633555.64	0.00	0.00	2663930.25		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Herbaspirillum;Herbaspirillum sp. meg3;Herbaspirillum sp. meg3
Ga0586324 5001939 1 618	0.00	0.00	0.00	0.00	0.00	0.00	0.00	293998.65	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified Myxococcales;Enhygromyxa;Enhygromyxa salina;Enhygromyxa salina SWB007
Ga0586324 5005209 31 615	0.00	0.00	0.00	3648000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		membrane protease subunit (stomatin/prohibitin family)	Archaea;Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;unclassified Thaumarchaeota;Aigarchaeota archaeon JGI 0000106-J15;Aigarchaeota archaeon JGI 0000106-J15 (contamination screened)
Ga0586324 5029923 2 616	78700000.00	91868000.00	44653888.97	119225000.00	137597700.00	29131026.30	199446757.44	315919000.00	261006300.00	138677000.00	320434400.00	105150000.00		predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;Halothiobacillus;Halothiobacillus sp. LS2;Halothiobacillus sp. LS2
Ga0586324 5032467 3 425	0.00	0.00	12926316.73	0.00	1122700.00	0.00	0.00	0.00	0.00	0.00	3071200.00	2010000.00		hypothetical protein	
Ga0586324 5049212 1 570	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10648000.00	7387500.00		hypothetical protein	
Ga0586324 5053283 3 614	0.00	0.00	0.00	0.00	3718300.00	0.00	0.00	5142300.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter thiogenes;Geobacter thiogenes ATCC BAA-34
Ga0586324 5074524 3 614	1940000.00	0.00	0.00	0.00	0.00	0.00	3306000.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micromonosporales;Micromonosporaceae;Plantactinospora;Plantactinospora sp. CNZ320;Plantactinospora sp. CNZ320
Ga0586324 5077614 2 541	0.00	0.00	21731800.00	24320000.00	0.00	0.00	12608400.00	10614000.00	13608000.00	0.00	0.00	0.00		hypothetical protein	
Ga0586324 5077777 2 613	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1155000.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter thiogenes;Geobacter thiogenes ATCC BAA-34
Ga0586324 5079091 3 614	0.00	0.00	0.00	0.00	0.00	392521.44	0.00	0.00	0.00	0.00	0.00	0.00		uncharacterized caspase-like protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter lanceolatus;Curvibacter lanceolatus ATCC 14669
Ga0586324 5087987 105 611	0.00	0.00	0.00	3296500.00	3903700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		Fe-S oxidoreductase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324 5090206 3 611	0.00	1060800.00	0.00	0.00	0.00	9686800.00	0.00	0.00	558148.32	0.00	594894.08	0.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Azospirillaceae;Azospirillum;Azospirillum doebereinerae;Azospirillum doebereinerae DSM 13131
Ga0586324 5092157 2 208	0.00	843200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		arylsulfatase A-like enzyme	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;Nitrosospira;Nitrosospira sp. Nsp2;Nitrosospira sp. Nsp2
Ga0586324 5106902 2 610	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3546400.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Smithella;Smithella sp. SCADC;Smithella sp. SCADC
Ga0586324 5117163 1 612	0.00	3685600.00	0.00	1111500.00	0.00	0.00	0.00	1945900.00	0.00	0.00	0.00	2610000.00		methionine synthase II (cobalamin-independent)	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methyloglobulus;Methyloglobulus morosus;Methyloglobulus morosus KoM1
Ga0586324 5127387 2 385	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2114100.00	3518900.00	0.00	0.00		hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324 5127473 91 609	291986.00	437214.16	0.00	0.00	270765.37	0.00	0.00	0.00	0.00	1301300.00	664975.52	728991.00		predicted AlkP superfamily pyrophosphatase or phosphodiesterase	Bacteria;Actinobacteria;Actinomycetia;Propionibacteriales;Nocardioidaceae;Nocardioides;Nocardioides sp. OAS665;Nocardioides sp. OAS665
Ga0586324 5168570 2 412	4960000.00	0.00	26235800.00	9785000.00	6952500.00	27750300.00	21454800.00	12810000.00	0.00	17787000.00	14344000.00	10200000.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324 5179700 3 608	25200000.00	16320000.00	23308200.00	21755000.00	23587000.00	22827500.00	1012844.40	16531000.00	16200000.00	0.00	11176000.00	12000000.00		hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodovulum;Rhodovulum sp. PH10;Rhodovulum sp. PH10
Ga0586324 5188501 1 606	0.00	3862400.00	0.00	0.00	3512300.00	0.00	0.00	0.00	0.00	4750900.00	5104000.00	0.00		hypothetical protein	
Ga0586324 5197326 202 606	0.00	0.00	0.00	0.00	0.00	1014120.62	1251546.72	933300.00	0.00	0.00	0.00	975000.00		TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sediminicola;Sulfurisoma sediminicola DSM 26916
Ga0586324 5199782 3 608	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3300000.00	0.00		predicted double-glycine peptidase	Bacteria;Firmicutes;Negativicutes;Selenomonadales;Sporomusaceae;Anaeroarcus;Anaeroarcus burkinensis;Anaeroarcus burkinensis DSM 6283
Ga0586324 5200960 1 606	2510000.00	5984000.00	2827217.10	4170500.00	6359941.00	4287600.00	3534000.00	4495700.00	7452000.00	0.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5213357 2 607	2340000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta lutea;Spirochaeta lutea JC230
Ga0586324 5223885 104 607	0.00	2210000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1478400.00	0.00	0.00		septal ring factor EnvC (AmiA/AmiB activator)	
Ga0586324 5225718 1 369	1600000.00	1434800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324 5229989 2 604	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1717100.00	0.00	0.00		DmsE family decaheme c-type cytochrome	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Imhoffiella;Imhoffiella purpurea;Imhoffiella purpurea AK35
Ga0586324 5236916 2 604	0.00	0.00	4980264.22	2593500.00	3811000.00	4009700.00	0.00	0.00	0.00	0.00	0.00	3022500.00		hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Intrasporangiaceae;Intrasporangium;Intrasporangium oryzae;Intrasporangium oryzae NRRL B-24470
Ga0586324 5297773 2 601	964019.00	0.00	0.00	0.00	0.00	491184.28	467484.36	756400.00	0.00	1301300.00	0.00	0.00		hypothetical protein	
Ga0586324 5299391 2 601	4430000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta cellobiosiphila;Spirochaeta cellobiosiphila DSM 17781
Ga0586324 5302596 3 602	5680000.00	0.00	0.00	10640000.00	0.00	0.00	0.00	1555500.00	0.00	6714400.00	5086400.00	0.00		hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-N07;Aminicenantes bacterium SCGC AAA252-N07 (contamination screened)
Ga0586324 5303111 3 602	0.00	0.00	0.00	0.00	3986100.00	40891000.00	5130000.00	0.00	0.00	0.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756
Ga0586324 5303965 1 297	0.00	7276000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter delicatus;Curvibacter delicatus NBRC 14919
Ga0586324 5313817 3 602	0.00	4290800.00	9796200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324 5318697 3 380	0.00	0.00	0.00	2460500.00	3759500.00	0.00	0.00	2366800.00	3402000.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324 5323120 3 602	2110000.00	1020000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324 5336629 1 600	712183.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfacinum;Desulfacinum infernum;Desulfacinum infernum DSM 9756

Ga0586324_5346249_78_578	0.00	0.00	0.00	0.00	0.00	16515200.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium tropiciagri;Bradyrhizobium tropiciagri SEMIA 6148
Ga0586324_5359152_3_599	0.00	0.00	0.00	9975000.00	1143300.00	1961993.85	1580895.00	3056100.00	3790800.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Acetobacteroides;Acetobacteroides hydrogenigenes;Acetobacteroides hydrogenigenes DSM 24657
Ga0586324_5363178_2_598	0.00	7888000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	34596100.00	18779200.00	0.00	hypothetical protein	Bacteria;Deferribacteres;Deferribacteres;Deferribacteraceae;Deferribacter;Deferribacter desulfuricans;Deferribacter desulfuricans SSM1
Ga0586324_5366788_1_492	0.00	0.00	4802344.96	3230000.00	1843700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Hymenobacteraceae;Adhaeribacter;Adhaeribacter pallidiroseus;Adhaeribacter pallidiroseus HMF7616
Ga0586324_5375570_41_598	0.00	0.00	805360.24	0.00	0.00	1883649.87	0.00	0.00	0.00	0.00	0.00	7267500.00	hypothetical protein	Bacteria;Chloroflexi;Caldilineae;Caldilineales;Caldilineaceae;Caldilinea;Caldilinea aerophila;Caldilinea aerophila STL-6-O1, DSM 14535
Ga0586324_5380116_166_597	0.00	2094400.00	0.00	1425000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_5380774_1_213	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1179200.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;unclassified Bacteroidetes;Bacteroidetes Order II. Incertae sedis;Rhodothermaceae;Rhodothermus;Rhodothermus marinus;Rhodothermus marinus SG0.5JP17-172
Ga0586324_5393624_1_597	0.00	3774000.00	0.00	1016500.00	852749.36	0.00	0.00	0.00	0.00	3542000.00	0.00	0.00	formyltetrahydrofolate synthetase	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobacteraceae;Desulfatirhabdium;Desulfatirhabdium butyrativorans;Desulfatirhabdium butyrativorans DSM 18734
Ga0586324_5396188_2_550	0.00	0.00	0.00	0.00	7049000.00	4624700.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_5429381_258_596	0.00	0.00	0.00	0.00	0.00	0.00	908646.64	0.00	0.00	0.00	0.00	0.00	rubrerythrin	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;unclassified Myxococcales;Enhaerominea;Enhaerominea salina;Enhaerominea salina SWB007
Ga0586324_5424176_3_404	9930000.00	8500000.00	58214200.00	0.00	0.00	48592800.00	0.00	2757200.00	0.00	3657500.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. OAE819;Bradyrhizobium sp. OAE819
Ga0586324_5436841_3_575	2170000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_5437854_1_597	0.00	6147200.00	0.00	0.00	0.00	15046300.00	23484000.00	6649000.00	12150000.00	0.00	0.00	13575000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Syntrophus;Syntrophus aciditrophicus;Syntrophus aciditrophicus SB
Ga0586324_5445327_1_594	37660000.00	7110069.80	0.00	0.00	1558000.00	16171000.00	0.00	1053300.00	18956453.75	8162000.00	33088000.00	8490000.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_5452194_1_594	0.00	5168000.00	0.00	0.00	0.00	8167900.00	0.00	8993760.00	8845000.00	5807700.00	8008000.00	6151200.00	basic membrane lipoprotein Med (substrate-binding protein (PBP1-ABC) superfamilv)	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_5463285_1_594	0.00	0.00	0.00	0.00	0.00	0.00	2485200.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermacetogenium;Thermacetogenium phaeum;Thermacetogenium phaeum PB
Ga0586324_5467169_2_337	0.00	0.00	0.00	0.00	2090900.00	0.00	0.00	1043100.00	0.00	0.00	2914560.00	2670000.00	hypothetical protein	
Ga0586324_5472342_1_489	7190000.00	7820000.00	0.00	8588000.00	5376600.00	0.00	3328800.00	3660000.00	3183300.00	0.00	6899200.00	3795000.00	opacity protein-like surface antigen	Bacteria;Acidobacteria;Blastocatellia;unclassified Blastocatellia;unclassified Blastocatellia;Chloracidobacterium;Chloracidobacterium thermophilum;Chloracidobacterium thermophilum B
Ga0586324_5472643_2_595	0.00	0.00	0.00	0.00	0.00	0.00	8276400.00	4135800.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Ralstonia;blood disease bacterium A2-HR MARDI;blood disease bacterium A2-HR MARDI
Ga0586324_5489267_2_592	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	538810.73	0.00	0.00	hypothetical protein	
Ga0586324_5495458_79_594	0.00	0.00	2043858.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus sp. YR651;Cupriavidus sp. YR651
Ga0586324_5500600_1_474	3720000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_5514866_2_592	0.00	1842800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_5515547_3_593	22000000.00	0.00	38565550.00	16737941.70	16603664.89	0.00	0.00	707600.00	0.00	18326000.00	0.00	687770.25	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium lacus;Methylosarcina lacus LW14
Ga0586324_5526562_3_593	6300000.00	4584135.00	3232909.27	2859500.00	2430800.00	4247900.00	2207963.40	1305400.00	602865.99	3395700.00	1742400.00	2070000.00	hypothetical protein	
Ga0586324_5526862_1_591	1580000.00	1584400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2587500.00	FtsP/CotA-like multicopper oxidase with cupredoxin domain	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Massilia;Massilia sp. WF1;Massilia sp. WF1
Ga0586324_5540973_2_592	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	468382.50	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidipila;Acidipila sp.;Acidipila sp. EB88
Ga0586324_5546971_1_591	0.00	10880000.00	0.00	0.00	11115000.00	0.00	0.00	5471700.00	0.00	5621000.00	9680000.00	5205000.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_5559611_2_535	0.00	0.00	51007800.00	29450000.00	1493500.00	91707000.00	65892000.00	25498000.00	35883000.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_5564881_1_591	0.00	0.00	0.00	716892.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted 2n-deoxenkent orotease	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_5576234_136_591	0.00	2638400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type branched-subunit amino acid transport system substrate-binding protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta cellobiosiphila;Spirochaeta cellobiosiphila DSM 17781
Ga0586324_5577485_2_589	0.00	4365600.00	5558099.27	13680000.00	2585300.00	11314500.00	8344800.00	7320000.00	0.00	7469000.00	7532800.00	6030000.00	alkylation response protein AidB-like acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfarcinum;Desulfarcinum infernum;Desulfarcinum infernum DSM 9756
Ga0586324_5579163_3_590	0.00	0.00	0.00	890028.40	0.00	4525800.00	1557390.48	0.00	2551500.00	0.00	0.00	2667562.50	outer membrane receptor protein involvel in Fe transport	Bacteria;Acidobacteria;Acidobacteriia;Bryobacterales;Bryobacteraceae;Bryobacter;Bryobacter aggregatus;DSM 18758 ;Bryobacter aggregatus DSM 18758
Ga0586324_5594715_3_395	15900000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella denitrificans;Sulfuricella denitrificans skB26
Ga0586324_5602001_2_589	0.00	1523200.00	2961937.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2250000.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Motilibacterales;Motilibacteraceae;Motilibacter;Motilibacter deuceda;Motilibacter deuceda DSM 45328
Ga0586324_5602447_128_589	0.00	0.00	0.00	0.00	0.00	6669600.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter sp. PAE-UM;Curvibacter sp. PAE-UM
Ga0586324_5610397_92_589	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	222284.37	0.00	0.00	signal transduction histidine kinase	Bacteria;Planctomycetes;Candidatus Brocadiae;Candidatus Brocadiales;Candidatus Brocadiaceae;Candidatus Brocadia;Candidatus Brocadia fulgida;Candidatus Brocadia fulgida Brocadia fulgida enrichment bioreactor
Ga0586324_5614727_276_587	0.00	91120000.00	25503900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	138000000.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Xanthobacteraceae;Pseudolabrys;Pseudolabrys taiwanensis;Pseudolabrys taiwanensis CC-B84
Ga0586324_5616021_2_589	0.00	10668000.00	13970561.98	2413000.00	2616200.00	0.00	3990000.00	1769000.00	2219400.00	2006620.00	8098631.12	945000.00	hypothetical protein	
Ga0586324_5643928_1_588	0.00	1489200.00	0.00	6773500.00	9774700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	S-layer protein (TIGR01567 familv)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina sp. Kolkseie;Methanosarcina sp. Kolkseie
Ga0586324_5674008_2_586	37600000.00	1502800.00	34511900.00	16435000.00	32826100.00	29576500.00	13725600.00	0.00	0.00	14168000.00	98560000.00	13492500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. Y-H1;Bradyrhizobium sp. Y-H1
Ga0586324_5682518_248_586	0.00	0.00	0.00	0.00	2605900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophorhabdales;Syntrophorhabdaceae;Syntrophorhabdus;Syntrophorhabdus aromaticivorans;Syntrophorhabdus aromaticivorans UI
Ga0586324_5684259_3_584	553648.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type sugar transport system substrate-binding protein	Bacteria;Chloroflexi;Chloroflexia;Chloroflexiales;Oscillochloridaceae;Oscillochloris;Oscillochloris trichodes;Oscillochloris trichodes DG6
Ga0586324_5685683_7_585	0.00	0.00	0.00	3771500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_5689281_3_584	82890000.00	113288000.00	90643000.00	87875000.00	8621000.00	10044100.00	98268000.00	77634700.00	18225000.00	74074000.00	69064200.00	68880000.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Zoogloeaceae;Zoogloea;Zoogloea sp. LCS8751;Zoogloea schiffanensis LCS8751
Ga0586324_5700756_2_406	19200000.00	4270400.00	3343274.16	5823500.00	5500200.00	155800.66	15344400.00	209230.00	3458700.00	5505500.00	9072800.00	12832500.00	2',3'-cyclic-nucleotide 2'-phosphodiesterase (5'-nucleotidase familv)	Bacteria;Actinobacteria;Actinomycetia;Propionibacterales;Nocardioidaceae;Nocardioides;Nocardioides sp. Root122;Nocardioides sp. Root122
Ga0586324_5706123_1_585	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4147200.00	0.00	0.00	0.00	glutamate synthase domain-containing protein 2	Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Thermoanaerobacterales Family III. Incertae Sedis;Caldicellulosiruptor;Caldicellulosiruptor bescii;Caldicellulosiruptor bescii DSM 6725
Ga0586324_5718944_3_305	0.00	0.00	0.00	0.00	3378400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase familv)	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Acidobacterium;unclassified Acidobacterium;Acidobacterium strain C40
Ga0586324_5722911_1_582	22100000.00	24548000.00	30176800.00	2888000.00	3223900.00	0.00	0.00	1262700.00	14256000.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Archaea;Euryarchaeota;Archaeoglobi;Archaeoglobales;Archaeoglobaceae;Geoglobus;Geoglobus ahangari;Geoglobus ahangari 234
Ga0586324_5743807_3_581	10900000.00	16524000.00	9458400.00	22610000.00	18643000.00	7265100.00	6840000.00	8479000.00	12798000.00	20790000.00	21648000.00	13875000.00	hypothetical protein	
Ga0586324_5754796_2_583	0.00	2087600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1654400.00	0.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiocystis;Thiocystis violascens;Thiocystis violascens 611, DSM 198
Ga0586324_5756862_1_583	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3124000.00	0.00	DNA-directed RNA polymerase beta' subunit	
Ga0586324_5759810_3_581	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	570251.25	lactate dehydrogenase-like 2-hydroxyacid dehydrogenase	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Thioclava;unclassified Thioclava;Thioclava electrotrophica elox9
Ga0586324_5774728_2_580	3420000.00	0.00	0.00	0.00	0.00	0.00	6405000.00	7411500.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Ramlibacter;Ramlibacter tataouinensis;Ramlibacter tataouinensis S-10
Ga0586324_5784655_201_527	0.00	0.00	3069763.13	0.00	6907800.00	4742400.00	0.00	3029400.00	0.00	0.00	0.00	0.00	RNA recognition motif-containing protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Cytophaga;Cytophaga aurantiaca;Cytophaga aurantiaca DSM 3654
Ga0586324_5787153_3_281	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2077500.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sterolibacteriaceae;Sulfurisoma;Sulfurisoma sedimnicola;Sulfurisoma sedimnicola DSM 26916
Ga0586324_5808256_52_579	311000000.00	0.00	136809000.00	28215000.00	0.00	17904700.00	61788000.00	0.00	0.00	0.00	11616000.00	46200000.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiobaca;Thiobaca trueperi;Thiobaca trueperi DSM 13587
Ga0586324_5816093_3_578	4180000.00	7969600.00	0.00	0.00	8490056.89	0.00	75087000.00	3625280.93	1214551.44	1878800.00	2590000.00	3765300.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. OAE829
Ga0586324_5827156_2_580	12300000.00	10132000.00	12836400.00	17100000.00	0.00	15284500.00	0.00	10126000.00	10530000.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Saprospiria;Saprospirales;Lewinellaceae;Lewinella;Lewinella antarctica;Lewinella antarctica DSM 105096
Ga0586324_5827524_3_578	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	985600.00	0.00	0.00	hypothetical protein	
Ga0586324_5839191_2_577	0.00	0.00	0.00	0.00	0.00	4195200.00	0.00	0.00	0.00	0.00	0.00	0.00	PAS domain S-box-containing protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylobacteriaceae;Microvirga;Microvirga massiliensis;Microvirga massiliensis JC119
Ga0586324_5841570_3_578	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	356536.89	0.00	0.00	0.00	acetyltransferase-like isoleucine patch superfamily enzyme	
Ga0586324_5850781_1_579	0.00	0.00	0.00	0.00	4429000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type transport system substrate-binding protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Levilinea;Levilinea saccharolytica;Levilinea saccharolytica DSM 16555
Ga0586324_5863745_1_576	0.00	0.00	0.00	0.00	1957000.00	9607400.00	0.00	1695800.00	0.00	0.00	2974400.00	0.00	alkylation response protein AidB-like acyl-CoA dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfosoma;Desulfosoma caldarium;Desulfosoma caldarium DSM 22027
Ga0586324_5869787_1_576	0.00	651203.36	0.00	0.00	0.00	0.00	0.00	0.00	366785.82	0.00	0.00	445089.00	hypothetical protein	
Ga0586324_5872343_2_463	0.00	1054000.00	1102123.17	1092500.00	1122700.00	0.00	0.00	0.00	381630.69	1386000.00	1152800.00	1537500.00	hypothetical protein	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae;Anaerolinea;Anaerolinea thermophila;Anaerolinea thermophila UNI-1
Ga0586324_5884550_1_576	4400000.00	0.00	0.00	0.00	2018800.00	0.00	0.00	0.00	0.00	0.00	0.00	3750000.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Silvibacterium;Silvibacterium bohemicum;Acidobacteriaceae bacterium S15
Ga0586324_5897807_3_332	3550000.00	1802000.00	0.00	2413000.00	2255700.00	0.00	0.00	1549400.00	1474200.00	1463000.00	2094400.00	1110000.00	hypothetical protein	
Ga0586324_5902702_3_575	0.00	0.00	636612.25	2394000.00	0.00	0.00	0.00	0.00	0.00	1848000.00	1839200.00	0.00	hypothetical protein	
Ga0586324_5910313_1_297	0.00	0.00	43187516.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TusE/DsrC/DsvC family sulfur relav protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thioflavicoccus;Thioflavicoccus mobilis;Thioflavicoccus mobilis 8321
Ga0586324_5931602_2_574	0.00	0.00	0.00	1194800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	tripartite-type tricarboxylate transporter receptor subunit TctC	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Curvibacter;Curvibacter sp. PAE-UM;Curvibacter sp. PAE-UM
Ga0586324_5939419_1_573	0.00	2373200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	L-ascorbate metabolism protein UlaG (beta-lactamase superfamily)	Bacteria;Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;unclassified Candidatus Latescibacteria;Latescibacteria bacterium SCGC AAA257-K07;Latescibacteria bacterium SCGC AAA257-K07 (contamination screened)
Ga0586324_5944697_3_575	0.00	0.00	5414872.07	0.00	0.00	4883100.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriales;Acidobacteriaceae;Candidatus Koribacter;Candidatus Koribacter versatilis;Candidatus Koribacter versatilis Ellin345
Ga0586324_5945592_3_575	0.00	0.00	0.00	0.00	0.00	3045109.10	0.00	0.00	0.00	0.00	0.00	0.00	outer membrane receptor for Fe3+-dicitrate	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolibacteraceae;Draconiibacterium;Draconiibacterium sedimnis;Draconiibacterium sedimnis JN14CK-3
Ga0586324_5965526_142_573	0.00	0.00	0.00	3809500.00	0.00	31998200.00	19699200.00	0.00	11016000.00	5898200.00	0.00	0.00	hypothetical protein	
Ga0586324_5967043_3_362	0.00	0.00	0.00	1351705.90	0.00	0.00	0.00	0.00	2802600.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASRB2, DSM 11109
Ga0586324_5968870_3_572	0.00	0.00	0.00	2137500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	heme/copper-type cytochrome/quinol oxidase subunit 2	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus;Desulfobulbus propionicus;Desulfobulbus propionicus 1p3, DSM 2032
Ga0586324_5976279_3_572	6800000.00	0.00	616276.69	0.00	7910400.00	0.00	0.00	0.00	0.00	0.00	4056800.00	3915000.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Cytophagaceae;Dyadobacter;Dyadobacter sp. SG02;Dyadobacter sp. SG02
Ga0586324_5983049_3_572	15300000.00	9860000.00	0.00	0.00	0.00	0.00	0.00	0.00	7144200.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_5984516_3_572	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	257979.75	hypothetical protein	
Ga0586324_5988059_1_573	0.00	884000.00	4346956.78	0.00	0.00	1359208.90	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;unclassified Candidatus Aminicenantes;Aminicenantes bacterium SCGC AAA252-D06;Aminicenantes bacterium SCGC AAA252-D06 (contamination screened)
Ga0586324_6009366_1_396	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2602500.00	hypothetical protein	Bacteria;Actinobacteria;Actinomycetia;Nakamurellales;Nakamurellaceae;Nakamurella;Nakamurella multipartita;Nakamurella multipartita Y-104, DSM 44233
Ga0586324_6016906_1_570	0.00	1523200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Blastocatellia;Blastocatellales;Pyrinomonadaceae;Pyrinomonas;Pyrinomonas methylaliphatogenes;Pyrinomonas methylaliphatogenes K22
Ga0586324_6018169_137_571	5260000.00	0.00	0.00	1406000.00	12772000.00	5240400.00	260934.60	0.00	4203900.00	1647800.00	0.00	6375000.00	methanogenic/sarcinoid protein MtbC1	Bacteria;Proteobacteria;Gammaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfomonile;Desulfomonile tiedjei;Desulfomonile tiedjei DCB-1, DSM 6799
Ga0586324_6024456_178_570	0.00	5256400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized protein YofA (UPF0365 familv)	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Pirellula;Pirellula staleyi;Pirellula staleyi DSM 6068
Ga0586324_6039124_3_569	0.00	0.00	0.00	0.00	0.00	0.00	0.00	713700.00	0.00	0.00	0.00	0.00	DNA-directed RNA polymerase beta' subunit	Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Candidatus Magnetobacterium;Candidatus Magnetobacterium casensis;Candidatus Magnetobacterium casensis MYR-1
Ga0586324_6040357_2_571	26780000.00	27125200.00	30852400.00	15798500.00	41962200.00	61693800.00	35248800.00	34227000.00	33890400.00	35258300.00	28168800.00	27502500.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Pauci;Pauci;Pauci

Ga0586324_6500964_200_553	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1490400.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Thiobacillaceae;Thiobacillus;Thiobacillus denitrificans;Thiobacillus denitrificans DSM 12475
Ga0586324_6518123_115_552	0.00	2427497.32	45715600.00	21394000.00	2934700.00	0.00	6634800.00	37393000.00	38370056.40	0.00	24904000.00	6067500.00		predicted porin	
Ga0586324_6534138_3_551	0.00	0.00	0.00	3315500.00	2441100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		alkyl sulfatase BDS1-like metallo-beta-lactamase superfamily hydrolase	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Chromatiaceae;Thiodictyon;Candidatus Thiodictyon syntrophicum;Candidatus Thiodictyon syntrophicum Cad16
Ga0586324_6555273_3_551	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1632400.00	1478400.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Gallionellaceae;Sideroxydans;Sideroxydans lithotrophicus;Sideroxydans lithotrophicus ES-1
Ga0586324_6564511_2_550	0.00	3230000.00	1883657.25	0.00	0.00	2183313.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_6594640_2_550	0.00	0.00	0.00	0.00	0.00	12108500.00	0.00	0.00	0.00	0.00	5491200.00	2737500.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Bryobacterales;Solibacteraceae;Candidatus Solibacter;Candidatus Solibacter usitatus;Candidatus Solibacter usitatus Ellin6076
Ga0586324_6600004_3_551	24457442.00	29700761.20	3673859.96	4379500.00	18677463.80	21618055.38	4661421.24	16555400.00	8950500.00	20254081.54	20319200.00	22702500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Marinobacter;Marinobacter manganoxydans;Marinobacter manganoxydans MnI7-9
Ga0586324_6614850_3_548	0.00	1475600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	arylsulfatase A-like enzyme	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas;Methylomonas lenta;Methylomonas lenta R-45370
Ga0586324_6642143_2_532	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1443200.00	0.00	0.00	hypothetical protein	
Ga0586324_6645759_69_482	817096.00	3821600.00	0.00	0.00	0.00	4367000.00	0.00	2360700.00	0.00	0.00	0.00	0.00	0.00	nucleotide-binding universal stress UsoA family protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_6648023_1_549	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	475910.25	hypothetical protein	Bacteria;Planctomycetes;Phycisphaerae;Sedimentisphaerales;Anaerohalosphaeraceae;Anaerohalosphaera;Anaerohalosphaera lusitana;Phycisphaerae bacterium ST-NAGAB-D1
Ga0586324_6650458_1_549	0.00	14348000.00	18916800.00	0.00	0.00	0.00	0.00	0.00	0.00	14553000.00	0.00	12150000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_6652733_2_547	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2513200.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_6665884_3_548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	847000.00	0.00	0.00	hypothetical protein	
Ga0586324_6666956_105_548	0.00	4467600.00	5798900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4611200.00	0.00	0.00	hypothetical protein	
Ga0586324_6678079_116_547	618337.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_6683257_193_546	0.00	0.00	0.00	6317500.00	8054600.00	0.00	0.00	3751500.00	5054400.00	4504500.00	3792800.00	3052500.00	0.00	Tfp pilus assembly protein PilF	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_6684052_397_546	0.00	0.00	0.00	291439.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_6685601_3_548	0.00	2346000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta cellobiosiphila;Spirochaeta cellobiosiphila DSM 17781
Ga0586324_6702973_3_545	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4198800.00	0.00	3896200.00	0.00	0.00	0.00	predicted porin	
Ga0586324_6704802_3_545	10600000.00	15640000.00	14187600.00	12540000.00	7529300.00	33983200.00	6201600.00	4953200.00	5580900.00	4874100.00	5368000.00	19950000.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_6705497_73_546	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	406060.29	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas denitrificans;Dechloromonas denitrificans ATCC BAA-841
Ga0586324_6716505_1_546	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5921300.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_6727311_3_446	0.00	16292800.00	5425287.57	6536000.00	30024500.00	5319800.00	6384000.00	15262200.00	21011400.00	20335700.00	19324800.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax temperans;Acidovorax temperans CB2
Ga0586324_6759811_1_396	0.00	1122000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_6765189_1_543	0.00	0.00	0.00	5567000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	arylsulfatase A-like enzyme	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Methylobacteriaceae;Methylobacterium;Methylobacterium pseudosasicola;Methylobacterium pseudosasicola BL36
Ga0586324_6782896_73_543	0.00	0.00	0.00	0.00	370050.16	0.00	1236717.60	1055300.00	0.00	0.00	0.00	601796.25	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;unclassified Burkholderiales;Rhizobacter;Rhizobacter sp. SG703;Rhizobacter sp. SG703
Ga0586324_6785386_3_545	4700000.00	0.00	0.00	10640000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1740000.00	0.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Sediminispirochaeta;Sediminispirochaeta smaragdinae;Sediminispirochaeta smaragdinae DSM 11293
Ga0586324_6806423_119_544	0.00	0.00	26010600.00	0.00	20703000.00	25606500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sulfurreducens;Geobacter sulfurreducens AM-1
Ga0586324_6806427_1_542	0.00	2080800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales;Acidobacteriaceae;Edaphobacter;Edaphobacter modestus;Edaphobacter modestus DSM 18101
Ga0586324_6808879_134_544	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3862500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Polyangiaceae;Sorangium;Sorangium cellulosum;Sorangium cellulosum So ce0T47
Ga0586324_6814055_72_542	56300000.00	42160000.00	94021000.00	59185000.00	7158500.00	84958000.00	4035600.00	58499000.00	52326000.00	53053000.00	57816000.00	49500000.00	0.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_6814835_2_541	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1640900.00	2276100.00	0.00	0.00	0.00	0.00	predicted porin	
Ga0586324_6821322_1_519	0.00	0.00	0.00	4351000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	anaerobic selenocysteine-containing dehydrogenase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_6825143_2_541	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1765800.00	0.00	768916.72	1462500.00	0.00	hypothetical protein	
Ga0586324_6831133_2_439	0.00	782000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_6837861_2_541	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	880000.00	273993.75		hypothetical protein	
Ga0586324_6842115_3_275	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1293600.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter sp. DSM 9736;Geobacter sp. DSM 9736
Ga0586324_6845717_1_543	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1777500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax sp. JS42;Acidovorax sp. JS42
Ga0586324_6848699_2_310	0.00	0.00	1276664.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ABC-type branched-subunit amino acid transport system substrate-binding protein	
Ga0586324_6849609_3_542	0.00	1720400.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_6850044_2_541	0.00	0.00	0.00	5643000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	RNA polymerase sigma factor (sigma-70 family)	Bacteria;Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Sphingobacteriaceae;Mucilaginibacter;Mucilaginibacter sp. OK268;Mucilaginibacter sp. OK268
Ga0586324_6871856_2_541	0.00	0.00	0.00	0.00	5280100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_6881028_2_541	0.00	5644000.00	0.00	8065500.00	6499300.00	0.00	5266800.00	510524.25	5540400.00	3634400.00	0.00	3285000.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriia;unclassified Acidobacteriia;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_6891663_2_541	0.00	0.00	593038.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaeta;Spirochaeta cellobiosiphila;Spirochaeta cellobiosiphila DSM 17781
Ga0586324_6935371_2_540	0.00	0.00	946870.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;Anaeromyxobacteraceae;Anaeromyxobacter;Anaeromyxobacter sp. K;Anaeromyxobacter sp. K
Ga0586324_6965096_3_539	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1960200.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriia;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_6970513_1_537	1340000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase in catechol pathway	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_6976588_1_537	0.00	0.00	0.00	0.00	0.00	0.00	616100.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium erythrophlei;Bradyrhizobium erythrophlei GAS242
Ga0586324_6992251_3_536	0.00	0.00	0.00	0.00	0.00	0.00	589328.93	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_7001686_1_537	4740000.00	10852800.00	15538800.00	6650000.00	0.00	0.00	10431000.00	0.00	0.00	0.00	0.00	0.00	0.00	S-layer protein (TIGR01567 family)	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_7006101_3_536	6420000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Aquimarina;Aquimarina sp. Aq107;Aquimarina sp. Aq107
Ga0586324_7021604_2_535	4130000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Cytophagia;Cytophagales;Fulvivirgaceae;Chryseolinea;Chryseolinea flava;Chryseolinea flava SDU1-6
Ga0586324_7030339_3_536	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2787400.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Firmicutes;Negativicutes;Acidaminococcales;Acidaminococcaceae;Acidaminococcus;Acidaminococcus masiliensis;Acidaminococcus masiliensis Marseille-P2828
Ga0586324_7030911_1_378	0.00	0.00	0.00	0.00	21012000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_7040853_2_535	0.00	3468000.00	7093800.00	7248500.00	0.00	0.00	0.00	0.00	6188400.00	0.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_7052797_3_536	0.00	2937600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	HEAT repeat protein	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Nostocales;Calothrichaceae;Calothrix;Calothrix sp. NIES-2098;Calothrix sp. NIES-2098
Ga0586324_7073423_1_534	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1960200.00	0.00	0.00	0.00	0.00	0.00	glutamate synthase domain-containing protein 2	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Syntrophobacter;Syntrophobacter fumaroxidans;Syntrophobacter fumaroxidans MPOB
Ga0586324_7105759_1_534	0.00	0.00	0.00	0.00	0.00	0.00	5843800.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Paraburkholderia;Paraburkholderia ginsengiterrae;Paraburkholderia ginsengiterrae DCY85-1
Ga0586324_7124842_1_258	49330000.00	13334800.00	110348000.00	22505500.00	37347800.00	13418600.00	17282400.00	13725000.00	22275000.00	15708000.00	0.00	7800000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium macuxiense;Bradyrhizobium macuxiense BR 10355
Ga0586324_7138375_2_532	0.00	0.00	0.00	3106500.00	0.00	0.00	0.00	1433500.00	0.00	0.00	2692800.00	3772500.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. BS;Bradyrhizobium sp. BS
Ga0586324_7157085_2_532	0.00	566338.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	TRAP-type mannitol/chloroaromatic compound transport system substrate-binding protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium lablabi;Bradyrhizobium lablabi GA5499
Ga0586324_7184268_2_532	0.00	0.00	0.00	0.00	0.00	0.00	1384700.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfarcinum;Desulfarcinum infernum;Desulfarcinum infernum DSM 9756
Ga0586324_7192212_1_531	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2525600.00	3115200.00	0.00	0.00	pimeloyl-ACP methyl ester carboxylesterase	Bacteria;Calditrichaeota;Calditrichae;Calditrichales;Calditrichaceae;Calditrichia;Calditrichia abyssi;Calditrichia abyssi LF13, DSM 13497
Ga0586324_7195914_2_529	0.00	2108000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriia;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_7213556_2_529	0.00	0.00	7825700.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriia;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_7224035_2_529	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	711458.64	0.00	0.00	0.00	0.00	aspartyl aminopeptidase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_7243134_1_528	5840000.00	9662800.00	0.00	12723832.60	8631400.00	863336.05	2864459.76	10900700.00	8286300.00	4768244.25	14643200.00	10027500.00	0.00	hypothetical protein	
Ga0586324_7262128_3_452	0.00	0.00	842416.90	0.00	0.00	571092.44	0.00	0.00	0.00	0.00	0.00	712578.75	0.00	rubrerythrin	Archaea;Euryarchaeota;Methanomicrobia;Methanomicrobiales;Methanoregulaceae;Methanoregula;Methanoregula formicica;Methanoregula formicica SMSP, DSM 22288
Ga0586324_7289967_1_441	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8316000.00	0.00	0.00	phasin family protein	Bacteria;Proteobacteria;Betaproteobacteria;Rhodocyclales;Azonexaceae;Dechloromonas;Dechloromonas aeitata;Dechloromonas aeitata CKB
Ga0586324_7284450_1_528	0.00	0.00	0.00	0.00	0.00	0.00	0.00	642671.82	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_7296191_1_510	0.00	0.00	0.00	10165000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	polyhydroxyalkanoate synthesis repressor PhaR	Bacteria;Proteobacteria;Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;unclassified Betaproteobacteria;uncultured beta proteobacterium;unclassified betaproteobacterium ENR4
Ga0586324_7307291_1_435	0.00	0.00	0.00	0.00	0.00	1109678.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized membrane protein YphA (DoxX/SURF4 family)	Bacteria;Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus;Opitutus sp. ER46;Opitutus sp. ER46
Ga0586324_7319541_2_526	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3615000.00	0.00	methyl-accepting chemotaxis protein	Bacteria;Acidobacteria;Vicinamibacteria;unclassified Vicinamibacteria;Vicinamibacteraceae;Luteitalea;Luteitalea pratensis;Luteitalea pratensis DSM 100886
Ga0586324_7324349_184_528	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1425600.00	0.00	0.00	RNA recognition motif-containing protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_7329544_2_526	0.00	0.00	0.00	0.00	8425400.00	5280100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Marinilabiliaceae;Saccharicrinis;Saccharicrinis fermentans;Saccharicrinis fermentans DSM 9555
Ga0586324_7356142_3_491	0.00	0.00	0.00	0.00	470033.35	0.00	0.00	1622600.00	1044900.00	2371600.00	1214400.00	900000.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodovulum;Rhodovulum sp. PH10;Rhodovulum sp. PH10
Ga0586324_7356590_1_525	0.00	7398400.00	1396617.21	11685000.00	15038000.00	0.00	0.00	5154500.00	1798200.00	8331400.00	0.00	2032500.00	0.00	hypothetical protein	
Ga0586324_7363109_3_524	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2116700.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_7364953_1_219	0.00	0.00	0.00	0.00	0.00	3283200.00	0.00	0.00	0.00	0.00	3317600.00	0.00	0.00	nucleotide-binding universal stress UsoA family protein	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanotrichaceae;Methanothrix;Methanothrix soehngenii;Methanothrix soehngenii GP-6
Ga0586324_7373386_225_524	0.00	0.00	0.00	1159000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Cupriavidus;Cupriavidus necator;Cupriavidus necator NH9
Ga0586324_7378358_2_526	0.00	0.00	0.00	0.00	0.00	0.00	16917600.00	0.00	0.00	0.00	0.00	0.00	0.00	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae;Desulfobacca;Desulfobacca acetoxidans;Desulfobacca acetoxidans ASR82, DSM 11109
Ga0586324_7423889_1_525	0.00	6392000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Acidobacteria;Acidobacteria;Acidobacteriia;Acidobacteriaceae;unclassified Acidobacteriaceae;Acidobacteriaceae bacterium KBS 96;Acidobacteriaceae bacterium KBS 96, DSM 24297
Ga0586324_7430453_3_524	0.00	0.00	0.00	0.00	1534700.00	984691.01	0.00	0.00	1004400.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Chromatiales;Thiocapsaceae;Thiocapsa;Thiocapsa roseopersicina;Thiocapsa roseopersicina DSM 217
Ga0586324_7454960_153_524	0.00	0.00	0.00	13110000.00	1545000.00	0.00	0.00	0.00	10773000.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophobacteraceae;Desulfarcinum;Desulfarcinum hydrothermale;Desulfarcinum hydrothermale DSM 13146
Ga0586324_7456080_76_522	0.00	0.00	0.00	11495000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio;unclassified Desulfovibrio;Desulfovibrio sp. DF1
Ga0586324_7458741_2_475	0.00	0.00	0.00	0.00	4871900.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomicrobium;Methylomicrobium lacus;Methylosarcina lacus LW14
Ga0586324_7480506_1_522	1170000.00	6228800.00	1676518.29	0.00	0.00	0.00	0.00	0.00	0.00	2227500.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_7480949_51_482	0.00	0.00	0.00	5871

Ga0586324_7991814_3_509	0.00	0.00	0.00	7115500.00	8559300.00	0.00	0.00	3684400.00	2713500.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_8001321_2_481	2160000.00	3257200.00	9739900.00	0.00	0.00	0.00	0.00	0.00	1587600.00	7168700.00	0.00	9075000.00	hypothetical protein	
Ga0586324_8002305_3_506	0.00	10281600.00	6812300.00	8132000.00	21630000.00	7463600.00	10960094.52	7902889.77	13632300.00	9548000.00	20215605.52	8325000.00	predicted porin	
Ga0586324_8005696_31_507	0.00	0.00	0.00	0.00	9836500.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_8006368_1_411	2270000.00	4658000.00	0.00	0.00	0.00	6788700.00	0.00	0.00	0.00	0.00	5728800.00	0.00	hvoothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Azospirillaceae;Skermanella;Skermanella aerolata;Skermanella aerolata KACC 11604
Ga0586324_8014833_3_506	0.00	1196800.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1665000.00	hypothetical protein	Bacteria;Bacteroidetes;Sphingobacteria;Sphingobacteriales;Sphingobacteriaceae;Mucilaginibacter;Mucilaginibacter sp. OV119;Mucilaginibacter sp. OV119
Ga0586324_8039342_1_507	1860000.00	13736000.00	27418100.00	25460000.00	15553000.00	18976600.00	0.00	6100000.00	6868800.00	18480000.00	24472800.00	23835000.00	Ca2+ binding RTX toxin-like protein	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax;Acidovorax sp. JS42;Acidovorax sp. JS42
Ga0586324_8040324_3_506	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3854400.00	0.00	TonB-dependent SusC/RagA subfamily outer membrane receptor	Bacteria;Bacteroidetes;Bacteroidia;Marinilabiliales;Prolixibacteraceae;Draconibacterium;Draconibacterium sediminis;Draconibacterium sediminis JN14CK-3
Ga0586324_8053228_1_507	7060000.00	258414.28	1404397.87	0.00	0.00	0.00	9895200.00	366074.42	24440598.18	12940696.23	2883726.56	0.00	predicted porin	
Ga0586324_8066310_3_506	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2475000.00	hvoothetical protein	
Ga0586324_8066638_3_506	2060000.00	2427600.00	5547008.17	6403000.00	3378400.00	6431400.00	0.00	0.00	3029400.00	5621000.00	6837600.00	3517500.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Roseiarcaceae;Roseiarcus;Roseiarcus fermentans;Roseiarcus fermentans DSM 24875
Ga0586324_8074151_2_166	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	258130.18	0.00	0.00	hypothetical protein	
Ga0586324_8076464_182_505	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1466100.00	0.00	0.00	0.00	plastocyanin	Archaea;Euryarchaeota;Methanomicrobia;Methanosarcinales;Methanosarcinaceae;Methanosarcina;Methanosarcina sp. DSM 11855;Methanosarcina sp. DSM 11855
Ga0586324_8091791_262_504	1730000.00	1169600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_8107284_3_506	0.00	2305200.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hvoothetical protein	Bacteria;Bacteroidetes;Chitinophaala;Chitinophaaales;Chitinoohaaraceae;Sediminibacterium;Sediminibacterium maanilacihabitans;Vibrionimonas maanilacihabitans DSM 22423
Ga0586324_8134037_1_504	0.00	0.00	0.00	0.00	0.00	2196886.84	0.00	0.00	0.00	0.00	0.00	0.00	uncharacterized protein (DUF2252 family)	Bacteria;Actinobacteria;Actinomycetia;Micrococcales;Cellulomonadaceae;Cellulomonas;Cellulomonas sp. HLT2-17;Cellulomonas sp. HLT2-17
Ga0586324_8168256_2_502	0.00	863600.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	
Ga0586324_8173697_1_504	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6415200.00	0.00	predicted porin	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Polaromonas;Polaromonas jejuensis;Polaromonas jejuensis NBRC 106434
Ga0586324_8180559_2_502	874759.00	1700000.00	1990908.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Bacteroidetes;Chitinophagia;Chitinophagales;Chitinophagaceae;Sediminibacterium;Sediminibacterium magnilacihabitans;Vibrionimonas magnilacihabitans DSM 22423
Ga0586324_8188900_3_503	0.00	1258000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	hvoothetical orotein	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfurihabdus;Sulfurihabdus autotrophica;Sulfurihabdus autotrophica DSM 100309
Ga0586324_8191844_3_503	0.00	0.00	0.00	0.00	0.00	0.00	1723011.96	0.00	0.00	0.00	0.00	0.00	predicted porin	
Ga0586324_8192136_3_503	0.00	0.00	10865900.00	6251000.00	1390500.00	6550500.00	0.00	0.00	3037500.00	750977.15	0.00	0.00	outer membrane protein OmpA-like peptidoglycan-associated protein	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;unclassified Alteromonadaceae;Alteromonadaceae bacterium 2719K.STB50.0a.01;Alteromonadaceae bacterium 2719K.STB50.0a.01
Ga0586324_8209022_3_431	0.00	0.00	0.00	0.00	0.00	0.00	0.00	719800.00	0.00	0.00	0.00	0.00	regulator of protease activity HflC (stomatin/prohibitin superfamily)	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter metallireducens;Geobacter metallireducens GS-15
Ga0586324_8223907_73_501	0.00	0.00	0.00	0.00	2678000.00	0.00	0.00	3104900.00	3790800.00	3957800.00	0.00	3097500.00	hypothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylosarcina;Methylosarcina fibrata;Methylosarcina fibrata AML-C10
Ga0586324_8226485_3_503	0.00	0.00	0.00	3562500.00	4233300.00	0.00	8527200.00	4995900.00	5864400.00	4897200.00	5068800.00	0.00	hvoothetical protein	
Ga0586324_8237060_247_501	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2235600.00	4211900.00	4699200.00	2707500.00	hypothetical protein	Bacteria;Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae;Rhodopirellula;Rhodopirellula sp. SWK7;Rhodopirellula sp. SWK7
Ga0586324_8262125_1_501	6710000.00	4515200.00	0.00	0.00	566619.48	2285012.90	0.00	2531500.00	2405700.00	31493000.00	353019.04	0.00	hypothetical protein	Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobia subdivision 3;Pedosphaera;Pedosphaera parvula;Pedosphaera parvula Ellin514
Ga0586324_8276734_48_500	2470000.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Spy/CpxP family protein refolding chaperone	Bacteria;Planctomycetes;Planctomycetia;Gemmatales;Gemmataceae;Fimbriglobus;Fimbriglobus ruber;Fimbriglobus ruber SP5
Ga0586324_8278434_1_501	0.00	0.00	0.00	0.00	0.00	0.00	1581068.28	0.00	0.00	0.00	0.00	0.00	cytochrome c-type biogenesis protein CcmH/NrfG	Bacteria;Cyanobacteria;unclassified Cyanobacteria;Nostocales;Fortieaceae;Aulosira;Aulosira laxa;Aulosira laxa NIES-50
Ga0586324_8302785_1_501	20540000.00	24364400.00	6024100.00	14630000.00	16191600.00	3822050.01	2325600.00	20636300.00	8861400.00	24817100.00	9398400.00	15202500.00	hvoothetical protein	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Marinobacter;Marinobacter sp. ;Marinobacter sp. MIT1353
Ga0586324_8309713_403_498	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4320000.00	hypothetical protein	
Ga0586324_8315782_2_499	0.00	0.00	787484.99	0.00	0.00	0.00	4751923.56	319702.83	0.00	0.00	608108.16	0.00	hypothetical protein	Bacteria;Proteobacteria;Alphaproteobacteria;Hyphomicrobiales;Bradyrhizobiaceae;Bradyrhizobium;Bradyrhizobium sp. Ai1a-2;Bradyrhizobium sp. Ai1a-2
Ga0586324_8321491_2_499	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5544000.00	0.00	0.00	predicted porin	Bacteria;Proteobacteria;Gammaproteobacteria;Acidiferrobacterales;Acidiferrobacteraceae;Sulfuricaulis;Sulfuricaulis limicola;Sulfuricaulis limicola HA5
Ga0586324_8334022_10_498	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	817500.00	rhodanese-related sulfurtransferase	Bacteria;Proteobacteria;Betaproteobacteria;Nitrosomonadales;Sulfuricellaceae;Sulfuricella;Sulfuricella sp. T08;Sulfuricella sp. T08
Ga0586324_8336218_2_499	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2063600.00	141033.20	0.00	AcrR family transcriptional reeulator	Bacteria;Actinobacteria;Nitrilirudotaria;Eelibacterales;Eelibacteraceae;Eelibacter;Eelibacter rhizosphaerae;Eelibacter rhizosphaerae EGI 80759
Ga0586324_8336674_136_498	0.00	0.00	0.00	0.00	0.00	10401400.00	0.00	0.00	0.00	0.00	0.00	0.00	hypothetical protein	Bacteria;Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter;Geobacter lovleyi;Geobacter lovleyi SZ

Supplementary Table 3. Pairwise comparison of key functional proteins identified by metaproteomics.

KO number	Description	Comparison									
		S-O- vs. S+O-		S-O+vs. S+O+		S-O- vs. S-O+		S+O- vs. S+O+		S-O- vs. S+O+	
		log2FoldChange	*padj*	log2FoldChange	*padj*	log2FoldChange	*padj*	log2FoldChange	*padj*	log2FoldChange	*padj*
K00437	[NiFe] hydrogenase large subunit	1.67	0.79	68633.75	0.86	0.15	0.98	-1.00	0.78	0.71	0.85
K00674	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	-17.58	0.00	23009.43	0.58	-0.16	0.15	29.44	0.00	-1.25	0.69
K01834	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	-19.25	0.00	20300.91	0.00	-1.43	0.67	NA	NA	-19.16	0.00
K15633	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	NA	NA	46407.24	0.00	17.31	0.00	18.56	0.00	18.48	0.00
K15635	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	-0.45	0.00	2885.15	0.00	-15.96	0.00	-0.34	0.00	-0.83	0.00
K06178	23S rRNA pseudouridine2605 synthase	-16.38	0.00	29163.57	0.00	1.89	0.00	NA	NA	-16.29	0.00
K00065	2-deoxy-D-gluconate 3-dehydrogenase	-18.40	0.00	0.00	NA	-18.42	0.00	NA	NA	-18.31	0.00
K00042	2-hydroxy-3-oxopropionate reductase	-0.39	0.36	58576.80	0.21	0.09	0.95	-0.65	0.51	-1.10	0.26
K12261	2-hydroxyacyl-CoA lyase 1	16.14	0.00	0.00	NA	NA	NA	-16.07	0.00	NA	NA
K01649	2-isopropylmalate synthase	15.79	0.00	42747.62	0.53	17.60	0.00	2.40	0.00	18.14	0.00
K00658	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)	1.19	0.76	9580.01	0.00	-30.00	0.00	-2.06	0.00	-0.85	0.80
K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	NA	NA	10633.54	0.00	NA	NA	17.02	0.00	16.94	0.00
K11381	2-oxoisovalerate dehydrogenase E1 component	-16.05	0.00	0.00	NA	-16.07	0.00	NA	NA	-15.96	0.00
K14652	3,4-dihydroxy 2-butanone 4-phosphate synthase/GTP cyclohydrolase II	NA	NA	17881.60	0.00	29.70	0.00	NA	NA	NA	NA
K03786	3-dehydroquinate dehydratase-2	NA	NA	7952.36	0.00	NA	NA	29.63	0.00	29.55	0.00
K03856	3-deoxy-7-phosphoheptulonate synthase	18.56	0.00	10601.55	0.00	15.51	0.00	-2.38	0.00	16.15	0.00
K08093	3-hexulose-6-phosphate synthase	-2.17	0.48	367544.63	0.47	-0.31	0.95	4.03	0.15	1.86	0.07
K00074	3-hydroxybutyryl-CoA dehydrogenase	-0.23	0.96	41052.80	0.84	-0.85	0.82	0.24	0.97	-0.03	1.00
K00052	3-isopropylmalate dehydrogenase	16.53	0.00	12634.16	0.00	17.01	0.00	-16.46	0.00	NA	NA
K00606	3-methyl-2-oxobutanoate hydroxymethyltransferase	NA	NA	14254.83	0.00	17.19	0.00	NA	NA	NA	NA
K01969	3-methylcrotonyl-CoA carboxylase beta subunit	0.90	0.00	16300.01	0.93	1.13	0.00	0.63	0.87	1.54	0.62
K00059	3-oxoacyl-[acyl-carrier protein] reductase	0.41	0.93	59235.58	0.95	0.08	0.97	0.08	0.98	0.44	0.79
K01607	4-carboxymuconolactone decarboxylase	-1.39	0.72	24044.72	NA	-2.76	0.39	-0.80	0.83	-2.26	0.00
K00205	4Fe-4S ferredoxin	NA	NA	57219.30	0.00	19.19	0.00	NA	NA	NA	NA
K14534	4-hydroxybutyryl-CoA dehydratase/vinylacetyl-CoA-Delta-isomerase	0.12	0.98	147455.78	NA	1.60	0.67	-19.08	0.00	-30.00	0.00
K00215	4-hydroxy-tetrahydrodipicolinate reductase	1.36	0.00	9182.22	0.00	-16.53	0.00	-1.06	0.00	0.27	0.06
K01714	4-hydroxy-tetrahydrodipicolinate synthase	-0.15	0.97	102190.62	0.18	1.15	0.12	0.61	0.88	0.39	0.74
K01588	5-(carboxyamino)imidazole ribonucleotide mutase	NA	NA	9649.46	0.00	NA	NA	16.88	0.00	16.80	0.00
K00320	5,10-methylenetetrahydromethanopterin reductase	0.03	0.97	4523272.16	0.00	-0.42	0.35	-1.29	0.00	-1.29	0.01
K10713	5,6,7,8-tetrahydromethanopterin hydro-lyase	-0.34	0.70	909390.17	0.91	-0.69	0.38	-0.05	0.87	-0.46	0.54
K15023	5-methyltetrahydrofolate corrinoid/iron sulfur protein methyltransferase	1.55	0.00	84015.35	0.82	-0.09	0.89	-1.92	0.53	-0.45	0.91
K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	-16.26	0.00	69140.96	0.67	2.73	0.40	30.00	0.00	1.44	0.67
K07538	6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase	-0.12	0.98	56005.69	NA	2.41	NA	-3.41	0.00	-3.52	0.16
K07539	6-oxo-cyclohex-1-ene-carbonyl-CoA hydrolase	-1.77	0.02	117952.20	0.59	-1.54	0.15	0.88	0.00	-0.93	0.26
K00033	6-phosphogluconate dehydrogenase	-30.00	0.00	40453.04	0.82	0.91	0.88	18.19	0.00	1.51	0.63
K01990	ABC-2 type transport system ATP-binding protein	NA	NA	31428.41	0.59	17.82	0.00	29.37	0.00	29.81	0.00
K00925	acetate kinase	19.07	0.00	1887.48	0.00	14.27	0.00	-19.00	0.00	NA	NA
K00023	acetoacetyl-CoA reductase	0.77	0.91	26741.58	0.01	-1.78	0.58	-0.44	0.91	0.26	0.95
K01907	acetoacetyl-CoA synthetase	18.37	0.00	28185.40	0.00	NA	NA	0.01	0.92	18.35	0.00
K04767	acetoin utilization protein AcuB	19.76	0.00	0.00	NA	NA	NA	-19.69	0.00	NA	NA
K01652	acetolactate synthase-1/2/3 large subunit	1.10	0.86	87888.38	0.71	1.96	0.54	1.42	0.68	2.46	0.42
K01653	acetolactate synthase-1/3 small subunit	1.30	0.67	0.00	NA	-28.52	0.00	-16.17	0.00	-28.58	0.00
K00632	acetyl-CoA acyltransferase	NA	NA	19334.13	0.00	17.63	0.00	NA	NA	NA	NA
K00626	acetyl-CoA C-acetyltransferase	0.38	0.76	273841.16	0.01	1.77	0.03	-0.68	0.56	-0.32	0.78
K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	-0.53	0.74	448709.56	0.01	-0.55	0.11	-1.75	0.17	-2.24	0.00
K00193	acetyl-CoA decarbonylase/synthase complex subunit beta	-0.27	0.63	2206607.44	0.00	-0.71	0.11	-1.07	0.00	-1.36	0.00
K00194	acetyl-CoA decarbonylase/synthase complex subunit delta	0.03	0.96	805307.40	0.00	-0.25	0.59	-1.08	0.00	-1.05	0.00
K00195	acetyl-CoA decarbonylase/synthase complex subunit epsilon	1.05	0.01	14231.50	0.00	-0.41	0.12	-18.57	0.00	-17.55	0.00
K00197	acetyl-CoA decarbonylase/synthase complex subunit gamma	1.22	0.00	1365269.44	0.00	0.56	0.13	-1.40	0.00	-0.18	0.68
K14138	acetyl-CoA synthase	1.53	0.00	1343606.58	0.04	0.26	0.30	-1.90	0.00	-0.41	0.33
K01895	acetyl-CoA synthetase	-0.48	0.07	5519292.35	0.00	-0.66	0.01	-0.75	0.00	-1.28	0.00
K00930	acetylglutamate kinase	-15.97	0.00	14762.30	0.48	0.14	0.57	16.66	0.00	0.69	0.28
K00821	acetylornithine/N-succinyldiaminopimelate aminotransferase	NA	NA	2592.72	0.00	NA	NA	14.99	0.00	14.91	0.00
K01681	aconitate hydratase	-15.67	0.00	57195.49	0.01	3.50	0.02	16.01	0.00	0.31	0.03
K01682	aconitate hydratase 2/2-methylisocitrate dehydratase	1.57	0.05	43651.23	0.88	-0.25	0.96	-2.03	0.00	-0.51	0.60
K01251	adenosylhomocysteinase	-1.82	0.01	266423.68	0.21	-0.32	0.66	1.17	0.07	-0.69	0.10
K00939	adenylate kinase	1.02	0.12	1790168.21	0.00	1.80	0.08	-1.91	0.00	-0.96	0.21
K01756	adenylosuccinate lyase	-17.52	0.00	25839.07	0.00	0.58	0.00	NA	NA	-17.43	0.00
K01939	adenylosuccinate synthase	-1.78	0.57	46535.58	0.81	0.05	0.94	1.41	NA	-0.41	0.92
K00394	adenylylsulfate reductase subunit A	1.18	0.00	11718565.35	0.20	0.52	0.00	-0.89	0.01	0.26	0.43
K00395	adenylylsulfate reductase subunit B	-0.22	0.68	773444.02	0.79	-0.37	0.61	0.13	0.49	-0.13	0.78
K12543	adhesin transport system outer membrane protein	0.57	0.89	324668.98	0.02	2.49	0.43	4.32	0.00	4.80	0.06
K03274	ADP-L-glycero-D-manno-heptose 6-epimerase	NA	NA	5959.28	0.00	NA	NA	16.19	0.00	16.11	0.00
K01872	alanyl-tRNA synthetase	-1.10	0.00	69121.25	0.62	-0.93	0.80	1.62	0.07	0.47	0.68
K00114	alcohol dehydrogenase (cytochrome c)	-1.16	0.76	45572.82	0.50	-1.23	0.72	1.77	0.57	0.66	0.92
K00138	aldehyde dehydrogenase	-0.41	0.92	14858.45	0.00	-0.89	0.00	-30.00	0.00	-18.11	0.00
K00128	aldehyde dehydrogenase (NAD+)	17.44	0.00	3253.71	0.00	15.06	0.00	-17.37	0.00	NA	NA
K03738	aldehyde:ferredoxin oxidoreductase	-1.08	0.02	431771.64	0.13	-1.50	0.00	-0.52	0.24	-1.63	0.00
K10232	alpha-glucoside transport system substrate-binding protein	-0.61	0.60	342959.91	0.03	0.15	0.91	-0.26	0.80	-0.89	0.32
K01426	amidase	-1.72	0.00	0.00	NA	-17.95	0.00	-16.08	0.00	-17.84	0.00
K00764	amidophosphoribosyltransferase	NA	NA	5004.02	0.00	NA	NA	15.93	0.00	15.86	0.00
K03392	aminocarboxymuconate-semialdehyde decarboxylase	16.30	0.00	82962.21	0.00	NA	NA	3.63	0.00	19.91	0.00
K00605	aminomethyltransferase	-18.39	0.00	0.00	NA	-18.41	0.00	NA	NA	-18.30	0.00
K22010	AmiR/NasT family two-component response regulator	0.30	0.01	44500.70	0.33	1.05	0.00	-1.26	0.68	-1.04	0.75
K03320	Amt family ammonium transporter	NA	NA	53053.07	0.46	18.68	0.00	30.00	0.00	29.18	0.00
K00766	anthranilate phosphoribosyltransferase	NA	NA	20838.11	0.00	NA	NA	17.99	0.00	17.91	0.00
K04749	anti-sigma B factor antagonist	-1.65	0.00	68161.33	0.00	-19.60	0.00	1.78	0.00	0.09	0.61
K01584	arginine decarboxylase	NA	NA	6366.49	0.00	NA	NA	29.32	0.00	29.23	0.00
K01478	arginine deiminase	0.19	0.78	73415.94	0.00	0.58	0.00	1.23	0.01	1.39	0.00
K01940	argininosuccinate synthase	-16.68	0.00	51519.80	0.23	1.06	0.02	18.56	0.00	1.85	0.00
K08356	arsenite oxidase large subunit	NA	NA	6560.22	0.00	NA	NA	16.33	0.00	16.25	0.00
K01551	arsenite-transporting ATPase	-17.66	0.00	0.00	NA	-17.68	0.00	NA	NA	-17.57	0.00
K07289	AsmA protein	NA	NA	51741.31	0.00	17.83	0.00	18.50	0.00	18.42	0.00
K09758	aspartate 4-decarboxylase	NA	NA	2647.87	0.00	27.93	0.00	NA	NA	NA	NA
K00812	aspartate aminotransferase	NA	NA	4167.81	0.00	NA	NA	15.67	0.00	15.59	0.00
K00609	aspartate carbamoyltransferase catalytic subunit	-1.30	0.00	16564.48	0.80	-1.06	0.75	1.32	0.68	-0.08	0.98
K00133	aspartate-semialdehyde dehydrogenase	-15.17	0.00	18112.45	0.92	1.35	0.00	16.81	0.00	1.61	0.00
K01876	aspartyl-tRNA synthetase	-1.16	0.75	114823.83	0.35	1.10	0.27	3.09	0.25	1.89	0.02
K02434	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B	-15.28	0.00	22631.47	0.00	-15.30	0.00	18.11	0.00	2.80	0.00
K03593	ATP-binding protein involved in chromosome partitioning	19.42	0.00	133753.19	0.82	30.00	0.00	0.53	0.90	30.00	0.00
K03694	ATP-dependent Clp protease ATP-binding subunit ClpA	2.32	0.00	32193.63	0.31	0.77	0.43	-0.41	0.04	1.88	0.00
K03695	ATP-dependent Clp protease ATP-binding subunit ClpB	0.29	0.79	294904.69	0.74	0.59	0.54	0.63	0.21	0.90	0.09
K03696	ATP-dependent Clp protease ATP-binding subunit ClpC	-0.21	NA	50063.35	0.76	-0.39	0.95	1.02	0.79	0.85	0.88
K03544	ATP-dependent Clp protease ATP-binding subunit ClpX	30.00	0.00	108836.37	0.18	19.57	0.00	-0.56	0.90	18.71	0.00
K01358	ATP-dependent Clp protease protease subunit	NA	NA	11750.44	0.38	14.62	0.00	29.05	0.00	29.77	0.00
K03667	ATP-dependent HslUV protease ATP-binding subunit HslU	20.63	0.00	183062.42	0.00	NA	NA	0.45	0.00	21.05	0.00
K01338	ATP-dependent Lon protease	-2.38	0.41	160979.77	0.54	1.72	0.76	5.76	0.00	3.26	0.26
K21449	autotransporter adhesin	17.46	0.00	24964.60	0.13	17.47	0.00	-1.01	0.23	16.43	0.00
K03594	bacterioferritin	0.33	0.96	62446.80	0.63	0.78	0.84	-0.49	0.93	-0.21	0.97
K07335	basic membrane protein A	-0.36	0.53	585200.82	0.00	-0.37	0.12	-0.52	0.29	-0.89	0.00
K05349	beta-glucosidase	-29.61	0.00	7025.19	0.00	0.18	0.96	NA	NA	-29.66	0.00
K03561	biopolymer transport protein ExbB	0.62	0.19	145016.19	0.82	0.50	0.51	-0.15	0.91	0.42	0.69
K03559	biopolymer transport protein ExbD	-18.67	0.00	0.00	NA	-18.69	0.00	NA	NA	-18.59	0.00
K00826	branched-chain amino acid aminotransferase	0.06	0.72	0.00	NA	-17.57	0.00	-17.49	0.00	-17.46	0.00
K01999	branched-chain amino acid transport system substrate-binding protein	-0.59	0.05	4047015.01	0.87	-0.54	0.05	0.22	0.27	-0.38	0.18
K00248	butyryl-CoA dehydrogenase	0.31	0.95	37262.59	0.94	-0.26	0.95	-0.56	0.92	-0.23	0.95
K11688	C4-dicarboxylate-binding protein DctP	-18.29	0.00	20157.81	0.00	-2.77	0.00	17.60	0.00	-0.72	0.00
K21449	Ca2+-binding RTX toxin-like protein	17.46	0.00	24964.60	0.13	17.47	0.00	-1.01	0.23	16.43	0.00
K01955	carbamoyl-phosphate synthase large subunit	-15.37	0.00	48515.64	0.28	0.85	0.80	19.04	0.00	3.59	0.00
K01673	carbonic anhydrase	2.08	0.02	552246.75	NA	2.93	0.00	-0.56	NA	1.35	NA
K00198	carbon-monoxide dehydrogenase catalytic subunit	1.09	0.02	1069467.30	0.00	0.19	0.82	-2.24	0.00	-1.20	0.01
K03520	carbon-monoxide dehydrogenase large subunit	30.00	0.00	63196.23	0.08	17.39	0.00	2.06	0.49	19.07	0.00
K03519	carbon-monoxide dehydrogenase medium subunit	29.85	0.00	43666.24	0.43	29.75	0.00	1.84	0.53	18.61	0.00
K03797	carboxyl-terminal processing protease	-30.00	0.00	83398.12	0.09	-0.39	0.94	19.54	0.00	1.21	0.72
K01061	carboxymethylenebutenolidase	NA	NA	21367.65	0.00	NA	NA	18.04	0.00	17.95	0.00
K03782	catalase-peroxidase	-0.71	0.62	252715.64	0.99	-0.32	0.64	0.72	NA	-0.09	NA
K14393	cation/acetate symporter	NA	NA	226209.75	0.52	20.40	0.00	20.10	0.00	20.06	0.00
K03798	cell division protease FtsH	-3.74	0.18	71900.41	0.11	-0.74	NA	-2.50	0.57	-6.28	0.00
K03531	cell division protein FtsZ	-0.28	0.80	40560.85	0.90	-1.32	0.71	-1.04	0.11	-1.36	0.00
K04077	chaperonin GroEL	0.43	0.08	64384886.01	0.99	0.41	0.14	0.18	0.14	0.57	0.05
K22447	chaperonin GroEL (HSP60 family)	0.13	0.89	123206.84	0.03	-0.02	0.98	-0.65	0.14	-0.51	0.36
K04078	chaperonin GroES	-0.30	0.89	188508.31	0.09	-3.93	0.00	-2.33	0.00	-2.71	0.02
K06596	chemosensory pili system protein ChpA (sensor histidine kinase/response regulator)	NA	NA	27747.04	0.04	13.25	0.00	30.00	0.00	30.00	0.00
K02557	chemotaxis protein MotB	3.28	0.16	11345.38	0.00	-28.70	0.00	-1.16	0.72	2.19	0.64
K03529	chromosome segregation protein	NA	NA	18616.18	0.93	16.67	0.00	29.72	0.00	28.69	0.00
K01644	citrate lyase subunit beta/citryl-CoA lyase	-0.90	0.83	19368.02	0.69	-2.51	0.38	-0.56	0.89	-1.48	0.12
K01647	citrate synthase	1.63	0.80	250683.15	0.02	2.39	0.49	-1.29	0.71	0.31	0.94
K11645	class I fructose-bisphosphate aldolase	-0.21	0.98	128957.75	NA	0.70	0.87	-0.16	0.98	-0.35	0.95
K00440	coenzyme F420 hydrogenase subunit alpha	1.62	0.19	662512.69	0.95	0.43	0.80	-1.06	0.12	0.58	0.70
K00441	coenzyme F420 hydrogenase subunit beta	-19.34	0.00	0.00	NA	-19.36	0.00	NA	NA	-19.25	0.00
K00443	coenzyme F420 hydrogenase subunit gamma	NA	NA	11766.91	0.00	NA	NA	17.17	0.00	17.09	0.00
K13195	cold-inducible RNA-binding protein	-0.22	0.97	59620.21	0.06	0.64	0.87	1.36	0.67	1.05	0.76
K03704	CspA family cold shock protein	2.58	0.00	24341.35	0.99	2.39	0.41	-0.09	0.98	2.42	0.38
K01937	CTP synthase	NA	NA	6637.27	0.00	NA	NA	29.35	0.00	29.31	0.00
K07537	cyclohexa-1,5-dienecarbonyl-CoA hydratase	27.28	0.00	1152.14	0.00	13.49	0.00	-28.52	0.00	NA	NA
K04487	cysteine desulfurase	NA	NA	61592.04	0.84	30.00	0.00	18.30	0.00	18.24	0.00
K01738	cysteine synthase A	18.73	0.00	10232.15	0.00	15.45	0.00	-2.59	0.00	16.11	0.00
K00405	cytochrome c oxidase cbb3-type subunit 2	NA	NA	49636.26	0.00	NA	NA	19.25	0.00	19.17	0.00

K00406	cytochrome c oxidase cbb3-type subunit 3	NA	NA	6475.65	0.00	NA	NA	16.31	0.00	16.23	0.00
K02275	cytochrome c oxidase subunit 2	18.89	0.00	24583.71	0.74	29.22	NA	-1.25	0.70	30.00	0.00
K00428	cytochrome c peroxidase	0.02	0.97	340352.05	0.39	-0.90	0.14	-1.18	0.00	-1.20	0.00
K00058	D-3-phosphoglycerate dehydrogenase	1.29	0.75	81522.07	0.00	0.37	0.94	-2.67	0.00	-1.47	0.67
K00809	deoxyhypusine synthase	-16.50	0.00	0.00	NA	-16.52	0.00	NA	NA	-16.41	0.00
K03273	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase	NA	NA	4452.22	0.00	NA	NA	15.77	0.00	15.69	0.00
K00382	dihydrolipoamide dehydrogenase	-14.87	0.00	69561.26	0.00	3.30	0.00	19.01	0.00	4.11	0.00
K05878	dihydroxyacetone kinase-like protein	18.16	0.00	0.00	NA	NA	NA	-18.09	0.00	NA	NA
K01687	dihydroxy-acid dehydratase	19.30	0.00	22629.88	0.47	28.26	0.00	-1.50	0.64	29.84	0.00
K02469	DNA gyrase subunit A	NA	NA	13288.53	0.00	NA	NA	30.00	0.00	29.43	0.00
K02470	DNA gyrase subunit B	NA	NA	6384.65	0.00	16.03	0.00	NA	NA	NA	NA
K06915	DNA helicase HerA-like ATPase	-3.21	0.22	45197.34	0.00	1.57	0.69	-13.91	0.00	-30.00	0.00
K02342	DNA polymerase III subunit epsilon	-18.59	0.00	2217.60	0.00	-18.61	0.00	14.76	0.00	-3.86	0.00
K02338	DNA polymerase-3 subunit beta	0.91	0.89	110002.23	0.04	2.44	0.43	0.38	0.92	1.30	0.69
K03168	DNA topoisomerase-1	NA	NA	27706.35	0.00	NA	NA	18.40	0.00	18.33	0.00
K03622	DNA-binding protein	-30.00	0.00	98609.69	0.00	-30.00	0.00	20.24	0.00	1.02	0.78
K03746	DNA-binding protein H-NS	0.24	0.91	37522.96	0.00	-19.67	0.00	-1.06	0.77	-0.90	0.81
K03530	DNA-binding protein HU-beta	0.37	0.94	217314.38	0.07	0.91	NA	-0.15	0.91	0.10	0.98
K21900	DNA-binding transcriptional LysR family regulator	NA	NA	26015.61	0.00	16.10	0.00	17.88	0.00	17.80	0.00
K03041	DNA-directed RNA polymerase subunit A'	1.24	NA	32466.74	0.00	0.90	NA	-2.48	0.00	-1.27	0.71
K03042	DNA-directed RNA polymerase subunit A"	0.17	0.17	232214.33	0.00	-0.41	0.00	3.81	0.00	3.95	0.00
K03040	DNA-directed RNA polymerase subunit alpha	1.10	0.79	598083.81	0.22	1.45	0.69	0.95	0.00	2.07	0.51
K03045	DNA-directed RNA polymerase subunit B"	-19.24	0.00	0.00	NA	-19.26	0.00	NA	NA	-19.16	0.00
K03043	DNA-directed RNA polymerase subunit beta	0.31	0.37	2290147.78	0.00	0.43	0.10	1.04	0.00	1.33	0.00
K03046	DNA-directed RNA polymerase subunit beta'	-0.50	0.37	2087422.55	0.16	-0.31	0.62	0.83	0.00	0.33	0.50
K03047	DNA-directed RNA polymerase subunit D	-17.21	0.00	14842.50	0.80	-1.15	0.72	16.79	0.00	-0.48	0.56
K10543	D-xylose transport system substrate-binding protein	-2.02	0.00	1220505.49	0.00	-1.71	0.00	1.31	0.00	-0.76	0.00
K03522	electron transfer flavoprotein alpha subunit	1.58	0.00	124881.64	0.24	0.79	0.23	-3.34	0.21	-1.83	0.56
K03521	electron transfer flavoprotein beta subunit	2.24	0.00	21174.61	0.84	0.44	0.00	-2.09	0.46	0.10	0.98
K03231	elongation factor 1-alpha	-0.74	0.02	439797.30	0.76	-1.36	0.00	-0.49	0.07	-1.25	0.00
K02355	elongation factor G	-1.00	0.25	842099.09	0.12	1.60	0.04	3.13	0.00	2.16	0.00
K02357	elongation factor Ts	-30.00	0.00	46466.66	0.39	-0.60	0.90	18.64	0.00	0.88	0.81
K02358	elongation factor Tu	0.03	0.90	10971717.26	0.11	0.59	0.00	0.96	0.00	0.96	0.00
K21449	ELWxxDGT repeat protein	17.46	0.00	24964.60	0.13	17.47	0.00	-1.01	0.23	16.43	0.00
K01689	enolase	-0.68	0.46	421869.25	0.00	-0.93	0.02	1.26	0.09	0.55	0.00
K00208	enoyl-[acyl-carrier protein] reductase I	-0.22	0.81	67836.30	0.89	-0.01	0.98	0.02	1.00	-0.24	0.95
K04027	ethanolamine utilization protein EutM	0.34	0.85	89997.89	0.28	-1.34	0.18	-0.67	0.58	-0.38	0.78
K03701	excinuclease ABC subunit A	0.39	0.96	82729.60	0.28	1.59	0.64	2.41	0.42	2.83	0.33
K14127	F420-non-reducing hydrogenase iron-sulfur subunit	15.50	0.00	948.94	0.00	13.28	0.00	-15.43	0.00	NA	NA
K14126	F420-non-reducing hydrogenase large subunit	NA	NA	89700.92	0.00	19.84	0.00	NA	NA	NA	NA
K04564	Fe-Mn family superoxide dismutase	-0.32	0.83	219392.75	0.44	-0.22	0.74	-0.01	0.99	-0.39	0.63
K00528	ferredoxin--NADP+ reductase	NA	NA	15043.38	0.00	17.26	0.00	NA	NA	NA	NA
K02217	ferritin	1.05	0.00	39943.67	0.96	1.07	0.00	0.44	0.91	1.40	0.67
K09013	Fe-S cluster assembly ATP-binding protein	29.13	0.00	23322.93	0.00	17.90	0.00	-29.68	0.00	NA	NA
K03773	FKBP-type peptidyl-prolyl cis-trans isomerase FklB	NA	NA	33428.08	0.00	18.42	0.00	NA	NA	NA	NA
K02390	flagellar hook protein FlgE	18.50	0.00	24358.21	0.00	NA	NA	-0.33	0.00	18.14	0.00
K02406	flagellin	-0.14	0.83	1508496.94	0.96	0.05	0.98	0.57	0.44	0.36	0.68
K09165	flavin-binding protein dodecin	1.35	0.72	94477.65	0.95	0.90	0.82	-0.35	0.92	0.92	0.88
K00124	formate dehydrogenase iron-sulfur subunit	16.95	0.00	15087.93	0.00	17.27	0.00	-16.88	0.00	NA	NA
K00123	formate dehydrogenase major subunit	NA	NA	10047.73	0.00	16.68	0.00	NA	NA	NA	NA
K00125	formate dehydrogenase subunit beta	-1.88	0.62	77627.24	0.44	-2.74	0.06	0.04	0.99	-1.95	0.17
K01938	formate--tetrahydrofolate ligase	0.77	0.24	1146473.89	0.17	-0.25	0.80	-0.12	0.87	0.62	0.33
K00200	formylmethanofuran dehydrogenase subunit A	-16.67	0.00	0.00	NA	-16.69	0.00	NA	NA	-16.58	0.00
K00201	formylmethanofuran dehydrogenase subunit B	-17.66	0.00	14175.68	0.40	-2.51	0.35	17.07	0.00	-0.62	0.00
K00202	formylmethanofuran dehydrogenase subunit C	-2.19	0.00	0.00	NA	-18.62	0.00	-16.29	0.00	-18.51	0.00
K10552	fructose transport system substrate-binding protein	-16.23	0.00	9815.06	0.72	-0.19	0.06	28.57	0.00	-0.82	0.79
K03841	fructose-1,6-bisphosphatase I	15.70	0.00	0.00	NA	NA	NA	-15.63	0.00	NA	NA
K01623	fructose-bisphosphate aldolase class I	16.48	0.00	8781.99	0.00	16.49	0.00	-16.41	0.00	NA	NA
K01624	fructose-bisphosphate aldolase class II	-1.54	0.69	422674.15	0.41	1.14	0.40	2.36	0.42	0.74	0.58
K22349	FtsP/CotA-like multicopper oxidase with cupredoxin domain	NA	NA	6351.87	0.00	NA	NA	16.28	0.00	16.20	0.00
K02111	F-type H+-transporting ATPase subunit alpha	0.30	0.31	4601571.02	0.71	-0.34	0.38	-0.57	0.02	-0.29	0.31
K02109	F-type H+-transporting ATPase subunit b	1.42	0.05	95604.74	0.44	0.80	0.05	-0.20	0.86	1.20	0.00
K02112	F-type H+-transporting ATPase subunit beta	0.67	0.00	4612297.97	0.01	0.60	0.00	-0.39	0.09	0.27	0.37
K02113	F-type H+-transporting ATPase subunit delta	-1.26	0.72	16118.48	0.79	-1.77	0.56	0.19	0.96	-1.08	0.00
K02114	F-type H+-transporting ATPase subunit epsilon	19.38	0.00	0.00	NA	NA	NA	-19.31	0.00	NA	NA
K02115	F-type H+-transporting ATPase subunit gamma	18.99	0.00	34313.63	0.02	18.10	0.00	-2.53	0.00	16.40	0.00
K01676	fumarate hydratase class I	-15.32	0.00	0.00	NA	-15.34	0.00	NA	NA	-15.23	0.00
K03711	Fur family ferric uptake transcriptional regulator	NA	NA	34596.31	0.00	18.47	0.00	NA	NA	NA	NA
K01711	GDPmannose 4,6-dehydratase	NA	NA	18642.81	0.00	17.11	0.00	15.96	0.00	15.88	0.00
K09969	general L-amino acid transport system substrate-binding protein	-1.02	0.08	319327.75	1.00	0.17	0.81	1.45	0.02	0.37	0.38
K11477	glc operon protein GlcG	NA	NA	22854.21	0.52	27.74	0.00	30.00	0.00	29.92	0.00
K01053	gluconolactonase	-0.66	0.13	48488.08	0.55	-2.76	0.57	0.52	0.90	-0.20	0.96
K00820	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	1.91	0.50	77584.65	0.73	4.03	0.17	1.18	0.83	3.05	0.27
K17315	glucose/mannose transport system substrate-binding protein	-1.17	0.32	331452.22	0.71	-0.58	0.16	1.02	0.40	-0.20	0.77
K00975	glucose-1-phosphate adenylyltransferase	NA	NA	29871.78	0.00	16.98	0.00	17.74	0.00	17.67	0.00
K00973	glucose-1-phosphate thymidylyltransferase	NA	NA	47553.77	0.00	NA	NA	19.18	0.00	19.11	0.00
K01039	glutaconate CoA-transferase subunit A	-0.38	0.94	85114.83	0.93	-0.98	0.80	-0.21	0.95	-0.56	0.93
K01040	glutaconate CoA-transferase subunit B	-2.38	0.43	128132.75	0.89	-0.64	0.62	1.88	0.53	-0.52	0.22
K01615	glutaconyl-CoA decarboxylase	29.37	0.00	0.00	NA	NA	NA	-29.87	0.00	NA	NA
K01295	glutamate carboxypeptidase	NA	NA	37118.65	0.00	NA	NA	18.83	0.00	18.75	0.00
K00262	glutamate dehydrogenase (NADP+)	0.49	0.24	567778.63	0.28	-0.69	0.17	-0.44	0.21	0.01	0.99
K00620	glutamate N-acetyltransferase/amino-acid N-acetyltransferase	16.74	0.00	23317.50	0.91	16.97	0.00	0.32	0.13	17.04	0.00
K01776	glutamate racemase	NA	NA	7517.37	0.00	NA	NA	16.52	0.00	16.44	0.00
K00265	glutamate synthase (NADPH/NADH) large chain	-0.52	0.90	84554.72	0.09	0.31	0.80	2.26	0.42	1.72	0.00
K00266	glutamate synthase (NADPH/NADH) small chain	0.25	0.06	52570.81	0.85	-1.57	0.64	-2.00	0.00	-1.78	0.00
K10001	glutamate/aspartate transport system substrate-binding protein	0.23	0.96	47998.61	0.95	0.40	0.95	0.24	0.95	0.34	0.95
K01845	glutamate-1-semialdehyde 2,1-aminomutase	-2.36	0.00	21513.87	0.50	-4.30	0.10	-0.14	0.05	-2.53	0.00
K00147	glutamate-5-semialdehyde dehydrogenase	-18.13	0.00	257077.62	NA	2.94	NA	19.53	0.00	1.39	0.01
K01425	glutaminase	-0.03	0.98	24981.91	0.08	-0.57	0.61	-1.43	0.02	-1.52	0.08
K01915	glutamine synthetase	-1.49	0.00	1739451.89	0.21	0.32	0.60	2.44	0.00	0.94	0.00
K16173	glutaryl-CoA dehydrogenase (non-decarboxylating)	0.79	0.88	47992.45	0.00	0.39	0.94	-3.05	0.00	-2.40	0.46
K00799	glutathione S-transferase	NA	NA	53297.66	0.12	28.65	0.00	19.21	0.00	19.15	0.00
K13889	glutathione transport system substrate-binding protein	-17.06	0.00	2150.05	0.00	-17.08	0.00	14.72	0.00	-2.38	0.00
K00134	glyceraldehyde 3-phosphate dehydrogenase	-0.45	0.55	835229.34	0.12	-0.68	0.39	0.57	0.13	0.13	0.83
K00018	glycerate dehydrogenase	NA	NA	2317.78	0.00	NA	NA	14.82	0.00	14.75	0.00
K00864	glycerol kinase	0.24	0.83	714308.65	0.91	0.27	0.79	0.25	0.30	0.40	0.66
K17321	glycerol transport system substrate-binding protein	0.28	0.96	136349.44	0.74	-0.01	1.00	-0.19	0.96	0.08	0.95
K00113	glycerol-3-phosphate dehydrogenase subunit C	NA	NA	45085.31	0.47	16.71	0.00	30.00	0.00	30.00	0.00
K02002	glycine betaine/proline transport system substrate-binding protein	-29.15	0.00	9272.46	0.00	-29.15	0.00	16.82	0.00	1.38	0.64
K00283	glycine dehydrogenase subunit 2	NA	NA	34482.25	0.96	17.40	0.00	30.00	0.00	29.77	0.00
K00600	glycine hydroxymethyltransferase	-30.00	0.00	67785.17	0.11	0.12	0.98	18.34	0.00	-0.37	0.93
K00104	glycolate oxidase	0.69	0.86	28373.87	0.67	0.33	0.94	-0.05	0.92	0.57	0.88
K01879	glycyl-tRNA synthetase beta chain	NA	NA	5571.35	0.00	15.83	0.00	NA	NA	NA	NA
K01951	GMP synthase (glutamine-hydrolysing)	1.16	0.00	19112.80	0.75	0.31	0.95	0.00	0.99	1.13	0.00
K03979	GTP-binding protein	NA	NA	12192.78	0.75	28.67	0.00	16.52	0.00	16.44	0.00
K06207	GTP-binding protein	1.06	0.80	252328.07	0.28	3.07	0.55	-1.77	0.56	-0.88	0.88
K06942	GTP-binding protein YchF	14.45	0.00	3975.43	0.00	15.34	0.00	-14.38	0.00	NA	NA
K12132	HAMP domain-containing protein	14.98	0.00	28479.21	0.87	29.83	0.00	2.68	0.32	30.00	0.00
K03388	heterodisulfide reductase subunit A	-0.01	0.99	77970.79	0.49	-0.33	0.69	-1.75	0.56	-1.79	0.57
K03389	heterodisulfide reductase subunit B	16.48	0.00	29490.27	0.00	18.24	0.00	-16.41	0.00	NA	NA
K11254	histone H4	-1.09	0.37	481684.87	0.93	-1.11	0.35	0.13	0.94	-0.96	0.54
K00003	homoserine dehydrogenase	0.98	0.00	17337.22	0.44	1.39	0.29	-0.22	0.70	0.72	0.13
K03666	host factor-I protein	-0.58	0.00	67785.09	0.89	-0.44	0.72	0.66	0.87	0.00	1.00
K13993	HSP20 family protein	0.96	0.04	222513.78	0.05	-0.61	0.59	0.02	0.95	0.93	0.06
K06281	hydrogenase large subunit	0.67	0.52	464425.59	0.37	0.31	0.75	-0.78	0.41	-0.12	0.91
K10535	hydroxylamine dehydrogenase	-18.38	0.00	0.00	NA	-18.41	0.00	NA	NA	-18.30	0.00
K05601	hydroxylamine reductase	0.70	0.88	323543.38	0.86	1.18	0.77	0.79	0.08	1.44	0.67
K07045	hypothetical protein	-16.62	0.00	0.00	NA	-16.64	0.00	NA	NA	-16.53	0.00
K09924	hypothetical protein	0.24	0.03	659.85	0.00	-2.39	0.00	-15.31	0.00	-15.10	0.00
K21449	hypothetical protein	17.46	0.00	24964.60	0.13	17.47	0.00	-1.01	0.23	16.43	0.00
K12132	hypothetical protein	14.98	0.00	28479.21	0.87	29.83	0.00	2.68	0.32	30.00	0.00
K06907	hypothetical protein	0.95	0.00	673157.22	0.62	-0.12	0.94	-0.39	0.23	0.53	0.00
K21572	hypothetical protein	1.25	0.00	199291.38	0.27	0.34	0.15	-1.49	0.08	-0.27	0.81
K21619	hypothetical protein	17.80	0.00	18853.48	0.00	17.59	0.00	-17.73	0.00	NA	NA
K20370	hypothetical protein	18.49	0.00	0.00	NA	NA	NA	-18.42	0.00	NA	NA
K01693	imidazoleglycerol-phosphate dehydratase	-17.42	0.00	19829.59	0.00	-17.44	0.00	30.00	0.00	0.43	0.92
K09607	immune inhibitor A	-1.45	0.06	390686.87	0.09	-2.00	0.02	0.77	0.24	-0.74	0.51
K00088	IMP dehydrogenase	0.11	0.98	125338.34	0.61	0.91	0.82	0.57	0.56	0.75	0.85
K04764	integration host factor subunit alpha	19.04	0.00	27308.76	0.00	18.12	0.00	-18.97	0.00	NA	NA
K09004	intracellular sulfur oxidation DsrE/DsrF family protein	15.68	0.00	1204481.50	0.01	22.23	0.00	7.42	0.00	23.08	0.00
K02014	iron complex outermembrane receptor protein	0.34	0.13	3859883.90	0.05	0.26	0.39	0.54	0.01	0.87	0.00
K02012	iron(III) transport system substrate-binding protein	1.18	0.00	4698.15	0.00	-0.11	0.34	-16.80	0.00	-15.66	0.00
K00031	isocitrate dehydrogenase	-1.48	0.00	7470.58	0.00	-3.78	0.17	-18.38	0.00	-19.89	0.00
K01637	isocitrate lyase	-30.00	0.00	76279.55	0.90	0.07	0.98	30.00	0.00	-0.01	1.00
K07303	isoquinoline 1-oxidoreductase beta subunit	-0.16	0.97	24292.69	0.00	-30.00	0.00	0.27	0.94	0.14	0.98
K00253	isovaleryl-CoA dehydrogenase	NA	NA	47518.33	0.00	NA	NA	19.18	0.00	19.10	0.00
K15987	K(+)-stimulated pyrophosphate-energized sodium pump	29.86	0.00	204830.08	NA	30.00	NA	3.65	0.16	20.44	0.00
K00053	ketol-acid reductoisomerase	0.66	0.88	212228.79	0.70	2.16	0.50	1.85	0.00	2.42	0.42
K02863	large subunit ribosomal protein L1	-0.63	0.89	235356.01	0.73	1.63	0.10	2.70	0.34	2.07	0.00
K02864	large subunit ribosomal protein L10	2.22	0.46	5457.87	0.00	-0.36	0.94	-30.00	0.00	-16.21	0.00
K02867	large subunit ribosomal protein L11	-3.41	0.21	42299.94	0.78	-1.34	0.71	2.97	0.29	-0.46	0.94
K02874	large subunit ribosomal protein L14	0.69	NA	220534.17	0.00	0.61	NA	1.93	0.00	2.58	0.06

K02879	large subunit ribosomal protein L17	18.56	0.00	0.00	NA	NA	NA	-18.49	0.00	NA	NA
K02884	large subunit ribosomal protein L19	NA	NA	898286.98	0.00	23.06	0.00	19.56	0.00	19.47	0.00
K02886	large subunit ribosomal protein L2	-30.00	0.00	52393.32	0.87	-0.08	0.99	18.11	0.00	-0.17	0.96
K02890	large subunit ribosomal protein L22	-16.17	0.00	8291.43	0.00	0.29	0.00	NA	NA	-16.08	0.00
K02892	large subunit ribosomal protein L23	-18.16	0.00	169040.74	0.00	1.45	0.00	20.20	0.00	2.01	0.00
K02897	large subunit ribosomal protein L25	NA	NA	43407.84	0.00	NA	NA	19.06	0.00	18.98	0.00
K02906	large subunit ribosomal protein L3	-17.31	0.00	33132.29	0.00	-17.33	0.00	18.66	0.00	1.31	0.00
K02907	large subunit ribosomal protein L30	0.21	0.97	45507.64	0.19	-0.17	0.97	-0.88	0.09	-0.71	0.85
K02910	large subunit ribosomal protein L31e	16.17	0.00	0.00	NA	NA	NA	-16.10	0.00	NA	NA
K02926	large subunit ribosomal protein L4	-16.24	0.00	24311.54	0.25	1.05	0.00	16.89	0.00	0.59	0.36
K02931	large subunit ribosomal protein L5	-0.03	0.99	332394.16	0.02	1.94	0.57	3.01	0.01	2.99	0.30
K02933	large subunit ribosomal protein L6	-1.95	0.05	184119.82	0.02	0.78	0.54	3.92	0.00	2.00	0.05
K02935	large subunit ribosomal protein L7/L12	30.00	0.00	21402.78	0.00	17.77	0.00	-30.00	0.00	NA	NA
K02939	large subunit ribosomal protein L9	-30.00	0.00	224128.69	0.00	1.41	0.68	20.89	0.00	2.73	0.35
K01424	L-asparaginase	0.81	0.00	49857.42	0.85	0.44	0.04	-0.40	0.84	0.36	0.85
K03744	LemA protein	-0.24	0.85	198600.80	0.57	1.01	0.21	1.23	0.00	0.98	0.10
K01255	leucyl aminopeptidase	15.95	0.00	27113.96	1.00	30.00	0.00	1.34	0.67	30.00	0.00
K20523	lipid-binding SYLF domain-containing protein	0.36	0.93	77627.43	0.01	-0.03	0.99	2.12	0.03	2.33	0.45
K10206	LL-diaminopimelate aminotransferase	17.06	0.00	0.00	NA	NA	NA	-16.99	0.00	NA	NA
K01897	long-chain acyl-CoA synthetase	0.44	0.00	2602.27	0.00	-0.95	0.00	-16.05	0.00	-15.65	0.00
K06076	long-chain fatty acid transport protein	0.15	0.88	6412298.98	0.00	1.86	0.00	2.71	0.00	2.86	0.00
K01752	L-serine dehydratase	-1.44	NA	79437.27	0.21	-0.15	0.96	-1.62	0.62	-3.16	NA
K01843	lysine 2,3-aminomutase	16.57	0.00	0.00	NA	NA	NA	-16.50	0.00	NA	NA
K00024	malate dehydrogenase	-0.53	0.85	237347.83	0.00	1.43	0.28	0.83	0.58	0.35	0.82
K00029	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)	-1.30	0.00	44218.38	0.62	-0.39	0.00	-0.10	0.98	-1.41	0.67
K00140	malonate-semialdehyde dehydrogenase (acetylating)/methylmalonate-semialdehyde dehydro	-17.69	0.00	0.00	NA	-17.71	0.00	NA	NA	-17.60	0.00
K15986	manganese-dependent inorganic pyrophosphatase	-1.70	0.02	479566.51	0.36	-1.35	0.00	0.25	0.80	-1.50	0.00
K03585	membrane fusion protein (multidrug efflux system)	NA	NA	8094.68	0.00	NA	NA	16.63	0.00	16.55	0.00
K04087	membrane protease subunit HflC	-1.14	0.00	64470.36	NA	0.35	NA	1.56	0.00	0.38	0.01
K04088	membrane protease subunit HflK	17.40	0.00	32095.99	0.64	16.73	0.00	0.63	0.87	30.00	0.00
K10944	methane/ammonia monooxygenase subunit A	-23.41	0.00	464436.64	NA	-1.07	NA	NA	NA	-23.32	0.00
K10945	methane/ammonia monooxygenase subunit B	1.43	NA	236522.12	0.13	-0.63	0.41	-2.79	NA	-1.41	0.00
K14081	methanol corrinoid protein	-0.95	0.00	287757.68	0.02	-2.14	0.00	-2.31	0.00	-3.28	0.00
K04480	methanol--5-hydroxybenzimidazolylcobamide Co-methyltransferase	-0.57	0.25	806715.77	0.05	-1.80	0.00	-1.76	0.00	-2.39	0.00
K01874	methionyl-tRNA synthetase	-17.53	0.00	6986.58	0.00	-1.33	0.00	NA	NA	-17.45	0.00
K00400	methyl coenzyme M reductase system subunit A2	-0.04	0.99	21803.85	0.00	-1.99	0.53	-0.27	0.28	-0.40	0.92
K03406	methyl-accepting chemotaxis protein	-2.33	0.66	227573.27	0.09	0.55	0.90	4.25	0.11	1.82	0.59
K00399	methyl-coenzyme M reductase alpha subunit	-2.44	0.00	377608.88	0.06	-1.32	0.39	-0.80	0.25	-3.25	0.00
K00401	methyl-coenzyme M reductase beta subunit	-0.53	0.00	18320421.28	0.35	-0.96	0.00	-0.38	0.02	-0.93	0.00
K00402	methyl-coenzyme M reductase gamma subunit	-0.76	0.02	5340193.12	0.31	-1.76	0.00	-1.15	0.00	-1.96	0.00
K01491	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	2.59	0.01	78275.78	0.74	0.28	0.85	-2.92	0.30	-0.39	0.93
K00297	methylenetetrahydrofolate reductase (NADPH)	30.00	0.00	21196.96	0.00	17.25	0.00	-1.63	0.60	16.26	0.00
K00319	methylenetetrahydromethanopterin dehydrogenase	-0.74	0.43	473418.28	0.97	-1.21	0.15	-0.29	0.51	-1.00	0.23
K10540	methyl-galactoside transport system substrate-binding protein	0.19	0.09	0.00	NA	-15.19	0.00	-15.24	0.00	-15.09	0.00
K01849	methylmalonyl-CoA mutase	-0.67	0.00	0.00	NA	-19.26	0.00	-18.45	0.00	-19.15	0.00
K01847	methylmalonyl-CoA mutase	-16.86	0.00	0.00	NA	-16.88	0.00	NA	NA	-16.77	0.00
K01848	methylmalonyl-CoA mutase N-terminal domain/subunit	-0.01	0.99	27781.44	0.14	-2.02	0.17	-3.12	0.00	-3.23	0.00
K07050	misacylated tRNA(Ala) deacylase	-1.10	0.00	7740.36	0.00	-18.75	0.00	-1.06	0.00	-2.20	0.00
K04043	molecular chaperone DnaK	-1.05	0.32	2310208.09	0.52	-0.87	0.44	0.67	0.13	-0.46	0.70
K04079	molecular chaperone HtpG	-2.61	0.00	463872.15	0.01	-0.61	0.04	1.66	0.00	-0.97	0.00
K04080	molecular chaperone IbpA	-0.98	0.89	92720.54	0.35	-1.21	0.77	1.18	0.74	0.23	0.95
K02020	molybdate transport system substrate-binding protein	NA	NA	70918.99	0.00	NA	NA	19.77	0.00	19.69	0.00
K03924	MoxR-like ATPase	-2.61	0.00	24325.79	0.70	-2.98	0.30	-1.13	0.00	-3.77	0.00
K10112	multiple sugar transport system ATP-binding protein	-3.76	0.03	55305.55	0.90	-3.34	0.32	0.26	0.90	-3.50	0.02
K10111	multiple sugar transport system ATP-binding protein	-30.00	0.00	3705.30	0.00	-30.00	0.00	15.50	0.00	-1.12	0.73
K02026	multiple sugar transport system permease protein	NA	NA	8169.16	0.00	16.38	0.00	NA	NA	NA	NA
K02027	multiple sugar transport system substrate-binding protein	-1.77	0.00	133804.32	0.78	-2.23	0.00	-0.36	0.68	-2.18	0.00
K01858	myo-inositol-1-phosphate synthase	-1.41	0.62	4637.70	0.00	-0.27	0.95	-27.93	0.00	-15.73	0.00
K02600	N utilization substance protein A	0.53	0.00	88104.32	0.99	1.51	0.67	1.09	0.19	1.56	0.05
K00346	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	-18.88	0.00	27674.71	0.65	-2.63	0.36	30.00	0.00	-0.91	0.79
K00145	N-acetyl-gamma-glutamyl-phosphate reductase	NA	NA	12338.53	0.00	30.00	0.00	NA	NA	NA	NA
K13075	N-acyl homoserine lactone hydrolase	-0.18	0.97	18886.68	0.94	-1.88	0.57	-1.27	0.69	-1.57	0.77
K00324	NAD(P) transhydrogenase subunit alpha	-20.02	0.00	112716.87	0.11	-0.29	0.82	18.69	0.00	-1.33	0.25
K00331	NADH-quinone oxidoreductase subunit B	18.75	0.00	16747.48	0.00	30.00	0.00	-18.68	0.00	NA	NA
K00332	NADH-quinone oxidoreductase subunit C	NA	NA	19906.00	0.00	NA	NA	17.93	0.00	17.85	0.00
K00333	NADH-quinone oxidoreductase subunit D	17.83	0.00	0.00	NA	NA	NA	-17.76	0.00	NA	NA
K00336	NADH-quinone oxidoreductase subunit G	NA	NA	7612.64	0.00	NA	NA	16.53	0.00	16.46	0.00
K00344	NADPH2:quinone reductase	NA	NA	11256.21	0.00	NA	NA	17.10	0.00	17.03	0.00
K00370	nitrate reductase alpha subunit	-1.25	0.75	24659.96	0.49	-2.64	0.38	0.50	0.90	-0.80	0.41
K00371	nitrate reductase beta subunit	0.71	0.68	241748.49	0.00	1.93	0.01	0.07	0.96	0.74	0.44
K02567	nitrate reductase NapA	NA	NA	6441.08	0.00	28.13	0.00	NA	NA	NA	NA
K15576	nitrate/nitrite transport system substrate-binding protein	NA	NA	26539.18	0.00	16.80	0.00	17.58	0.00	17.50	0.00
K03385	nitrite reductase (cytochrome c-552)	0.23	0.96	78141.01	0.01	2.24	0.04	-0.53	0.89	-0.31	0.22
K15864	nitrite reductase (NO-forming)/hydroxylamine reductase	-19.39	0.00	38045.32	0.49	-1.92	0.00	18.08	0.00	-1.36	0.02
K02585	nitrogen fixation protein NifB	-1.15	0.72	4618.59	0.00	-1.83	0.00	0.84	0.78	-0.32	0.02
K04751	nitrogen regulatory protein P-II 1	2.06	0.00	388533.39	0.18	1.08	0.01	-1.16	0.05	0.88	0.04
K04752	nitrogen regulatory protein P-II 2	2.52	0.00	310863.58	0.15	2.00	0.00	-0.84	0.09	1.66	0.00
K00376	nitrous-oxide reductase	-2.71	0.34	193538.88	0.31	0.57	0.73	2.29	0.43	-0.43	0.43
K02051	NitT/TauT family transport system substrate-binding protein	-29.86	0.00	58736.49	0.96	0.37	0.94	18.51	0.00	0.42	0.92
K09759	nondiscriminating aspartyl-tRNA synthetase	-15.70	0.00	0.00	NA	-15.72	0.00	NA	NA	-15.62	0.00
K07001	NTE family protein	NA	NA	15838.05	0.00	14.31	0.00	17.41	0.00	17.33	0.00
K00940	nucleoside-diphosphate kinase	-18.26	0.00	24959.83	0.00	-0.44	0.00	15.49	0.00	-2.80	0.00
K01740	O-acetylhomoserine (thiol)-lyase	0.81	0.85	34974.54	0.90	-0.71	0.91	-0.97	0.78	-0.19	0.98
K02523	octaprenyl-diphosphate synthase	NA	NA	13474.51	0.00	NA	NA	30.00	0.00	30.00	0.00
K10823	oligopeptide transport system ATP-binding protein	-17.11	0.00	37118.65	0.00	-17.13	0.00	18.83	0.00	1.69	0.00
K15580	oligopeptide transport system substrate-binding protein	-0.77	0.86	41519.88	0.00	0.32	0.95	-17.65	0.00	-30.00	0.00
K03286	OOP family OmpA-OmpF porin	-0.29	0.73	3571615.88	0.06	0.27	0.57	1.03	0.02	0.75	0.02
K19691	osomolarity two-component system, sensor histidine kinase NIK1	NA	NA	29679.23	0.00	NA	NA	18.50	0.00	18.43	0.00
K16079	outer membrane immunogenic protein	0.87	0.84	815547.83	0.05	1.91	0.58	0.11	0.42	1.01	0.78
K12686	outer membrane lipase/esterase	-0.37	0.96	13702.32	0.27	-1.75	0.72	1.04	0.74	0.59	0.87
K03634	outer membrane lipoprotein carrier protein	NA	NA	0.00	NA	NA	NA	NA	NA	NA	NA
K12340	outer membrane protein	-0.45	0.92	71522.19	0.12	-1.96	0.51	2.11	0.48	1.64	0.00
K07274	outer membrane protein	1.10	0.79	89204.88	0.00	1.67	0.00	-0.37	0.92	0.66	0.16
K06142	outer membrane protein	3.55	0.00	26143.35	0.17	-3.03	0.00	-2.95	0.32	0.43	0.92
K17713	outer membrane protein assembly factor BamB	NA	NA	19586.64	0.00	NA	NA	30.00	0.00	30.00	0.00
K07287	outer membrane protein assembly factor BamC	NA	NA	23330.65	0.00	NA	NA	18.14	0.00	18.07	0.00
K07277	outer membrane protein insertion porin family	-0.63	0.54	240262.77	0.56	0.40	0.61	1.67	0.03	0.99	0.00
K01577	oxalyl-CoA decarboxylase	-16.74	0.00	0.00	NA	-16.76	0.00	NA	NA	-16.65	0.00
K03497	ParB family chromosome partitioning protein	-7.14	0.00	16633.06	0.00	-8.00	0.00	3.56	0.00	-3.64	0.00
K01728	pectate lyase	-0.04	0.83	3196.49	0.00	-15.81	0.00	-0.46	0.00	-0.53	0.00
K02032	peptide/nickel transport system ATP-binding protein	0.26	0.04	41403.15	0.00	-18.01	0.00	0.74	0.00	0.96	0.00
K02035	peptide/nickel transport system substrate-binding protein	-0.74	0.04	1376513.92	0.02	-0.64	0.02	0.61	0.03	-0.15	0.56
K03640	peptidoglycan-associated lipoprotein	-0.45	0.20	166532.39	0.22	-2.22	0.00	-0.91	0.00	-1.37	0.00
K03769	peptidyl-prolyl cis-trans isomerase C	1.47	0.81	73569.37	0.72	0.81	0.90	0.47	0.91	1.89	0.56
K03770	peptidyl-prolyl cis-trans isomerase D	NA	NA	40581.94	0.50	29.84	0.00	18.55	0.00	18.45	0.00
K03771	peptidyl-prolyl cis-trans isomerase SurA	NA	NA	14876.08	0.29	14.57	0.00	29.38	0.00	29.99	0.00
K03386	peroxiredoxin (alkyl hydroperoxide reductase subunit C)	0.55	0.94	92974.26	0.09	0.20	0.96	0.47	0.91	1.10	0.76
K03564	peroxiredoxin Q/BCP	29.51	0.00	22717.61	0.00	NA	NA	1.59	0.58	18.04	0.00
K21449	PGF-CTERM protein	17.46	0.00	24964.60	0.13	17.47	0.00	-1.01	0.23	16.43	0.00
K03969	phage shock protein A	0.68	0.92	9138.99	NA	0.21	0.96	-0.95	NA	-0.30	0.96
K06907	phage tail sheath protein FI	0.95	0.00	673157.22	0.62	-0.12	0.94	-0.39	0.23	0.53	0.00
K00625	phosphate acetyltransferase	0.70	0.88	31211.60	0.95	-0.64	0.87	-1.42	0.79	-0.69	0.85
K00634	phosphate butyryltransferase	NA	NA	26926.37	0.00	15.68	0.00	18.06	0.00	17.99	0.00
K06217	phosphate starvation-inducible PhoH-like protein	NA	NA	16925.41	0.00	NA	NA	17.69	0.00	17.61	0.00
K02036	phosphate transport system ATP-binding protein	NA	NA	7750.75	0.00	NA	NA	16.57	0.00	16.49	0.00
K02040	phosphate transport system substrate-binding protein	-2.33	0.00	252676.25	0.00	-0.94	0.03	3.48	0.00	1.14	0.00
K07221	phosphate-selective porin OprO/OprP	2.15	0.46	0.00	NA	-30.00	0.00	-18.63	0.00	-30.00	0.00
K01610	phosphoenolpyruvate carboxykinase (ATP)	-1.71	0.00	6208.43	0.00	-0.74	0.00	-14.94	0.00	-16.69	0.00
K01596	phosphoenolpyruvate carboxykinase (GTP)	-30.00	0.00	17064.30	0.36	-1.47	0.64	29.54	0.00	0.82	0.88
K01835	phosphoglucomutase	NA	NA	17318.45	0.00	17.47	0.00	NA	NA	NA	NA
K00927	phosphoglycerate kinase	0.81	0.30	396500.71	0.01	2.24	0.00	0.90	0.01	1.65	0.02
K15778	phosphomannomutase/phosphoglucomutase	NA	NA	82656.44	0.00	19.40	0.00	17.65	0.00	17.59	0.00
K03147	phosphomethylpyrimidine synthase	-3.00	0.00	16872.03	0.71	-0.58	0.47	1.82	0.51	-1.19	0.71
K00602	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	-1.49	0.00	20207.33	0.00	-0.30	0.00	-16.42	0.00	-17.95	0.00
K01923	phosphoribosylaminoimidazole-succinocarboxamide synthase	NA	NA	30151.36	NA	30.00	NA	16.72	0.00	16.65	0.00
K01814	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	NA	NA	14183.62	0.00	15.38	0.00	16.95	0.00	16.87	0.00
K00855	phosphoribulokinase	18.38	0.00	299802.24	0.78	30.00	0.00	2.69	0.00	21.08	0.00
K00831	phosphoserine aminotransferase	30.00	0.00	20953.81	0.00	17.74	0.00	-30.00	0.00	NA	NA
K02704	photosystem II CP47 chlorophyll apoprotein	1.50	0.00	255411.36	0.40	4.85	0.00	1.48	0.65	2.99	0.31
K02703	photosystem II P680 reaction center D1 protein	30.00	0.00	0.00	NA	NA	NA	-30.00	0.00	NA	NA
K02706	photosystem II P680 reaction center D2 protein	1.82	0.00	43430.68	0.00	0.56	0.90	-19.95	0.00	-18.16	0.00
K02280	pilus assembly protein CpaC	1.47	0.06	167360.29	0.10	1.10	0.74	3.83	0.01	5.32	0.00
K02283	pilus assembly protein CpaF	NA	NA	46370.86	0.10	18.19	0.00	17.77	0.00	17.70	0.00
K08086	pilus assembly protein FimV	NA	NA	4635.05	0.00	NA	NA	15.82	0.00	15.75	0.00
K02030	polar amino acid transport system substrate-binding protein	-1.57	0.02	387365.48	0.61	-0.68	0.46	1.40	0.00	-0.25	0.77
K00962	polyribonucleotide nucleotidyltransferase	0.52	0.72	704449.98	0.72	1.47	0.18	1.27	0.00	1.83	0.06
K01698	porphobilinogen synthase	NA	NA	26794.06	0.67	30.00	0.00	16.74	0.00	16.66	0.00
K11206	predicted amidohydrolase	NA	NA	10091.16	0.00	12.82	0.00	16.84	0.00	16.76	0.00
K07004	predicted extracellular nuclease	0.09	0.98	3900.41	0.00	-30.00	0.00	-1.74	0.00	-1.74	0.58
K07092	predicted peroxiredoxin	NA	NA	21303.65	0.80	16.78	0.00	17.01	0.00	16.93	0.00
K07006	predicted pyridoxine 5'-phosphate oxidase superfamily flavin-nucleotide-binding protein	-17.53	0.00	9843.79	0.00	-0.83	0.00	NA	NA	-17.44	0.00
K07045	predicted TIM-barrel fold metal-dependent hydrolase	-16.62	0.00	0.00	NA	-16.64	0.00	NA	NA	-16.53	0.00

K07744	predicted transcriptional regulator	0.03	0.99	8281.53	0.00	-0.57	0.60	-30.00	0.00	-16.94	0.00
K03070	preprotein translocase subunit SecA	2.78	0.00	229719.40	0.06	1.22	0.31	-0.17	0.72	2.53	0.00
K03072	preprotein translocase subunit SecD	17.69	0.00	19593.67	0.96	28.84	0.00	-0.96	0.77	29.77	0.00
K04802	proliferating cell nuclear antigen	-1.42	0.00	6540.82	0.00	-2.61	0.36	-17.15	0.00	-18.60	0.00
K01881	prolyl-tRNA synthetase	NA	NA	7750.75	0.00	NA	NA	16.57	0.00	16.49	0.00
K01966	propionyl-CoA carboxylase beta chain	3.37	0.00	42494.76	0.00	3.56	0.00	-0.82	0.37	2.53	0.00
K01908	propionyl-CoA synthetase	-0.44	0.51	82499.12	0.34	0.87	0.28	0.84	0.16	0.39	0.58
K04773	protease-4	NA	NA	12572.94	0.55	27.25	0.00	29.94	0.00	29.84	0.00
K03432	proteasome alpha subunit	0.14	0.81	160964.34	0.95	-1.55	0.01	-1.49	0.00	-1.41	0.00
K03433	proteasome beta subunit	-0.21	0.07	0.00	NA	-16.65	0.00	-16.29	0.00	-16.54	0.00
K0627	protein phosphatase 1 regulatory subunit	NA	NA	79140.69	0.00	NA	NA	19.92	0.00	19.84	0.00
K22169	proton-translocating NADH-quinone oxidoreductase chain N	NA	NA	11856.50	0.00	16.92	0.00	NA	NA	NA	NA
K02003	putative ABC transport system ATP-binding protein	-28.70	0.00	0.00	NA	-28.70	0.00	NA	NA	-28.59	0.00
K01989	putative ABC transport system substrate-binding protein	NA	NA	3284.83	0.00	NA	NA	15.33	0.00	15.25	0.00
K10546	putative multiple sugar transport system substrate-binding protein	-0.26	0.57	1020653.61	0.99	-0.53	0.14	-0.08	0.87	-0.37	0.23
K07572	putative nucleotide binding protein	-16.77	0.00	0.00	NA	-16.79	0.00	NA	NA	-16.68	0.00
K07283	putative salt-induced outer membrane protein	NA	NA	3704.17	0.00	15.24	0.00	NA	NA	NA	NA
K02052	putative spermidine/putrescine transport system ATP-binding protein	NA	NA	36537.08	0.00	NA	NA	18.80	0.00	18.72	0.00
K02055	putative spermidine/putrescine transport system substrate-binding protein	-16.69	0.00	0.00	NA	-16.71	0.00	NA	NA	-16.60	0.00
K07795	putative tricarboxylic transport membrane protein	0.12	0.92	516720.04	0.00	1.29	0.01	2.55	0.00	2.62	0.00
K11073	putrescine transport system substrate-binding protein	-18.86	0.00	0.00	NA	-18.88	0.00	NA	NA	-18.78	0.00
K06215	pyridoxal 5'-phosphate synthase pdxS subunit	30.00	0.00	110316.00	0.60	19.80	0.00	-0.95	0.87	30.00	NA
K00756	pyrimidine-nucleoside phosphorylase	-0.39	0.92	194380.52	0.00	-30.00	0.00	4.87	0.00	4.38	0.09
K00895	pyrophosphate--fructose-6-phosphate 1-phosphotransferase	-1.56	0.00	77670.11	0.99	-1.58	0.65	0.14	0.29	-1.47	0.00
K00163	pyruvate dehydrogenase E1 component	17.72	0.00	0.00	NA	NA	NA	-17.65	0.00	NA	NA
K00162	pyruvate dehydrogenase E1 component beta subunit	-16.67	0.00	6659.90	0.00	-16.69	0.00	16.35	0.00	-0.35	0.01
K00169	pyruvate ferredoxin oxidoreductase alpha subunit	-0.68	0.92	100681.84	0.80	0.01	1.00	1.67	0.75	0.88	0.88
K00170	pyruvate ferredoxin oxidoreductase beta subunit	18.75	0.00	9229.50	0.00	NA	NA	-1.99	0.00	16.74	0.00
K00172	pyruvate ferredoxin oxidoreductase gamma subunit	19.07	0.00	219748.19	0.00	21.13	0.00	-19.00	0.00	NA	NA
K00873	pyruvate kinase	-17.55	0.00	43164.11	0.98	0.34	0.95	18.10	0.00	0.53	0.50
K01006	pyruvate,orthophosphate dikinase	0.33	0.57	486184.50	0.32	-0.24	0.72	-0.80	0.07	-0.49	0.23
K01007	pyruvate,water dikinase	0.14	0.90	38119.39	0.93	-1.59	0.64	-1.27	0.70	-1.13	0.75
K03737	pyruvate-ferredoxin/flavodoxin oxidoreductase	0.02	0.99	171254.12	0.88	-0.22	0.87	0.00	1.00	0.00	1.00
K16885	quinone-modifying oxidoreductase subunit QmoA	2.78	0.02	328979.93	0.66	2.51	0.03	0.21	0.88	2.90	0.00
K16886	quinone-modifying oxidoreductase subunit QmoB	1.89	0.00	653111.61	0.18	1.26	0.10	0.16	0.54	1.99	0.00
K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	-1.70	0.01	360134.08	0.99	-0.88	0.45	1.07	NA	-0.74	NA
K07463	RecJ-like exonuclease	30.00	0.00	0.00	NA	NA	NA	-30.00	0.00	NA	NA
K03554	recombination associated protein RdgC	18.58	0.00	10359.59	0.00	16.73	0.00	-18.51	0.00	NA	NA
K03553	recombination protein RecA	-0.23	0.80	175589.79	0.01	0.56	0.40	0.54	0.02	0.29	0.67
K10559	rhamnose transport system substrate-binding protein	-30.00	0.00	29653.63	0.00	-0.10	0.98	17.84	0.00	0.91	0.79
K08300	ribonuclease E	-30.00	0.00	55817.18	0.53	-1.06	0.86	18.98	0.00	0.49	0.91
K12574	ribonuclease J	-1.63	0.22	2339.92	0.00	-2.26	0.09	-15.15	0.00	-16.74	0.00
K00989	ribonuclease PH	-15.43	0.00	0.00	NA	-15.45	0.00	NA	NA	-15.34	0.00
K00525	ribonucleoside-diphosphate reductase alpha chain	-17.62	0.00	62577.92	0.16	0.64	0.00	18.68	0.00	1.02	0.00
K10439	ribose transport system substrate-binding protein	-1.22	0.00	542522.63	0.31	-1.31	0.00	0.32	0.20	-0.91	0.00
K00948	ribose-phosphate pyrophosphokinase	NA	NA	19358.80	0.39	17.29	0.00	27.88	0.00	27.83	0.00
K02838	ribosome recycling factor	-18.99	0.00	0.00	NA	-19.01	0.00	NA	NA	-18.90	0.00
K01601	ribulose-bisphosphate carboxylase large chain	3.79	0.00	193450.46	0.00	3.44	0.00	-0.90	0.27	2.87	0.00
K01783	ribulose-phosphate 3-epimerase	-17.35	0.00	195461.62	0.49	3.52	0.28	29.96	0.00	1.07	0.76
K03086	RNA polymerase primary sigma factor	0.16	0.22	63581.27	0.34	-0.90	0.80	1.31	0.05	1.44	0.03
K03599	RNA polymerase-associated protein	NA	NA	53297.66	0.12	28.65	0.00	19.21	0.00	19.15	0.00
K03569	rod shape-determining protein MreB	1.29	0.02	228760.58	0.52	1.85	0.01	1.40	0.25	2.65	0.01
K00789	S-adenosylmethionine synthetase	-2.79	0.32	214805.86	0.53	0.21	0.77	3.35	0.21	0.59	0.28
K04771	serine protease Do	-1.39	0.28	561344.58	0.00	-0.39	0.75	5.32	0.00	3.89	0.00
K07180	serine protein kinase	0.73	0.47	112515.49	0.33	1.56	0.02	0.16	0.91	0.85	0.42
K07258	serine-type D-Ala-D-Ala carboxypeptidase	-18.48	0.00	0.00	NA	-18.50	0.00	NA	NA	-18.40	0.00
K03598	sigma-E factor negative regulatory protein RseB	NA	NA	17969.43	0.00	NA	NA	30.00	0.00	29.79	0.00
K03106	signal recognition particle subunit SRP54	-1.82	0.78	34756.01	0.00	-29.94	0.00	2.81	0.28	0.89	0.80
K02058	simple sugar transport system substrate-binding protein	-1.65	0.18	144316.49	0.90	-1.74	0.12	0.16	0.92	-1.51	0.00
K03111	single-strand DNA-binding protein	20.43	0.00	0.00	NA	NA	NA	-20.36	0.00	NA	NA
K02945	small subunit ribosomal protein S1	1.38	0.11	495333.61	0.35	3.21	0.00	2.86	0.00	4.24	0.00
K02946	small subunit ribosomal protein S10	-1.27	0.84	67117.78	0.76	-0.84	0.90	1.74	0.74	0.48	0.94
K02948	small subunit ribosomal protein S11	-0.41	0.93	39208.43	0.82	-1.30	0.82	-0.21	0.00	-0.67	0.86
K02956	small subunit ribosomal protein S15	NA	NA	32533.67	0.56	17.85	0.00	29.78	0.00	29.75	0.00
K02967	small subunit ribosomal protein S2	1.29	NA	228610.71	0.07	1.85	0.59	1.41	0.00	2.58	0.40
K02982	small subunit ribosomal protein S3	-3.36	NA	325558.31	0.24	-0.11	0.96	3.73	0.00	0.33	NA
K02984	small subunit ribosomal protein S3Ae	-16.60	0.00	0.00	NA	-16.61	0.00	NA	NA	-16.50	0.00
K02986	small subunit ribosomal protein S4	0.16	0.97	141744.43	0.50	-0.21	0.98	1.41	0.01	1.51	0.66
K02988	small subunit ribosomal protein S5	-18.27	0.00	73931.21	0.94	0.32	0.95	18.86	0.00	0.58	0.70
K02992	small subunit ribosomal protein S7	-1.36	0.00	403003.91	0.88	0.49	0.42	2.01	0.00	0.63	0.19
K02994	small subunit ribosomal protein S8	-29.10	0.00	27572.29	0.51	2.35	0.40	29.54	0.00	1.06	0.83
K02996	small subunit ribosomal protein S9	NA	NA	41104.73	0.00	NA	NA	18.97	0.00	18.89	0.00
K05813	sn-glycerol 3-phosphate transport system substrate-binding protein	-17.92	0.00	41971.96	0.00	-17.94	0.00	19.00	0.00	1.05	0.00
K06324	spore coat protein A	0.72	0.53	210509.95	0.32	-0.22	0.87	-1.38	0.05	-0.68	0.58
K21677	squalene-associated FAD-dependent desaturase	15.31	0.00	0.00	NA	NA	NA	-15.24	0.00	NA	NA
K00688	starch phosphorylase	-18.32	0.00	5490.05	0.00	-2.50	0.38	NA	NA	-18.23	0.00
K04047	starvation-inducible DNA-binding protein	1.24	0.83	48396.51	0.93	1.42	0.80	0.22	0.95	1.37	0.67
K11085	subfamily B ATP-binding cassette protein MsbA	NA	NA	3162.13	0.00	15.01	0.00	NA	NA	NA	NA
K00239	succinate dehydrogenase / fumarate reductase flavoprotein subunit	2.42	0.46	72068.01	0.81	-0.10	0.98	-3.12	0.28	-0.83	0.89
K01902	succinyl-CoA synthetase alpha subunit	-0.57	0.90	70657.85	0.41	0.27	0.95	-0.88	0.80	-1.47	0.78
K01903	succinyl-CoA synthetase beta subunit	-29.98	0.00	20335.56	0.00	1.42	0.66	NA	NA	-29.82	0.00
K00958	sulfate adenylyltransferase	0.11	0.89	884661.92	0.00	0.10	0.91	-1.09	0.00	-1.04	0.01
K06020	sulfate-transporting ATPase	NA	NA	11445.39	0.55	27.74	NA	16.80	0.00	16.70	0.00
K17229	sulfide dehydrogenase [flavocytochrome c] flavoprotein subunit	NA	NA	16421.03	0.00	NA	NA	30.00	0.00	30.00	0.00
K17218	sulfide:quinone oxidoreductase	-5.42	0.02	483106.22	0.82	1.32	0.06	7.02	0.00	1.57	0.02
K05301	sulfite dehydrogenase	-18.77	0.00	741518.01	0.00	2.13	0.01	22.75	0.00	3.95	0.00
K11180	sulfite reductase alpha subunit	0.42	0.44	3353409.30	0.75	1.23	0.01	1.06	0.00	1.48	0.00
K11181	sulfite reductase beta subunit	0.46	0.25	2707265.26	0.00	0.51	0.11	-0.06	0.85	0.36	0.27
K15515	sulfoacetaldehyde dehydrogenase	NA	NA	7964.72	0.00	16.35	0.00	NA	NA	NA	NA
K17222	sulfur-oxidizing protein SoxA	-18.73	0.00	4528310.68	0.06	5.59	0.00	24.98	0.00	6.22	0.00
K17224	sulfur-oxidizing protein SoxB	0.88	0.83	323318.82	0.44	2.73	0.59	3.85	0.00	4.76	0.06
K17223	sulfur-oxidizing protein SoxX	NA	NA	158812.59	0.00	19.85	0.00	19.73	0.00	19.65	0.00
K17226	sulfur-oxidizing protein SoxY	16.98	0.00	13224.84	0.00	NA	NA	0.31	0.00	17.26	0.00
K17227	sulfur-oxidizing protein SoxZ	NA	NA	215479.51	0.00	21.08	0.00	16.97	0.00	16.88	0.00
K05919	superoxide reductase	-0.40	0.55	145398.88	0.00	-0.89	0.05	-1.12	0.00	-1.58	0.00
K05795	tellurium resistance protein TerD	-17.56	0.00	0.00	NA	-17.58	0.00	NA	NA	-17.47	0.00
K00577	tetrahydromethanopterin S-methyltransferase subunit A	1.00	0.81	284542.10	0.00	2.25	0.51	-2.73	0.00	-1.72	0.60
K00584	tetrahydromethanopterin S-methyltransferase subunit H	-0.31	0.41	372286.04	0.65	-0.99	0.11	-0.75	0.05	-1.09	0.00
K22447	thermosome	0.13	0.89	1232062.84	0.03	-0.02	0.98	-0.65	0.14	-0.51	0.36
K11065	thiol peroxidase	NA	NA	5460.38	0.00	28.81	0.00	NA	NA	NA	NA
K03673	thiol:disulfide interchange protein DsbA	-18.24	0.00	63800.64	0.54	0.02	0.98	18.76	0.00	0.51	0.25
K03671	thioredoxin 1	30.00	0.00	74819.09	0.00	19.60	0.00	-30.00	0.00	NA	NA
K01754	threonine dehydratase	NA	NA	60922.80	0.63	18.16	0.00	18.69	0.00	18.62	0.00
K01868	threonyl-tRNA synthetase	NA	NA	11957.30	0.00	NA	NA	17.19	0.00	17.11	0.00
K03568	TldD protein	NA	NA	10142.60	0.01	14.63	0.00	16.55	0.00	16.50	0.00
K00616	transaldolase	-0.67	0.92	281733.04	0.20	0.33	0.95	0.39	0.92	-0.22	0.96
K03124	transcription initiation factor TFIIB	-0.86	0.00	13411.33	0.00	-1.19	0.00	-17.36	0.00	-18.25	0.00
K03120	transcription initiation factor TFIID TATA-box-binding protein	0.60	0.89	52615.00	0.52	1.26	0.20	-0.87	0.88	-0.26	0.95
K03628	transcription termination factor Rho	-0.16	0.74	1068436.86	0.99	-0.18	0.80	0.24	0.54	0.07	0.91
K02601	transcriptional antiterminator NusG	1.07	0.00	26176.43	0.65	-0.39	0.56	-1.54	0.00	-0.51	0.38
K13525	transitional endoplasmic reticulum ATPase	-2.17	0.53	99342.50	0.16	-1.88	0.60	1.11	0.15	-1.02	0.78
K00615	transketolase	-1.81	0.00	1586040.58	0.00	-0.72	0.25	0.10	0.03	-1.77	0.00
K02519	translation initiation factor IF-2	0.52	0.89	41538.16	0.89	2.20	0.00	1.55	0.76	2.03	0.50
K02520	translation initiation factor IF-3	NA	NA	52927.78	0.89	30.00	0.00	18.16	0.00	18.08	0.00
K09800	translocation and assembly module TamB	NA	NA	21069.60	0.00	NA	NA	18.01	0.00	17.93	0.00
K07080	TRAP transporter TAXI family solute receptor	-2.42	0.00	257735.54	0.26	-2.02	0.00	0.93	0.01	-1.50	0.00
K21395	TRAP-type C4-dicarboxylate transport system substrate-binding protein	1.16	0.87	2956.36	0.00	-1.28	0.80	-29.76	0.00	-29.76	0.00
K03545	trigger factor	2.63	0.00	23734.51	0.52	2.21	0.43	1.19	0.00	3.77	0.00
K01803	triosephosphate isomerase	-0.26	0.96	42182.42	0.24	1.68	0.01	-0.57	0.92	-0.88	0.78
K21395	tripartite ATP-independent transporter DctP family solute receptor	1.16	0.87	2956.36	0.00	-1.28	0.80	-29.76	0.00	-29.76	0.00
K04085	tRNA 2-thiouridine synthesizing protein A	NA	NA	24782.46	0.00	30.00	0.00	NA	NA	NA	NA
K07237	tRNA 2-thiouridine synthesizing protein B	NA	NA	2915.89	0.00	NA	NA	28.21	0.00	28.14	0.00
K07235	tRNA 2-thiouridine synthesizing protein D	0.74	0.00	104081.59	0.01	2.17	0.00	2.60	0.00	3.30	0.00
K06001	tryptophan synthase beta chain	0.28	0.96	51652.15	0.89	0.50	0.91	-0.17	0.98	0.16	0.97
K01867	tryptophanyl-tRNA synthetase	NA	NA	4121.36	0.00	NA	NA	28.76	0.00	28.68	0.00
K23077	TusE/DsrC/DsvC family sulfur relay protein	0.31	0.88	414387.57	0.03	0.75	0.40	-0.30	0.83	0.03	0.98
K02660	twitching motility protein PilJ	16.22	0.00	121045.34	0.06	18.66	0.00	3.72	0.00	19.88	0.00
K02669	twitching motility protein PilT	-12.57	0.00	111329.42	0.62	5.99	0.02	19.90	0.00	7.27	0.00
K02670	twitching motility protein PilU	NA	NA	27551.99	0.67	17.55	0.00	28.94	0.00	29.82	0.00
K02658	twitching motility two-component system response regulator PilH	NA	NA	2361.22	0.00	NA	NA	14.85	0.00	14.77	0.00
K13587	two-component system cell cycle sensor histidine kinase/response regulator CckA	NA	NA	727.17	0.00	12.89	0.00	NA	NA	NA	NA
K07712	two-component system nitrogen regulation response regulator GlnG	NA	NA	13992.16	0.55	27.94	0.00	30.00	0.00	30.00	0.00
K02482	two-component system NtrC family sensor kinase	NA	NA	3794.62	0.00	28.43	0.00	NA	NA	NA	NA
K14981	two-component system response regulator ChvI	-18.61	0.00	29422.95	0.00	-0.33	0.00	NA	NA	-18.52	0.00
K02650	type IV pilus assembly protein PilA	NA	NA	23159.58	0.00	17.89	0.00	NA	NA	NA	NA
K02652	type IV pilus assembly protein PilB	-16.66	0.00	0.00	NA	-16.69	0.00	NA	NA	-16.58	0.00
K02656	type IV pilus assembly protein PilF	NA	NA	14874.38	0.83	16.26	0.00	16.49	0.00	16.41	0.00
K02662	type IV pilus assembly protein PilM	17.55	0.00	88160.65	0.21	19.29	0.00	0.85	0.18	18.36	0.00
K02663	type IV pilus assembly protein PilN	-16.11	0.00	133290.18	0.13	3.87	0.00	18.89	0.00	2.71	0.00
K02664	type IV pilus assembly protein PilO	NA	NA	12565.02	0.88	28.79	0.00	29.57	0.00	29.39	0.00
K02666	type IV pilus assembly protein PilQ	-0.22	0.55	2563983.19	0.00	0.50	0.27	1.63	0.00	1.37	0.00
K11901	type VI secretion system protein ImpB	-16.63	0.00	0.00	NA	-16.65	0.00	NA	NA	-16.54	0.00

K11900	type VI secretion system protein ImpC	-0.94	0.00	39796.02	0.40	-2.22	0.00	-0.65	0.26	-1.60	0.01
K11907	type VI secretion system protein VasG	-0.22	0.12	29554.81	0.00	0.16	0.83	-1.18	0.00	-1.44	0.00
K11903	type VI secretion system secreted protein Hcp	18.61	0.00	1741.86	0.00	NA	NA	-4.25	0.00	14.33	0.00
K01866	tyrosyl-tRNA synthetase	NA	NA	1812.82	0.00	NA	NA	27.27	0.00	26.97	0.00
K00413	ubiquinol-cytochrome c reductase cytochrome c1 subunit	-0.01	1.00	32573.81	0.73	2.08	0.51	1.04	0.85	1.06	0.75
K00411	ubiquinol-cytochrome c reductase iron-sulfur subunit	NA	NA	123917.49	0.00	NA	NA	20.57	0.00	20.49	0.00
K00012	UDPglucose 6-dehydrogenase	NA	NA	20618.92	0.88	30.00	0.00	29.70	0.00	29.68	0.00
K08678	UDP-glucuronate decarboxylase	-18.37	0.00	0.00	NA	-18.39	0.00	NA	NA	-18.28	0.00
K02473	UDP-N-acetylglucosamine 4-epimerase	NA	NA	2699.49	0.00	NA	NA	15.04	0.00	14.97	0.00
K09702	uncharacterized protein	-18.08	0.00	1597.77	0.00	-18.10	0.00	14.29	0.00	-3.82	0.00
K09807	uncharacterized protein YggE	-1.97	0.00	0.00	NA	-17.53	0.00	-15.42	0.00	-17.43	0.00
K11959	urea transport system substrate-binding protein	-0.94	0.82	48145.89	0.94	-0.44	0.60	0.57	0.92	-0.41	0.92
K02302	uroporphyrin-III C-methyltransferase/precorrin-2 dehydrogenase/sirohydrochlorin ferrochelatase	NA	NA	10044.38	0.00	NA	NA	29.12	0.00	29.10	0.00
K00963	UTP--glucose-1-phosphate uridylyltransferase	NA	NA	63201.20	0.49	18.15	0.00	18.75	0.00	18.69	0.00
K02117	V/A-type H+-transporting ATPase subunit A	-0.07	0.81	1502380.58	0.00	-0.56	0.00	-0.95	0.00	-1.04	0.00
K02118	V/A-type H+-transporting ATPase subunit B	-0.11	0.85	1426580.53	0.00	-0.45	0.03	-0.80	0.03	-0.92	0.00
K02119	V/A-type H+-transporting ATPase subunit C	1.07	0.03	216138.22	0.18	0.96	0.03	-0.38	0.32	0.70	0.17
K02121	V/A-type H+-transporting ATPase subunit E	-0.91	0.01	440133.54	0.13	-0.98	0.00	-0.40	0.45	-1.35	0.00
K02122	V/A-type H+-transporting ATPase subunit F	-17.18	0.00	0.00	NA	-17.20	0.00	NA	NA	-17.09	0.00
K02123	V/A-type H+-transporting ATPase subunit I	2.87	0.01	35195.51	0.00	1.62	0.00	-19.65	0.00	-16.82	0.00
K01805	xylose isomerase	16.36	0.00	2616.81	0.00	NA	NA	-1.41	0.00	14.92	0.00
K01621	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	-13.69	0.00	5025.29	0.48	0.11	0.31	28.57	0.00	1.74	0.53
K07263	zinc protease	NA	NA	30885.96	0.83	17.54	0.00	30.00	0.00	30.00	0.00
K00765	ATP phosphoribosyltransferase	NA	NA	17624.61	0.00	NA	NA	17.75	0.00	17.67	0.00
K23107	1-deoxyxylulose-5-phosphate synthase	NA	NA	17605.24	0.00	NA	NA	17.75	0.00	17.67	0.00
K03735	ethanolamine ammonia-lyase large subunit	-17.85	0.00	11722.85	0.00	-0.89	0.00	NA	NA	-17.76	0.00
K01810	glucose-6-phosphate isomerase	NA	NA	77196.78	0.00	19.26	0.00	17.71	0.00	17.63	0.00
K03149	thiazole synthase	NA	NA	16475.66	0.00	NA	NA	17.65	0.00	17.58	0.00
K02665	type IV pilus assembly protein PilP	NA	NA	27296.61	0.65	29.56	0.00	17.82	0.00	17.73	0.00
K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma	-17.56	0.00	0.00	NA	-17.58	0.00	NA	NA	-17.48	0.00
K22222	tubulin-like protein CetZ	-17.56	0.00	0.00	NA	-17.58	0.00	NA	NA	-17.48	0.00
K03071	preprotein translocase subunit SecB	NA	NA	13905.14	0.00	NA	NA	17.41	0.00	17.33	0.00
K16787	energy-coupling factor transport system ATP-binding protein	NA	NA	12736.34	0.00	NA	NA	17.28	0.00	17.20	0.00
K00368	nitrite reductase (NO-forming)	-17.38	0.00	0.00	NA	-17.41	0.00	NA	NA	-17.30	0.00
K07041	uncharacterized protein	NA	NA	12697.60	0.00	NA	NA	17.28	0.00	17.20	0.00
K03500	16S rRNA (cytosine967-C5)-methyltransferase	NA	NA	12619.65	0.00	NA	NA	17.27	0.00	17.19	0.00
K08691	malyl-CoA/(S)-citramalyl-CoA lyase	-17.36	0.00	0.00	NA	-17.38	0.00	NA	NA	-17.28	0.00
K03390	heterodisulfide reductase subunit C2	-17.30	0.00	0.00	NA	-17.33	0.00	NA	NA	-17.22	0.00
K06911	quercetin 2,3-dioxygenase	NA	NA	11732.42	0.00	NA	NA	17.16	0.00	17.09	0.00
K03183	demethylmenaquinone methyltransferase / 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase	-17.26	0.00	0.00	NA	-17.28	0.00	NA	NA	-17.17	0.00
K02314	replicative DNA helicase	29.55	0.00	11334.16	0.00	NA	NA	0.54	0.88	17.04	0.00
K13812	bifunctional enzyme Fae/Hps	NA	NA	11142.35	0.00	NA	NA	17.09	0.00	17.01	0.00
K19064	lysine 6-dehydrogenase	-17.18	0.00	0.00	NA	-17.20	0.00	NA	NA	-17.09	0.00
K00259	alanine dehydrogenase	NA	NA	10817.79	0.00	NA	NA	17.05	0.00	16.97	0.00
K08301	ribonuclease G	NA	NA	9510.56	0.00	NA	NA	16.86	0.00	16.78	0.00
K02031	peptide/nickel transport system ATP-binding protein	-16.86	0.00	0.00	NA	-16.88	0.00	NA	NA	-16.77	0.00
K17725	sulfur dioxygenase	NA	NA	16786.99	0.96	29.50	0.00	16.74	0.00	16.66	0.00
K19804	lipopolysaccharide assembly protein B	NA	NA	8374.36	0.00	NA	NA	16.68	0.00	16.60	0.00
K02188	cobalt-precorrin-5B (C1)-methyltransferase	-16.73	0.00	0.00	NA	-16.75	0.00	NA	NA	-16.65	0.00
K21417	acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit beta	-16.67	0.00	0.00	NA	-16.69	0.00	NA	NA	-16.58	0.00
K02454	general secretion pathway protein E	-16.66	0.00	0.00	NA	-16.69	0.00	NA	NA	-16.58	0.00
K12339	S-sulfo-L-cysteine synthase	-16.62	0.00	0.00	NA	-16.64	0.00	NA	NA	-16.53	0.00
K13628	iron-sulfur cluster assembly protein	NA	NA	7439.41	0.00	NA	NA	16.51	0.00	16.43	0.00
K01258	tripeptide aminopeptidase	NA	NA	24537.92	0.00	17.45	0.00	16.51	0.00	16.43	0.00
K06044	(1->4)-alpha-D-glucan 1-alpha-D-glucosylmutase	NA	NA	7324.14	0.00	NA	NA	16.48	0.00	16.41	0.00
K00705	4-alpha-glucanotransferase	NA	NA	7324.14	0.00	NA	NA	16.48	0.00	16.41	0.00
K07275	outer membrane protein	-16.56	0.00	15743.82	0.00	0.82	0.00	NA	NA	-16.47	0.00
K12538	outer membrane protein, type I secretion system	NA	NA	7027.92	0.00	NA	NA	16.43	0.00	16.35	0.00
K03590	cell division protein FtsA	-16.43	0.00	14745.38	0.00	0.85	0.00	NA	NA	-16.34	0.00
K01995	branched-chain amino acid transport system ATP-binding protein	NA	NA	6981.19	0.00	12.69	0.00	16.28	0.00	16.20	0.00
K01998	branched-chain amino acid transport system permease protein	NA	NA	6348.57	0.00	NA	NA	16.28	0.00	16.20	0.00
K00681	gamma-glutamyltranspeptidase / glutathione hydrolase	-16.36	0.00	0.00	NA	-16.38	0.00	NA	NA	-16.28	0.00
K01608	tartronate-semialdehyde synthase	NA	NA	14831.10	0.00	16.49	0.00	16.21	0.00	16.13	0.00
K02343	DNA polymerase III subunit gamma/tau	NA	NA	5900.70	0.00	NA	NA	16.17	0.00	16.09	0.00
K09065	N-acetylornithine carbamoyltransferase	-16.22	0.00	0.00	NA	-16.24	0.00	NA	NA	-16.13	0.00
K06869	uncharacterized protein	-0.26	0.02	0.00	NA	-16.21	0.00	-15.81	0.00	-16.11	0.00
K01782	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase	NA	NA	5484.48	0.00	NA	NA	16.07	0.00	15.99	0.00
K01280	tripeptidyl-peptidase II	0.31	0.00	0.00	NA	-16.17	0.00	-16.34	0.00	-16.06	0.00
K00677	UDP-N-acetylglucosamine acyltransferase	-16.15	0.00	0.00	NA	-16.17	0.00	NA	NA	-16.06	0.00
K01945	phosphoribosylamine---glycine ligase	-16.05	0.00	0.00	NA	-16.07	0.00	NA	NA	-15.97	0.00
K02674	type IV pilus assembly protein PilY1	NA	NA	5102.28	0.00	NA	NA	15.96	0.00	15.88	0.00
K00549	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	NA	NA	4868.90	0.00	NA	NA	15.90	0.00	15.82	0.00
K01126	glycerophosphoryl diester phosphodiesterase	NA	NA	7935.58	0.81	27.60	0.00	15.83	0.00	15.75	0.00
K04567	lysyl-tRNA synthetase, class II	NA	NA	4165.45	0.00	NA	NA	15.67	0.00	15.59	0.00
K02410	flagellar motor switch protein FliG	NA	NA	3716.16	0.00	NA	NA	15.51	0.00	15.43	0.00
K02990	small subunit ribosomal protein S6	NA	NA	3689.24	0.00	NA	NA	15.50	0.00	15.42	0.00
K01042	L-seryl-tRNA(Ser) seleniumtransferase	-15.53	0.00	0.00	NA	-15.55	0.00	NA	NA	-15.44	0.00
K00872	homoserine kinase	NA	NA	3364.67	0.00	NA	NA	15.36	0.00	15.28	0.00
K09949	UDP-2,3-diacylglucosamine hydrolase	-15.19	0.00	9606.68	0.00	1.48	0.00	NA	NA	-15.10	0.00
K04748	nitric oxide reductase NorQ protein	NA	NA	33243.22	0.00	NA	NA	18.66	0.00	18.57	0.00
K16898	ATP-dependent helicase/nuclease subunit A	-15.01	0.00	0.00	NA	-15.03	0.00	NA	NA	-14.92	0.00
K07646	two-component system, OmpR family, sensor histidine kinase KdpD	-14.95	0.00	0.00	NA	-14.97	0.00	NA	NA	-14.86	0.00
K02340	DNA polymerase III subunit delta	-14.87	0.00	0.00	NA	-14.89	0.00	NA	NA	-14.79	0.00
K04065	hyperosmotically inducible periplasmic protein	NA	NA	23685.26	0.46	17.10	0.00	16.95	0.00	16.89	0.00
K03565	regulatory protein	-14.83	0.00	0.00	NA	-14.85	0.00	NA	NA	-14.74	0.00
K03546	DNA repair protein SbcC/Rad50	4.37	0.00	0.00	NA	-14.83	0.00	-19.06	0.00	-14.73	0.00
K00055	aryl-alcohol dehydrogenase	NA	NA	1847.22	0.00	NA	NA	14.50	0.00	14.42	0.00
K01792	glucose-6-phosphate 1-epimerase	NA	NA	10186.99	0.00	16.44	0.00	14.35	0.00	14.27	0.00
K02304	precorrin-2 dehydrogenase	NA	NA	1452.73	0.00	NA	NA	14.15	0.00	14.07	0.00
K01736	chorismate synthase	NA	NA	1428.17	0.00	NA	NA	14.13	0.00	14.05	0.00
K00790	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	NA	NA	1099.35	0.00	NA	NA	13.75	0.00	13.67	0.00
K01962	acetyl-CoA carboxylase carboxyl transferase subunit alpha	NA	NA	1058.72	0.00	NA	NA	13.69	0.00	13.62	0.00
K02078	acyl carrier protein	NA	NA	898.57	0.00	NA	NA	13.46	0.00	13.38	0.00
K20920	polysaccharide biosynthesis protein VpsM	-16.99	0.00	101265.45	0.00	1.51	0.00	19.68	0.00	2.66	0.00
K10822	nonribosomal peptide-acid-transporting ATPase	NA	NA	22925.84	0.53	16.50	0.00	17.47	0.00	17.34	0.00
K08884	serine/threonine protein kinase, bacterial	14.98	0.00	28479.21	0.87	29.83	0.00	2.68	0.32	30.00	0.00
K03768	peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	-0.85	0.83	0.00	NA	-30.00	0.00	-16.44	0.00	-30.00	0.00
K02487	type IV pili sensor histidine kinase	NA	NA	19211.39	0.00	NA	NA	30.00	0.00	30.00	0.00
K01023	arylsulfate sulfotransferase	1.05	0.78	10211.07	0.00	0.28	0.96	-17.35	0.00	-29.96	0.00
K07337	penicillin-binding protein activator	NA	NA	12427.37	0.70	15.48	0.00	28.72	0.00	29.62	0.00
K22187	alpha-ketoglutaric semialdehyde dehydrogenase	NA	NA	8127.60	0.00	NA	NA	29.63	0.00	29.58	0.00
K07175	PhoH-like ATPase	NA	NA	19669.70	0.86	29.98	0.00	29.30	0.00	29.39	0.00
K02303	uroporphyrin-III C-methyltransferase	NA	NA	10044.38	0.00	NA	NA	29.12	0.00	29.10	0.00
K01622	fructose 1,6-bisphosphate aldolase/phosphatase	-29.14	0.00	0.00	NA	-29.14	0.00	NA	NA	-29.00	0.00
K08070	2-alkenal reductase	NA	NA	5242.07	0.00	NA	NA	28.93	0.00	28.90	0.00
K01991	polysaccharide biosynthesis/export protein	30.00	0.00	20858.76	0.76	29.18	0.00	-0.86	0.88	28.87	0.00
K06346	spoIIJ-associated protein	NA	NA	3706.15	0.00	NA	NA	28.59	0.00	28.55	0.00
K01586	diaminopimelate decarboxylase	19.16	0.00	18263.66	0.36	30.00	0.00	-4.70	0.04	27.58	0.00
K03518	aerobic carbon-monoxide dehydrogenase	NA	NA	1872.33	0.00	NA	NA	27.57	0.00	27.33	0.00
K01130	arylsulfatase	0.89	0.46	41346.12	0.89	-1.90	0.57	-2.34	0.01	-1.46	0.00
K07192	flotillin	-1.60	0.00	9069.14	0.00	-17.60	0.00	0.81	0.00	-0.83	0.00
K03657	ATP-dependent DNA helicase UvrD/PcrA	-15.01	0.00	4887.96	0.00	-1.25	0.00	15.46	0.00	0.42	0.00
K05520	deglycase	-17.25	0.00	16484.16	0.00	-17.27	0.00	17.65	0.00	0.37	0.01
K00020	3-hydroxyisobutyrate dehydrogenase	-0.44	0.22	58576.80	0.21	0.05	0.98	-0.65	0.51	-1.14	0.23
K11179	tRNA 2-thiouridine synthesizing protein E	1.46	0.00	118951.34	0.25	0.38	0.83	-2.51	0.00	-1.07	0.29
K00611	ornithine carbamoyltransferase	1.08	0.00	58814.32	0.00	1.94	0.00	-0.83	0.00	0.21	0.38
K18584	actin-related protein 3	0.42	0.92	151012.11	0.00	3.35	0.22	1.97	0.00	2.41	0.39
K02120	V/A-type H+/Na+-transporting ATPase subunit D	1.05	0.81	9252.41	0.78	-2.38	0.63	-4.22	0.10	-3.13	0.49
K02044	phosphonate transport system substrate-binding protein	1.77	0.15	27492.98	0.56	-0.74	0.56	-3.71	0.18	-1.94	0.51
K02878	large subunit ribosomal protein L16	-30.00	0.00	33859.99	0.66	-2.98	0.56	18.12	0.00	-1.92	0.59
K00335	NADH-quinone oxidoreductase subunit F	-0.58	0.89	45464.86	0.87	-0.79	0.83	0.42	0.91	-0.21	0.59
K00135	succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase	-16.94	0.00	3566.94	0.00	-16.96	0.00	28.26	0.00	-1.53	0.60
K05592	ATP-dependent RNA helicase DeaD	0.07	0.99	17162.37	0.26	1.75	0.73	-0.90	0.00	-0.81	0.79
K03684	ribonuclease D	0.70	0.54	345860.60	0.01	0.44	0.72	-0.45	0.00	0.27	0.82
K18933	tyrosine decarboxylase / aspartate 1-decarboxylase	-0.82	0.90	26015.43	0.58	-2.11	0.68	0.05	0.99	-0.73	0.84
K00027	malate dehydrogenase (oxaloacetate-decarboxylating)	2.26	0.46	45376.21	0.60	0.50	0.91	-2.85	0.30	-0.56	0.93
K11187	peroxiredoxin 5	-1.10	0.76	24813.51	0.88	-0.95	0.79	0.84	0.88	-0.35	0.93
K09860	outer membrane protein FlgP	-29.68	0.00	7794.08	0.01	-1.14	0.72	15.88	0.00	-0.30	0.94
K17285	methanethiol oxidase	-19.95	0.00	111921.66	0.59	-1.96	NA	30.00	0.00	0.09	0.98
K01302	carboxypeptidase Q	NA	NA	3072.53	0.00	14.97	0.00	NA	NA	NA	NA
K05962	two-component system, LuxR family, sensor histidine kinase TtrS	29.41	0.00	60213.02	0.00	30.00	0.00	-29.93	0.00	NA	NA
K01028	3-oxoacid CoA-transferase subunit A	NA	NA	7346.74	0.00	29.36	0.00	NA	NA	NA	NA
K03079	L-ribulose-5-phosphate 3-epimerase	19.08	0.00	0.00	NA	NA	NA	-19.01	0.00	NA	NA
K02474	UDP-N-acetyl-D-glucosamine/UDP-N-acetyl-D-galactosamine dehydrogenase	NA	NA	10538.29	0.00	16.75	0.00	NA	NA	NA	NA
K09691	homopolymeric O-antigen transport system ATP-binding protein	NA	NA	28609.65	0.00	18.19	0.00	NA	NA	NA	NA
K11891	type VI secretion system protein ImpL	NA	NA	1680.56	0.00	14.10	0.00	NA	NA	NA	NA
K01497	GTP cyclohydrolase II	NA	NA	16595.14	0.00	30.00	0.00	NA	NA	NA	NA
K0701	putative glutamine amidotransferase	15.75	0.00	0.00	NA	NA	NA	-15.67	0.00	NA	NA
K03044	DNA-directed RNA polymerase subunit B'	16.16	0.00	21672.07	0.00	17.79	0.00	-16.09	0.00	NA	NA
K00712	poly(glycerol-phosphate) alpha-glucosyltransferase	NA	NA	1325.14	0.00	13.76	0.00	NA	NA	NA	NA
K00184	dimethyl sulfoxide reductase iron-sulfur subunit	NA	NA	7009.85	0.00	16.16	0.00	NA	NA	NA	NA
K02851	UDP-GlcNAc:undecaprenyl-phosphate/decaprenyl-phosphate GlcNAc-1-phosphate transferase	NA	NA	8682.00	0.00	16.47	0.00	NA	NA	NA	NA

K01170	tRNA-intron endonuclease, archaea type	16.52	0.00	0.00	NA	NA	NA	-16.45	0.00	NA	NA
K01933	phosphoribosylformylglycinamidine cyclo-ligase	17.11	0.00	4005.13	0.00	15.35	0.00	-17.04	0.00	NA	NA
K05594	ElaB protein	NA	NA	57238.03	0.00	19.20	0.00	NA	NA	NA	NA
K01092	myo-inositol-1(or 4)-monophosphatase	NA	NA	1593.93	0.00	14.03	0.00	NA	NA	NA	NA
K08264	heterodisulfide reductase subunit D	18.00	0.00	0.00	NA	NA	NA	-17.93	0.00	NA	NA
K13924	two-component system, chemotaxis family, CheB/CheR fusion protein	17.78	0.00	0.00	NA	NA	NA	-17.71	0.00	NA	NA
K03615	H+/Na+-translocating ferredoxin:NAD+ oxidoreductase subunit C	-0.99	0.80	16346.23	0.51	-1.01	0.10	-0.48	0.90	-1.43	NA
K02837	peptide chain release factor 3	15.97	0.00	0.00	NA	NA	NA	-15.90	0.00	NA	NA
K01926	redox-sensing transcriptional repressor	30.00	0.00	25667.15	0.00	30.00	0.00	-30.00	0.00	NA	NA
K01417	extracellular elastinolytic metalloproteinase	NA	NA	976.66	0.00	13.32	0.00	NA	NA	NA	NA
K02316	DNA primase	NA	NA	11559.49	0.00	16.88	0.00	NA	NA	NA	NA
K13819	NifU-like protein	NA	NA	3750.70	0.00	15.26	0.00	NA	NA	NA	NA
K11076	putrescine transport system ATP-binding protein	NA	NA	8250.84	0.00	16.40	0.00	NA	NA	NA	NA
K00374	nitrate reductase gamma subunit	NA	NA	5179.79	0.00	15.73	0.00	NA	NA	NA	NA
K16887	quinone-modifying oxidoreductase, subunit QmoC	16.78	0.00	0.00	NA	NA	NA	-16.71	0.00	NA	NA
K00015	glyoxylate reductase	14.98	0.00	0.00	NA	NA	NA	-14.91	0.00	NA	NA
K14170	chorismate mutase / prephenate dehydratase	NA	NA	3403.20	0.00	15.12	0.00	NA	NA	NA	NA
K04518	prephenate dehydratase	NA	NA	3403.20	0.00	15.12	0.00	NA	NA	NA	NA
K00412	ubiquinol-cytochrome c reductase cytochrome b subunit	NA	NA	8454.79	0.00	16.43	0.00	NA	NA	NA	NA
K20976	histidine phosphotransfer protein HptB	NA	NA	0.00	NA	NA	NA	NA	NA	NA	NA
K06147	ATP-binding cassette, subfamily B	NA	NA	3162.13	0.00	15.01	0.00	NA	NA	NA	NA
K17758	ADP-dependent NAD(P)H-hydrate dehydratase	18.77	0.00	0.00	NA	NA	NA	-18.70	0.00	NA	NA
K17759	NAD(P)H-hydrate epimerase	18.77	0.00	0.00	NA	NA	NA	-18.70	0.00	NA	NA
K01733	threonine synthase	NA	NA	1529.32	NA	27.13	NA	NA	NA	NA	NA
K17836	beta-lactamase class A	NA	NA	2477.53	0.00	14.66	0.00	NA	NA	NA	NA
K00566	tRNA-uridine 2-sulfurtransferase	11.72	0.00	0.00	NA	NA	NA	-11.65	0.00	NA	NA
K03821	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC	17.65	0.00	0.00	NA	NA	NA	-17.57	0.00	NA	NA
K01638	malate synthase	15.58	0.00	0.00	NA	NA	NA	-15.51	0.00	NA	NA
K03703	excinuclease ABC subunit C	17.07	0.00	0.00	NA	NA	NA	-17.00	0.00	NA	NA
K03641	TolB protein	NA	NA	0.00	NA	NA	NA	NA	NA	NA	NA
K06886	hemoglobin	14.61	0.00	0.00	NA	NA	NA	-14.54	0.00	NA	NA
K07250	4-aminobutyrate aminotransferase / (S)-3-amino-2-methylpropionate transaminase / 5-aminov	29.26	0.00	0.00	NA	NA	NA	-30.00	0.00	NA	NA
K00823	4-aminobutyrate aminotransferase	29.26	0.00	0.00	NA	NA	NA	-30.00	0.00	NA	NA
K07214	iron(III)-enterobactin esterase	NA	NA	22315.58	0.00	17.83	0.00	NA	NA	NA	NA
K01159	crossover junction endodeoxyribonuclease RuvC	16.13	0.00	0.00	NA	NA	NA	-16.06	0.00	NA	NA
K00931	glutamate 5-kinase	NA	NA	111451.99	NA	30.00	NA	NA	NA	NA	NA
K07638	two-component system, OmpR family, osmolarity sensor histidine kinase	17.55	0.00	0.00	NA	NA	NA	-17.48	0.00	NA	NA
K18682	ribonucrease Y	NA	NA	0.00	NA	NA	NA	NA	NA	NA	NA
K16306	fructose-bisphosphate aldolase / 2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase	30.00	0.00	10148.71	0.00	16.70	0.00	-30.00	0.00	NA	NA
K01890	phenylalanyl-tRNA synthetase beta chain	NA	NA	10864.99	0.00	16.79	0.00	NA	NA	NA	NA
K01209	alpha-L-arabinofuranosidase	14.68	0.00	0.00	NA	NA	NA	-14.61	0.00	NA	NA
K07536	2-ketocyclohexanecarboxyl-CoA hydrolase	NA	NA	18367.87	0.00	17.55	0.00	NA	NA	NA	NA
K12257	SecD/SecF fusion protein	17.69	0.00	0.00	NA	NA	NA	-17.62	0.00	NA	NA
K04044	molecular chaperone HscA	NA	NA	1462.26	0.00	13.90	0.00	NA	NA	NA	NA
K00763	nicotinate phosphoribosyltransferase	21.39	0.00	0.00	NA	NA	NA	-21.32	0.00	NA	NA
K07482	transposase, IS30 family	14.35	0.00	0.00	NA	NA	NA	-14.28	0.00	NA	NA
K06959	protein Tex	15.44	0.00	0.00	NA	NA	NA	-15.37	0.00	NA	NA
K06200	carbon starvation protein	NA	NA	15355.24	0.00	17.29	0.00	NA	NA	NA	NA
K15256	tRNA (cmo5U34)-methyltransferase	NA	NA	14091.47	0.00	17.17	0.00	NA	NA	NA	NA
K14128	F420-non-reducing hydrogenase small subunit	NA	NA	13823.18	0.00	17.14	0.00	NA	NA	NA	NA
K00784	ribonuclease Z	NA	NA	7964.72	0.00	16.35	0.00	NA	NA	NA	NA
K06413	stage V sporulation protein K	NA	NA	5123.36	0.00	15.71	0.00	NA	NA	NA	NA
K02904	large subunit ribosomal protein L29	18.18	0.00	0.00	NA	NA	NA	-18.11	0.00	NA	NA
K10701	acetophenone carboxylase	16.04	0.00	0.00	NA	NA	NA	-15.97	0.00	NA	NA
K01473	N-methylhydantoinase A	16.04	0.00	0.00	NA	NA	NA	-15.97	0.00	NA	NA
K00343	NADH-quinone oxidoreductase subunit N	NA	NA	11856.50	0.00	16.92	0.00	NA	NA	NA	NA
K01744	aspartate ammonia-lyase	17.16	0.00	0.00	NA	NA	NA	-17.09	0.00	NA	NA
K02659	twitching motility protein PilI	NA	NA	9546.78	0.00	16.61	0.00	NA	NA	NA	NA
K05501	TetR/AcrR family transcriptional regulator	NA	NA	13371.23	0.00	17.09	0.00	NA	NA	NA	NA
K01692	enoyl-CoA hydratase	18.07	0.00	0.00	NA	NA	NA	-18.00	0.00	NA	NA
K05607	methylglutaconyl-CoA hydratase	18.07	0.00	0.00	NA	NA	NA	-18.00	0.00	NA	NA
K06865	ATPase	NA	NA	2369.12	0.00	14.60	0.00	NA	NA	NA	NA
K18332	NADP-reducing hydrogenase subunit HndD	NA	NA	5541.15	0.00	15.82	0.00	NA	NA	NA	NA
K07246	tartrate dehydrogenase/decarboxylase / D-malate dehydrogenase	18.97	0.00	0.00	NA	NA	NA	-18.90	0.00	NA	NA

NA, Not available

Supplementary Table 4. Comparison of stoichiometric fluxes and marker protein abundances using two-way ANOVA.

Modeling				Proteomics			
Reactions	Treatments			Maker proteins	Treatments		
	F (1,8) (*p*-value)				F (1,8) (*p*-value)		
	SO_4^{2-}	O_2	Interaction		SO_4^{2-}	O_2	Interaction
Aerobic Heterotroph	5.1	3633 (***)	5.1	Cytochrome c oxidase (ccoN)	72.8 (***)	141.9 (***)	72.8 (***)
Lactate Fermentation	113.7 (***)	34.8 (***)	44.1 (***)	L-lactate dehydrogenase (Ldh)	1.7	0.02	0.1
Hydrogenic acetogenesis	16.2 (**)	4545 (***)	24.5 (**)	Acetate kinase (Ack)	0.6	0.6	1.4
Sulfidogenic lactate oxidation	50.4 (***)	50.4 (***)	50.4 (***)	Sulfide reductase (Srd)	0.7	0.2	0.08
Sulfidogenic hydrogen oxidation	14784 (***)	14784 (***)	14784 (***)	Dissimilatory sulfite reductase (Dsr)	10.6 (**)	0.03	0
Hydrogenic Methanogenesis	1147 (***)	1064 (***)	1141 (***)	Ferredoxin oxidoreductase (Frt)	0.8	0.6	4.9
Acetoclastic Methanogenesis	1728 (***)	19020 (***)	1744 (***)	Phosphate acetyltransferase (Pta)	9.1 (*)	0.01	0.7
Methane oxidation	2.1	145.8 (***)	2.1	Methane/ammonia monooxygenase (Pmo)	5.2	17.9 (**)	1.7
Butyrate production	6.2	217.2 (***)	6.2	3-hydroxyisobutyrate dehydrogenase (HIBADH)	2	0	0

* for *padj* < 0.05, ** for *padj* < 0.01 and *** for *padj* < 0.001.