



Anaerobic C4-dicarboxylate transporter DcuB	0	0	0	0	0	0	0	0	0	0.214657	0	0.110198	0
Anaphase-promoting complex (APC), Cdc16 subunit	0	5.76781	2.74283	0	0	0	0	0	0	0	0	0	0
Anhydro-N-acetylmuramic acid kinase (EC 2.7.1.-)	314.004	0	165.8117	0	0	0	0	0	0	0	0	0	0.984643
Arabinan endo-1,5-alpha-L-arabinosidase A precursor (EC 3.2.1.99)	0.224626	0	0.117807	0	0	0	0	0	0	0	0	0	0
Archaeal DNA polymerase I (EC 2.7.7.7)	0	186.5248	88.8695	0	0	0	93.8248	23.1537	52.20475	0	0	0	0
Archaeal DNA polymerase II large subunit (EC 2.7.7.7)	0	0	0	0	0	0	618.456	0	303.202	0	0	0	0
Archaeal transcription factor E	0	63.7771	30.3121	0	0	0	0	0	0	0	0	0	0
Archaeosine tRNA-ribosyltransferase (EC 2.4.2.-) type 1 / archaeosine tRNA-ribosyltransferase (EC 2.4.2.-) P1	0	0	0	0	0	0	0	0	6.37487	3.28163	0	0	0
Arginine deiminase (EC 3.5.3.6)	0.278462	0	0.146042	0	0	0	0	0	0	0	0	0	0
Argininosuccinate synthase (EC 3.4.5.5)	0	49.655	23.7192	0	0	0	0	0	0	0	0	0	0
Aromatic hydrocarbon utilization transcriptional regulator CatR (LysR family)	0	15.293	7.20662	0	0	0	0	0	0	0	0	0	0
Arsenic resistance protein ArsH	0	37.5215	17.843	47.0642	0	27.3625	0	0	0	0	0	0	0
Arsenical pump-driving ATPase (EC 3.6.3.16)	0	0	0	39.9592	0	23.4061	0	0	0	0	0	0	0
Arsenical resistance operon trans-acting repressor ArsD	0	0	0	58.4566	0	33.9859	0	0	0	0	0	0	0
Arylimalonate decarboxylase	0	0	0	0	0	0	0	1.5427	0.78525	0	0	0	0
Asparagine synthase (EC 6.3.5.4)	0	0	0	0.531547	0.222513	0	0	0	0	0	0	0	0
Aspartate aminotransferase	0	0	0	0	0	0	15.3634	7.78844	0	0	0	0	0
Aspartate ammonia-lyase (EC 4.3.1.1)	0	546.866	259.741	0	0	0	0	0	0	0	0	0.976288	0
Aspartate carbanoyltransferase (EC 2.1.3.2)	0.87403	2.68942	2.644123	0	0	0	0	0	0	0	0	0	0
Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	0	67.403	31.2199	0	0	0	0	5.43757	2.7183	0	0	0.241903	0
Aspartokinase (EC 2.7.2.4)	0	103.9696	49.159	0	0	0	0	64.1796	32.8704	0	0	0.806974	0
Aspartyl-tRNA synthetase (EC 6.1.1.12)	0	0	0	0	0	0	846.743	4.84292	420.96384	0	0	0	0
Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.6)	5.91803	0	3.10376	0	0	0	0	0	0	0	0	0.559243	0
ASPIC/Urbv domain-containing protein	0	0	0	0	0	0	0	0	1.15206	0	0.591429	0	0
ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17)	1418.87	0	735.279	0	0	0	0	0	0	0	0	0.382279	0
ATP synthase epsilon chain (EC 3.6.3.14)	0	0	0	0	0	0	0	175.980424	89.980633	0	0	0	0
ATP synthase F0 sector subunit a	0	0	0	0	0	0	0	0	0	38.5595	0	20.3402	0
ATP synthase F0 sector subunit b	0	0	0	0	0	0	0	0	0	1277.507	0	639.578	0
ATP synthase F0 sector subunit c	0	0	0	14.6746	6.14301	0	0	0	0	0	0	0	0
ATP-binding protein p271	0.190361	0	0.0998364	0	0	0	0	0	0	0	0	0	0
ATP-binding region, ATPase-like	0	0	0	0	0	0	6.46197	3.2892	0	0	0	0	0
ATP-dependent Clp protease ATP-binding subunit ClpA	2161.779	37.7572	1056.614738	0	0	0	0	0	0	0	0	293.003784	0
ATP-dependent Clp protease ATP-binding subunit ClpC	0	41.427659	19.855402	50.5776	30.4241	0	284.90693	145.14963	0	0	0	0	0
ATP-dependent DNA helicase	0.3623	0	0.190011	0	0	0	0	0	0	0	0	0	0
ATP-dependent DNA helicase RecQ	55.9459	0	29.4149	0	0	0	0	0	0	83.069278	39.272929	0.956048	0
ATP-dependent DNA helicase SCS0183	0.185641	0	0.0973611	0	0	0	0	0	0	0	1.75433	0.96834	0
ATP-dependent DNA helicase UvrD/PcrA, actinomycete paralog	0.208954	0	0.109588	0	0	0	0	0	0	0	0	0	0
ATP-dependent DNA ligase (EC 6.5.1.1)	0	0	0	0	0	0.370991	0	0.182124	0	0	0	0	0
ATP-dependent DNA ligase I	0	0.212646	0.101122	0	0	0	0	0	0	0	0	0	0
ATP-dependent helicase	0	0	0	0	0	0	12.77586	6.50303	0	0	0	0	0
ATP-dependent helicase hrpA	0	0	0	0	0	0	16.4176	8.3567	0	0	0	0	0
ATP-dependent hsl protease ATP-binding subunit HslU	0	67.587	322.368	0	0	0	0	0	0	0	0	1.00632	0
ATP-dependent protease La (EC 3.4.2.153) Type I	0	127.028604	64.929277	0	0	0	0	0	15.5154	0	7.7932	1.099142	0
ATP-dependent protease La (EC 3.4.2.153) Type II	0	0	0	0	0	0	0	61.1312	41.9377	0	0	0	0
ATP-dependent RNA helicase	0	0	0	0	0	0	0	1373.6481	873.8974	0	0	1089.87	0
ATP-dependent RNA helicase A	0	0	0	0	0	0	0	14.0785	6.99584	0	0	0	0
ATP-dependent RNA helicase, DEAD box family	0	0	0	0	0	0	0	0	0	7.37814	0	3.78769	0
ATP-dependent RNA helicase, eIF-4A family	0	0	0	0	0	57.9112	0	29.1944	0	0	0	0	0
ATP/GTP-binding protein	0	0	0	0	0	0	0	0	0	0.262844	0.127908	0	0
ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3	0	0	21.9959	0	12.6897	0	0	0	0	0	0	0	0
ATPase component of general energizing module of ECF transporters	0	0	0	0	0	0	0	0	0	246.96	2.19271	0	0
ATPase involved in DNA repair	0	0	0	0	0	56.265	0	27.5743	0	0	0	0	0
ATPase type IV secretion complex and secretion of T-DNA complex (VirB11)	0	0	0.400138	0.232635	0	0	0	0	0	0	0	0	0
ATPase YjeE	0.228047	0	0.119601	0	0	0	0	0	0	0	0	0	0
Autotransporter adhesin	0	0	0	0	0	0.866696	0.575422	0	0	0	0	0	0
Auxin-responsive GH3 protein homolog, putative	0	0	0	0	0	0	345.724	0	170.568	0	0	0	0
B12 binding domain of Methylmalonyl-CoA mutase (EC 5.4.99.2)	0	20.9318	15.9188	0	0	0	0	0	0	0	0	0	0
Bacillopeptidase F	162.187	0	0	0	0	0	0	0	0	0	0	0	0
Bacillosamine/Legionaminic acid biosynthesis aminotransferase PglE; 4-keto-6-deoxy-N-Acetyl-D-hexosamin	0	0	0	0	0	0	22.3221	11.4865	0	0	0	0	0
Bacterial proteasome-activating AAA-ATPase (PAN)	0	0	0	0	0	0	0	0	0.350277	0	0.179821	0	0
Bacterioferritin	297.261	93.9246	203.1818	0	0	0	0	0	0	0	0	0.353703	0
Barstar, RNase (barnase) inhibitor	0	0	0	96.3939	0	56.0681	0	0	0	0	0	0	0
Beta-N-acetyl-glucosaminidase (EC 3.2.1.52)	3539.55	0	1974.473	0	0	0	0	0	0	0	0	0	0
Beta-adrenergic receptor kinase 1 (EC 2.7.11.15)	0	0	0	10033.5	0	0	0	0	0	943.903	2097.56	0	0
Beta-carotene ketolase (EC 1.14.-.-)	0	0	0	0	0	0	0	2.056767	1.031764	0	0	0	0
Beta-galactosidase (EC 3.2.1.23)	0	0	0	0	0	0	4.22643	76.4276	40.97579	1.95552	0.951619	0	0
Beta-glucanase precursor (EC 3.2.1.73)	0	0	0.198309	0.115294	0	0	0	0	0	0	0	0	0
Beta-glucoside ABC transport system, sugar-binding protein	0	0	0	0	1427.45	0	708.129	0	0	0	0	0	0
Beta-hexosaminidase (EC 3.2.1.52)	0	63.4776	0	0	0	0	0	0	0	0	0	0	0
Beta-hexosaminidase precursor	0	0	0	0	0	0	0	0	0	43.8178	0	22.4745	0
Beta-lactamase (EC 3.5.2.6)	0	0	322.7954	187.5779	302.831	153.0783	0	0	0	0	0.733281	0	0
Beta-ureidopropionase (EC 3.5.1.6)	0	0	2.96507	3.47068	0	0	0	0	0	0	0	0.626983	0
BH2577 unknown conserved protein	0	0	0	0	0	0	0	12.2016	6.26388	0	0	0	0
Bifunctional autolysin Aht / N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) / endo-beta-N-acetylglucosam	0	0	0	0	0	0	0	421.708	258.2133	0	0	0	0
Biotin PGA outer membrane secretin PglA	7.62646	3.6267	0	0	0	0	0	0	0	0	0	0	0
Biosynthetic arginine decarboxylase (EC 4.1.1.19)	0	0	0	0	0	0	0	0	0	0.285811	0.139085	0	0
Biotin synthesis protein BiotC	9.32506	0	4.89061	0	0	0	0	0	0	0	0	0	0
Biotin-protein ligase (EC 6.3.4.9, EC 6.3.4.10, EC 6.3.4.11, EC 6.3.4.15)	0	0	0	0	0	18.68459	9.28867	0	0	0	0	0	0
Bipolar DNA helicase HerA	0	0	0	0	0	460.903	253.178	0	0	0	0	0	0
Bir3456, hypothetical protein	0	0	0	0	0	15.34	8.28432	0	0	0	0	0	0
Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1)	1165.31	0	616.344	0	0	621.674	304.796	0	0	0	0	5.345865	0
Branched-chain amino acid transport system carrier protein	8.36982	0	4.38962	0	0	0	0	0	0	0	0	0	0
C4-dicarboxylate transport sensor protein	211.2211	0	46.7902	0	0	0	0	0	0	0	0	0	0
Calmodulin-binding protein CRAG, contains DENN domain	61.9657	0	33.1626	0	0	0	0	0	0	0	0	0	0
cAMP-binding proteins - catapalt gene activator and regulatory subunit of cAMP-dependent protein kinas	0	0	0	0	0	0	0	56.9802	29.0035	0	0.347699	0.169202	0
Carbamate kinase (EC 2.7.2.2)	0	0	0	0	0	0	0	6.11056	3.26342	0	0	0	0
Carbon monoxide dehydrogenase CooS subunit (EC 1.2.99.2)	0	0	0	0	0	0	0.231783	0.17198	0	0	0	0	0
Carbon-nitrogen hydrolase	0	0	0	0	0	0	0	0	0	0	0	0	0
Carbonic anhydrase (EC 4.2.1.1)	0.262209	0	0.137518	0	0	0	0	0	0	0	0	0	0
Carboxy-terminal processing protease	0	0	16.31899	9.48765	0	0	0	0	0	0	0	0	0
Card-like transcriptional regulator	0	0	0	0	0	0	0	0	830.474	0	425.895	0	0
Cardiolipin synthase (EC 2.7.8.-)	0	0	499.677	299.56	0	0	0	0	0	0	0	0.673123	0
Cartilage oligomeric matrix protein	0	248.2424	117.9314	0	0	0	0	0	0	0	0	0	0
Catalase (EC 1.11.1.6)	0	30.9961	14.5709	0	0	0	0	0	0	0	0	2.339523	0
Catechol 1,2-dioxygenase (EC 1.13.11.1)	0	0	0	5.48466	2.29595	0	0	0	0	0	0	0	0
Cation transport ATPase	0	0	0	0	0	0	0	0	0.270926	0	0.139085	0	0
Cation-transporting ATPase, E1-E2 family	0	0	0	0	0	0	0	56.6446	0	0	29.0795	0	0
CBS domain protein	0	0	0	9.39751	3.93392	0	0	0	0	0	0	0.529884	0
CBS domain protein	0	0	0	0	0	0	0	32.788	0	0	0	0	0
CcxA-related protein	53.2671	0	28.163	0	0	0	0	0	0	0	0	0.161269	0
CDP-6-deoxy-delta-3,4-glucose reductase-like	0	0	377.868	0	0	0	0	0	0	0	0	0.445011	0
Cell division control protein CDC48 homolog	0	0	0.262962	0	0	0	0	0	0	0	0	0	0
Cell division inhibitor related protein	0	0	0	0	1.25452	0	0.615959	0	0	0	0	0	0
Cell division protein FtsI (EC 2.4.1.129)	219.7134	0	114.9104	0	0	1.44209	0.734038	14.6222	96.67653	55.013189	0.472105	0	0
Cell division protein FtsJ / Ribosomal RNA large subunit methyltransferase E (EC 2.1.1.-)	0	7.93754											



Eukaryotic translation initiation factor 3 subunit 10, putative	0	0	0	0	0	0	0	228.32	309.17	0	0	0	0	0
Excinuclease ABC subunit A paralog of unknown function	0	0	0	0	0	0	0	0	75.6521	0	0	0	0	0
Exodeoxyribonuclease III (EC 3.1.11.2)	1488.156	0	812.33	0	0	0	0	0	0	0	0	0	0	0.306306
Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)	0	1.56418	0.743832	0	0	0	0	0	0	0	0	0	0	0
Exonuclease SbcD	0	0	0	0	942.588	395.428	0	33.6111	17.2013	0	0	0	0	0
Exported zinc metalloprotease YfgC precursor	0	101.4962	48.6942	0	0	0	0	0	0	0	0	0	0	1.143881
Extensin-like protein	0.187971	0	0.0985832	0	0	0	0	0	0	0	0	0	0	0
Extracellular deoxyribonuclease PA3909 (required for catabolism of external DNA)	0	5.27695	2.08867	0	0	0	0	0	0	0	0	0	0	0
Extracellular Matrix protein PeIA	0	700.935	339.54	0	0	0	0	0	0	0	0	0	0	2.431971
extracellular solute-binding protein, family 3	0	0	0	0	0	0	0	79.9303	42.5584	0	0	0	0	0
extracellular solute-binding protein, family 5	0	1969.93	933.49	0	0	0	0	718.588	389.209	0	0	0	0	0
FAD dependent oxidoreductase	0	0	0	0	0	0	26.0888	0	12.8094	0	0	0	0	0
FAD linked oxidase domain protein	0	0	0	0	0	0	0	62.3263	31.7247	0	0	0	0	0
Fap amyloid fiber secretin	0.297518	0	0.156036	0	0	0	0	0	0	0	0	0	0	0
Fe-S oxidoreductase	0	0	0	0	0	0	0	1068.26158	542.66259	0	0	0	0	0
Fe-S oxidoreductase	0	0	0	0	0	0	0	43.351	22.1436	0	0	0	0	0
Fe-S cluster-containing hydrogenase components 2	0	0	0	0	0	0	0	106.588	52.2922	0	0	0	0	0
Ferredoxin	0	36.1667	16.7265	0	0	0	0	0	25.2663	0	0	0	0	0.21134
Ferredoxin / Ferredoxin-NADP(+) reductase, actinobacterial (eukaryote-like) type (EC 1.18.1.2)	0	0	0	0	0	0	0	0	0	277.233	128.428	0	0	0
Ferric iron ABC transporter, iron-binding protein	0	51.1962	24.346	0	0	0	0	0	0	0	0	0	0	0.704504
Ferric uptake regulation protein FUR	0	0	0	0	112.513	47.463	0	35.0438	17.0051	0	0	0	0	1.232019
Ferrichrome-iron receptor	963.909	0	506.362	1047.1548	0	0	0	622.26547	0	0	0	0	0	4.953707
Fibrillarin	0	13.3713	6.21074	0	0	0	0	0	0	0	0	0	0	0
Fibronectin type III domain protein	299.33	904.296	587.556	0	0	0	0	222.94773	114.11502	0	0	0	0	0
Flagellar biosynthesis protein FlIC	0	0	0	0	0	0	1.3645	0	0.669955	0	0	0	0	0
Flagellar hook-basal body complex protein FlIE	165.752	0	87.1201	0	0	0	0	0	0	0	0	0	0	1.93367
Flagellar motor protein	0	0	0	0	0	0	0	62.5277	31.8754	0	0	0	0	0
Flagellin FlaB1	0	0	0	0	0	0	0	501.39723	251.56083	0	0	0	0	0
Flagellum-specific ATP synthase FlII	0	0	0	544.741	0	332.527	0	6.22048	3.16629	0	0	0	0	0.843103
Flap structure-specific endonuclease (EC 3....-)	0	430.468	368.714	0	0	0	0	0	0	0	0	0	0	0
Flavodoxin reductases (ferredoxin-NADPH reductases) family 1	263.99	0	0	0	0	0	0	0	0	0	0	0	0	0.601019
Fmu (Sun) /eukaryotic nucleolar NOL1/Nop2p; tRNA and rRNA cytosine-C5-methylases	0	22.1189	13.5711	0	0	0	0	0	0	0	0	0	0	1.18779
Formaldehyde activating enzyme / D-arabino-3-hexulose 6-phosphate formaldehyde-lyase (EC 4.1.2.43)	0	0	0	0	0	0	0	0.470219	0.239346	0	0	0	0	0
Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)	0.174806	0	0.0916785	151.4319	0	89.2001	0	0	0	0	0	0	0	0.74894
Formate dehydrogenase chain D (EC 1.2.1.2)	0	0	0	3.0833	0	1.62965	0	0	0	0	0	0	0	0.295976
Formate dehydrogenase O alpha subunit (EC 1.2.1.2) @ selenocysteine-containing	19.4229	0	10.1325	0	0	0	0	51.3885	26.2527	0	0	0	0	0
Formate dehydrogenase O beta subunit (EC 1.2.1.2)	0	0	0	0	0	0	0	246.198	124.304	0	0	0	0	0
Formate efflux transporter (TC 2.A.44 family)	0	0	0	148.764	0	96.612	0	0	0	0	0	0	0	0
Formate-tetrahydrofolate ligase (EC 6.3.4.3)	0	0	0	0	0	0	0	971.884	503.982	0	0	0	0	0
Formiminotetrahydrofolate cyclodeaminase (EC 4.3.1.4)	0	0	0	315.602	0	167.519	0	0	0	0	0	0	0	0
Formylmethanofuran dehydrogenase (tungsten) operon gene F (polyferredoxin)	0	6.93195	3.08027	0	0	0	0	0	0	0	0	0	0	0
Fosmidomycin resistance protein	0	0	0	11.3546	6.92715	0	0	0	0	0	0	0	0	0.344201
Fructokinase (EC 2.7.1.4)	0	0	0.286461	0	0	0	0	0	0	558.024	0	0	298.615	0
Fructosamine kinase family protein, At3g51080 homolog	0	0	0	0	0	0	0	112.42	57.9529	0	0	0	0	0
Fructosamine-3-kinase (EC 2.7.1.-)	0	0	0	0	0	0	0	109.591	55.9015	0	0	0	0	0
Fructose-1,6-bisphosphatase, Bacillus type (EC 3.1.3.11)	0	0	0	0	0	0	0	22.8855	11.6505	0	0	0	0	0
Fructose-1,6-bisphosphatase, type V, archaeal (EC 3.1.3.11)	0	0	0	0	0	0	632.165	0	136.06	0	0	0	0	0
Fructose-bisphosphate aldolase class II (EC 4.1.2.13)	0	303.866	144.8924	0	0	0	0	0	0	111.91266	0.231799	57.673991	0.619044	0
Fumarate reductase, flavoprotein subunit precursor (EC 1.3.99.1)	0	0	0	0	0	0	4.67949	0	2.29758	0	0	0	0	0
Fusobacterium membrane protein	0	0	0	0	0	0	0	17.32111	7.5035	0	0	0	0	0
Gag/pol polyprotein	0	0	0	0	0	0	0	0	13.4397	6.89952	0	0	0	0
Galactitol utilization operon repressor	0	0	0	0	0	0	0	0	131.358	0	0	67.4351	0	0
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	0	0	0	0	0	0	0	186.972	97.0636	0	0	0	0	0
Galactose/methyl galactoside ABC transport system, permease protein MglC (TC 3.A.1.2.3)	0	47.3463	21.2791	0	0	0	0	0	0	0	0	0	0	0
Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	0	0	0	189.7955	0	199.118	0	0	0	0	0	0	0	0.951294
Gamma-glutamyl-GABA hydrolase (EC 3.5.1.94)	0.197908	0	0.103795	0	0	0	0	0	0	0	0	0	0	0
Gamma-glutamyl-putrescine synthetase (EC 6.3.1.11)	442.576	0	233.113	0	0	0	0	0	0	0	0	0	0	0
GDP-mannose 4,6 dehydratase (EC 4.2.1.47)	0	198.832	96.3596	0	0	0	0	0	0	0	0	0	0	0
General secretion pathway protein A	0	0	0	0	0	0	0	8.63963	4.39766	0	0	0	0	0
General secretion pathway protein F	0	28.3479	13.4806	0	0	0	0	0	0	0	0	0	0	0.147641
Geranyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.5)	0	0	0	0	0	0	0	0	0	0.428716	0.208627	0	0	0
Geranylgeranyl diphosphate synthase (EC 2.5.1.29)	0	0	0	38.7168	16.5082	0	0	0	0	0	0	0	0	0
Geranylgeranyl pyrophosphate synthase	0	0	0	41.3796	16.1897	0	0	0	0	0	0	0	0	0
Geranylgeranyl pyrophosphate synthetase (EC 2.5.1.29)	0	0	0	0	0	0	0	0	0	113.9523	0	58.5308	0	0
Gfa-like protein	0.183368	0	0.0961689	0	0	0	0	0	0	0	0	0	0	0
GGDEF domain/EAL domain protein	0	0	0.246458	0	0	0	0	0	0	0	0	0	0	0
Gil423 protein	0	0	0	0	0	0	0	567.008	288.368	0	0	0	0	0
Glucanase permease	0.224626	0	0.117807	0	0	0	0	0	0	0	0	0	0	0
Glucanate utilization system GntI transcriptional repressor	1.26666	0	0.664325	0	0	0	0	0	0	0	0	0	0	0
Glucanokinase (EC 2.7.1.12)	0	450.193	218.81	0	0	0	0	225.59	95.2343	0	0	0	0	0.238238
Glucose 1-dehydrogenase (EC 1.1.1.47)	0	0	0	0	0	0	0	51.6719	26.3015	0	0	0	0	0
Glucose ABC transport system, inner membrane component 1	0.395816	0	0.207589	0	0	0	0	0	0	0	0	0	0	0
Glucose dehydrogenase, PQQ-dependent (EC 1.1.5.2)	0.206079	0	0.16212	0	0	0	0	0	0	0	0	0	0	0
Glutamate Aspartate periplasmic binding protein precursor GltI (TC 3.A.1.3.4)	445.319	0	229.826	0	0	0	0	0	0	83.2203	41.9754	5.414724	0	0
Glutamate-cysteine ligase (EC 6.3.2.2), divergent, of Alpha- and beta-proteobacteria type	0	12.196	5.395666	0	0	0	0	0	0	0	0	0	0	1.192844
Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)	6.36223	7.97158	10.4518	0	0	0	0	0	0	0	0	0	0	0
Glutamate-aspartate carrier protein	0.221306	0	0.116066	0	0	0	0	0	0	0	0	0	0	0
Glutamine synthetase type I (EC 6.3.1.2)	9.6878	0	6.45739	0	0	0	0	0	0	6.24512	0	3.20604	1.358951	0
Glutamine-dependent 2-keto-4-methylthiobutyrate transaminase	0	0	0	0	0	0	77.7862	0	38.1923	0	0	0	0	0
Glutamyl-tRNA reductase (EC 1.2.1.70)	0	0	0	3428.99	0	1992.52	0.345755	0	0.169762	0	0	0	69.744852	0
Glutamyl-tRNA synthetase (EC 6.1.1.17)	0	0	0	0	0	0	56.0609	28.5356	167.951	0	0	88.5251	0	0
Glutamyl-tRNA(Gln) amidotransferase asparaginase subunit (EC 6.3.5.7)	0	54.7857	26.0407	0	0	0	0	3.93809	2.00452	0	0	0	0	0
Glutamyl-tRNA(Gln) synthetase (EC 6.1.1.24)	0	0	0	0	0	0	0	0	0	13.9527	0	7.16286	0	0
Glutathione reductase (EC 1.8.1.7)	10.1226	0	5.3089	0	0	0	0	0	0	0	0	0	0	0.985397
Glutathione S-transferase family protein	399.89167	0	211.47841	0	0	0	0	0	0	0	0	0	0	0.75745
Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)-like	0	0	0	0	0	0	0	14.4913	7.37619	0	0	0	0	0
Glutathione synthetase (EC 6.3.2.3)	47.5232	0	24.9658	0	0	0	0	0	0	0	0	0	0	1.051857
Glycerate kinase (EC 2.7.1.31)	0	0	0	2.99629	0	1.5618	0	0	0	0	0	0	0	0
Glycerol kinase (EC 2.7.1.30)	0	280.8472	383.9734	0	0	0	605.64656	0	297.24811	0	0	0	0	0.47432
Glycerol-1-phosphate dehydrogenase (EC 1.1.1.261)	0	0	0	0	0	0	0	29.3015	15.376	0	0	0	0	0
Glycerol-3-phosphate ABC transporter, permease protein UgpA (TC 3.A.1.1.3)	155.0456	0	102.7277	212.918	0	126.5161	0	0	0	0	0	0	0	2.443186
Glycerol-3-phosphate acyltransferase (EC 2.3.1.15)	0.179701	0	0.0942455	0	0	0	0	0	0	0	0	0	0	0
Glycerol-3-phosphate regulon repressor, DeoR family	0	0	0	1.92446	0	0	1.11885	0	0	0	0	0	0	0.146267
Glycine cleavage system H protein	0	1302.22	622.969	0	0	0	0	0	0	0	0	0	0	0.579295
Glycine cleavage system transcriptional activator	41.4885	787.76	513.947	0	0	0	0	268.4	140.664	0	0	0	0	1.856575
Glycine dehydrogenase (glycine cleavage system P1 protein) (EC 1.4.4.2)	0.327125	0	0.171563	0	0	0	0	125.57	62.9237	0	0	0	0	0
Glycine dehydrogenase (glycine cleavage system P2 protein) (EC 1.4.4.2)	0	1507.55	767.472	0	0	0	0	0	0	0	0	0	0	0
Glycine-rich cell wall structural protein precursor	0	0	0											

Histidine kinase of the competence regulon ComD	0	0	0	0	0	0	0	0	730.711	0	0	376.778	0
Histidinol-phosphate aminotransferase (EC 2.6.1.9)	1114.2646	0	599.344807	0	0	0	0	3.56015	1.812146	0	0	0	0.688951
Histidinol-phosphate aminotransferase (EC 2.6.1.9)	0	0	0	656.398	0	0	0	0	0	0	0	0	1.389317
Histone acetyltransferase HPA2 and related acetyltransferases	0	0	0	0	64.4946	0	0	0	0	0	0	0	5.423561
Hnr protein	0	0	0	0	2.56391	0	0	0	0	0	0	0	0
HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-)	11886.37	0	6267.86	0	0	0	0	0	0	0	14.7192	0	0.83338
HTH DNA-binding protein	0	57.7926	30.0045	0	0	0	0	0	0	0	0	0	0
HtrA protease/chaperone protein	0	0	0	16.5058	0	0	9.59625	3.2165	0	1.525594	0	0	2.830939
Hydantoin racemase (EC 5.1.99.-)	0	0	0	0	0	0	0	382.525	0	187.216	0	0	0
Hydrogenase metallocenter assembly protein HvpF	0	0	0	0	0	0	0	3.29028	0	1.615495	0	0	0
Hydrolase (HAD superfamily)	0	0	0	0	0	0	0	0	29.2994	14.91367	0	0	0
Hydrolase, alpha/beta fold family	476.625	0	249.9408	0	0	0	0	0	0	0	0	0	0.198032
Hydrolase, CoCε/NonD family	0	0	0	0	0	0	0	20.8388	11.6451	0	0	0	0
Hydrolase, HAD subfamily IIIA	0	0	0	0	0	0	0	0	0	3.81864	0	0	2.03576
Hydrolase, UxaA family	0	0	0	0	0	0	0	118.4272	60.6026	0	0	0	0
Hydroxybenzoyl-CoA reductase subunit #1 FIG predicted	0	0	0	0	0	0	0	0	0	2.92957	0	0	0
Hydroxylamine oxidoreductase (Fragment)	0	0	0	0	0	0	0	85.3209	42.749	0	0	0	0
Hydroxylamine reductase (EC 1.7.-.-)	0	0	0	0	0	0	0	0	0	0.475661	0	0	0.244189
Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)	275.0808	0	143.7304	0	0	0	0	0	0	0	0	0	0.458679
Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34)	0	0	0	0	0	0	0	0	0	1911.548	0	0	2153.06
Hydroxymethylpyrimidine ABC transporter, transmembrane component	0	0	0	118.407	0	0	65.8723	0	0	0	0	0	0
Hydroxymethylpyrimidine phosphate synthase THC (EC 4.1.99.17)	0	41.6809	20.5222	0	0	0	0	0	0	0	0	0	0.275855
Hypothetical ATP-binding protein UPF00042, contains P-loop	199.985	0	104.649	0	0	0	0	0	0	0	0	0	0.167052
Hypothetical lipoprotein	0	0	0	0	0	0	0	3.87313	1.971458	0	0	0	0
Hypothetical lipoprotein yghG precursor	0.359401	0	0.188491	0	0	0	0	0	0	0	0	0	0
Hypothetical membrane spanning protein	0	0	0	0	0	0	0	1.9499	0.957384	0	0	0	0
Hypothetical mobile element-associated protein	0	0	0	0	0	0	0	0	0	1.72357	0	0	0.884824
Hypothetical nudix hydrolase YezB	0	27.9233	13.2787	0	0	0	0	0	0	0	0	0	0
Hypothetical oxidoreductase YqhD (EC 1.1.-.-)	0	1.8007	0.856306	0	0	0	0	0	0	0	0	0	0.667184
Hypothetical phage protein	0	0	0	82.0145	0	0	47.6821	0	0	0	0	0	0
Hypothetical protein SAV252	0	0	0	0	0	0	0	31.9994	16.288	0	0	0	0
hypothetical protein sometimes fused to ribosomal protein S6 glutaminyl transferase / Ribosomal protein S1	0	0	0	0	0	0	0	0.302573	0.154013	0	0	0	0
Hypothetical protein UPF0052	271.941	0	142.662	0	0	0	0	0	0	318.58	0	0	0
Hypothetical protein YbgA	0	0	0	0	0	0	0	322.815	165.838	0	0	0	0
Hypothetical protein YbgI	277.254	0	145.6242	0	0	0	0	0	0	0	0	0	1.009579
Hypothetical protein-transmembrane prediction	0	0	0	0	0	0	0	0	0	422.148	0	0	215.544
Hypothetical protein-transmembrane region and signal peptide prediction	0	0	0	0	0	0	0	16.0705	8.18004	0	0	0	0
Hypothetical protein, putative ABC transporter associated permease	0	0	0	0	0	0	0	30.0345	15.2614	0	0	0	0
Hypothetical protein, putative ABC transporter associated permease	0	0	0	0	0	0	0	318.58	413.706	0	0	0	0
Hypothetical protein; FIG008059	0	0	0	0	0	0	0	14.7718	7.67403	0	0	0	0
Hypothetical protein; FIG002842	0	0	0	23.6368	0	0	13.7421	0	0	0	0	0	0.328786
Hypothetical protein; FIG003307	0	0	0	0	0	0	0	736.028	376.007	0	0	0	0
Hypothetical protein; FIG00347935	0	11.4338	5.5667	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00348156	0	0	0	1046.75	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00350121	16.2811	0	8.53388	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00350294	118.431	0	42.7471	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00350342	0	281.313	133.7759	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00351164	2.36448	0	1.24007	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00351471	0	0	0.841478	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00431079	0	0	0	0	0	0	0	46.1118	24.1315	0	0	0	0
Hypothetical protein; FIG00441227	1388.885	0	333.121	0	0	2980.56	1288.98	0	0	0	0	0	0.141655
Hypothetical protein; FIG00452163	0	0	0	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00452747	0	0	0	0	0	0	0	0	0	79.8705	0	0	41.0633
Hypothetical protein; FIG00465763	0	0	0	0	0	0	0	0	0	0	972.139	0	473.051
Hypothetical protein; FIG00481472	0	0	0	0	0	0	0	0	0	0	13.28968	0	6.46719
Hypothetical protein; FIG00512995	0	0	0	0	0	0	0	0.203049	0	0	0	0	0
Hypothetical protein; FIG00520126	1.03873	0	0.544772	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00521049	0	511.873	229.687	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00530012	0	5.2709	2.50653	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00536986	87.9139	0	46.1362	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00537682	17.99187	0	9.43599	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG005429	0.165166	0	0.088627	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00544776	2.13661	0	1.03644	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00545606	0	0	0	0	0	0	0	0	0	0.214657	0	0	0.110198
Hypothetical protein; FIG00547247	0	0	0	0	0	0	0	0	0	6.4089	0	0	3.29012
Hypothetical protein; FIG00577025	0	0	0	0	0	0	0	17.0331	8.67001	0	0	0	0
Hypothetical protein; FIG00577033	0	0	0	0	0	0	0	40.3166	11.8153	0	0	0	0
Hypothetical protein; FIG00577375	0	46.3151	23.4333	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00581088	0	0	0	0	0	0	1.87078	0.952221	0	0	0	0	0
Hypothetical protein; FIG00581358	0	0	0	0	0	0	0	0	0	0.221342	0	0	0.107712
Hypothetical protein; FIG00581518	0	0	0	0	0	0	146.6979	0	71.6316	0	0	0	0
Hypothetical protein; FIG00581832	0	2.6903	1.57254	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00582348	0	0	0	0	0	0	0	1106.016	567.491	0	0	0	0
Hypothetical protein; FIG00582897	4.80148	0	2.58387	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00585670	0	0	0	0	0	0	0	0	0	0	0	0	2.07954
Hypothetical protein; FIG00607773	0	0	0	0	0	0	4.25662	2.166661	0	0	0	0	0
Hypothetical protein; FIG00627631	0	0	0	0	0	0	0	0	0	1020.103	0	0	490.226
Hypothetical protein; FIG00637996	0	0	0	0	0	0	0	0	0	0.262844	0	0	0.127908
Hypothetical protein; FIG00638088	0	0	0	0.46998	0	0.19674	0	0	0	0	0	0	0
Hypothetical protein; FIG00638504	0	0	0	492.549	0	284.167	0	0	0	0	0	0	0
Hypothetical protein; FIG00640476	0	0	0	0	0	0	24.747	0	12.1506	0	0	0	0
Hypothetical protein; FIG00640568	0.208954	0	0.109588	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00646873	0	0	45.3812	0	0	84.5355	0	0	0	0	0	0	0
Hypothetical protein; FIG00648199	0	0	0	0	0	0	0.208211	0.105982	0	0	0	0	0
Hypothetical protein; FIG00648345	0	0	0	0	0	0	18.7009	0	9.18198	0	0	0	0
Hypothetical protein; FIG00653436	0	0	0	0	0	0	3.24661	1.65256	0	0	0	0	0
Hypothetical protein; FIG00659888	0	0	0	0	0	0	4.02909	0	4.02566	0	0	0	0
Hypothetical protein; FIG00663041	0	0	0	0	0	0	138.364	70.4471	0	0	0	0	0
Hypothetical protein; FIG00680164	0	0	0	0	0	0	33.5741	15.3408	0	0	0	0	0
Hypothetical protein; FIG00688519	0	0	0	0	0	0	11.5897	5.89928	0	0	0	0	0
Hypothetical protein; FIG00693527	0	0	0	0	0	0	0	0	25.5734	0	0	0	13.1082
Hypothetical protein; FIG00729359	0	0	0	0	0	0	0	0	153.3273	0	0	0	0
Hypothetical protein; FIG00731616	0	0	0	763.473	0	443.849	0	0	0	0	0	0	0
Hypothetical protein; FIG00734443	0.214953	0	0.112734	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00758552	0	0	0.437909	0	0	0.254594	0	0	0	0	0	0	0
Hypothetical protein; FIG00759958	0	0	0	0	0	0	16.3998	7.59729	0	0	0	0	0
Hypothetical protein; FIG00764857	0	161.797	82.131	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00772051	0	0	0	0	0	0	11.09944	6.35674	0	0	0	0	0
Hypothetical protein; FIG00772742	0	0	0	0	0	0	0.238534	0.121416	0	0	0	0	0
Hypothetical protein; FIG00772929	0	0	0	0	0	0	18.67302	9.49582	0	0	0	0	0
Hypothetical protein; FIG00775401	32.942	0	17.7203	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00781076	0	0	0	0	0	0	0	0	0	57.1881	0	0	29.0511
Hypothetical protein; FIG00784450	0.18115	0	0.0950056	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00795790	0	4.78685	2.27635	0	0	0	0	0	0	0	0	0	0
Hypothetical protein; FIG00796651	0	0	0	0	0	0	16.8082	0	9.2376	0	0	0	0
Hypothetical protein; FIG00809930	0	0	0	0	0	0	0	0	0	0.255987	0	0	0.124572
Hypothetical protein; FIG00818530	0	0	0	0	0	0	0	0	0	91.9087	0	0	47.3801
Hypothetical protein; FIG00818702	0	0	0	0	0	0	0	0	0	7.24728</			



L-fucose isomerase (EC 5.3.1.25)	0	0	0	0	0	0	0	12.4128	6.93861	0	0	0	0
L-fucose mutarotase, type 2	0	0	0	0	0	0	0	0.529503	0.700758	0	0	0	0
L-lactate dehydrogenase (EC 1.1.1.27)	0	0	0	0	0	0	0	0	0	40.0114	0	20.5406	0
L-lactate dehydrogenase (EC 1.1.1.3)	0	512.922	244.339	0	256.884	0	103.3453	0	0	0	0	0	0
L-proline glycine betaine ABC transport system permease protein ProV (TC 3.A.1.12.1)	0	0	0	0	0	0	0	57.9145	0	28.5075	0	0	0
L-proline glycine betaine ABC transport system permease protein ProW (TC 3.A.1.12.1)	0	0	0	0	0	0	0	0	0	252.823	0	129.869	0
L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1)	0.206079	0	0.10808	0	0	0	0	0	0	0	0	0	0
L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81)	365.257	0	192.7315	0	0	0	0	0	0	0	0	0	0.264264
L-threonine 3-O-phosphate decarboxylase (EC 4.1.1.81) / Cobyric acid A,C-diamide synthase	0.412157	0	0.216159	0	0	0	0	0	0	0	0	0	0
Lactose permease	0.247385	0	0.129743	0	0	0	0	0	0	0	0	0	0
Lanthionine biosynthesis protein LanB	0	0	0	0	0	0	0	0	0	152.90088	0	78.49437	0
Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type	577.09536	1944.7	1579.567362	3.06477	0	1.78182	142.096	0	73.6906	0	0	0	2.614193
LemA protein	0	0	0	0	0	0	123.6203	0	54.174	0	0	0	0
Leucyl aminopeptidase	0	336.317	159.948	0	0	0	0	11.3017	5.65889	0	0	0	0
Lipopolysaccharide ABC transporter, ATP-binding protein LpH	0	0	0	0	0	0	0	0	0	0	0	0	0
Lipopolysaccharide cholinephosphotransferase Lcd3 (EC 2.7.8.-)	0	0	0	0	0	0	0	0.279193	0.142112	0	0	0	0
Lipoprotein, putative	0	0	0	0	0	77654.1	0	0	0	0	0	0	1.686073
LmbE family protein	0	0	0	0	0	0	0	0	0	60.4906	0	31.0984	0
Low-specificity D-threonine aldolase	0	0	0	0	108.3187	45.0062	0	0	0	0	0	0	0.715692
LSU ribosomal protein L10p (P0)	0	0	0	0	6037.54	2048.07	0	0	0	0	0	0	0
LSU ribosomal protein L11e (L5p)	0	0	0	0	0	0	60.2769	33.8137	0	0	0	0	0
LSU ribosomal protein L12a (P1/P2)	0	68.0466	468.093	0	0	0	0	0	0	0	0	0	0
LSU ribosomal protein L14p (L23e)	0	0	0	0	0	0	366.443	187.521	201.127	0	103.862	0	0
LSU ribosomal protein L15e	0	0	0	0	0	0	25.3255	13.0743	0	0	0	0	0
LSU ribosomal protein L15p (L27Ae)	0	0	0	0	0	0	0	0	2.1363	0	1.09671	0	0
LSU ribosomal protein L16p (L10e)	0	263.77508	125.48276	0	0	0	0	0	93.1496	0	0	0	0.53954
LSU ribosomal protein L17e (L22p)	0	311.4333	148.20293	0	0	0	7.60676	3.69389	0	0	0	0	0
LSU ribosomal protein L17p	0	0	0	0	0	0	0	0	0	46.0726	0	23.6522	0
LSU ribosomal protein L18p (L5e)	0	0	0	0	0	0	0	0	0	315.246	0	161.255	0
LSU ribosomal protein L20p	0	0	0	0	0	2.04246	0	1.00283	9.88091	0	5.07253	0	0
LSU ribosomal protein L21e	0	1335.84	636.461	0	0	0	0	0	0	0	0	0	0
LSU ribosomal protein L24p (L26e)	0	189.086	91.0965	0	0	0	114.607	59.1316	105.193	0	53.3181	0	0
LSU ribosomal protein L26e (L24p)	0	0	0	0	0	0	0	0	4.0718	0	2.09033	0	0
LSU ribosomal protein L30e	0	35.8147	17.0847	0	0	0	0	0	0	0	0	0	0
LSU ribosomal protein L31p	0	0	0	0	0	0	0.171811	0.0874534	0	0	0	0	0
LSU ribosomal protein L35e (L29p)	0	0	0	0	0	0	34.4867	17.5541	0	0	0	0	0
LSU ribosomal protein L36e	0	0	0	0	0	0	0	0	1.2809	0	0.657574	0	0
LSU ribosomal protein L36p	0	0	0	0	0	0	0	0	114.749	0	61.9341	0	0
LSU ribosomal protein L3e (L3p)	0	0	0	0	0	0	0	30.1795	13.4391	0	0	0	0
LSU ribosomal protein L6p (L9e)	0	169.7396	128.8363	0	0	0	15.0108	7.64064	0	0	0	0	0.241532
Lysine-arginine-ornithine-binding periplasmic protein precursor (TC 3.A.1.3.1)	0	19.0998	9.08274	0	0	0	0	0	0	0	0	0	0
Lysine-epsilon oxidase (EC 1.4.3.20) antimicrobial protein Loda	0	0	0	0	0	0	0	0	0	1.122654	0	0.54632	0
LysR family transcriptional regulator	0.264266	0	0.207895	0	206.51	68.6652	0	0	5.95312	0	0	0	1.67562
Lysin endopeptidase (EC 3.4.21.50)	0	182.445	87.6218	0	0	0	0	0	0	0	0	0	0
Lysin-RNA synthetase (class I) (EC 6.1.1.6)	0	0	0	0	0	0	2353.71	0	1916.46	0	0	0	0
Lysin-RNA synthetase (class II) (EC 6.1.1.6)	0.200559	0	0.105185	0.850196	44.9154	19.295222	0	0.463565	0.235959	0	759.445	369.571	0.2396
Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	0.105674	16.5783	5543.64407	0	0	0	0	0	0	0	0	0	0
Major facilitator:Oxalate:Formate Antiporter	0.222402	0	0.116641	0	0	0	0	0	0	0	0	0	0
Malate Na(+)-symporter	0	0	0	0	0	0	0	0.316338	0.161019	0	0	0	0
Malate:quinone oxidoreductase (EC 1.1.5.4)	0	0	0	0	0	0	0	0	0	250.253	0	129.5539	0
Malonyl-CoA-acyl carrier protein transacylase (EC 2.3.1.39)	129.27717	0	58.6531689	0	0	0	0	0	0	0	0	0	1.293696
Maltodextrin phosphorylase (EC 2.4.1.1)	0	0	0	0	0	0	0	0	0	208.169	0	109.33	0
Maltose phosphorylase (EC 2.4.1.8) / Trisaccharide phosphorylase (EC 2.4.1.64)	0.313431	0	0.164382	0	0	0	0	0	0	0	0	0	0
Maltose/maltodextrin ABC transporter, permease protein MalG	0	0	0	9.40816	0	5.50927	0	0	0	0	0	0	0.179957
Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE	0	0	0	0	0	0	175.408	90.6673	0	0	0	0	0
Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19)	0	634.869	310.061	6.41229	0	3.74513	0	0	0	0	0	0	0.786916
Manganese superoxide dismutase (EC 1.15.1.1)	0	0	0	0	0	0	0.964484	0.490931	300.668	0	0	0	970.632
Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	0	0	0	0	0	0	0	0	81.688	0	42.1951	0	0
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	0	16.57694	10.2671	0	0	0	0	0	0	0	0	0	0
Mannosyltransferase	3.35077	0	0	0	0	0	0	0	0	0	0	0	0
MCE-FAMILY PROTEIN MCE4B	0	0	0	0	0	0	0	0	0	3.23273	0	1.57315	0
Mediator of hyperadherence YidE	0	0	0	77.2725	0	32.3474	0	0	0	0	0	0	0
Membrane bound hydrogenase, MdhH subunit	0	0	0	0	0	0	120.052	0	58.9445	0	0	0	0
Membrane protein ydfI	0	0	0	0	0	0	0	0.323779	0	1.38462	0	3.55409	0
Membrane protein, suppressor for copper-sensitivity ScsD	0	0	0	0	0	0	0	4.21581	2.14589	0	0	0	0
Membrane-associated phospholipid phosphatase	0	0	0	0	0	0	0	76.4082	39.6127	0	0	0	0.161269
Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)	0	0.829725	0.394569	0	0	0	0	0	0	0	0	0	0
Metal-dependent protease	0	776.319	385.239	0	0	0	15.7067	7.82231	0	0	0	0	0
Metallo-beta-lactamase family protein, RNA-specific	0	599.74	285.546	0	0	0	0	0	0	0	0	0	0.415825
Metalloprotease, insulinase family	1330.159	0	658.489	0	0	0	0	0	0	0	0	0	0
Methanol:corrinoid methyltransferase	0	121.234	58.1856	0	0	0	0	0	0	0	0	0	0
Methionine ABC transporter ATP-binding protein	0	10.7208	5.11851	0.342661	0.143443	0	0	0	0	0	0	0	1.243278
Methionine biosynthesis and transport regulator MtaR, LysR family	0	0	0	0	0	18.1478	0	8.72282	0	0	0	0	0
Methionine gamma-lyase (EC 4.4.1.11)	0	296.238	141.368	0	0	0	0	0	0	0	0	0	17.337988
Methionyl-RNA synthetase, clonistral paralogue	0	0.222781	0.110941	0	0	0	0	0	0	0	0	0	0
Methyl-accepting chemotaxis protein	0.65425	0	0.343127	0	0	0	0	0	0	0	0	0	0
Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63)	180.389	0	96.5794	0	0	0	0	0	0	0	0	0	0.161269
Methylmalonyl-CoA mutase (EC 5.4.99.2)	0	0	0	0	0	7.02571	19.71192	3.31652	0	0	0	0	0
Methyltransferase	0	0	0	0	0	0	49.37018	25.18656	0	0	0	0	0
Methyltransferase FkbM	0	0	0	0	0	0	3.70652	1.88666	0	0	0	0	0
Methyltransferase TM1293	0	0	0	0	0	0	1.40703	0.550918	0	0	0	0	0
Mevlonate kinase (EC 2.7.1.36)	0	7.27366	3.46326	0	0	0	0	0.289046	0.147127	0	0	0	0
MFS permease protein	0	0	0	4.94341	0	2.87403	0	0	0	0	0	0	0.927154
Mg-chelatase subunit ChlD	0.529013	0	0.277445	0	0	0	0	0	0	0	0	0	0
Mg/Co/Ni transporter MgtE / CBS domain	0.463146	0	0.242901	0	0	0	0	0	0	0	0	0	0
Mg++ transporter	0	0	0	0	0	0	1.31619	0.669955	0	0	0	0	0
Microbial collagenase, secreted (EC 3.4.24.3)	0	230.6572	202.0411	0	0	0	0	0	0	0	0	0	0
MIND superfamily P-loop ATPase containing an inserted ferredoxin domain	0	0.253651	0.120621	0	0	0	1.36979	126.402	66.614952	0	0	0	0
MilS128 protein	0	0	0	0	0	0	51.6809	28.2178	0	0	0	0	0
Mir3099 protein	0	0	485.047	0	0	0	0	0	0	0	0	0	0
Mir6856 protein	0	0	0	0	0	0	66.2179	32.7367	0	0	0	0	0
MiRc	0	3.1665	1.32865	0	0	0	0	0	0	0	0	0	0.154154
MmgG/PrpD family protein	0	0	0	0	0	0	1037.19	440.127	0	0	0	0	0
Molecular chaperone (small heat shock protein)	0	0	0	0	0	0	0	0	4.27124	0	12.6008	0	0
MORN repeat family protein	0	538.166561	265.060163	0	0	0	0	0	0	0	0	0	0
MOSC domain protein	0	0	0	362.864	155.6893	0	0	0	0	0	0	0	0
MoxR-like ATPase in aerotolerance operon	0	0	0	0	0	0	172.242	87.4307	0	0	0	0	0
MSHA biogenesis protein MshM	0	0	0	0	0	0	88.5613	45.0262	0	0	0	0	0
Multi antimicrobial extrusion protein (Na+)/(drug antiporter), MATE family of MDR efflux pumps	0	0	0	0.265774	0	0.111256	0	0	0	1166.06	0	549.409	0
Multi-sensor hybrid histidine kinase	0	0	0	0	0	0	16.4423	8.36929	0	0	0	0	0
Multidrug efflux membrane fusion protein MexE	0	0	0	0	0	4.40117	0	2.16093	0	0	0	0	0
Multidrug resistance protein 1	0	0	0	12.93819	0	7.52208	0	0	0	0	0	0	0
Multidrug resistance protein B (ErmB)	0.136551	0	0.0716151	0	0	0.19674	0	0	0	0	0	0	0
Multidrug transporter MtdD	0	0	0	241.054	101.325	0	0	0	0	0	0	0	0
Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-) / Penicillin-binding protein 3A/18 (I)	0	0	0										







Putative integral membrane protein	0	0	0	0	0	396.668	415.864	406.493	0	0	0	0	0
Putative integration host factor IHF alpha subunit	0	0	0	0	0	0	0.588982	0.299797	0	0	0	0	0
Putative isobutyryl-CoA mutase, chain B	0	19.9538	13.6302	0	0	0	0	0	0	0	0	0	0
Putative lipoprotein LspB	0	0	0	0	1855.832	657.457	0	0	0	0	0	0	0
Putative major facilitator superfamily (MFS) transporter	0.174806	0	0.0916785	0	0	0	0	0	0	0	0	0	0
Putative membrane-bound ClpP-class protease associated with aq_911	0	754.316	374.706	0	0	0	0	0	0	0	0	0	0.767273
Putative methionine aminopeptidase	0	0	0.210369	0	0	0	0	0	0	0	0	0	0
Putative multi-domain protein	0	0	0	0	0	0	0	19.0827	9.77398	0	0	0	0
Putative nucleotide-binding protein	0	92.5516	45.5178	0	0	0	0	0	0	0	0	0	0
Putative oligopeptide ABC transport system membrane protein	0	0	0	3630.509	0	486.958	0	0	0	0	0	0	0
Putative opine dehydrogenase	0	0	0	0	0	0	1.05954	0.539314	0	0	0	0	0
Putative peptidoglycan binding domain 1	0	0	0	0	0	0	0	0	0.418581	0	0	0.214886	0
Putative periplasmic protein kinase ArgK and related GTPases of G3E family	0	0	0	0	0	0	0	0	0.263259	0	0	0.135148	0
Putative phage excisionase	0	0	94.6336	0	0	126.8891	0	0	0	0	0	0	0
Putative phosphatidylglycerophosphate synthase	0.371897	0	0.195045	0	0	0	0	0	0	0	0	0	0
Putative phosphoenolpyruvate synthase/pyruvate dikinase, C-terminal domain	0	789.112	378.85	0	0	0	3.9825	2.16747	0	0	0	0	0
Putative phosphotransferase system protein	0	376.284	0	0	0	0	0	0	0	0	0	0	0
Putative plasmid-related protein	0	0	0	0	0	0	0	0	98.864	0	0	50.4175	0
Putative protein phosphatase	0	0	0	2988.16	1252.64	0	0	0	0	0	0	0	0
Putative pyridine nucleotide-disulphide oxidoreductase	0	0	0	0	0	0	0	0	0.667304	0	0	0.342572	0
Putative secretion accessory protein EsaA/YxeB	0	0	0	0	0	0	0	0	78.8728	0	0	40.4755	0
Putative senescence marker protein-30 (SMP-30) (Regucalcin) (RC)	0	0	0.0938701	0	0	0	0	0	0	0	0	0	0
Putative sensory transduction histidine kinase	5.05702	0	2.6522	0	0	0	0	0	0	0	0	0	0
Putative stomatin/prohibitin-family membrane protease subunit aq_911	0	203.1329	100.8688	0	0	564.501	2501.10578	1798.995079	0	0	0	0	0.207164
Putative sucrose phosphorylase (EC 2.4.1.7)	0	0	0	0.695401	0.291104	0	0	0	0	0	0	0	0
Putative sugar isomerase	0	0	0	0	0	0	129.099	66.3288	0	0	0	0	0
Putative superfamily I DNA helicases	0	0	0	0	0	0	315.094	132.1598	0	0	0	0	0
putative TonB-dependent receptor	0	0	0	0.336472	0.140852	0	0	0	0	0	0	0	0
Putative transcriptional regulator	0	0	0	0	0	0	0.94496	0.4527	0	0	0.547693	0.266525	0
Putative transferase	0	0	0	0	0	0	0	0	0	0	0	0	0
Putative transmembrane protein	0	0.134637	0.0640255	92.8901	0	54.1418	0	0	0	0	0	0	4.163868
Putative transporter	0.211911	0	0.111339	0	0	0	0	0	0	0	0	0	0
Putative transporting ATPase	0	0	0	45.7063	0	26.573	0	0	0	0	0	0	0
Putative transportable element	19.896	0	10.7401	0	0	0	0	0	0	0	0	0	0
Putative tRNA-m1A22 methylase	32.7803	0	17.1919	0	0	0	0	0	0	0	0	0	0
Putative two-component system response regulator	0.423822	0	0.222277	0	0	0	35.6473	18.8042	0	0	0	0	0
Putative two-component system sensor protein, no kinase domain	0	0	0	0	0	0	9.8022	4.97854	0	0	0	0	0
Putative UDP-glucuronosyltransferase	0	0	0	0	0	0	0	0	405.755	0	0	801.3	0
Putative uncharacterized protein S007g030556	0.409901	0	0.214976	0	0	0	0	0	0	0	0	0	0
Putative virion core protein (lumpy skin disease virus)	0	0	0	0	0	0	602.4901	306.67349	0	0	0	0	0
Pva1 protein	0	0	0	0	0	0	0	0	17.758	0	0	10.0931	0
Pyridine nucleotide-disulphide oxidoreductase family protein	0	0	0	0	0	0	24.0314	12.22088	0	0	0	0	0
Pyrogallol hydroxytransferase (EC 1.9.1.2)	0	0	0	0	0	0	25.0853	12.7687	0	0	0	0	0
Pyrophosphate-energized proton pump (EC 3.6.1.1)	0	154.5689	73.9344	0	0	0	0	0	0	0	0	0	0
Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	0	0	0	300.907	0	176.175	0	0	0	0	0	0	0
Pyruvate formate-lyase (EC 2.3.1.54)	0	0	0	0	0	0	11.7767	6.12643	0	0	0	0	0
Pyruvate formate-lyase activating enzyme (EC 1.9.7.1.4)	0	0	0	0	0	0	26.1353	13.06767	0	0	0	0	0
Pyruvate,phosphate dikinase (EC 2.7.9.1)	0	8.476432	4.030901	0	0	0	0	0	108.3285	0	0	61.3515	0
Pyruvate:ferredoxin oxidoreductase, alpha subunit (EC 1.2.7.1)	0	243.357	111.545	0	0	0	0	0	0	0	0	0	0
Pyruvate:ferredoxin oxidoreductase, beta subunit (EC 1.2.7.1)	0	0	0	0	0	0	1.35701	0.690729	0	0	0	0	0
Pyruvate:ferredoxin oxidoreductase, gamma subunit (EC 1.2.7.1)	0	224.58798	106.78721	0	0	0	0	0	0	0	0	0	0
Quaternary ammonium compound-resistance protein SugE	1584.616	343.855	941.378	0	0	0	0	0	0	0	0	0	0
Queuosine Biosynthesis QueC ATPase	0	81.2319	38.6771	0	0	0	0	0	0	0	0	1.011531	0
Radical SAM domain protein	73.9163	236.295	150.8757	11.10326	0	6.5647	10.5296	2.53422	0	0	0	0.541941	0
RecA protein	0	37.5581	17.8604	0	0	0	0.200563	0.102088	402.141	0	207.5167	0.848083	0
RecD-like DNA helicase YrrC	0	0	0	0	0	0	40.6957	22.73605	0	0	0	0	0
Recombination protein RecK	0	0	0	132.43	0	77.7802	0	0	0	0	0	0.478989	0
Redox-sensing transcriptional regulator QorR	0	6.55408	3.11674	0	0	0	0	0	0	0	1634.008	755.957	0
Reductases with broad range of substrate specificities	0	0	0	0	0	0	0	0	0	0	0	0	0
Regulatory protein, MarR	104.8612	0	47.6514	0	0	0	0	0	0	0	0	0	0
Replication-associated protein	0	0	0	0	0	0	1.58811	0.808362	0	0	0	0	0
Repressor CsoR of the copZa operon	0	0	188.8313	0	0	109.784	0	0	0	0	0	0	0
Resolvasin, N-terminal domain	0	0	0	0	0	0	27.1439	0	12.5058	0	0	0	0
Resolvasin/Integrase TlnR protein	0	14.9034	7.06372	0	0	0	0	0	0	0	0	0	0
Response regulator	12.3859	0	6.49589	0	0	0	0	0	0	0	0	0	0.40215
Response regulator of the LytR/AlgR family	0	0	0	3.27425	0	1.9036	0	0	0	0	0	0	0
Response regulator receiver	0	0	0	0	0	0	0	0	0	470.945	0	0	0
Retron-type reverse transcriptase	0	0	0	0	525.939	218.531	661.363	608.542	707.6049	23824.7	1342.575	0	0.802072
Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)	0	18920.2708	12592.62	3955.41	0	43140.8	6744.593	30243.585	0	0	0	9651.41	0
Retrotransposon protein, putative, LINE subclass	0	0	0	0	0	0	0	0	112.27	0	0	113.62	0
Retrotransposon protein, putative, Ty1-copia subclass	99.783	0	52.3688	0	0	0	0	0	378.305	0	201.5603	0	0
Retrotransposon protein, putative, Ty3-gypsy subclass	0	467.023	339.927	0.242269	0	0.140852	0	0	3671.67	0	1890.785	0	0
Retrotransposon protein, putative, unclassified	145.625	0	76.3978	0	0.44546	0.186475	0	0	1428.257	0	748.405	0	0
Retrotransposon, putative, centromere-specific	0	0	0	0	0	0	0	0	14.5701	0	7.47981	0	0
Reverse transcriptase	0	235.683	321.7316	0	0	0	0	0	0	0	0	0	0
Rhamnolacturonides degradation protein RhlN	0	0	0	0	0	0	15.0764	7.88074	0	0	0	0	0
Rhamnolacturonase (EC 2.7.1.5)	0	0	0	0	0	0	435.685	208.964	0	0	0	0	0
Rhs family protein	0	0	0	0	0	0	17.18446	8.74705	0	0	0	0	0
Ribonuclease BN (EC 3.1.-.-)	0	0	0	0	0	0	0	0	9.30844	0	4.77865	0	0
Ribonuclease HII (EC 3.1.26.4)	3.11654	0	1.60365	0	0	0	0	0	0	0	0	0	0
Ribonuclease III family protein	0	0	0	0	0	0	0	0	85.2358	0	43.7393	0	0
Ribonuclease J1 (endonuclease and 5' exonuclease)	0	0	0	0	0	0	0	0	467.823	0	239.986	0	0
Ribonuclease P protein component 1 (EC 3.1.26.5)	0	0	0	0	0	0	38.2961	19.4931	0	0	0	0	0
Ribonuclease PH (EC 2.7.7.56)	0	17.44458	8.28221	0	0	0	0	0	0	0	0	1.104813	0
Ribonuclease Y (EC 3.1.-.-)	0	0	0	0	0	0	0	0	117.9399	0	63.0805	0	0
Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1)	0.815125	0	0.42645	0	0	0	0	0	0	0	0	0	0
Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1) @ interin-containing	0	0	0	0	0	0	0	0	79.8504	0	43.1825	0	0
Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)	0.90627	0	4.77062	2185.14	0	1308.94	0	3.40095	1.73112	55.2917	0	28.5182	1.211452
Ribonucleotide reductase transcriptional regulator NrdR	0.206079	0	0.10808	0	0	0	15.155	7.34718	0	0	0	0	0
Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1)	0	90.5387	43.0549	0	0	0	328.7639	179.1278	0	0	0	0	0.72263
Ribose ABC transporter (permease)	0	71.6863	54.5552	0	0	0	0	0	0	0	0	0	0
Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	0	14.5222	7.10904	0	0	0	38.5768	20.3557	31.1547	0	17.6815	0.243779	0
Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)	0	0	0	48.5986	0	28.8662	0	0	0	0	0	0	0
Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)	0	0	0	47.8035	0	31.6237	0	0	0	0	0	0	0
Ribosome recycling factor	682.04	164.387	432.1989	0	0	0	0	0	0	0	0	0	0.200622
Ribulokinase (EC 2.7.1.16)	0	50.4516	23.9918	0	0	0	0	0	0	0	0	0	0
Ribulose biphosphate carboxylase large chain (EC 4.1.1.39)	0	0	0	0	0	0	2.55776	1.30193	0	0	0	0	0
Rieske (2Fe-2S) region	0	0	0	0	0	0	0	0	20.5407	0	9.90577	0	0
RNA 3'-terminal phosphate cyclase (EC 6.5.1.4)	0	0	0	0	0	0	0	0	225.422	0	125.1996	0	0
RNA binding methyltransferase FtsI like	0	0	0	0.272127	0.113916	0	0	0	0	0.281708	0.137088	0	0
RNA methyltransferase, TrmA family	0	0	0	0	0	3.04701	1.27552	0	0	0	0	0	0
RNA polymerase associated protein RapA (EC 3.6.1.-)	0.271725	0	0.142508	0	0	0	0	0	0	0	0	0	0
RNA polymerase principal sigma factor HrdD	0	0	0.179401	0	0	0	0	0	0	0	0	0	0
RNA polymerase sigma factor for flagellar operon	0	181.424	86.1666	0	0	0	0	0	0	0	0	1.227755	0
RNA polymerase sigma factor RpoH	35.8202	0	18.5574	0	0	0	0	0	0	0	0	0	0
RNA-binding protein	0	0	0	0									



Translation initiation factor eIF1B-related protein	0	0	0	0	0	0	0	4.90445	3.49498	0	0	0	0
Transmembrane protein MT2276, clustered with lipote gene	0	0	0	0	0	0	0	0	0	0	0.324212	0	0
Transmembrane protein Tmp5	0	0	0	0	0	0	0	49.7547	21.89833	0	0	0	0
Transposase	33079.633	145.1721	17407.0887	315.75667	0	193.79029	133.5779	0	65.5538	0	0	0	68.121658
Transposase DDE domain protein	0	0	0	0	0	0	0	18.44648	9.34922	0	0	0	0
Transposase EC0136	0	0	0	0	0	0	189.5688	0	92.4456	0	0	0	0
Transposase in ISPg1	0	0	0	119.706	0	151.031	0	0	0	0	0	0	0
Transposase, IS4	5.75396	0	0	0	0	0	0	0	0	8.83903	0	4.53767	0
Transposase, mutator type	0	0	0	0	0	0	0.98915	0	1.33557	0	0	0	0
Transposon protein, putative, CACTA, En/Spm sub-class	27.3335	0	13.2934	0	0	0	0	0	0	0	0	0	0
TRAP dicarboxylate transporter, DctM subunit, unknown substrate 3	0	0	0	0	0	0	0	43.75736	23.996773	0	0	0	0
TRAP dicarboxylate transporter, DctM subunit, unknown substrate 5	0	0	0	0	0	0	0	52.89188	26.1668	0	0	0	0
TRAP dicarboxylate transporter, DctM subunit, unknown substrate 6	0	0	0	0	0	0	0	44.344	20.9375	0	0	0	0
TRAP transporter solute receptor, TAXI family precursor, unknown substrate 2	0	0	0	0	0	0	0	207.543	116.327	0	0	0	0
TRAP transporter solute receptor, unknown substrate 1	0	0	0	0	0	0	0	81.504	32.421	0	0	0	0
TRAP transporter solute receptor, unknown substrate 3	0	75.5782	36.1042	0	0	0	233.631	35.3945	132.4117	0	0	0	0
TRAP transporter solute receptor, unknown substrate 6	0	0	0	0	0	0	0	25.98133	12.98333	0	0	0	0
TRAP transporter, 4TM/12TM fusion protein, unknown substrate 2	0	0	0	0	0	0	0	127.467	63.1483	0	0	0	0
TRAP-type C4-dicarboxylate transport system, large permease component	0	0	0	0	0	0	0	0.867925	0.373816	0	0	0	0
TRAP-type C4-dicarboxylate transport system, periplasmic component	0	0	0	0	0	0	2.02309	2037.6852	1039.44592	0	0	0	0
Trehalose synthase (EC 5.4.99.16)	677.006	0	355.108	0	0	0	0	0	0	0	0	0	3.207508
Tricarboxylate transport membrane protein TctA	0.178985	0	0.0938701	0	0	0	0.744271	0	0.36543	0	0	0	0
Tricarboxylate transport protein TctC	0	0	0	0	0	0	0	68.123	34.7087	0	0	0	0
Trimethylamine-N-oxide reductase (EC 1.6.6.9)	0	0	0	1.16245	0	0.675832	0	0	0	0	0	0	0
Trimethylamine:corrinoid methyltransferase; pyrrolysine-containing	0	0	0	0	0	0	0	142.6433	72.7442	0	0	0	0
Triosephosphate isomerase (EC 5.3.1.1)	0	44.5056	21.3041	0	0	0	0	0	0	0	0	0	0
Tripeptide aminopeptidase (EC 3.4.11.4)	0	0	0	0	0	0	0	3.8388	6.47623	0	0	0	0
Trk system potassium uptake protein TrkA	0	0	0	0	0	0	0	4.41948	2.259214	0	0	0	0
tRNA N2,N2-dimethyl(Guanine26-N2)-methyltransferase (EC 2.1.1.32)	0	0	0	0	0	0	0	0	0	70.6624	0	36.2757	0
tRNA-dependent lipid II-Ala-L-alanine ligase	0	0	0	0	0	0	0	10.1207	8.1359	0	0	0	0
tRNA-(6A)37 methyltransferase	0	0	0	0	0	0	0	0	0	58.7232	0	31.6281	0
Tryptophan 2-monooxygenase (EC 1.13.12.3)	0	44.7027	21.258	0	0	0	0	0	0	0	0	0	0
Tryptophan synthase beta chain like (EC 4.2.1.20)	0	0	0	0	0	0	587.4324	494.4672	480.32008	0	0	0	0
TspB protein	0	0	0	0	0	0	4.46029	0	2.20437	127.805	55.9689	47.447	0
Tungsten-containing aldehyde:ferredoxin oxidoreductase (EC 1.2.7.5)	0	193.0028	89.25551	0	0	0	0	226.34529	116.71013	0	0	0	0
Tungsten-containing formate dehydrogenase alpha subunit	0	0	0	0	0	0	0	16.1258	7.87906	0	0	0	0
Twin-arginine translocation protein TatC	0	2255.87	1501.13	0	0	0	0	0	0	0	0	0	0.427856
Two component transcriptional regulator VraR	0	0	0	0	0	0	0	0	0	428.316	0	222.619	0
Two component transcriptional regulator, winged helix family	0	0	0	0	0	0	0	0	0	0.395147	0	0.192282	0
Two component transcriptional regulatory protein DevR	0	0	0	4.13866	0	8.55328	0	0	0	0	0	0	0
Two component, sigma54 specific, transcriptional regulator, Fis family	0	39.2097	18.6458	0	0	0	0	0	0	0	0	0	0
Two-component response regulator CreC	0	65.8038	32.0288	0	0	0	0	0	0	0	0	0	0
Two-component sensor histidine kinase	0	0	0	0	0	0	0	2.20069	0.902827	0	0	0	0
Two-component system sensor histidine kinase/response regulator, hybrid ('one-component system')	0	0	0	0	0	0	0	2.6884	1.368419	0	0	0	0
Type cbb3 cytochrome oxidase biogenesis protein cbbG, involved in Cu oxidation	14.6387	0	6.81725	0	0	0	0	0	0	0	0	0	1.0413224
Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	3.82969	0	2.00851	110.898	0	64.6862	0	0	0	0	0	0	0.383048
Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)	63.72077	0	33.41892	0	0	6.91041	2.86883	4.87171	4.96585	0.270078	2.680729	10.631895	0
Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	0	90.114	431.094	0	0	0	0	0	0	0	0	0	0.229543
Type I secretion outer membrane protein, TolC precursor	0.368239	0	0.193126	1439.15	0	839.702	0	0	0	0	0	0	0.698055
Type I signal peptidase	0	100.162	47.7372	0	0	0	0	0	0	0	0	0	0
Type II restriction enzyme HpaII (Endonuclease HpaII) (EC 3.1.21.4)	4991.95	0	2619.6	0	0	0	0	0	0	0	0	0	0
Type II restriction enzyme, methylese subunit YeeA	7.184251	731.123	350.361848	0	0	0	0	0	0	0	0	0	0
Type II secretory pathway, ATPase PufE/Flp plus assembly pathway, ATPase PilB	0	0	0	11.3539	0	7.52445	0	0	0	0	0	0	0.859371
Type III restriction-modification system methylation subunit (EC 2.1.1.72)	0	0	0	0	0	0	0	0	0	47.2334	22.9425	0	0
Type IV fibrillar assembly, ATPase PilB	0	10.5988	5.04019	0	0	0	0	312.6458	159.2867	0	0	0	0.3662
Type IV pilus biogenesis protein PilM	0	0	0	0	0	0	0	21.7664	11.0793	0	0	0	0
Type IV pilus biogenesis protein PilP	62.5372	0	32.7982	0	0	0	0	0	0	0	0	0	0
Type IV pilus biogenesis protein PilQ	95.2618	0	0	0	0	0	0	0	0	0	0	0	1.293975
Tyrosine recombinase XerC	0	0	0	0	0	0	0	1330.02	676.826	0	0	0	0
Tyrosyl-tRNA synthetase (EC 6.1.1.1)	0	95.56158	47.52163	0	0	0	0	48.2934	24.6013	0	0	0	0.29761
Ubiquitin-specific protease	17225.2	0	9652.09	0	0	0	0	0	0	0	0	0	0.35467
UDP-2,3-diacetylglucosamine diphosphatase (EC 3.6.1.54)	8.64668	0	4.53483	0	0	0	0	0	0	0	0	0	0
UDP-3-O-glucosamine N-acyltransferase (EC 2.3.1.1)	0	0	0	0	0	0	3.81062	0	3.01161	0	0	0	0
UDP-3-O-glucosamine N-acyltransferase (EC 2.3.1.191)	28.0434	0	14.7076	0	0	0	0	0	0	0	0	0	0.326303
UDP-galactopyranose mutase (EC 5.4.99.9)	0	0	0	0	0	4.8862	0	2.39908	0	0	0	0	0
UDP-glucose 4-epimerase (EC 5.1.3.2)	0	101.476	47.7731	0	0	0	0	26.9314	13.70831	0	0	0	9.170099
UDP-glucose dehydrogenase (EC 1.1.1.22)	0	0	0	0	0	0	0	17.681248	9.037581	0	0	0	0
UDP-N-acetylnovoyglucosamine reductase (EC 1.1.1.158)	0	48.87219	23.50806	0	0	0	34.567364	17.593386	0	0	0	0	0.187187
UDP-N-acetylglucosamine 4,6-dehydratase (EC 4.2.1.1)	0	0	0	0	0	0	48.3832	24.6275	0	0	0	0	0
UDP-N-acetylmuramyl-L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.1)	0	453.757	225.6563	0.278791	0.116706	0	0	0	0	0	0	0	0.714503
UDP-N-acetylmuramylalanyl-D-glutamyl-2,6-diaminopimelate ligase (EC 6.3.2.13)	0.481201	25.1603	12.504771	0	0	0	0	0	0	0	0	0	0.389552
Uncharacterized 9.4 kDa protein	0.724599	0	0.304018	0	0	0	0	0	0	0	0	0	0
Uncharacterized ATP-dependent helicase AF1149	0	0	0	0	0	0	203.758	109.035	0	0	0	0	0
Uncharacterized conserved protein, contains double-stranded beta-helix domain	0.255257	0	0.133871	0	0	0	0	0	0	0	0	0	0
Uncharacterized mitochondrial protein AtMq0030	0	0	0	0	0	0	0	0	26.9387	0	0	0	0
Uncharacterized protein (ATP-grasp superfamily)	0	4.46995	2.12565	0	0	0	0	0	0	0	0	0	0
Uncharacterized protein AF_0817 precursor	0	0	0	0	0	0	104.1553	7.00228	0	0	0	0	0
Uncharacterized protein MJ0274	0	0	0	0	0	0	0	0	125.6793	0	64.9775	0	0
Uncharacterized protein MJ1313	0	0	0	0	0	0	19.7092	10.0322	0	0	0	0	0
Uncharacterized protein similar to VCAD109	19.30071	0	9.88419	0	0	0	0	0	0	0	0	0	0
Uncharacterized protein, homolog of B subtilis YhgC	0	0	0	0	0	0	0	0	32.32798	0	16.82796	0	0
Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)	0	19.2796	9.16824	0	0	0	0	0	0	0	0	0	0.671048
Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)	0	0	0	0	0	0	0	0	147.4101	0	75.5595	0	0
UPF0246 protein YaaA	0	0	0	0	0	0	0	0	0	0.294385	0.143257	0	0
Uracil phosphoribosyltransferase (EC 2.4.2.9)	1.472956	0	0.772504	0	0	0	0	0	84.3862	0	43.3211	0	0
Urea ABC transporter, urea binding protein	109.1722	0	32.7732	0	0	0	0	0	0	0	0	0	0
Urea carboxylase (EC 6.3.4.6)	0	1.62852	0.774428	0	0	0	9.29636	4.731594	0	0	0	0	0
Urease accessory protein UreF	0	0	0	0	0	0	0	0	111.756	0	33.8892	0	0
Uridine phosphorylase (EC 2.4.2.3)	0	0	0	131.8725	0	84.8683	0	0	0	0	0	0	0
Uridylate kinase (EC 2.7.4.-)	25.3642	0	13.3156	0	0	0	0	0	0	0	0	0	0
Uridyltransferase (EC 2.7.7.59)	0	0	0	42.6961	0	78.1409	0	5.91807	3.01235	0	0	0	2.773962
Uroporphyrinogen decarboxylase (URO-D)	0	0	0	4.4214	0	2.9931	0	0	0	0	0	0	0
Uroporphyrinogen-III decarboxylase	0	0	0	0	0	0	0	5.48748	1.714	0	0	0	0
Uroporphyrinogen-III decarboxylase-like protein	0	0	0	0	0	0	0	0	167.378	0	85.9262	0	0
Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)	0	51.1944	24.345	0	0	0	11.83777	0.602554	0	0	0	0	0.215578
V-type ATP synthase subunit I (EC 3.6.3.14)	0	3.43712	1.35694	0	0	0	0	0	0	0	0	0	0
Valyl-tRNA synthetase (EC 6.1.1.9)	0.454207	10.53887	5.116793	0	0	0	356.9169	175.7908	38.0946	1.9849	24.304029	0.962629	0
Vibriolysin, extracellular zinc protease (EC 3.4.24.25)	0	0	35.8943	0	0	0	0	0	0	0	0	0	0
Vitamin-B12 independent methionine synthase family protein	0	12.20161	5.85716	0	0	0	0	0	0	0	0	0	0
Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family	304.6137	0	71.5458	0	0	0	0	0	0	0	0	0	0.231231
Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)	0	23.08889	10.96756	0	0	0	0	0	0	0	0	0	1.103275
Xanthine permease	0	0	0	1460.746	0	814.7104	0	0	0	0	0	0	0
Xanthine phosphoribosyltransferase (EC 2.4.2.22)	0	0	0										