Table S1. Genes regulated by EIIA^{Ntr}. List of all genes from a microarray using wild-type and the *ptsN* mutant *Salmonella*. Genes displayed 2-fold or more changes are marked with red (increase in the *ptsN* mutant) and green (decrease in the *ptsN* mutant) colors.

Gene	*P*-value (ptsN/WT)	Fold (ptsN/WT)	Probe Comment
STM0001_25_59	0.46	1.74	1251519|thrL|thr operon leader peptide|+
STM0002_1688_1722	0.00	-8.34	1251520|thrA|bifunctional aspartokinase I/homeserine dehydrogenase II|+
STM0003_329_363	0.84	-1.05	1251521|thrB|homoserine kinase|+
STM0004_1040_1074	0.04	-1.83	1251522|thrC|threonine synthase|+
STM0005_257_291	0.07	1.51	1251523|yaaA|hypothetical protein|-
STM0006_784_818	0.03	1.43	1251524|yaaJ|putative alanine/glycine transport protein|-
STM0007_113_147	0.04	1.38	1251525|talB|transaldolase B|+
STM0008_17_51	0.91	-1.01	1251526|mogA|molybdenum cofactor biosynthesis protein|+
STM0009_197_231	0.01	1.92	1251527|yaaH|hypothetical protein|-
STM0010_641_675	0.36	1.07	1251528|htgA|hypothetical protein|-
STM0012_982_1016	0.06	1.40	1251530|dnaK|molecular chaperone DnaK|+
STM0013_797_831	0.02	2.14	1251531|dnaJ|chaperone protein DnaJ|+
STM0014_673_707	0.04	1.16	1251532|STM0014|putative transcriptional regulator|+
STM0017_385_419	0.03	1.23	1251535|STM0017|hypothetical protein|-
STM0018_1933_1967	0.02	1.76	1251536|STM0018|putative exochitinase|+
STM0019_2846_2880	0.20	1.09	1251537|STM0019|putative hydroxymethyltransferase|+
STM0020_241_275	0.01	1.45	1251538|STM0020|putative cytoplasmic protein|+
STM0021_433_467	0.02	1.73	1251539|bcfA|fimbrial subunit|+
STM0022_193_227	0.04	3.01	1251540|bcfB|fimbrial chaparone|+
STM0024_233_267	0.94	1.01	1251542|bcfD|fimbrial subunit|+
STM0025_81_115	0.01	2.19	1251543|bcfE|fimbrial subunit|+
STM0027_353_387	0.19	-1.15	1251545|bcfG|fimbrial chaparone|+
STM0028.1n_241_275	0.02	1.90	2673738|STM0028.1n|hypothetical protein|+
STM0029_334_371	0.06	-1.61	1251547|STM0029|putative transcriptional regulator|-
STM0030_214_248	0.03	1.92	1251548|STM0030|putative transcriptional regulator|+
STM0031_217_251	0.03	1.51	1251549|STM0031|putative transcriptional regulator|-
STM0033_829_863	0.03	2.46	1251551|STM0033|putative 5'-nucleotidase|-
STM0035_895_929	0.03	-1.64	1251553|STM0035|putative arylsulfatase|+
STM0036_224_258	0.56	-1.07	1251554|STM0036|putative arylsulfatase regulator|+
STM0037_815_849	0.03	1.24	1251555|STM0037|putative cytoplasmic protein|+
STM0039_232_266	0.39	1.07	1251557|nhaA|pH-dependent sodium/proton antiporter|+
STM0040_361_395	0.46	1.09	1251558|nhaR|transcriptional activator NhaR|+
STM0041_1377_1411	0.29	1.12	1251559|STM0041|putative glycosyl hydrolase|-
STM0042_767_801	0.98	-1.00	1251560|STM0042|putative sodium galactoside symporter|-

STM0043_49_83	0.01	-2.11	1251561|rpsT|30S ribosomal protein S20|-
STM0044_170_207	0.06	-1.39	1251562|yaaY|putative cytoplasmic protein|+
STM0045_553_587	0.99	1.00	1251563|ribF|bifunctional riboflavin kinase/FMN adenylyltransferase|+
STM0046_2362_2396	0.02	-1.53	1251564|ileS|isoleucyl-tRNA synthetase|+
STM0047_33_67	0.06	1.19	1251565|lspA|lipoprotein signal peptidase|+
STM0048_9_43	0.07	1.11	1251566|slpA|FKBP-type peptidyl-prolyl cis-trans isomerase|+
STM0049_517_551	0.32	-1.09	1251567|ispH|4-hydroxy-3-methylbut-2-enyl diphosphate reductase|+
STM0050_1100_1134	0.06	1.48	1251568|STM0050|putative nitrite reductase|+
STM0051_385_419	0.40	1.20	1251569|rihC|ribonucleoside hydrolase RihC|+
STM0052_617_651	0.00	-1.52	1251570|STM0052|putative transcriptional regulator|-
STM0053_749_783	0.07	2.27	1251571|STM0053|putative transcriptional regulator|-
STM0054_370_404	0.03	1.43	1251572|STM0054|putative oxalacetate decarboxylase subunit beta|-
STM0055_1194_1228	0.13	1.25	1251573|STM0055|pyruvate carboxylase subunit B|-
STM0056_101_135	0.76	1.06	1251574|STM0056|oxaloacetate decarboxylase subunit gamma|-
STM0057_1302_1336	0.04	2.72	1251575|STM0057|putative citrate-sodium symporter|-
STM0060_129_163	0.26	1.55	1251578|citE2|putative citrate lyase beta chain|+
STM0061_1482_1516	0.92	1.01	1251579|citF2|putative citrate lyase alpha chain/citrate-ACP transferase|+
STM0062_89_123	0.14	1.22	1251580|citX2|putative cytoplasmic protein|+
STM0063_65_99	0.99	-1.00	1251581|citG2|triphosphoribosyl-dephospho-CoA synthase|+
STM0064_289_323	0.04	-1.38	1251582|dapB|dihydrodipicolinate reductase|+
STM0067_2485_2519	0.14	-1.61	1251585|carB|carbamoyl phosphate synthase large subunit|+
STM0068_237_271	0.06	1.42	1251586|caiF|DNA-binding transcriptional activator CaiF|+
STM0069_209_243	0.95	1.00	1251587|caiE|carnitine racemase stimulation factor|-
STM0070_449_483	0.82	1.02	1251588|caiD|carnitinyl-CoA dehydratase|-
STM0071_1195_1229	0.44	1.27	1251589|caiC|putative crotonobetaine/carnitine-CoA ligase|-
STM0072_731_765	0.37	1.17	1251590|caiB|crotonobetainyl-CoA:carnitine CoA-transferase|-
STM0073_1104_1138	0.03	1.68	1251591|caiA|crotonobetainyl-CoA dehydrogenase|-
STM0074_663_697	0.69	-1.06	1251592|caiT|L-carnitine/gamma-butyrobetaine antiporter|-
STM0075_449_483	0.03	2.30	1251593|fixA|putative electron transfer flavoprotein FixA|+
STM0078_3_37	0.20	1.54	1251596|fixX|putative ferredoxin|+
STM0079_726_760	0.18	1.25	1251597|yaaU|putative transport protein|+
STM0080_33_67	0.02	1.36	1251598|STM0080|putative outer membrane lipoprotein|+
STM0081_289_323	0.02	3.68	1251599|STM0081|putative secreted protein|+
STM0082_217_251	0.01	3.65	1251600|STM0082|putative secreted protein|-
STM0084_1787_1821	0.04	1.61	1251602|STM0084|putative sulfatase|+

STM0085_433_467	0.98	1.00	1251603|yabF|glutathione-regulated potassium-efflux system ancillary protein KefF|+
STM0086_1440_1474	0.01	1.37	1251604|kefC|glutathione-regulated potassium-efflux system protein KefC|+
STM0087_345_379	0.04	1.89	1251605|folA|dihydrofolate reductase|+
STM0088_33_67	0.03	-1.52	1251606|apaH|diadenosine tetraphosphatase|-
STM0089_129_163	0.17	1.18	1251607|apaG|ApaG|-
STM0090_641_675	0.19	-1.10	1251608|ksgA|dimethyladenosine transferase|-
STM0091_641_675	0.00	-1.38	1251609|pdxA|4-hydroxythreonine-4-phosphate dehydrogenase|-
STM0092_352_386	0.29	-1.25	1251610|surA|peptidyl-prolyl cis-trans isomerase SurA|-
STM0093_1874_1908	0.01	-1.99	1251611|imp|organic solvent tolerance protein|-
STM0094_353_387	0.03	1.26	1251612|djlA|Dna-J like membrane chaperone protein|+
STM0095_65_99	0.28	1.11	1251613|rluA|23S rRNA/tRNA pseudouridine synthase A|-
STM0096_2436_2470	0.03	-1.25	1251614|hepA|ATP-dependent helicase HepA|-
STM0097_1625_1659	0.01	1.65	1251615|polB|DNA polymerase III|-
STM0098_465_499	0.04	1.64	1251616|STM0098|putative secreted protein|-
STM0100_2_36	0.01	2.25	1251618|STM0100|putative cytoplasmic protein|+
STM0101_226_260	0.82	-1.04	1251619|araD|L-ribulose-5-phosphate 4-epimerase|-
STM0102_1464_1498	0.02	-1.47	1251620|araA|L-arabinose isomerase|-
STM0103_871_905	0.01	-1.59	1251621|araB|ribulokinase|-
STM0104_217_251	0.65	-1.06	1251622|araC|DNA-binding transcriptional regulator AraC|+
STM0105_321_355	0.10	-1.48	1251623|yabI|hypothetical protein|+
STM0106_345_379	0.04	-1.55	1251624|thiQ|thiamin transporter ATP-binding subunit|-
STM0107_1348_1382	0.18	-1.26	1251625|thiP|thiamin transporter membrane protein|-
STM0108_49_83	0.62	1.28	1251626|tbpA|thiamin transporter substrate binding subunit|-
STM0109_868_902	0.60	-1.04	1251627|yabN|putative periplasmic binding protein|-
STM0110_49_83	0.12	1.41	1251628|leuD|isopropylmalate isomerase small subunit|-
STM0111_438_472	0.98	1.00	1251629|leuC|isopropylmalate isomerase large subunit|-
STM0112_605_639	0.20	-1.35	1251630|leuB|3-isopropylmalate dehydrogenase|-
STM0113_1469_1503	0.09	2.11	1251631|leuA|2-isopropylmalate synthase|-
STM0114_11_45	0.62	1.37	1251632|leuL|leu operon leader peptide|-
STM0115_641_675	0.66	-1.08	1251633|leuO|leucine transcriptional activator|+
STM0116_855_889	0.79	1.04	1251634|ilvI|acetolactate synthase 3 catalytic subunit|+
STM0117_417_451	0.02	-2.16	1251635|ilvH|acetolactate synthase 3 regulatory subunit|+
STM0118_214_248	0.04	-1.27	1251636|fruR|DNA-binding transcriptional regulator FruR|+
STM0119_17_51	0.86	-1.03	1251637|yabB|hypothetical protein|+
STM0120_273_307	0.01	-1.94	1251638|mraW|S-adenosyl-methyltransferase MraW|+

STM0121_34_68	0.02	-1.61	1251639|ftsL|cell division protein FtsL|+
STM0122_1280_1314	0.77	1.04	1251640|ftsI|division specific transpeptidase|+
STM0123_617_651	0.01	-2.12	1251641|murE|UDP-N-acetylmuramoylalanyl-D-glutamate--2 6-diaminopimelate ligase|+
STM0124_456_490	0.02	-1.83	1251642|murF|UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase|+
STM0125_308_342	0.00	-1.51	1251643|mraY|phospho-N-acetylmuramoyl-pentapeptide-transferase|+
STM0126_606_640	0.04	-1.69	1251644|murD|UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase|+
STM0127_694_728	0.03	-1.28	1251645|ftsW|essential cell division gene|+
STM0128_165_199	0.09	-1.18	1251646|murG|N-acetylglucosaminyl transferase|+
STM0129_589_623	0.01	-2.34	1251647|murC|UDP-N-acetylmuramate--L-alanine ligase|+
STM0130_609_643	0.00	-1.83	1251648|ddl|D-alanine--D-alanine ligase|+
STM0131_449_483	0.02	-1.47	1251649|ftsQ|cell division protein FtsQ|+
STM0132_792_826	0.00	-1.81	1251650|ftsA|cell division protein FtsA|+
STM0133_361_395	0.26	-1.21	1251651|ftsZ|cell division protein FtsZ|+
STM0134_473_507	0.10	-1.19	1251652|lpxC|UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase|+
STM0135_425_459	0.11	1.63	1251653|yacA|SecA regulator SecM|+
STM0136_2347_2381	0.01	-1.80	1251654|secA|preprotein translocase subunit SecA|+
STM0137_351_389	0.05	-1.74	1251655|mutT|nucleoside triphosphate pyrophosphohydrolase marked preference for dGTP|+
STM0137.1N_7_41	0.97	-1.00	2673762|STM0137.1N|-|-
STM0138_89_123	0.01	1.46	1251656|yacG|zinc-binding protein|-
STM0139_513_547	0.57	-1.04	1251657|yacF|hypothetical protein|-
STM0140_513_547	0.34	-1.14	1251658|coaE|dephospho-CoA kinase|-
STM0141_477_511	0.86	1.03	1251659|guaC|guanosine 5'-monophosphate oxidoreductase|+
STM0142_652_686	0.35	1.19	1251660|hofC|type IV pilin biogenesis protein|-
STM0144_65_99	0.83	1.05	1251662|ppdD|putative major pilin subunit|-
STM0145_49_83	0.58	-1.03	1251663|nadC|quinolinate phosphoribosyltransferase|-
STM0146_193_227	0.32	1.08	1251664|ampD|N-acetyl-anhydromuranmyl-L-alanine amidase|+
STM0147_545_579	0.01	1.37	1251665|ampE|regulatory protein AmpE|+
STM0148_737_771	0.83	-1.02	1251666|STM0148|putative cytoplasmic protein|-
STM0149_472_506	0.93	1.01	1251667|STM0149|Na+/galactoside symporter|-
STM0150_503_537	0.01	-2.94	1251668|aroP|aromatic amino acid transporter|-
STM0151_161_195	0.00	5.54	1251669|pdhR|transcriptional regulator PdhR|+
STM0152_1793_1827	0.01	2.52	1251670|aceE|pyruvate dehydrogenase subunit E1|+
STM0153_1275_1309	0.03	1.99	1251671|aceF|dihydrolipoamide acetyltransferase|+

STM0154_1034_1068	0.03	1.59	1251672|lpdA|dihydrolipoamide dehydrogenase|+
STM0155_27_61	0.03	1.35	1251673|STM0155|putative outer membrane protein|+
STM0156_681_715	0.95	1.01	1251674|STM0156|putative periplasmic protein|-
STM0157_1474_1508	0.12	1.57	1251675|yacH|putative outer membrane protein|-
STM0158_2239_2273	0.05	-1.47	1251676|acnB|bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase|+
STM0159_321_355	0.11	1.25	1251677|STM0159|putative restriction endonuclease|-
STM0160_117_151	0.04	1.27	1251678|yacL|hypothetical protein|+
STM0161_705_739	0.06	1.93	1251679|kdgT|2-keto-3-deoxygluconate permease|+
STM0163_545_579	0.01	-1.45	1251681|pdxA|4-hydroxythreonine-4-phosphate dehydrogenase 2|+
STM0164_97_131	0.10	1.19	1251682|STM0164|putative transcriptional regulator|+
STM0165_321_355	0.12	-1.59	1251683|speD|S-adenosylmethionine decarboxylase|-
STM0166_337_371	0.43	1.43	1251684|speE|spermidine synthase|-
STM0168_1268_1302	0.04	-1.96	1251686|cueO|multicopper oxidase|+
STM0169_1680_1714	0.30	1.27	1251687|gcd|glucose dehydrogenase|-
STM0170_65_99	0.91	-1.02	1251688|hpt|hypoxanthine-guanine phosphoribosyltransferase|+
STM0171_225_259	0.43	-1.11	1251689|yadF|carbonic anhydrase|-
STM0172_289_323	0.03	1.22	1251690|yadG|putative ABC-type multidrug transport system ATPase component|+
STM0173_609_643	0.08	-1.13	1251691|yadH|putative transport protein|+
STM0174_801_835	0.11	1.48	1251692|stiH|putative fimbrial protein precuror|-
STM0175_1948_1982	0.65	1.09	1251693|stiC|putativie fimbrial usher|-
STM0176_625_659	0.04	1.47	1251694|stiB|putative fimbrial chaperone|-
STM0177_213_247	0.06	1.51	1251695|stiA|putative fimbrial subunit|-
STM0178_294_328	0.07	1.38	1251696|yadI|putative PTS enzyme|+
STM0179_279_313	0.01	-2.01	1251697|yadE|putative xylanase/chitin deacetylase|+
STM0180_145_179	0.77	-1.07	1251698|panD|aspartate alpha-decarboxylase|-
STM0181_321_355	0.99	1.01	1251699|panC|pantoate--beta-alanine ligase|-
STM0182_229_263	0.11	-1.21	1251700|panB|3-methyl-2-oxobutanoate hydroxymethyltransferase|-
STM0183_377_411	0.29	-1.18	1251701|folK|2-amino-4-hydroxy-6-hydroxymethyldihyropteridine pyrophosphokinase|-
STM0184_524_558	0.03	-2.08	1251702|pcnB|poly(A) polymerase I|-
STM0185_513_547	0.25	-1.28	1251703|yadB|glutamyl-Q tRNA(Asp) synthetase|-
STM0186_17_51	0.42	-1.13	1251704|dksA|DnaK transcriptional regulator DksA|-
STM0187_251_285	0.09	1.16	1251705|sfsA|sugar fermentation stimulation protein A|-
STM0188_211_245	0.00	1.52	1251706|ligT|2'-5' RNA ligase|-

STM0189_1572_1606	0.01	-1.88	1251707|hrpB|ATP-dependent RNA helicase HrpB|+
STM0190_1780_1814	0.92	1.00	1251708|mrcB|penicillin-binding protein 1b|+
STM0191_1959_1993	0.02	-3.06	1251709|fhuA|ferrichrome outer membrane transporter|+
STM0192_729_763	0.22	-1.41	1251710|fhuC|iron-hydroxamate transporter ATP-binding subunit|+
STM0193_249_283	0.01	2.61	1251711|fhuD|iron-hydroxamate transporter substrate-binding subunit|+
STM0194_2011_2045	0.05	2.35	1251712|fhuB|iron-hydroxamate transporter permease subunit|+
STM0195_65_99	0.91	-1.05	1251713|stfA|putative fimbrial subunit|+
STM0198_305_339	0.02	2.62	1251716|stfE|putative minor fimbrial subunit|+
STM0199_117_151	0.50	-1.28	1251717|stfF|putative minor fimbrial subunit|+
STM0200_335_369	0.18	1.17	1251718|stfG|putative minor fimbrial subunit|+
STM0201_705_739	0.04	2.15	1251719|STM0201|putative outer membrane protein|+
STM0202_698_732	0.04	1.56	1251720|hemL|glutamate-1-semialdehyde aminotransferase|-
STM0203_943_977	0.01	-1.65	1251721|yadQ|chloride channel protein|+
STM0204.S_273_307	0.01	1.90	1251722|yadR|hypothetical protein|+
STM0205_449_483	0.57	1.06	1251723|yadS|hypothetical protein|-
STM0206_270_304	0.30	2.07	1251724|btuF|vitamin B12-transporter protein BtuF|-
STM0207_289_323	0.06	-1.43	1251725|pfs|5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase|-
STM0208_1351_1385	0.04	1.63	1251726|dgt|deoxyguanosinetriphosphate triphosphohydrolase|+
STM0209_1101_1135	0.04	2.06	1251727|htrA|serine endoprotease|+
STM0210_639_673	0.00	-3.24	1251728|cdaR|carbohydrate diacid transcriptional activator CdaR|+
STM0211_289_323	0.01	-2.60	1251729|yaeH|putative cytoplasmic protein|-
STM0212_879_913	0.23	1.08	1251730|STM0212|putative inner membrane protein|+
STM0213_641_675	0.78	1.03	1251731|dapD|2 3 4 5-tetrahydropyridine-2-carboxylate N-succinyltransferase|-
STM0214_2634_2668	0.14	1.22	1251732|glnD|PII uridylyl-transferase|-
STM0215_593_627	0.04	-1.34	1251733|map|methionine aminopeptidase|-
STM0216_609_643	0.06	-1.55	1251734|rpsB|30S ribosomal protein S2|+
STM0217_689_723	0.04	-2.28	1251735|tsf|elongation factor Ts|+
STM0218_65_99	0.02	-2.03	1251736|pyrH|uridylate kinase|+
STM0219_241_275	0.05	-1.31	1251737|frr|ribosome recycling factor|+
STM0220_478_512	0.66	-1.06	1251738|dxr|1-deoxy-D-xylulose 5-phosphate reductoisomerase|+
STM0221_389_423	0.01	-2.10	1251739|uppS|undecaprenyl pyrophosphate synthase|+
STM0222_705_739	0.07	-1.27	1251740|cdsA|CDP-diglyceride synthase|+
STM0223_482_516	0.01	-1.72	1251741|yaeL|zinc metallopeptidase|+
STM0224_1416_1450	0.02	-1.51	1251742|yaeT|outer membrane protein assembly factor YaeT|+
STM0225_97_131	0.03	-1.53	1251743|hlpA|periplasmic chaperone|+
STM0226_363_397	0.74	-1.05	1251744|lpxD|UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase|+

STM0227_217_251	0.07	-1.49	1251745|fabZ|(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase|+
STM0228_385_419	0.15	-1.25	1251746|lpxA|UDP-N-acetylglucosamine acyltransferase|+
STM0229_214_248	0.08	1.26	1251747|lpxB|lipid-A-disaccharide synthase|+
STM0230_393_427	0.02	-1.57	1251748|rnhB|ribonuclease HIII|+
STM0232_553_587	0.07	-1.52	1251750|accA|acetyl-CoA carboxylase carboxyltransferase subunit alpha|+
STM0233_1213_1247	0.23	1.17	1251751|STM0233|putative endochitinase|+
STM0234_1303_1337	0.12	1.30	1251752|ldcC|lysine decarboxylase 2|+
STM0235_138_172	0.37	1.11	1251753|yaeR|hypothetical protein|+
STM0236_1078_1112	0.12	1.43	1251754|tilS|tRNA(Ile)-lysidine synthetase|+
STM0237_33_67	0.17	1.31	1251755|rof|Rho-binding antiterminator|-
STM0238_177_211	0.21	1.32	1251756|yaeP|hypothetical protein|-
STM0239_373_407	0.41	-1.19	1251757|yaeQ|putative cytoplasmic protein|+
STM0240_9_43	0.03	-1.39	1251758|yaeJ|hypothetical protein|+
STM0241_49_83	0.01	3.01	1251759|cutF|pseudo|+
STM0242_1184_1218	0.01	-2.53	1251760|proS|prolyl-tRNA synthetase|-
STM0243_313_347	0.02	-1.53	1251761|yaeB|putative regulatory protein|-
STM0244_185_219	0.44	1.15	1251762|rcsF|outer membrane lipoprotein|-
STM0245_289_323	0.01	2.55	1251763|metQ|DL-methionine transporter substrate-binding subunit|-
STM0246_329_363	0.01	4.10	1251764|yaeE|DL-methionine transporter permease subunit|-
STM0247_609_643	0.01	4.53	1251765|metN|DL-methionine transporter ATP-binding subunit|-
STM0248_49_83	0.24	1.38	1251766|yaeD|D D-heptose 1 7-bisphosphate phosphatase|+
STM0250_36_70	0.02	-2.30	1251768|ileV|tRNA|+
STM0255_257_291	0.12	1.34	1251773|dkgB|2 5-diketo-D-gluconate reductase B|+
STM0256_129_163	0.43	-1.11	1251774|yafC|putative transcriptional regulator|-
STM0257_1009_1043	1.00	1.00	1251775|STM0257|putative drug efflux protein|+
STM0258_225_259	0.02	1.17	1251776|yafD|hypothetical protein|+
STM0259_385_419	0.06	-1.39	1251777|yafE|putative methyltransferase|+
STM0260_369_403	0.00	-2.65	1251778|dniR|predicted membrane-bound lytic murein transglycosylase D|-
STM0261_521_555	0.07	1.84	1251779|gloB|predicted hydroxyacylglutathione hydrolase|-
STM0262_257_291	0.09	1.17	1251780|yafS|putative SAM-dependent methyltransferase|+
STM0263_129_163	0.30	1.08	1251781|rnhA|ribonuclease H|-
STM0264_49_83	0.62	-1.04	1251782|dnaQ|DNA polymerase III subunit epsilon|+
STM0266_185_219	0.08	-1.18	1251784|STM0266|putative cytoplasmic protein|-
STM0268_1301_1335	0.17	-1.20	1251786|STM0268|putative cytoplasmic protein|-
STM0270_625_659	0.75	1.10	1251788|STM0270|putative cytoplasmic protein|-
STM0271_129_163	0.18	1.16	1251789|STM0271|putative cytoplasmic protein|-

STM0273_273_307	0.05	1.40	1251791|STM0273|putative cytoplasmic protein|+
STM0274_894_928	0.05	1.54	1251792|STM0274|putative cytoplasmic protein|+
STM0275.s_73_107	0.03	1.65	1251794|STM0275.s|putative cytoplasmic protein|+
STM0277_161_195	0.02	1.68	1251796|STM0277|putative cytoplasmic protein|+
STM0278_127_161	0.42	1.25	1251797|STM0278|putative periplasmic protein|+
STM0280_81_115	0.07	1.40	1251799|STM0280|putative outer membrane lipoprotein|+
STM0281_345_379	0.26	1.15	1251800|STM0281|putative cytoplasmic protein|+
STM0283_117_151	0.00	2.35	1251802|STM0283|putative inner membrane protein|+
STM0284_58_95	0.05	1.77	1251803|STM0284|putative Shiga-like toxin A subunit|+
STM0285_3479_3513	0.75	-1.12	1251804|STM0285|putative inner membrane protein|+
STM0286_85_120	0.03	-1.44	1251805|STM0286|putative cytoplasmic protein|+
STM0288_241_275	0.03	1.12	1251807|STM0288|putative cytoplasmic protein|+
STM0289_1831_1865	0.01	2.37	1251808|STM0289|putative cytoplasmic protein|+
STM0290_113_150	0.05	2.29	1251809|STM0290|putative cytoplasmic protein|+
STM0291_3968_4002	0.36	1.16	1251810|STM0291|putative RHS-like protein|+
STM0292_359_397	0.15	1.46	1251811|STM0292|putative RHS-like protein|+
STM0293_57_95	0.36	1.14	1251812|STM0293|putative cytoplasmic protein|+
STM0294_61_98	0.00	2.15	1251813|STM0294|putative cytoplasmic protein|+
STM0294.1N_28_62	0.03	-1.41	2673758|STM0294.1N|hypothetical protein|-
STM0295_99_137	0.03	1.51	1251814|STM0295|putative cytoplasmic protein|+
STM0299_465_500	0.16	1.31	1251818|safA|putative outer membrane protein|+
STM0300_393_427	0.46	1.09	1251819|safB|putative fimbrial assembly chaperone|+
STM0301_1912_1946	0.40	1.10	1251820|safC|putative fimbrial usher|+
STM0302_181_215	0.58	-1.15	1251821|safD|putative fimbrial subunit|+
STM0303_321_355	0.13	-1.55	1251822|ybeJ|putative xylanase/chitin deacetylase|+
STM0304_161_195	0.23	-1.27	1251823|sinR|transcriptional regulator|+
STM0305_161_195	0.81	1.07	1251824|STM0305|putative cytoplasmic protein|+
STM0306_401_435	0.01	2.25	1251825|STM0306|SapA-like protein|-
STM0307_229_263	0.01	3.42	1251826|STM0307|VirG-like protein|-
STM0308_417_451	0.02	1.34	1251827|yafV|hypothetical protein|-
STM0309_1830_1864	0.93	1.01	1251828|fadE|acyl-CoA dehydrogenase|-
STM0310_353_387	0.03	-1.13	1251829|gmhA|phosphoheptose isomerase|+
STM0311_321_355	0.63	1.05	1251830|yafJ|putative glutamine amidotransferase|+
STM0312_273_307	0.00	-4.13	1251831|yafK|putative periplasmic protein|-
STM0313_761_795	0.07	1.21	1251832|dinP|DNA polymerase IV|+
STM0314_1038_1072	0.09	1.68	1251833|STM0314|pseudo|+

STM0315_289_323	0.28	-1.17	1251834|prfH|peptide chain release factor-like protein|+
STM0316_1387_1421	0.03	1.50	1251835|pepD|aminoacyl-histidine dipeptidase|-
STM0317_137_171	0.05	-1.95	1251836|gpt|xanthine-guanine phosphoribosyltransferase|+
STM0318_374_408	0.56	-1.04	1251837|frsA|fermentation/respiration switch protein|+
STM0319_241_275	0.04	1.58	1251838|crl|DNA-binding transcriptional regulator Crl|+
STM0320_190_224	0.00	2.72	1251839|phoE|outer membrane phosphoporin protein E|-
STM0321_361_395	0.09	-1.50	1251840|proB|gamma-glutamyl kinase|+
STM0322_348_382	0.74	-1.22	1251841|proA|gamma-glutamyl phosphate reductase|+
STM0325_579_613	0.01	1.52	1251844|STM0325|putative truncated IS3 transposase|-
STM0327_129_163	0.00	-2.33	1251846|STM0327|putative cytoplasmic protein|+
STM0328.s_435_469	0.04	1.33	1251847|STM0328.s|putative permease|+
STM0329_431_465	0.04	-1.35	1251848|STM0329|isopropylmalate isomerase large subunit|+
STM0330_337_371	0.86	-1.02	1251849|STM0330|putative 3-isopropylmalate isomerase|+
STM0332_609_643	0.11	1.54	1251851|STM0332|putative hydrolase/acyltransferase|+
STM0333_769_803	0.25	-1.12	1251852|STM0333|putative transcriptional regulator|+
STM0335_19_54	0.96	1.02	1251854|STM0335|putative outer membrane protein|+
STM0336_177_211	0.02	1.49	1251855|stbE|putative fimbrial chaparone|-
STM0338_1787_1821	0.94	-1.01	1251857|stbC|putative fimbrial usher|-
STM0339_193_227	0.04	2.35	1251858|stbB|putative fimbrial chaperone|-
STM0340_283_317	0.41	1.26	1251859|stbA|putative fimbrial major subunit|-
STM0341_275_309	0.02	2.96	1251860|STM0341|putative inner membrane protein|+
STM0342_49_83	0.47	-1.09	1251861|STM0342|putative periplasmic protein|+
STM0343_1128_1162	0.15	1.51	1251862|STM0343|hypothetical protein|+
STM0344_369_403	0.16	1.81	1251863|STM0344|putative response regulator|+
STM0345_385_419	0.91	-1.04	1251864|STM0345|putative inner membrane protein|+
STM0346_337_371	0.07	2.93	1251865|STM0346|putative outer membrane protein|+
STM0347_249_283	0.01	1.93	1251866|STM0347|putative response regulator|+
STM0348_45_79	0.03	3.27	1251867|STM0348|putative inner membrane protein|+
STM0349_65_99	0.16	1.38	1251868|STM0349|putative outer membrane lipoprotein|+
STM0350.S_1307_1341	0.65	1.08	1251869|STM0350.S|outer membrane efflux-like protein|-
STM0351_2377_2411	0.20	1.43	1251870|STM0351|putative cation efflux system protein|-
STM0352.S_607_641	0.15	1.71	1251871|STM0352.S|putative cation efflux pump|-
STM0353_1658_1692	0.03	-1.45	1251872|STM0353|putative cation transport ATPase|+
STM0354_365_399	0.95	-1.01	1251873|STM0354|putative transcriptional regulator|+
STM0355_62_96	0.04	-1.41	1251874|STM0355|putative copper chaperone|+
STM0356_479_513	0.00	-2.40	1251875|STM0356|putative inner membrane protein|+

STM0357_1088_1122	0.02	1.48	1251876|mod|DNA methylase|+
STM0359_2_40	0.02	2.25	1251878|STM0359|putative cytoplasmic protein|+
STM0360_949_983	0.40	1.24	1251879|STM0360|cytochrome BD2 subunit II|+
STM0361_16_50	0.89	1.03	1251880|STM0361|cytochrome BD2 subunit III|+
STM0362_65_99	0.72	1.09	1251881|STM0362|putative cytoplasmic protein|+
STM0363_118_152	0.00	2.39	1251882|STM0363|putative transcriptional regulator|+
STM0364_1398_1432	0.88	1.04	1251883|foxA|ferrioxamine receptor|+
STM0365_4_38	0.00	-4.16	1251884|yahN|putative transport protein|-
STM0366_95_129	0.32	-1.24	1251885|yahO|hypothetical protein|+
STM0367_1107_1141	0.00	-4.26	1251886|prpR|prp operon regulator|-
STM0368_65_99	0.09	-1.26	1251887|prpB|2-methylisocitrate lyase|+
STM0369_471_505	0.46	1.44	1251888|prpC|methylcitrate synthase|+
STM0370_1029_1063	0.06	1.41	1251889|prpD|2-methylcitrate dehydratase|+
STM0372_553_587	0.02	1.63	1251891|hemB|delta-aminolevulinic acid dehydratase|-
STM0373_2770_2804	0.82	1.02	1251892|yaiU|flagellar protein|+
STM0374_257_291	0.01	2.24	1251893|yaiV|putative DNA-binding transcriptional regulator|+
STM0375_132_166	0.08	-1.29	1251894|ampH|beta-lactamase/D-alanine carboxypeptidase|-
STM0376_1150_1184	0.13	1.40	1251895|sbmA|transport protein|+
STM0377_1008_1042	0.04	1.26	1251896|yaiW|putative outer membrane lipoprotein|+
STM0378_165_199	0.00	4.41	1251897|yaiY|putative inner membrane protein|-
STM0379_125_159	0.00	-2.93	1251898|yaiZ|putative inner membrane protein|+
STM0380_256_290	0.01	-1.64	1251899|ddlI|D-alanyl-alanine synthetase A|-
STM0381_625_659	0.29	1.23	1251900|STM0381|putative inner membrane protein|+
STM0382_213_247	0.02	1.31	1251901|STM0382|putative permease|+
STM0383_197_231	0.03	1.93	1251902|yaiB|hypothetical protein|+
STM0384_129_163	0.01	4.71	1251903|psiF|hypothetical protein|+
STM0385_1010_1044	0.33	-1.11	1251904|yaiC|hypothetical protein|+
STM0386_33_67	0.54	-1.04	1251905|proC|pyrroline-5-carboxylate reductase|-
STM0387_161_195	0.77	-1.04	1251906|yaiI|hypothetical protein|+
STM0388_257_291	0.03	-3.18	1251907|aroL|shikimate kinase III|+
STM0389_13_47	0.18	-1.49	1251908|yaiA|hypothetical protein|+
STM0390_25_59	0.01	-2.92	1251909|aroM|hypothetical protein|+
STM0391_153_187	0.72	1.09	1251910|yaiE|hypothetical protein|+
STM0392_657_691	0.51	-1.18	1251911|rdgC|recombination associated protein|-
STM0393_289_323	0.13	-1.32	1251912|yajF|fructokinase|+
STM0394_1038_1072	0.02	1.53	1251913|araJ|protein AraJ|-

STM0395_2702_2736	0.17	-1.29	1251914|sbcC|exonuclease subunit SbcC|-
STM0396_844_878	0.43	1.11	1251915|sbcD|exonuclease subunit SbcD|-
STM0397_513_547	0.67	-1.09	1251916|phoB|DNA-binding response regulator in two-component regulatory system with PhoR (or CreC)|+
STM0398_1097_1131	0.23	-1.38	1251917|phoR|phosphate regulon sensor protein|+
STM0399_977_1011	0.18	1.23	1251918|brnQ|branched-chain amino acid transporter|+
STM0400_884_918	0.38	-1.05	1251919|proY|putative proline transporter|+
STM0401_1251_1285	0.96	-1.01	1251920|malZ|maltodextrin glucosidase|+
STM0402_385_419	0.05	1.84	1251921|STM0402|putative thiol-alkyl hydroperoxide reductase|-
STM0403_129_163	0.30	1.22	1251922|yajB|acyl carrier protein phosphodiesterase|-
STM0404_578_612	0.04	-2.22	1251923|queA|S-adenosylmethionine:tRNA ribosyltransferase-isomerase|+
STM0405_961_995	0.55	-1.08	1251924|tgt|queuine tRNA-ribosyltransferase|+
STM0406_273_307	0.02	-2.43	1251925|yajC|preprotein translocase subunit YajC|+
STM0407_1041_1075	0.01	-2.92	1251926|secD|preprotein translocase subunit SecD|+
STM0408_609_643	0.00	-2.04	1251927|secF|preprotein translocase subunit SecF|+
STM0409_65_99	0.24	1.19	1251928|STM0409|hypothetical protein|+
STM0410_81_115	0.00	-1.37	1251929|STM0410|putative regulatory protein|+
STM0411_289_323	0.08	1.54	1251930|yajD|hypothetical protein|+
STM0412_93_127	0.39	1.16	2673775|STM0412|-|-
STM0413_257_291	0.00	-4.46	1251932|tsx|nucleoside channel|-
STM0414_325_359	0.02	1.28	1251933|yajI|hypothetical protein|-
STM0415_97_131	0.01	2.50	1251934|ybaD|hypothetical protein|+
STM0416_873_907	0.19	-1.18	1251935|ribD|bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase|+
STM0417_353_387	0.94	-1.02	1251936|ribH|riboflavin synthase subunit beta|+
STM0418_121_155	0.29	1.17	1251937|nusB|transcription antitermination protein NusB|+
STM0419_849_883	0.17	-1.32	1251938|thiL|thiamine monophosphate kinase|+
STM0420_225_259	0.07	-1.33	1251939|pgpA|phosphatidylglycerophosphatase A|+
STM0421_917_951	0.07	-1.83	1251940|yajO|putative oxidoreductase|-
STM0422_1200_1234	0.10	-1.29	1251941|dxs|1-deoxy-D-xylulose-5-phosphate synthase|-
STM0423_225_259	0.03	-1.24	1251942|ispA|geranyltranstransferase|-
STM0424_33_67	0.02	-1.34	1251943|xseB|exodeoxyribonuclease VII small subunit|-
STM0425_482_516	0.06	-1.48	1251944|thiI|thiamine biosynthesis protein ThiI|+
STM0426_433_467	0.05	1.30	1251945|phnV|2-aminoethylphosphonate transporter|-
STM0427_375_409	0.49	-1.22	1251946|phnU|2-aminoethylphosphonate transporter|-
STM0428_719_753	0.26	1.14	1251947|phnT|2-aminoethylphosphonate transporter|-

STM0430_513_547	0.21	1.17	1251949|phnR|2-aminoethylphosphonate transport protein|-
STM0431_281_315	0.73	1.06	1251950|phnW|2-aminoethylphosphonate transport|+
STM0432_257_291	0.90	-1.01	1251951|phnX|2-aminoethylphosphonate transport|+
STM0433_129_163	0.01	2.71	1251952|thiJ|hypothetical protein|-
STM0434_769_803	0.02	1.73	1251953|apbA|2-dehydropantoate 2-reductase|-
STM0435_97_131	0.02	-1.78	1251954|yajQ|nucleotide-binding protein|+
STM0436.S_1006_1040	0.03	1.60	1251955|yajR|putative transport protein|-
STM0436A_89_123	0.10	1.25	1251956|STM0436A|-|-
STM0438_769_803	0.02	2.14	1251958|STM0438|tetratricopeptide repeat protein|+
STM0439_849_883	0.03	2.38	1251959|cyoE|protoheme IX farnesyltransferase|-
STM0440_61_95	0.06	-1.76	1251960|cyoD|cytochrome o ubiquinol oxidase subunit IV|-
STM0441_229_263	0.00	-2.53	1251961|cyoC|cytochrome o ubiquinol oxidase subunit III|-
STM0442_1393_1427	0.01	-1.47	1251962|cyoB|cytochrome o ubiquinol oxidase subunit II|-
STM0443_129_163	0.00	-2.84	1251963|cyoA|cytochrome o ubiquinol oxidase subunit III|-
STM0444_1333_1367	0.03	1.22	1251964|ampG|muropeptide transporter|-
STM0445_293_327	0.03	-1.81	1251965|yajG|hypothetical protein|-
STM0446_257_291	0.11	1.50	1251966|bolA|transcriptional regulator BolA|+
STM0447_1036_1070	0.19	1.54	1251967|tig|trigger factor|+
STM0448_145_179	0.00	1.31	1251968|clpP|ATP-dependent Clp protease proteolytic subunit|+
STM0449_273_307	0.06	-1.18	1251969|clpX|ATP-dependent protease ATP-binding subunit|+
STM0450_1708_1742	0.01	2.33	1251970|lon|DNA-binding ATP-dependent protease La|+
STM0451_225_259	0.00	-4.14	1251971|hupB|transcriptional regulator HU subunit beta|+
STM0452_1577_1611	0.02	1.80	1251972|cypD|peptidyl-prolyl cis-trans isomerase (rotamase D)|+
STM0453_141_175	0.12	1.20	1251973|ybaV|putative DNA uptake protein|+
STM0454_189_223	0.00	-3.79	1251974|ybaW|putative esterase|+
STM0455_609_643	0.03	1.83	1251975|ybaX|queuosine biosynthesis protein QueC|-
STM0456_1422_1456	0.00	-2.92	1251976|ybaE|putative ABC transporter periplasmic binding protein|-
STM0457_721_755	0.42	1.07	1251977|cof|putative hydrolase|+
STM0458_953_987	0.06	1.91	1251978|STM0458|putative cysteine synthase/cystathionine beta-synthase|-
STM0459_353_387	0.07	1.46	1251979|ybaO|putative transcriptional regulator|+
STM0460_1342_1376	0.46	1.14	1251980|mdlA|putative multidrug transporter membrane\ATP-binding components|+
STM0461_1071_1105	0.26	-1.14	1251981|mdlB|putative multidrug transporter membrane\ATP-binding components|+
STM0461.1n_377_411	0.14	1.53	2673746|STM0461.1n|hypothetical protein|-
STM0462_171_205	0.01	1.81	1251982|glnK|nitrogen regulatory protein P-II 2|+

STM0463_1184_1218	0.03	1.40	1251983|amtB|ammonium transporter|+
STM0464_225_259	0.02	1.70	1251984|tesB|acyl-CoA thioesterase III|-
STM0465_17_51	0.05	1.67	1251985|ybaY|hypothetical protein|+
STM0466_342_376	0.51	-1.17	1251986|ybaZ|putative methyltransferase|-
STM0467_17_51	0.62	1.56	1251987|ffs|misc_RNA|+
STM0468_656_690	0.18	-1.27	1251988|ylaB|hypothetical protein|-
STM0469_5_39	0.03	-12.11	1251989|rpmE2|50S ribosomal protein L31 type B|+
STM0470_49_83	0.05	-4.97	1251990|rpmJ|50S ribosomal protein L36|+
STM0471_289_323	0.00	2.54	1251991|ylaC|putative inner membrane protein|-
STM0472_73_107	0.66	1.04	1251992|maa|maltose O-acetyltransferase|-
STM0473_125_159	0.05	1.61	1251993|hha|hemolysin expression-modulating protein|-
STM0474_145_179	0.00	1.99	1251994|ybaJ|hypothetical protein|-
STM0475_2623_2657	0.19	1.13	1251995|acrB|acridine efflux pump|-
STM0476_211_245	0.10	1.33	1251996|acrA|acridine efflux pump|-
STM0477_185_221	0.84	-1.02	1251997|acrR|DNA-binding transcriptional repressor|+
STM0478_2876_2910	0.28	-1.19	1251998|aefA|potassium efflux protein KefA|+
STM0479_585_619	0.05	1.58	1251999|STM0479|putative transposase|-
STM0480_25_59	0.05	1.21	1252000|ybaM|hypothetical protein|-
STM0481_97_131	0.88	1.05	1252001|priC|primosomal replication protein N''|-
STM0482_129_163	0.44	-1.14	1252002|ybaN|hypothetical protein|+
STM0483_289_323	0.02	-1.62	1252003|apt|adenine phosphoribosyltransferase|+
STM0484_1046_1080	0.54	-1.07	1252004|dnaX|DNA polymerase III subunits gamma and tau|+
STM0485_5_40	0.87	1.02	1252005|ybaB|hypothetical protein|+
STM0486_197_231	0.60	1.31	1252006|recR|recombination protein RecR|+
STM0487.S_1420_1454	0.96	1.01	1252007|htpG|heat shock protein 90|+
STM0488_129_163	0.01	-3.73	1252008|adk|adenylate kinase|+
STM0489_321_355	0.21	1.12	1252009|hemH|ferrochelatase|+
STM0490_673_707	0.01	-2.25	1252010|aes|acetyl esterase|-
STM0491_1106_1140	0.00	-1.59	1252011|gsk|inosine-guanosine kinase|+
STM0492_878_912	0.00	1.76	1252012|ybaL|putative cation:proton antiport protein|-
STM0493_238_272	0.59	-1.12	1252013|fsr|putative transport protein|-
STM0494_1110_1144	0.03	-1.91	1252014|ushA|bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic precursor|+
STM0495_113_147	0.05	1.26	1252015|ybaK|hypothetical protein|-
STM0496_641_675	0.37	1.28	1252016|ybaP|putative cytoplasmic protein|-
STM0497_205_239	0.03	2.41	1252017|STM0497|putative periplasmic protein|-

STM0498_2447_2481	0.15	-1.79	1252018|copA|copper transporter|-
STM0499_353_387	0.01	2.11	1252019|cueR|DNA-binding transcriptional activator of copper-responsive regulon genes|+
STM0500_113_147	0.01	1.78	1252020|ybbJ|hypothetical protein|-
STM0502_609_643	0.22	-1.19	1252022|ybbL|putative ABC transporter ATP-binding protein YbbL|+
STM0503_177_211	0.07	1.27	1252023|ybbM|putative transport protein|+
STM0504_665_699	0.29	1.32	1252024|ybbN|putative thioredoxin protein|-
STM0505_129_163	0.16	-1.12	1252025|ybbO|short chain dehydrogenase|-
STM0506_433_467	0.07	-1.46	1252026|tesA|multifunctional acyl-CoA thioesterase I and protease I and lysophospholipase L1|-
STM0507_73_107	0.00	2.24	1252027|ybbA|putative ABC transporter ATP-binding protein YbbA|+
STM0508_1752_1786	0.02	1.39	1252028|ybbP|putative inner membrane protein|+
STM0509_935_969	0.79	-1.06	1252029|STM0509|putative outer membrane protein|+
STM0510_492_526	0.06	-1.43	1252030|sfbA|putative ABC-type transport system ATPase component|+
STM0511_850_884	0.13	-1.23	1252031|sfbB|putative ABC-type transport system ATPase component|+
STM0512_385_419	0.01	-2.26	1252032|sfbC|putative ABC transporter permease component|+
STM0513_300_334	0.01	1.64	1252033|ybbB|tRNA 2-selenouridine synthase|-
STM0516_641_675	0.21	1.15	1252036|allR|DNA-binding transcriptional repressor|+
STM0518_305_339	0.26	-1.47	1252038|gip|hydroxypyruvate isomerase|+
STM0522_987_1021	0.26	1.29	1252042|allP|allantoin permease|+
STM0523_363_397	0.39	-1.30	1252043|allB|allantoinase|+
STM0525_1078_1112	0.03	2.82	1252045|glxK|glycerate kinase II|+
STM0526_161_195	0.58	1.18	1252046|ylbA|hypothetical protein|-
STM0528_195_229	0.15	1.88	1252048|allD|ureidoglycolate dehydrogenase|-
STM0529_1162_1196	0.05	1.18	1252049|fdrA|membrane protein FdrA|+
STM0531_389_423	0.69	-1.04	1252051|ylbF|putative cytoplasmic protein|+
STM0533_853_887	0.01	-2.73	1252053|purK|phosphoribosylaminoimidazole carboxylase ATPase subunit|-
STM0534_169_203	0.01	-4.50	1252054|purE|phosphoribosylaminoimidazole carboxylase catalytic subunit|-
STM0535_321_355	0.96	1.01	1252055|lpxH|UDP-2 3-diacylglucosamine hydrolase|-
STM0536_361_395	0.09	-1.70	1252056|ppiB|peptidyl-prolyl cis-trans isomerase B (rotamase B)|-
STM0537_515_549	0.07	1.25	1252057|cysS|cysteinyl-tRNA synthetase|+
STM0538_257_291	0.83	-1.05	1252058|STM0538|putative outer membrane protein|-
STM0539_377_411	0.16	-1.18	1252059|STM0539|putative inner membrane protein|-
STM0540_149_183	0.64	1.04	1252060|ybcI|putative membrane-bound metal-dependent hydrolase|-
STM0541_152_187	0.05	1.25	1252061|ybcJ|hypothetical protein|-

STM0542_609_643	0.07	1.26	1252062|folD|bifunctional 5 10-methylene-tetrahydrofolate dehydrogenase/ 5 10-methylene-tetrahydrofolate cyclohydrolase|-
STM0543_65_99	0.07	-2.16	1252063|fimA|fimbrin|+
STM0545_218_252	0.02	2.45	1252065|fimC|periplasmic chaperone|+
STM0547_969_1003	0.04	-1.32	1252067|fimH|minor fimbrial subunit|+
STM0550_41_75	0.13	1.37	1252070|fimY|putative regulatory protein|-
STM0552_167_201	0.02	1.39	1252072|fimW|putative fimbrial protein|-
STM0554_17_51	0.69	1.17	1252074|STM0554|integrase|-
STM0555_337_371	0.64	1.15	2673757|STM0555|pseudo|-
STM0558_665_699	0.05	1.76	1252078|yfdH|putative glycosyltransferase|-
STM0559_257_291	0.71	1.14	1252079|rfbI|putative glycosyl translocase|-
STM05559.T1_9_43	0.03	1.91	2673761|STM05559.T1|tRNA|+
STM0560_5_39	0.42	1.22	1252080|STM0560|pseudo|-
STM0561_43_77	0.03	1.21	1252081|STM0561|sensor kinase|-
STM0562_169_203	0.04	-1.26	2673759|STM0562|-|+
STM0563_241_275	0.00	1.77	1252083|STM0563|putative transcriptional regulator|-
STM0564_583_617	0.95	1.01	1252084|STM0564|pyridine nucleotide-disulfide oxidoreductase|+
STM0565_65_99	0.76	1.07	1252085|STM0565|putative periplasmic protein|+
STM0567_321_355	0.05	1.45	1252087|STM0567|putative DNA repair ATPase|-
STM0568_1292_1326	0.94	-1.01	1252088|pheP|phenylalanine transporter|+
STM0569_1017_1051	0.02	-1.37	1252089|ybdG|hypothetical protein|-
STM0570_1388_1422	0.15	-1.16	1252090|apeE|outer membrane esterase|+
STM0571_1731_1765	0.12	1.50	1252091|STM0571|putative inner membrane protein|+
STM0572_849_883	0.16	-1.24	1252092|STM0572|putative phosphosugar isomerase|-
STM0573_813_847	0.03	2.22	1252093|STM0573|putative inner membrane protein|-
STM0575_113_147	0.14	1.52	1252095|STM0575|putative inner membrane protein|-
STM0576_113_147	0.01	2.33	1252096|STM0576|putative PTS system mannose-specific enzyme IIAB|-
STM0577_33_67	0.41	1.10	1252097|STM0577|putative PTS system mannose-specific enzyme IIAB|-
STM0578_417_451	0.16	-1.48	1252098|nfnB|dihydropteridine reductase|-
STM0579_117_151	0.33	1.08	1252099|ybdF|hypothetical protein|-
STM0580_345_379	0.01	-1.92	1252100|STM0580|putative regulatory protein|-
STM0581_61_95	0.25	1.08	1252101|STM0581|putative regulatory protein|+
STM0582_3_37	0.68	-1.11	1252102|ybdJ|putative inner membrane protein|-
STM0583_696_730	0.03	-1.29	1252103|ybdK|putative cytoplasmic protein|-
STM0584_513_547	0.72	-1.15	1252104|entD|phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex|-

STM0585_2025_2059	0.18	-1.44	1252105|fepA|outer membrane ferric enterobactin receptor precursor|-
STM0588_3318_3352	0.20	-1.37	1252108|entF|enterobactin synthase subunit F|+
STM0589_394_428	0.06	1.97	1252109|fepE|ferric enterobactin/enterochelin transporter|+
STM0590_721_755	0.40	-1.17	1252110|fepC|iron-enterobactin transporter ATP-binding protein|-
STM0591_369_403	0.40	-1.13	1252111|fepG|iron-enterobactin transporter permease|-
STM0592_889_923	0.24	-1.22	1252112|fepD|iron-enterobactin transporter membrane protein|-
STM0593_310_344	0.87	-1.03	1252113|ybdA|enterobactin exporter EntS|+
STM0594_225_259	0.16	-1.33	1252114|fepB|iron-enterobactin transporter periplasmic binding protein|-
STM0595_241_275	0.36	1.19	1252115|entC|isochorismate synthase|+
STM0596_992_1026	0.97	-1.01	1252116|entE|enterobactin synthase subunit E|+
STM0597_769_803	0.01	1.42	1252117|entB|2 3-dihydro-2 3-dihydroxybenzoate synthetase|+
STM0598_705_739	0.62	-1.07	1252118|entA|2 3-dihydroxybenzoate-2 3-dehydrogenase|+
STM0599_187_221	0.23	-1.18	1252119|ybdB|hypothetical protein|+
STM0600_1299_1333	0.00	-9.62	1252120|cstA|carbon starvation protein|+
STM0601_67_101	0.00	-5.90	1252121|ybdD|putative cytoplasmic protein|+
STM0602_938_972	0.01	15.08	1252122|ybdH|putative glycerol dehydrogenase|-
STM0603_254_288	0.01	9.24	1252123|ybdL|putative aminotransferase|+
STM0604_257_291	0.43	1.20	1252124|ybdM|putative transcriptional regulator|-
STM0605_773_807	0.07	2.22	1252125|ybdN|putative 3'-phosphoadenosine 5'-phosphosulfate sulfotransferase|-
STM0606_681_715	0.02	2.18	1252126|ybdO|putative transcriptional regulator|-
STM0607_417_451	0.37	-1.11	1252127|dsbG|disulfide isomerase/thiol-disulfide oxidase|-
STM0608_65_99	0.99	-1.00	1252128|ahpC|alkyl hydroperoxide reductase subunit C|+
STM0609_935_969	0.15	1.38	1252129|ahpF|alkyl hydroperoxide reductase F52a subunit|+
STM0610_161_195	0.26	1.56	1252130|STM0610|putative anaerobic dehydrogenase component|+
STM0611_2113_2147	0.33	-1.11	1252131|STM0611|putative oxidoreductase protein|+
STM0612_201_235	0.19	-1.28	1252132|STM0612|putative hydrogenase protein|+
STM0613_725_759	0.20	-1.14	1252133|STM0613|putative hydrogenase protein|+
STM0614_209_243	0.05	1.66	1252134|ybdQ|putative universal stress protein|-
STM0615_816_850	0.03	-1.37	1252135|ybdR|putative dehydrogenase|+
STM0616_25_59	0.03	-1.63	1252136|rnk|nucleoside diphosphate kinase regulator|-
STM0617_497_531	0.01	2.83	1252137|rna|ribonuclease II|-
STM0618_1121_1155	0.53	-1.39	1252138|citT|citrate/succinate transport antiport protein|-
STM0619_785_819	0.47	-1.14	1252139|citG|triphosphoribosyl-dephospho-CoA synthase|-
STM0620_481_515	0.11	-1.21	1252140|citX|2'-(5''-triphosphoribosyl)-3'-dephospho-CoA:apo-citrate lyase|-
STM0622_193_227	0.03	-1.25	1252142|citE|citrate lyase beta chain|-

STM0624_798_832	0.49	1.07	1252144|citC|citrate lyase synthetase|-
STM0625_711_745	0.01	-1.59	1252145|dpiB|sensory histidine kinase|+
STM0626_465_499	0.02	-1.42	1252146|dpiA|DNA-binding response regulator in two-component regulatory system with citA|+
STM0628_369_403	0.02	1.33	1252148|pagP|palmitoyl transferase for Lipid A|+
STM0629_145_179	0.01	-2.83	1252149|cspE|cold shock protein E|+
STM0630_49_83	0.26	-1.16	1252150|ccrB|camphor resistance protein CrcB|-
STM0631_433_467	0.11	1.21	1252151|ybeM|putative hydrolase|+
STM0632_91_125	0.07	1.64	1252152|tatE|twin arginine translocase protein E|+
STM0633_617_651	0.19	-1.23	1252153|lipA|lipoyl synthase|-
STM0634_257_291	0.04	-1.68	1252154|ybeF|putative DNA-binding transcriptional regulator|-
STM0635.S_273_307	0.00	2.02	1252155|lipB|lipoyltransferase|-
STM0636_81_115	0.09	-1.26	1252156|ybeD|hypothetical protein|-
STM0638_643_677	0.05	-1.29	1252158|rlpA|rare lipoprotein A|-
STM0639_426_460	0.71	1.08	1252159|mrdB|cell wall shape-determining protein|-
STM0640_1223_1257	0.01	2.46	1252160|mrdA|penicillin-binding protein 2|-
STM0641_45_79	0.31	1.20	1252161|ybeA|hypothetical protein|-
STM0642_129_163	0.01	2.54	1252162|ybeB|hypothetical protein|-
STM0643_229_263	0.20	1.12	1252163|cobC|alpha ribazole-5'-P phosphatase|-
STM0644_240_274	0.02	-2.54	1252164|cobD|threonine-phosphate decarboxylase|+
STM0645_65_99	0.00	-1.71	1252165|nadD|nicotinic acid mononucleotide adenyltransferase|-
STM0646_145_179	0.67	-1.07	1252166|holA|DNA polymerase III subunit delta|-
STM0647_329_363	0.02	-1.68	1252167|rlpB|LPS-assembly lipoprotein RplB|-
STM0648_1720_1754	0.47	-1.17	1252168|leuS|leucyl-tRNA synthetase|-
STM0649.S_101_135	0.07	1.44	1252169|STM0649.S|putative hydrolase|+
STM0651_305_339	0.07	1.45	1252171|STM0651|2-keto-3-deoxygluconate permease|+
STM0652_1442_1476	0.49	-1.24	1252172|STM0652|putative sigma-54 dependent transcriptional regulator|+
STM0653_5_39	0.01	-1.84	1252173|ybeL|hypothetical protein|+
STM0654_833_867	0.05	2.28	1252174|ybeQ|tetratricopeptide repeat protein|-
STM0655_289_323	0.20	-1.17	1252175|ybeR|putative cytoplasmic protein|+
STM0656_755_789	0.14	-1.37	1252176|ybeS|putative molecular chaperone|+
STM0658_730_764	0.13	-1.15	1252178|ybeV|putative molecular chaperone|+
STM0660_832_866	0.83	1.09	1252180|STM0660|putative cytoplasmic protein|-
STM0661_401_435	0.02	-2.14	1252181|rihA|ribonucleoside hydrolase 1|-
STM0662_513_547	0.02	-1.99	1252182|gltL|glutamate/aspartate transporter|-
STM0663_321_355	0.01	-1.59	1252183|gltK|glutamate/aspartate transporter|-

STM0664_641_675	0.01	-1.35	1252184|gltJ|glutamate/aspartate transporter|-
STM0665_289_323	0.60	-1.06	1252185|gltI|glutamate and aspartate transporter subunit|-
STM0666_1212_1246	0.00	1.27	1252186|lnt|apolipoprotein N-acyltransferase|-
STM0667_129_163	0.04	-1.11	1252187|ybeX|putative transport protein|-
STM0668_401_435	0.32	1.18	1252188|ybeY|hypothetical protein|-
STM0669_727_761	0.45	-1.07	1252189|phoL|putative phosphate starvation-inducible protein|-
STM0670_714_748	0.16	1.14	1252190|miaB|rRNA modification protein|-
STM0671_705_739	0.33	-1.16	1252191|ubiF|2-octaprenyl-3-methyl-6-methoxy-1 4-benzoquinol hydroxylase|+
STM0672_273_307	0.37	1.24	1252192|STM0672|putative inner membrane protein|-
STM0675/STM0679_2_36	0.02	-1.76	1252195/1252199|metU/metT|tRNA|-
STM0678_9_43	0.01	-2.65	1252198|leuW|tRNA|-
STM0680_1114_1148	0.01	1.70	1252200|asnB|asparagine synthetase B|-
STM0681_9_43	0.11	-1.14	1252201|nagD|UMP phosphatase|-
STM0682_862_896	0.05	1.63	1252202|nagC|N-acetylglucosamine operon transcriptional repressor|-
STM0683_924_958	0.30	-1.15	1252203|nagA|N-acetylglucosamine-6-phosphate deacetylase|-
STM0684_689_723	0.07	-1.09	1252204|nagB|glucosamine-6-phosphate deaminase|-
STM0685_1498_1532	0.00	-2.26	1252205|nagE|N-acetyl glucosamine specific PTS system components IIABC|+
STM0686_1245_1279	0.89	-1.04	1252206|glnS|glutaminyl-tRNA synthetase|+
STM0687_728_762	0.03	-1.65	1252207|ybfM|putative outer membrane protein|+
STM0689_498_532	0.31	1.20	1252209|citA|citrate-proton symporter|-
STM0691_1197_1231	0.07	1.46	1252211|STM0691|tricarballylate dehydrogenase|-
STM0692_297_331	0.57	-1.05	1252212|STM0692|putative transcriptional regulator|-
STM0693_257_291	0.28	1.14	1252213|fur|ferric uptake regulator|-
STM0694_385_419	0.06	1.35	1252214|fldA|flavodoxin FldA|-
STM0695_13_47	0.08	-1.32	1252215|ybfE|LexA regulated protein|-
STM0696_137_171	0.70	-1.05	1252216|ybfF|hypothetical protein|-
STM0697_257_291	0.22	-1.17	1252217|seqA|replication initiation regulator SeqA|+
STM0698_642_676	0.02	-2.02	1252218|pgm|phosphoglucomutase|+
STM0699_305_339	0.27	-1.13	1252219|STM0699|putative cytoplasmic protein|-
STM0700_897_931	0.23	-1.16	1252220|potE|putrescine/ornithine antiporter|-
STM0702_129_163	0.26	1.09	1252222|kdpE|DNA-binding response regulator in two-component regulatory system with KdpD|-
STM0703_2262_2296	0.08	-1.31	1252223|kdpD|sensor protein KdpD|-
STM0704_227_261	0.06	1.18	1252224|kdpC|potassium-transporting ATPase subunit C|-
STM0705_1642_1676	0.47	1.13	1252225|kdpB|potassium-transporting ATPase subunit B|-

STM0707_48_86	0.01	1.93	1252227|STM0707|putative outer membrane protein|-
STM0708_141_175	0.00	2.34	1252228|ybfA|putative periplasmic protein|+
STM0709_551_585	0.20	-1.22	1252229|phrB|deoxyribodipyrimidine photolyase|+
STM0710_595_629	0.02	2.53	1252230|ybgH|putative POT family transport protein|-
STM0711_169_203	0.13	-1.24	1252231|ybgI|putative hydrolase-oxidase|+
STM0712_17_51	0.66	-1.17	1252232|ybgJ|putative carboxylase|+
STM0713_593_627	0.19	-1.26	1252233|ybgK|putative carboxylase|+
STM0714_385_419	0.13	-1.23	1252234|ybgL|hypothetical protein|+
STM0715_33_67	0.02	1.68	1252235|STM0715|putative cytoplasmic protein|+
STM0716_493_527	0.03	2.82	1252236|STM0716|putative phage integrase|+
STM0717_301_335	0.83	1.02	1252237|STM0717|putative inner membrane protein|+
STM0718_513_547	0.41	1.04	1252238|STM0718|putative cytoplasmic protein|+
STM0719_602_636	0.02	2.31	1252239|STM0719|putative UDP-galactopyranose mutase|+
STM0721_775_809	0.51	1.19	1252241|STM0721|putative glycosyl transferase|+
STM0722_137_171	0.05	2.13	1252242|STM0722|putative ABC transporter permease protein|+
STM0723_161_195	0.20	1.69	1252243|STM0723|putative ABC-type polysaccharide/polyol phosphate transport system ATPase component|+
STM0725_33_67	0.04	2.91	1252245|STM0725|putative glycosyltransferase|+
STM0726_1673_1707	0.02	2.23	1252246|STM0726|putative glycosyl transferase|+
STM0727_100_135	0.04	-1.89	1252247|STM0727|putative cytoplasmic protein|+
STM0728_545_579	0.94	1.01	1252248|neil|endonuclease VIII|+
STM0729_960_994	0.14	1.16	1252249|abrB|putative transport protein|-
STM0730_349_383	0.00	-4.30	1252250|gltA|type II citrate synthase|-
STM0731_49_83	0.11	-1.58	1252251|STM0731|putative inner membrane protein|+
STM0732_109_143	0.00	-14.72	1252252|sdhC|succinate dehydrogenase cytochrome b556 large membrane subunit|+
STM0733_49_83	0.00	-5.92	1252253|sdhD|succinate dehydrogenase cytochrome b556 small membrane subunit|+
STM0734_1664_1698	0.00	-7.14	1252254|sdhA|succinate dehydrogenase flavoprotein subunit|+
STM0735_669_703	0.00	-10.77	1252255|sdhB|succinate dehydrogenase iron-sulfur subunit|+
STM0736_1867_1901	0.00	-8.11	1252256|kgd|alpha-ketoglutarate decarboxylase|+
STM0737_754_788	0.00	-4.99	1252257|sucB|dihydrolipoamide acetyltransferase|+
STM0738_936_970	0.00	-12.44	1252258|sucC|succinyl-CoA synthetase subunit beta|+
STM0739_65_99	0.00	-8.47	1252259|sucD|succinyl-CoA synthetase subunit alpha|+
STM0740_586_620	0.87	-1.03	1252260|cydA|cytochrome d terminal oxidase polypeptide subunit II|+
STM0741_701_735	0.34	1.14	1252261|cydB|cytochrome d terminal oxidase polypeptide subunit III|+

STM0742_9_43	0.97	1.01	1252262|ybgT|putative outer membrane lipoprotein|+
STM0743_9_43	0.07	1.30	1252263|ybgE|hypothetical protein|+
STM0744_361_395	0.01	-1.40	1252264|ybgC|acyl-CoA thioester hydrolase YbgC|+
STM0745_169_203	0.04	-2.03	1252265|tolQ|colicin uptake protein TolQ|+
STM0746_193_227	0.14	-1.46	1252266|tolR|colicin uptake protein TolR|+
STM0747_1001_1035	0.89	-1.02	1252267|tolA|cell envelope integrity inner membrane protein TolA|+
STM0748_806_840	0.01	-1.80	1252268|tolB|translocation protein TolB|+
STM0749_129_163	0.02	-2.58	1252269|pal|peptidoglycan-associated outer membrane lipoprotein|+
STM0750_193_227	0.15	-1.30	1252270|ybgF|hypothetical protein|+
STM0756_397_431	0.05	1.57	1252276|nadA|quinolinate synthetase|+
STM0757_17_51	0.04	1.21	1252277|pnuC|nucleoside/purine/pyrimidine transporter|+
STM0758_833_867	0.33	1.17	1252278|ybgR|zinc transporter ZitB|-
STM0759_225_259	0.04	2.05	1252279|ybgS|hypothetical protein|-
STM0760_166_200	0.01	-1.32	1252280|aroG|phospho-2-dehydro-3-heoxyheptonate aldolase|+
STM0761_353_387	0.17	1.13	1252281|STM0761|fumarate hydratase|-
STM0762_577_611	0.65	-1.07	1252282|STM0762|fumarate hydratase|-
STM0763.s_769_803	0.13	-1.27	1252283|STM0763.s|transcriptional regulator|+
STM0764_769_803	0.03	2.34	1252284|STM0764|transcriptional regulator|-
STM0767_1309_1343	0.03	1.70	1252287|dcoA|pseudo|+
STM0769_65_99	0.37	-1.20	1252289|STM0769|putative cytoplasmic protein|+
STM0770_793_827	0.08	1.23	1252290|STM0770|putative ABC transport protein|+
STM0772_385_419	0.59	-1.09	1252292|gpmA|phosphoglyceromutase|-
STM0773_698_732	0.87	-1.03	1252293|galM|aldose 1-epimerase|-
STM0774_918_952	0.59	1.02	1252294|galK|galactokinase|-
STM0775_688_722	0.76	1.04	1252295|galT|galactose-1-phosphate uridylyltransferase|-
STM0776_18_52	0.35	-1.12	1252296|galE|UDP-galactose-4-epimerase|-
STM0777_801_835	0.02	2.41	1252297|STM0777|putative inner membrane protein|-
STM0778_757_791	0.14	-1.26	1252298|modF|putative molybdenum transport ATP-binding protein ModF|-
STM0779_113_147	0.54	1.09	1252299|modE|DNA-binding transcriptional dual regulator|-
STM0780_21_55	0.11	1.72	1252300|STM0780|hypothetical protein|+
STM0781_545_579	0.02	1.90	1252301|modA|molybdate transporter periplasmic protein|+
STM0782_593_627	0.00	-1.53	1252302|modB|molybdate ABC transporter permease protein|+
STM0783_180_214	0.38	-1.10	1252303|modC|molybdate transporter ATP-binding protein|+
STM0784_321_355	0.21	-1.25	1252304|ybhA|predicted hydrolase|-
STM0785_449_483	0.45	1.15	1252305|ybhE|6-phosphogluconolactonase|+
STM0786_1181_1215	0.01	-3.38	1252306|ybhC|putative pectinesterase|-

STM0787_1137_1171	0.00	-2.95	1252307|hutI|imidazolonepropionase|+
STM0788_785_819	0.01	-1.72	1252308|hutG|formimidoylglutamase|+
STM0789_129_163	0.00	-1.58	1252309|hutC|histidine utilization repressor|+
STM0790_798_832	0.01	-3.32	1252310|hutU|pseudo|+
STM0792_345_379	0.02	2.44	1252312|ybhB|predicted kinase inhibitor|-
STM0793_291_325	0.92	-1.03	1252313|bioA|adenosylmethionine--8-amino-7-oxononanoate transaminase|-
STM0794_490_524	0.14	1.60	1252314|bioB|biotin synthetase|+
STM0795_271_305	0.45	-1.17	1252315|bioF|8-amino-7-oxononanoate synthase|+
STM0796_360_394	0.07	1.57	1252316|bioC|predicted methyltransferase|+
STM0797_73_107	0.13	-1.72	1252317|bioD|dithiobiotin synthetase|+
STM0798_1343_1377	0.68	-1.05	1252318|uvrB|excinuclease ABC subunit B|+
STM0799.1N_97_131	0.02	2.06	2673729|STM0799.1N|-|+
STM0800_2067_2101	0.03	1.43	1252320|slrP|leucine-rich repeat protein|+
STM0801_385_419	0.03	-1.52	1252321|ybhK|putative cytoplasmic protein|-
STM0802_81_115	0.03	-1.43	1252322|moaA|molybdenum cofactor biosynthesis protein A|+
STM0803_65_99	0.30	-1.11	1252323|moaB|molybdopterin biosynthetic protein B|+
STM0804_361_395	0.01	-1.45	1252324|moaC|molybdenum cofactor biosynthesis protein C|+
STM0805_33_67	0.07	-1.35	1252325|moaD|molybdopterin synthase small subunit|+
STM0806_97_131	0.24	-1.16	1252326|MoaE|molybdopterin synthase large subunit|+
STM0807_257_291	0.26	-1.11	1252327|ybhL|putative permease|+
STM0808_545_579	0.02	1.44	1252328|ybhM|putative integral membrane protein|+
STM0809_410_444	0.18	1.38	1252329|STM0809|putative inner membrane protein|+
STM0810_145_179	0.15	1.58	1252330|STM0810|putative inner membrane protein|+
STM0811_241_275	0.01	1.64	1252331|ybhN|hypothetical protein|-
STM0812_1011_1045	0.01	1.65	1252332|ybhO|cardiolipin synthase 2|-
STM0814_63_97	0.00	-3.76	1252334|ybhQ|putative inner membrane protein|+
STM0815_236_270	0.01	-1.51	1252335|ybhR|putative transport protein|-
STM0816_388_422	0.02	1.40	1252336|ybhS|putative transport protein|-
STM0817_1578_1612	0.64	-1.06	1252337|ybhF|putative ABC-type multidrug transport system ATPase component|-
STM0819_553_587	0.46	-1.07	1252339|ybiH|putative DNA-binding transcriptional regulator|-
STM0820_1134_1168	0.06	-1.30	1252340|rhlE|ATP-dependent RNA helicase RhlE|+
STM0821_1514_1548	0.13	1.64	1252341|dinG|ATP-dependent DNA helicase DinG|+
STM0822_673_707	0.08	1.33	1252342|ybiB|hypothetical protein|+
STM0823_9_43	0.02	2.69	1252343|ybiJ|hypothetical protein|-
STM0825_109_143	0.24	1.51	1252344|ybiI|hypothetical protein|-

STM0826_385_419	0.65	1.05	1252345|ybiN|putative SAM-dependent methyltransferase|+
STM0827_1992_2026	0.33	-1.14	1252346|ybiO|predicted mechanosensitive channel|-
STM0828_65_99	0.04	-1.21	1252347|glnQ|glutamine ABC transporter ATP-binding protein|-
STM0829_257_291	0.04	1.13	1252348|glnP|glutamine ABC transporter permease protein|-
STM0830_481_515	0.04	1.66	1252349|glnH|glutamine ABC transporter periplasmic protein|-
STM0831_369_403	0.01	2.76	1252350|dps|DNA starvation/stationary phase protection protein Dps|-
STM0832_561_595	0.40	-1.10	1252351|ybiF|threonine and homoserine efflux system|-
STM0833_393_427	0.01	5.22	1252352|ompX|outer membrane protein X|+
STM0835_97_131	0.04	-1.25	1252354|STM0835|manganese transport regulator MntR|+
STM0836_114_148	0.37	1.10	1252355|ybiR|putative transporter|+
STM0838_1362_1396	0.01	-1.96	1252357|ybiT|putative ABC transporter ATPase component|+
STM0841_667_701	0.04	-1.38	1252360|ybiU|putative cytoplasmic protein|-
STM0842_553_587	0.86	1.03	1252361|ybiV(1)|putative hydrolase|+
STM0844_449_483	0.05	2.06	1252363|pflE|putative pyruvate formate lyase activating enzyme|-
STM0845_193_227	0.20	1.37	1252364|moeB|molybdopterin biosynthesis protein MoeB|-
STM0846_931_965	0.71	1.06	1252365|moeA|molybdopterin biosynthesis protein MoeA|-
STM0847_577_611	0.12	-1.66	1252366|ybiK|L-asparaginase|+
STM0848_1333_1367	0.02	-1.75	1252367|yliA|glutathione transporter ATP-binding protein|+
STM0849_828_862	0.05	-1.60	1252368|yliB|putative ABC transporter periplasmic binding protein|+
STM0850_677_711	0.24	-1.24	1252369|yliC|putative ABC transporter periplasmic binding protein|+
STM0851_465_499	0.02	-2.26	1252370|yliD|putative ABC transporter inner membrane component|+
STM0852_1223_1257	0.03	-2.04	1252371|yliG|putative FeS oxidoreductase|-
STM0853_273_307	0.02	1.45	1252372|bssR|biofilm formation regulatory protein BssR|+
STM0854_221_255	0.02	1.51	1252373|STM0854|putative cytoplasmic protein|+
STM0855_787_821	0.10	2.21	1252374|STM0855|putative electron transfer protein beta subunit|+
STM0856_569_603	0.26	1.14	1252375|STM0856|putative electron transfer protein alpha subunit|+
STM0857_949_983	0.89	1.01	1252376|STM0857|putative acyl-CoA dehydrogenase|+
STM0858_991_1025	0.15	1.50	1252377|STM0858|putative dehydrogenase|+
STM0859_481_515	0.05	2.08	1252378|STM0859|putative transcriptional regulator|-
STM0860_285_321	0.01	3.93	1252379|STM0860|putative inner membrane protein|-
STM0861_593_627	0.32	1.23	1252380|yliI|-|+
STM0862_90_124	0.69	1.03	1252381|yliJ|putative glutathione S-transferase|-
STM0863_556_590	0.03	1.80	1252382|dacC|D-alanyl-D-alanine carboxypeptidase fraction C|+
STM0864_345_379	0.77	1.08	1252383|deoR|DNA-binding transcriptional repressor|-
STM0865_49_83	0.11	1.42	1252384|ybjG|undecaprenyl pyrophosphate phosphatase|-
STM0866_810_844	0.41	-1.12	1252385|mdfA|multidrug translocase|+

STM0867_145_179	0.00	1.51	1252386|STM0867|putative hydrolase|-
STM0868_213_247	0.07	-1.18	1252387|STM0868|putative transport protein/regulator|-
STM0869_129_163	0.49	1.11	1252388|STM0869|putative regulatory protein|+
STM0870_879_913	0.03	-1.10	1252389|STM0870|hypothetical protein|-
STM0871_225_259	0.04	1.61	1252390|ybjM|putative inner membrane protein|+
STM0872_73_107	0.02	1.63	1252391|grxA|glutaredoxin 1|-
STM0873_21_55	0.78	-1.04	1252392|ybjC|predicted inner membrane protein|+
STM0874_577_611	0.57	1.06	1252393|mdaA|nitroreductase A|+
STM0876_321_355	0.27	-1.11	1252395|ybjN|putative cytoplasmic protein|+
STM0877_626_660	0.00	-2.43	1252396|potF|putrescine transporter subunit: periplasmic-binding component of ABC superfamily|+
STM0878_1039_1073	0.00	-2.36	1252397|potG|putrescine transporter ATP-binding subunit|+
STM0879_209_243	0.20	-1.16	1252398|potH|putrescine transporter subunit: membrane component of ABC superfamily|+
STM0880_753_787	0.01	-1.84	1252399|potI|putrescine transporter subunit: membrane component of ABC superfamily|+
STM0881_353_387	0.09	1.20	1252400|ybjO|putative inner membrane protein|+
STM0882_756_790	0.03	-1.33	1252401|rumB|23S rRNA metyluridine methyltransferase|+
STM0884_761_795	0.78	-1.04	1252402|ulaA|ascorbate-specific PTS system enzyme IIC|+
STM0885_185_219	0.03	1.39	1252403|STM0885|putative inner membrane protein|+
STM0886_745_779	0.04	1.37	1252404|STM0886|putative sulfatase|+
STM0887_129_163	0.01	1.46	1252405|artJ|arginine transport system component|-
STM0888_153_187	0.01	-2.06	1252406|artM|arginine transporter permease subunit ArtM|-
STM0889_609_643	0.01	-1.61	1252407|artQ|arginine transporter permease subunit ArtQ|-
STM0890_433_467	0.00	-3.46	1252408|artI|arginine transport system|-
STM0891_513_547	0.01	-1.77	1252409|artP|arginine transporter ATP-binding subunit|-
STM0892_401_435	0.99	1.00	1252410|ybjP|predicted lipoprotein|-
STM0894_109_143	0.02	-2.04	1252412|STM0894|putative excisionase|-
STM0897_349_383	0.04	-1.33	1252415|STM0897|hypothetical protein|-
STM0900_1129_1163	0.05	-2.03	1252419|STM0900|putative helicase|+
STM0901_865_899	0.37	-1.18	1252420|STM0901|putative phage DNA primase|+
STM0906_73_107	0.05	2.10	1252425|STM0906|hypothetical protein|+
STM0907_73_107	0.25	1.33	1252426|STM0907|putative chitinase|+
STM0908_53_88	0.09	1.61	1252427|STM0908|hypothetical protein|+
STM0909_321_355	0.14	-1.52	1252428|STM0909|hypothetical protein|+
STM0910_1302_1336	0.15	-1.27	1252429|STM0910|hypothetical protein|+

STM0912_1908_1942	0.59	-1.18	1252431|STM0912|ATP-dependent protease|+
STM0913.2N_198_232	0.35	-1.23	2673767|STM0913.2N|hypothetical protein|+
STM0914_429_463	0.90	-1.02	1252433|STM0914|putative phage tail component|+
STM0915_296_331	0.02	-1.33	1252434|STM0915|hypothetical protein|+
STM0916.1N_365_399	0.50	-1.05	2673747|STM0916.1N|hypothetical protein|+
STM0921_249_283	0.45	-1.09	1252440|STM0921|putative minor tail protein|+
STM0922_533_567	0.03	-1.60	1252441|STM0922|putative phage tail assembly protein|+
STM0928_608_642	0.11	-1.57	1252447|nanH|neuraminidase|-
STM0930_33_67	0.15	1.14	1252449|orfB|hypothetical protein|+
STM0931_321_355	0.34	-1.06	1252450|ybjR|putative aminidase|+
STM0932_399_433	0.01	-1.45	1252451|STM0932|putative nucleoside-diphosphate-sugar epimerase|-
STM0933_467_501	0.09	1.16	1252452|ybjT|putative nucleoside-diphosphate-sugar epimerase|-
STM0934_3_37	0.03	1.51	1252453|ltaA|L-allo-threonine aldolase PLP-dependent|-
STM0935_1024_1058	0.09	1.41	1252454|poxB|pyruvate dehydrogenase|-
STM0936_545_579	0.02	-1.66	1252455|hcr|HCP oxidoreductase NADH-dependent|-
STM0938_769_803	0.03	-1.18	1252457|ybjE|putative inner membrane protein|-
STM0939_916_950	0.01	-1.55	1252458|ybjD|hypothetical protein|+
STM0940_193_227	0.30	1.16	1252459|ybjX|VirK-like protein|-
STM0941_1016_1050	0.02	1.43	1252460|ybjY|macrolide transporter subunit MacA|+
STM0942_1428_1462	0.04	1.61	1252461|ybjZ|macrolide transporter ATP-binding /permease protein|+
STM0943_105_139	0.00	-6.01	1252462|cspD|stress response protein|-
STM0944_248_282	0.08	-1.47	1252463|clpS|ATP-dependent Clp protease adaptor protein ClpS|+
STM0945_1406_1440	0.11	-1.45	1252464|clpA|ATP-dependent Clp protease ATP-binding subunit|+
STM0946/STM2471/STM303	0.07	-1.17	1252465/1253993/1254555/1255002/1255837|tnpA_1/tnpA_3/tnpA_4/tnpA_5/tnpA_6|transposase|+
STM0947_193_227	0.27	1.24	1252466|STM0947|putative integrase|-
STM0948_129_163	0.08	-1.57	1252467|STM0948|putative cytoplasmic protein|-
STM0949_8_42	0.71	1.49	1252468|serW|tRNA|-
STM0950_401_435	0.06	-1.72	1252469|STM0950|S|sA|-
STM0952_833_867	0.00	1.67	1252471|STM0952|putative transcriptional regulator|+
STM0953_65_99	0.32	1.10	1252472|infA|translation initiation factor IF-1|-
STM0954_49_83	0.73	-1.10	1252473|STM0954|putative inner membrane protein|-
STM0955_353_387	0.61	-1.04	1252474|aat|leucyl/phenylalanyl-tRNA--protein transferase|-
STM0956_1379_1413	0.02	-1.43	1252475|cydC|cysteine/glutathione ABC transporter membrane/ATP-binding component|-

STM0957_1632_1666	0.80	1.04	1252476|cydD|cysteine/glutathione ABC transporter membrane/ATP-binding component|-
STM0958_705_739	0.88	1.03	1252477|trxB|thioredoxin reductase|-
STM0959_353_387	0.02	-1.90	1252478|lrp|leucine-responsive transcriptional regulator|+
STM0960_3841_3875	0.02	-2.04	1252479|ftsK|DNA translocase FtsK|+
STM0961_321_355	0.05	-1.31	1252480|lolA|outer-membrane lipoprotein carrier protein|+
STM0962_1185_1219	0.01	-1.32	1252481|ycaJ|recombination factor protein RarA|+
STM0963_550_584	0.16	1.37	1252482|serS|seryl-tRNA synthetase|+
STM0964_2342_2376	0.99	-1.00	1252483|dmsA|anaerobic dimethyl sulfoxide reductase subunit A|+
STM0965_583_617	0.86	-1.01	1252484|dmsB|anaerobic dimethyl sulfoxide reductase subunit B|+
STM0966_417_451	0.00	2.35	1252485|dmsC|anaerobic dimethyl sulfoxide reductase subunit C|+
STM0969_1127_1161	0.02	1.14	1252487|ycaM|putative amino-acid transporter|+
STM0970_161_195	0.01	2.26	1252488|pflA|pyruvate formate lyase-activating enzyme 1|-
STM0972_721_760	0.02	-1.40	1252490|STM0972|SopD-like protein|+
STM0973_2244_2278	0.83	-1.03	1252491|pflB|pyruvate formate lyase II|-
STM0974_497_531	0.04	-1.48	1252492|focA|formate transporter|-
STM0975_1482_1516	0.06	-1.35	1252493|ycaO|putative cytoplasmic protein|-
STM0976_317_351	0.17	-1.22	1252494|ycaP|putative inner membrane protein|+
STM0977_442_476	0.20	1.30	1252495|serC|phosphoserine aminotransferase|+
STM0978_1053_1087	0.68	-1.13	1252496|aroA|3-phosphoshikimate 1-carboxyvinyltransferase|+
STM0979_641_675	0.01	1.56	1252497|ycaL|putative Zn-dependent protease|+
STM0980_137_171	0.03	-1.80	1252498|cmk|cytidylate kinase|+
STM0981_851_885	0.02	-1.79	1252499|rpsA|30S ribosomal protein S1|+
STM0982_232_266	0.56	1.11	1252500|ihfB|integration host factor subunit beta|+
STM0984_1134_1168	0.02	-1.81	1252502|msbA|lipid transporter ATP-binding/permease protein|+
STM0985_417_451	0.04	-1.62	1252503|lpxK|tetraacyldisaccharide 4'-kinase|+
STM0986_898_932	0.03	-1.28	1252504|ycaQ|putative cytoplasmic protein|+
STM0987_83_117	0.24	1.21	1252505|ycaR|hypothetical protein|+
STM0988_277_311	0.03	1.54	1252506|kdsB|3-deoxy-manno-octulosonate cytidylyltransferase|+
STM0989_561_595	0.22	-1.13	1252507|STM0989|hypothetical protein|+
STM0990_132_167	0.02	-1.81	1252508|ycbC|hypothetical protein|-
STM0991_201_235	0.03	-1.48	1252509|smtA|putative metallothionein SmtA|+
STM0992_372_406	0.03	-1.51	1252510|mukF|condesin subunit F|+
STM0993_321_355	0.01	-1.96	1252511|mukE|condesin subunit E|+
STM0994_3804_3838	0.00	-3.30	1252512|mukB|cell division protein MukB|+
STM0995_1099_1133	0.00	1.91	1252513|ycbB|hypothetical protein|+

STM0996_109_143	0.04	-1.66	1252514|ycbK|putative outer membrane protein|+
STM0997_417_451	0.81	-1.05	1252515|ycbL|putative metallo-beta-lactamase|+
STM0998_944_978	0.75	-1.08	1252516|aspC|aromatic amino acid aminotransferase|-
STM0999_285_319	0.01	-2.61	1252517|ompF|outer membrane protein F precursor|-
STM1000_1338_1372	0.02	1.82	1252518|asnC|asparaginyl-tRNA synthetase|-
STM1001_281_315	0.00	-1.87	1252519|STM1001|putative leucine response regulator|-
STM1003_694_728	0.02	-1.97	1252521|STM1003|putative transcriptional regulator|+
STM1004_476_510	0.06	-1.11	1252522|pncB|nicotinate phosphoribosyltransferase|-
STM1005_1062_1096	0.12	1.44	1252523|STM1005|integrase|-
STM1006_145_179	0.10	1.91	1252524|STM1006|excisionase|-
STM1009/STM2632_2759_2	0.00	1.91	1252527/1254155|STM1009/STM2632|exodeoxyribonuclease|-
STM1010_127_161	0.10	1.35	1252528|STM1010|hypothetical protein|-
STM1010.1n_122_156	0.25	1.37	2673727|STM1010.1n|hypothetical protein|-
STM1011_144_178	0.01	1.95	1252529|STM1011|hypothetical protein|-
STM1012/STM2628_67_101	0.12	1.37	1252530/1254151|STM1012/STM2628|probable regulatory protein|-
STM1013/STM2627_57_91	0.04	1.84	1252531/1254150|STM1013/STM2627|probable regulatory protein|+
STM1014/STM2626_257_29	0.03	-1.24	1252532/1254149|STM1014/STM2626|probable regulatory protein|+
STM1015/STM2625_577_61	0.50	1.05	1252533/1254148|STM1015/STM2625|putative replication protein|+
STM1016/STM2624_193_22	0.01	-1.47	1252534/1254147|STM1016/STM2624|hypothetical protein|+
STM1017/STM2623_129_16	0.03	-1.29	1252535/1254146|STM1017/STM2623|hypothetical protein|+
STM1018_60_99	0.02	1.44	1252536|STM1018|hypothetical protein|+
STM1020_159_194	0.02	1.54	1252538|STM1020|hypothetical protein|+
STM1021_432_466	0.01	2.68	1252539|STM1021|hypothetical protein|+
STM1021.1n_77_111	0.02	1.19	2673724|STM1021.1n|hypothetical protein|+
STM1022_673_707	0.96	-1.00	1252540|STM1022|putative molecular chaperone|+
STM1023_225_259	0.16	-1.32	1252541|STM1023|hypothetical protein|+
STM1024_5_39	0.18	1.49	1252542|STM1024|hypothetical protein|+
STM1025_385_419	0.04	2.05	1252543|STM1025|hypothetical protein|-
STM1026_166_200	0.09	1.35	1252544|STM1026|hypothetical protein|-
STM1027_80_114	0.06	1.96	1252545|STM1027|hypothetical protein|+
STM1028_141_175	0.05	1.20	1252546|STM1028|lysozyme|+
STM1029_83_117	0.07	1.61	1252547|STM1029|hypothetical protein|+
STM1030_145_179	0.87	-1.02	1252548|STM1030|hypothetical protein|+
STM1031_1332_1366	0.01	-1.41	1252549|STM1031|hypothetical protein|+
STM1032_603_637	0.01	-1.64	1252550|STM1032|hypothetical protein|+
STM1033_1083_1117	0.43	-1.08	1252551|STM1033|Clp protease-like protein|+

STM1034_49_83	0.04	1.77	1252552|STM1034|putative RecA/RadA recombinase|+
STM1035_33_67	0.11	1.61	1252553|STM1035|ATP-binding sugar transporter-like protein|+
STM1036_249_283	0.74	-1.07	1252554|STM1036|probable minor tail protein|+
STM1037_366_400	0.02	-1.11	1252555|STM1037|probable minor tail protein|+
STM1038_9_43	0.08	-1.20	1252556|STM1038|probable major tail protein|+
STM1039_49_83	0.48	1.13	1252557|STM1039|probable minor tail protein|+
STM1040_229_263	0.03	-1.72	1252558|STM1040|probable minor tail protein|+
STM1041_2677_2711	0.17	-1.20	1252559|STM1041|probable minor tail protein|+
STM1042_226_260	0.03	1.67	1252560|STM1042|probable minor tail protein|+
STM1043_191_225	0.65	1.04	1252561|STM1043|attachment/invasion protein|+
STM1044_429_463	0.00	3.26	1252562|sodC|superoxide dismutase precursor|-
STM1045_301_335	0.04	-1.39	1252563|STM1045|probable minor tail protein|+
STM1046_225_259	0.02	-1.44	1252564|STM1046|probable tail assembly protein|+
STM1047_341_375	0.10	-1.15	1252565|STM1047|probable tail assembly protein|+
STM1048_2217_2251	0.18	1.25	1252566|STM1048|host specificity protein J|+
STM1048.1N_717_751	0.66	1.08	2673720|STM1048.1N|hypothetical protein|+
STM1049_1520_1554	0.20	1.13	1252567|STM1049|probable tail fiber protein|+
STM1050_329_364	0.03	1.82	1252568|STM1050|tail fiber assembly like-protein|+
STM1051_433_467	0.00	3.37	1252569|sse||secreted effector protein|+
STM1052_121_155	0.02	3.47	1252570|STM1052|pseudo|+
STM1053_129_163	0.04	1.28	1252571|STM1053|hypothetical protein|-
STM1054_228_263	0.02	1.64	1252572|STM1054|hypothetical protein|-
STM1055_105_139	0.07	1.39	1252573|STM1055|hypothetical protein|-
STM1056_57_91	0.01	1.34	1252574|STM1056|MsgA-like protein|-
STM1057_2446_2480	0.13	1.26	1252575|pepN|aminopeptidase N|+
STM1058_68_102	0.06	-1.28	1252576|pyrD|dihydroorotate dehydrogenase 2|+
STM1059_345_379	0.91	-1.02	1252577|ycbW|putative cytoplasmic protein|+
STM1060_895_929	0.01	1.38	1252578|STM1060|putative iron-sulfur protein|-
STM1061_1366_1400	0.07	1.50	1252579|ycbY|putative N6-adenine-specific DNA methylase|+
STM1062_1229_1263	0.03	-1.51	1252580|uup|ABC transporter ATPase component|+
STM1063_1183_1217	0.08	1.90	1252581|pqiA|paraquat-inducible protein A|+
STM1064_1522_1556	0.04	2.65	1252582|pqiB|paraquat-inducible protein B|+
STM1065_73_107	0.03	-1.18	1252583|ymbA|putative outer membrane protein|+
STM1066_81_115	0.20	1.30	1252584|rmf|ribosome modulation factor|+
STM1067_449_483	0.01	-2.29	1252585|fabA|3-hydroxydecanoyl-(acyl carrier protein) dehydratase|-
STM1068_1594_1628	0.02	-1.17	1252586|lonH|putative protease|-

STM1069_281_315	0.10	1.32	1252587|ycbG|hypothetical protein|+
STM1071_401_435	0.22	1.28	1252589|sulA|SOS cell division inhibitor|-
STM1072_113_147	0.00	-2.26	1252590|yccR|putative DNA transformation protein|+
STM1073_1427_1461	0.92	-1.01	1252591|yccS|putative transporter|-
STM1074_289_323	0.13	1.45	1252592|yccF|hypothetical protein|-
STM1075_1280_1314	0.12	1.46	1252593|helD|DNA helicase IV|+
STM1076_321_355	0.02	-1.70	1252594|mgsA|methylglyoxal synthase|-
STM1077_497_531	0.98	1.00	1252595|yccT|hypothetical protein|-
STM1078_119_153	0.84	1.03	1252596|STM1078|putative cytoplasmic protein|+
STM1079_81_115	0.16	1.24	1252597|yccV|putative inner membrane protein|-
STM1080_853_887	0.28	1.25	1252598|yccW|putative SAM-dependent methyltransferase|-
STM1081_257_291	0.08	1.83	1252599|STM1081|putative outer membrane protein|+
STM1082_457_491	0.89	-1.02	1252600|STM1082|bacterial regulatory protein|+
STM1083_241_275	0.14	1.11	1252601|yccX|putative phosphohydrolase|+
STM1084_235_269	0.29	-1.15	1252602|yccK|sulfurtransferase TusE|-
STM1085_561_595	0.00	8.43	1252603|yccA|hypothetical protein|-
STM1086_35_69	0.75	1.49	1252604|serT|tRNA|+
STM1087_5_39	0.07	1.33	1252605|pipA|pathogenicity island-encoded protein A|-
STM1089_259_293	0.08	1.19	1252607|STM1089|putative inner membrane protein|+
STM1090_129_163	0.02	-1.46	1252608|pipC|pathogenicity island-encoded protein C|-
STM1092_125_159	0.05	-1.76	1252610|orfX|putative cytoplasmic protein|+
STM1093_37_71	0.00	-7.71	1252611|STM1093|putative cytoplasmic protein|-
STM1095_1262_1296	0.23	1.21	1252613|copS|copper resistance protein|-
STM1096_357_391	0.68	1.11	1252614|copR|transcriptional regulatory protein YedW|-
STM1097_157_191	0.02	1.76	1252615|STM1097|hypothetical protein|+
STM1098_353_387	0.13	1.23	1252616|hpaC|4-hydroxyphenylacetate catabolism|-
STM1100_225_259	0.02	1.85	1252618|hpaR|4-hydroxyphenylacetate catabolism|-
STM1106_209_243	0.03	-1.61	1252624|hpaI|4-hydroxyphenylacetate catabolism|+
STM1107_962_996	0.02	-1.91	1252625|hpaX|4-hydroxyphenylacetate catabolism|+
STM1108_769_803	0.02	1.98	1252626|hpaA|4-hydroxyphenylacetate catabolism|+
STM1109_577_611	0.96	-1.00	1252627|STM1109|putative periplasmic protein|+
STM1110_33_67	0.09	2.63	1252628|STM1110|hypothetical protein|-
STM1111_97_131	0.05	-1.46	1252629|yccD|chaperone-modulator protein CbpM|-
STM1112_193_227	0.14	-1.16	1252630|cbpA|curved DNA-binding protein CbpA|-
STM1113_41_76	0.60	1.07	1252631|scsA|suppression of copper sensitivity protein A|+
STM1114_1016_1050	0.74	1.12	1252632|scsB|suppression of copper sensitivity protein|+

STM1116_53_87	0.06	-1.18	1252634|scsD|suppression of copper sensitivity protein|+
STM1117_307_341	0.00	-7.81	1252635|agp|glucose-1-phosphatase/inositol phosphatase|+
STM1118_129_163	0.41	1.13	1252636|yccJ|hypothetical protein|-
STM1119_81_115	0.28	-1.15	1252637|wraB|TrpR binding protein WrbA|-
STM1120_19_53	0.08	1.53	1252638|ycdF|pseudo|+
STM1121_95_129	0.02	3.35	1252639|ymdF|putative cytoplasmic protein|+
STM1122_481_515	0.10	-1.46	1252640|ycdC|putative transcriptional repressor|+
STM1123_33_67	0.01	-2.86	1252641|STM1123|putative periplasmic protein|-
STM1124_3228_3262	0.05	-2.49	2673752|putA|-|-
STM1125_798_832	0.01	-1.89	1252643|putP|major sodium/proline symporter|+
STM1126_449_483	0.01	-1.43	2673763|phoH|-|+
STM1127_129_163	0.00	1.88	1252645|STM1127|putative transcriptional regulator|-
STM1128_1298_1332	0.45	-1.10	1252646|STM1128|putative sodium/glucose cotransporter|-
STM1129_33_67	0.08	-1.18	1252647|STM1129|N-acetylmannosamine-6-phosphate 2-epimerase|-
STM1130_706_740	0.03	1.99	1252648|STM1130|putative inner membrane protein|+
STM1131_57_91	0.66	-1.10	1252649|STM1131|putative outer membrane protein|+
STM1132_482_516	0.89	1.02	1252650|STM1132|putative sialic acid transporter|+
STM1133_108_142	0.18	1.18	1252651|STM1133|putative dehydrogenase|+
STM1134_12_46	0.73	1.44	1252652|serX|tRNA|-
STM1135_769_803	0.01	1.74	1252653|ycdW|putative oxidoreductase|+
STM1136_33_67	0.46	-1.07	1252654|ycdX|putative hydrolase|+
STM1137_81_115	0.51	-1.08	1252655|ycdY|putative oxidoreductase component|+
STM1138_189_223	0.02	1.84	1252656|ycdZ|putative inner membrane protein|+
STM1139_353_387	0.56	1.03	1252657|csgG|putative curli operon transcriptional regulator|-
STM1141_94_128	0.01	-1.45	1252659|csgE|curli assembly protein CsgE|-
STM1142_345_379	0.04	-1.38	1252660|csgD|DNA-binding transcriptional activator in two-component regulatory system|-
STM1143_129_163	0.13	-1.31	1252661|csgB|curlin minor subunit|+
STM1144_209_243	0.01	2.41	1252662|csgA|cryptic curlin major subunit|+
STM1145_81_115	0.03	3.41	1252663|csgC|putative curli production protein precursor|+
STM1146_241_275	0.03	2.47	1252664|ymdA|putative periplasmic protein|+
STM1147_209_243	0.02	1.60	1252665|STM1147|hypothetical protein|+
STM1148.S_1129_1163	0.35	1.10	1252666|ymdC|putative phospholipase|+
STM1149_808_842	0.67	-1.05	1252667|mdoC|glucans biosynthesis protein|-
STM1150_793_827	0.17	-1.21	1252668|mdoG|glucan biosynthesis protein G|+
STM1151_2089_2123	0.05	-1.18	1252669|mdoH|glucosyltransferase MdoH|+

STM1152_129_163	0.19	-1.29	1252670|yceK|predicted lipoprotein|+
STM1153_65_99	0.01	-2.02	1252671|msyB|hypothetical protein|-
STM1154_760_794	0.76	1.04	1252672|yceE|drug efflux system protein MdtG|-
STM1155_457_491	0.31	1.07	1252673|htrB|lipid A biosynthesis lauroyl acyltransferase|-
STM1156_758_792	0.03	-2.18	1252674|yceA|hypothetical protein|+
STM1157_353_387	0.33	-1.11	1252675|yceI|hypothetical protein|-
STM1158_97_131	0.09	1.21	1252676|STM1158|putative inner membrane protein|-
STM1159_61_95	0.04	1.46	1252677|yceO|putative inner membrane protein|-
STM1160_504_538	0.87	1.04	1252678|solA|N-methyltryptophan oxidase|-
STM1161.S_53_87	0.85	1.01	1252679|bssS|biofilm formation regulatory protein BssS|-
STM1162_7_41	0.54	1.05	1252680|dinI|DNA damage-inducible protein I|-
STM1163_208_242	0.02	-1.66	1252681|pyrC|dihydroorotase|-
STM1164_37_71	0.04	1.52	1252682|yceB|predicted lipoprotein|-
STM1165_457_491	0.54	-1.15	1252683|grxB|glutaredoxin 2|-
STM1166_690_724	0.04	-1.31	1252684|yceL|multidrug resistance protein MdtH|-
STM1167_401_435	0.00	-2.08	1252685|rimJ|ribosomal-protein-S5-alanine N-acetyltransferase|+
STM1168_385_419	0.17	-1.44	1252686|yceH|hypothetical protein|+
STM1169_65_99	0.09	1.31	1252687|mviM|putative virulence protein|+
STM1170_1152_1186	0.62	-1.10	1252688|mviN|putative virulence protein|+
STM1171_13_47	0.41	1.21	1252689|flgN|putative FlgK/FlgL export chaperone|-
STM1172_257_291	0.11	1.48	1252690|flgM|anti-sigma28 factor FlgM|-
STM1173_129_163	0.95	1.02	1252691|flgA|flagellar basal body P-ring biosynthesis protein FlgA|-
STM1175_289_323	0.49	1.20	1252693|flgC|flagellar basal body rod protein FlgC|+
STM1181_163_197	0.74	-1.04	1252699|flgI|flagellar basal body P-ring protein|+
STM1183_1239_1273	0.01	-2.29	1252701|flgK|flagellar hook-associated protein FlgK|+
STM1184_225_259	0.95	1.01	1252702|flgL|flagellar hook-associated protein FlgL|+
STM1185_2877_2911	0.02	-1.70	1252703|rne|ribonuclease E|-
STM1186_121_155	0.16	1.38	1252704|STM1186|pseudo|+
STM1187_737_771	0.08	-1.26	1252705|rluC|23S rRNA pseudouridylate synthase C|+
STM1188_333_367	0.20	-1.43	1252706|STM1188|putative inner membrane lipoprotein|+
STM1189_391_425	0.09	-1.54	1252707|maf|Maf-like protein|-
STM1190_225_259	0.02	-2.30	1252708|yceD|hypothetical protein|+
STM1191_139_173	0.06	-2.19	1252709|rpmF|50S ribosomal protein L32|+
STM1192_633_667	0.64	1.11	1252710|plsX|fatty acid/phospholipid synthesis protein|+
STM1193_289_323	0.28	1.17	1252711|fabH|3-oxoacyl-(acyl carrier protein) synthase III|+
STM1194_673_707	0.03	1.29	1252712|fabD|acyl carrier protein S-malonyltransferase|+

STM1195_257_291	0.14	-1.38	1252713|fabG|3-ketoacyl-(acyl-carrier-protein) reductase|+
STM1196_202_236	0.54	-1.09	1252714|acpP|acyl carrier protein|+
STM1197_1075_1109	0.68	-1.08	1252715|fabF|3-oxoacyl-(acyl carrier protein) synthase III|+
STM1198_65_99	0.01	1.44	1252716|pabC|4-amino-4-deoxychorismate lyase|+
STM1199_760_794	0.13	1.42	1252717|yceG|hypothetical protein|+
STM1200_161_195	0.20	-1.25	1252718|tdk|thymidylate kinase|+
STM1201_646_680	0.99	1.00	1252719|holB|DNA polymerase III subunit delta'|+
STM1202_353_387	0.02	1.46	1252720|ycfH|predicted metallodependent hydrolase|+
STM1203_1011_1045	0.02	-1.81	1252721|ptsG|glucose-specific PTS system IIBC components|+
STM1204_2008_2042	0.01	2.07	1252722|fhuE|ferric-rhodotorulic acid outer membrane transporter|-
STM1205_225_259	0.03	-1.31	1252723|ycfF|purine nucleoside phosphoramidase|+
STM1206_173_207	0.40	-1.16	1252724|ycfL|putative outer membrane lipoprotein|+
STM1207_593_627	0.02	-1.41	1252725|ycfM|putative outer membrane lipoprotein|+
STM1209_91_125	0.12	-1.15	1252727|nagZ|beta-hexosaminidase|+
STM1210_65_99	0.13	-1.31	1252728|ycfP|hypothetical protein|+
STM1211_1170_1204	0.01	2.26	1252729|ndh|respiratory NADH dehydrogenase 2|+
STM1212_65_99	0.62	1.05	1252730|ycfJ|hypothetical protein|+
STM1213_63_97	0.00	2.42	1252731|ycfQ|putative transcriptional repressor|-
STM1214_21_55	0.00	12.69	1252732|ycfR|putative outer membrane protein|+
STM1215_673_707	0.02	1.44	1252733|ycfS|putative periplasmic protein|-
STM1216_2640_2674	0.79	1.02	1252734|mfd|transcription-repair coupling factor|-
STM1217.S_537_571	0.03	-1.35	1252735|ycfU|outer membrane-specific lipoprotein transporter subunit LolC|+
STM1218_49_83	0.00	-1.61	1252736|lolD|lipoprotein transporter ATP-binding subunit|+
STM1219_758_792	0.02	-2.12	1252737|ycfW|outer membrane-specific lipoprotein transporter subunit LolE|+
STM1220_449_483	0.00	-2.06	1252738|ycfX|N-acetyl-D-glucosamine kinase|+
STM1221_3_37	0.24	-1.16	1252739|cobB|NAD-dependent deacetylase|+
STM1222_912_946	0.10	-2.13	1252740|potD|spermidine/putrescine ABC transporter periplasmic substrate-binding protein|-
STM1223_145_179	0.62	1.11	1252741|potC|spermidine/putrescine ABC transporter membrane protein|-
STM1224_796_830	0.06	1.78	1252742|sifA|secreted effector protein|-
STM1225_649_683	0.37	-1.07	1252743|potB|spermidine/putrescine ABC transporter membrane protein|-
STM1226_650_684	0.19	1.21	1252744|potA|putrescine/spermidine ABC transporter ATPase protein|-
STM1227_519_553	0.01	-2.34	1252745|pepT|peptidase T|+
STM1228_432_466	0.88	-1.04	1252746|STM1228|putative periplasmic protein|+
STM1229_667_701	0.03	-1.28	1252747|ycfD|putative cytoplasmic protein|-
STM1230_1009_1043	0.19	1.43	1252748|phoQ|sensor protein PhoQ|-

STM1231_65_99	0.01	2.37	1252749|phoP|DNA-binding response regulator in two-component regulatory system with PhoQ|-
STM1232_1332_1366	0.01	-2.16	1252750|purB|adenylosuccinate lyase|-
STM1233_313_347	0.55	-1.12	1252751|ycfC|hypothetical protein|-
STM1234.S_940_974	0.02	-2.11	1252752|trmU|tRNA (5-methylaminomethyl-2-thiouridylate)-
STM1235_290_325	0.90	-1.02	1252753|ymfB|putative MutT-like protein|-
STM1236_33_67	0.48	-1.06	1252754|STM1236|putative periplasmic protein|-
STM1237_305_339	0.07	-1.30	1252755|ymfC|putative ribosomal large subunit pseudouridine synthase|-
STM1238_908_942	0.02	-2.11	1252756|icdA|isocitrate dehydrogenase|+
STM1239_502_536	0.91	-1.02	1252757|STM1239|putative cytoplasmic protein|+
STM1240_49_83	0.07	1.96	1252758|envF|putative envelope lipoprotein|-
STM1241.1N_42_76	0.84	1.02	2673773|STM1241.1N|-|+
STM1241_17_51	0.16	1.46	1252759|msgA|macrophage survival protein|-
STM1242_353_387	0.01	1.79	1252760|envE|putative envelope protein|-
STM1244_201_235	0.04	3.16	1252762|pagD|virulence protein PAGD precursor|-
STM1246_464_498	0.01	9.88	1252764|pagC|virulence membrane protein PAGC precursor|+
STM1247_35_69	0.56	-1.44	1252765|STM1247|tRNA|+
STM1248_117_151	0.00	-3.38	1252766|STM1248|pseudo|+
STM1249_165_199	0.71	-1.04	1252767|STM1249|putative periplasmic protein|-
STM1250_145_179	0.07	1.63	1252768|STM1250|putative cytoplasmic protein|+
STM1251_145_179	0.03	2.97	1252769|STM1251|putative molecular chaperone|+
STM1252_973_1007	0.04	2.13	1252770|STM1252|putative cytoplasmic protein|+
STM1253_21_55	0.14	1.50	1252771|STM1253|putative inner membrane protein|-
STM1254_65_99	0.16	1.54	1252772|STM1254|putative outer membrane lipoprotein|-
STM1256_385_419	0.48	1.06	1252774|STM1256|putative ABC transporter protein|+
STM1257_737_771	0.24	-1.07	1252775|STM1257|putative ABC transporter protein|+
STM1259_65_99	0.25	-1.19	1252777|STM1259|putative ABC-type transport system ATPase component|+
STM1260_327_361	0.03	1.36	1252778|STM1260|putative inner membrane protein|-
STM1261_115_149	0.26	-1.18	1252779|STM1261|putative cytoplasmic protein|+
STM1262_3_37	0.09	-1.43	1252780|STM1262|tRNA|+
STM1263_609_643	0.02	-4.52	1252781|STM1263|hypothetical protein|+
STM1264_65_99	0.03	-1.45	1252782|aadA|aminoglycoside adenyltransferase|+
STM1265_501_535	0.99	1.00	1252783|STM1265|putative response regulator|+
STM1266_641_675	0.32	-1.13	1252784|STM1266|putative transcriptional regulator|+
STM1267_97_131	0.03	-2.34	1252785|STM1267|putative cytoplasmic protein|-
STM1269_353_387	0.07	1.37	1252787|STM1269|chorismate mutase|+

STM1270_353_389	0.01	-1.18	1252788|yeaS|leucine export protein LeuE|+
STM1271_65_99	0.01	1.25	1252789|yeaR|putative cytoplasmic protein|+
STM1272_21_55	0.03	1.27	1252790|yoaG|putative cytoplasmic protein|+
STM1273_449_483	0.11	1.90	1252791|STM1273|putative nitric oxide reductase|+
STM1274_113_147	0.99	-1.00	1252792|yeaQ|hypothetical protein|+
STM1275_193_227	0.01	2.27	1252793|yaoF|putative hemolysin|+
STM1276_129_163	0.02	1.28	1252794|STM1276|putative periplasmic protein|+
STM1277_273_307	0.03	1.54	1252795|yeaO|putative cytoplasmic protein|-
STM1278_346_380	0.15	-1.34	1252796|yeaN|putative amino acid/amine transport protein|-
STM1279_689_723	0.00	1.81	1252797|yeaM|putative regulatory protein|+
STM1280_145_179	0.28	-1.10	1252798|yeaL|putative inner membrane protein|-
STM1281_5_39	0.02	1.78	1252799|STM1281|putative inner membrane protein|+
STM1282_73_107	0.01	2.88	1252800|yeaK|putative cytoplasmic protein|-
STM1283_1295_1329	0.09	1.32	1252801|yeaJ|putative methyl-accepting chemotaxis protein|-
STM1285_1416_1450	0.60	-1.06	1252803|yeaG|putative serine protein kinase|-
STM1286_673_707	0.01	-2.54	1252804|mipA|MltA-interacting protein A|+
STM1287_358_392	0.13	1.26	1252805|STM1287|arylsulfatase regulator|+
STM1288_609_643	0.48	-1.12	1252806|STM1288|putative aldehyde reductase|+
STM1289_609_643	0.96	-1.00	1252807|yeaD|aldose 1-epimerase|-
STM1290_801_835	0.01	-1.82	1252808|gapA|glyceraldehyde-3-phosphate dehydrogenase|-
STM1291_289_323	0.00	-3.16	1252809|yeaA|methionine sulfoxide reductase B|+
STM1292_161_195	0.01	-3.25	1252810|yeaC|putative cytoplasmic protein|+
STM1293_513_547	0.17	1.32	1252811|pncA|nicotinamidase/pyrazinamidase|-
STM1294_34_68	0.10	-1.28	1252812|ansA|cytoplasmic asparaginase II|-
STM1295_1634_1668	0.13	-1.28	1252813|sppA|protease 4|-
STM1296_365_399	0.42	1.17	1252814|ydjA|putative oxidoreductase|+
STM1297_661_695	0.07	1.45	1252815|selD|selenophosphate synthetase|+
STM1298_1783_1817	0.29	1.20	1252816|topB|DNA topoisomerase III|+
STM1299_665_699	0.02	-2.22	1252817|gdhA|glutamate dehydrogenase|-
STM1300_145_179	0.03	2.13	1252818|STM1300|putative periplasmic protein|+
STM1301_273_307	0.15	-1.35	1252819|STM1301|pyrimidine (deoxy)nucleoside triphosphate pyrophosphohydrolase|-
STM1302_641_675	0.22	1.23	1252820|xthA|exonuclease III|-
STM1303_484_518	0.20	-1.14	1252821|argD|bifunctional succinylornithine transaminase/acetylornithine transaminase|+
STM1304_932_966	0.00	-1.47	1252822|astA|arginine succinyltransferase|+

STM1305_1184_1218	0.03	-1.29	1252823|astD|succinylglutamic semialdehyde dehydrogenase|+
STM1308_241_275	0.15	1.27	1252826|spy|periplasmic protein|+
STM1309_869_903	0.01	1.81	1252827|STM1309|endonuclease of nucleotide excision repair|-
STM1310_537_571	0.06	1.55	1252828|nadE|NAD synthetase|-
STM1311_177_211	0.02	2.03	1252829|osmE|DNA-binding transcriptional activator|+
STM1312_241_275	0.06	1.49	1252830|celA|N N'-diacetylchitobiose-specific PTS system transporter subunit IIB|+
STM1314_137_171	0.00	-1.46	1252832|celC|N N'-diacetylchitobiose-specific PTS system transporter subunit IIA|+
STM1315_105_139	0.00	-1.49	1252833|celD|DNA-binding transcriptional dual regulator|+
STM1316_637_671	0.75	-1.12	1252834|celF|phospho-beta-glucosidase/cellobiose-6-phosphate hydrolase|+
STM1317_321_355	0.30	-1.09	1252835|celG|hypothetical protein|+
STM1318_1662_1696	0.05	1.93	1252836|katE|hydroperoxidase III|-
STM1319_20_56	0.02	1.25	1252837|cedA|cell division modulator|+
STM1320_537_571	0.13	-1.53	1252838|ydjN|kinase/transporter-like protein|-
STM1321_105_139	0.02	1.53	1252839|ydjM|hypothetical protein|-
STM1322_145_179	0.15	1.10	1252840|yniC|predicted hydrolase|-
STM1323_407_441	0.01	-1.83	1252841|yniB|putative regulatory protein|+
STM1324_769_803	0.01	-1.83	1252842|STM1324|putative cytoplasmic protein|-
STM1325_225_259	0.30	1.14	1252843|ydiZ|putative cytoplasmic protein|-
STM1326_433_467	0.13	1.30	1252844|pfkB|6-phosphofructokinase 2|-
STM1327_721_755	0.75	1.15	1252845|ydiY|putative outer membrane protein|+
STM1328_905_939	0.00	2.95	1252846|STM1328|putative outer membrane protein|-
STM1332_931_965	0.03	-1.50	1252850|rfc|O-antigen polymerase|-
STM1333_1522_1556	0.29	-1.21	1252851|thrS|threonyl-tRNA synthetase|+
STM1334.c_417_451	0.74	-1.08	1252852|infC|translation initiation factor IF-3|+
STM1335_109_144	0.02	-2.23	1252853|rpmI|50S ribosomal protein L35|+
STM1336_129_163	0.01	-2.18	1252854|rplT|50S ribosomal protein L20|+
STM1337_585_619	0.05	1.69	1252855|pheS|phenylalanyl-tRNA synthetase subunit alpha|+
STM1338_1933_1967	0.00	-1.48	1252856|pheT|phenylalanyl-tRNA synthetase subunit beta|+
STM1339_205_239	0.01	1.70	1252857|ihfA|integration host factor subunit alpha|+
STM1340_577_611	0.60	-1.13	1252858|btuC|vtamin B12-transporter permease|+
STM1341_397_431	0.00	-1.67	1252859|btuE|predicted glutathione peroxidase|+
STM1342_609_643	0.03	1.28	1252860|btuD|vitamin B12-transporter ATPase|+
STM1343_97_131	0.17	-1.19	1252861|nlpC|lipoprotein|+
STM1344_529_563	0.06	1.44	1252862|ydiV|hypothetical protein|+

STM1345_828_862	0.07	1.25	1252863|ydiU|hypothetical protein|+
STM1346_129_163	0.65	-1.15	1252864|ydiE|hypothetical protein|-
STM1347_336_370	0.06	-1.41	1252865|aroH|phospho-2-dehydro-3-deoxyheptonate aldolase|-
STM1348_513_547	0.24	-1.09	1252866|ydiA|hypothetical protein|-
STM1349_1444_1478	0.01	-1.51	1252867|pps|phosphoenolpyruvate synthase|+
STM1350_1442_1476	0.06	1.20	1252868|ydiD|short chain acyl-CoA synthetase|-
STM1351_137_171	0.08	1.58	1252869|ydiT|putative ferredoxin|-
STM1352_816_850	0.81	-1.02	1252870|ydiS|flavoprotein|-
STM1355_257_291	0.20	1.50	1252873|ydiP|putative transcriptional regulator|+
STM1356_345_379	0.04	1.62	1252874|ydiO|putative acyl-CoA dehydrogenase|-
STM1357.S_725_759	0.58	-1.13	1252875|ydiF|putative acetyl-CoA/acetoacetyl-CoA transferase beta subunit|-
STM1358_449_483	0.46	1.13	1252876|aroD|3-dehydroquinate dehydratase|-
STM1362_325_359	0.00	-3.10	1252880|ydiL|putative cytoplasmic protein|-
STM1363_49_83	0.07	2.01	1252881|rprA|misc_RNA|-
STM1364_712_746	0.04	1.18	1252882|ydiK|predicted inner membrane protein|-
STM1365_2362_2396	0.20	-1.29	1252883|ydiJ|putative oxidase|+
STM1366_185_219	0.16	1.21	1252884|STM1366|hypothetical protein|+
STM1367_11_49	0.21	-1.36	1252885|ydiH|putative cytoplasmic protein|+
STM1369_137_171	0.01	1.83	1252887|sufA|iron-sulfur cluster assembly scaffold protein|+
STM1370_1001_1035	0.01	2.17	1252888|sufB|cysteine desulfurase activator complex subunit SufB|+
STM1371_513_547	0.04	1.32	1252889|sufC|cysteine desulfurase ATPase component|+
STM1373_478_512	0.00	1.47	1252891|sufS|selenocysteine lyase|+
STM1375_195_229	0.32	-1.09	1252893|ynhG|hypothetical protein|+
STM1377_103_137	0.12	1.40	1252895|lpp|murein lipoprotein|-
STM1378_622_656	0.09	-1.32	1252896|pykF|pyruvate kinase|-
STM1379_377_411	0.00	-3.03	1252897|orf48|putative amino acid permease|-
STM1380_545_579	0.01	-2.60	1252898|orf32|putative proline iminopeptidase|-
STM1381_325_359	0.00	-2.85	1252899|orf245|putative cytoplasmic protein|-
STM1382_676_710	0.53	-1.08	1252900|orf408|putative regulatory protein|-
STM1383_2440_2474	0.05	2.68	1252901|ttrA|tetrathionate reductase complex subunit A|-
STM1384_432_466	0.92	1.01	1252902|ttrC|tetrathionate reductase complex subunit C|-
STM1387_161_195	0.01	-1.61	1252905|ttrR|response regulator|+
STM1388_177_211	0.09	-1.47	1252906|orf70|hypothetical protein|+
STM1389_449_483	0.05	-1.52	1252907|orf319|putative inner membrane protein|-
STM1390_129_163	0.02	1.81	1252908|orf242|putative regulatory protein|-
STM1391_129_163	0.04	1.58	1252909|ssrB|transcriptional activator|-

STM1394_559_593	0.29	1.13	1252912|ssaC|outer membrane secretin precursor|+
STM1395_757_791	0.30	1.22	1252913|ssaD|virulence protein|+
STM1396_153_187	0.18	1.55	1252914|ssaE|secretion system effector|+
STM1397_89_123	0.03	2.46	1252915|sseA|secretion system chaperone protein|+
STM1398_409_443	0.90	1.62	1252916|sseB|translocation machinery component|+
STM1399_385_419	0.31	1.13	1252917|sscA|secretion system chaparone|+
STM1400_1172_1206	0.04	1.58	1252918|sseC|translocation machinery component|+
STM1401_281_315	0.34	1.42	1252919|sseD|translocation machinery component|+
STM1402_9_43	0.34	1.46	1252920|sseE|secreted effector protein|+
STM1403_274_308	0.05	1.39	1252921|sscB|secretion system chaparone|+
STM1404_593_627	0.01	1.40	1252922|sseF|secreted effector protein|+
STM1405_577_611	0.15	1.38	1252923|sseG|secreted effector protein|+
STM1406_93_127	0.53	3.69	1252924|ssaG|type III secretion system apparatus protein|+
STM1407_2_36	0.01	2.44	1252925|ssaH|type III secretion system apparatus protein|+
STM1408_161_195	0.08	1.37	1252926|ssaI|type III secretion system apparatus protein|+
STM1409_49_83	0.16	1.50	1252927|ssaJ|needle complex inner membrane lipoprotein|+
STM1410_109_143	0.01	1.85	1252928|STM1410|putative cytoplasmic protein|+
STM1411_513_547	0.05	1.39	1252929|ssaK|type III secretion system apparatus protein|+
STM1412_658_692	0.05	2.02	1252930|ssaL|type III secretion system apparatus protein|+
STM1414_1087_1121	0.98	2.00	1252932|ssaV|secretion system apparatus protein SsaV|+
STM1416_257_291	0.05	1.55	1252934|ssaO|type III secretion system apparatus protein|+
STM1417_166_200	0.10	1.41	1252935|ssaP|type III secretion system apparatus protein|+
STM1418_529_563	0.18	1.62	1252936|ssaQ|type III secretion system protein|+
STM1419_273_307	0.37	1.58	1252937|ssaR|type III secretion system protein|+
STM1420_189_223	0.33	1.22	1252938|ssaS|type III secretion system apparatus protein|+
STM1421_305_339	0.01	1.38	1252939|ssaT|type III secretion system apparatus protein|+
STM1423_39_73	0.86	1.24	1252941|valW|tRNA|-
STM1424_38_72	0.58	-1.42	1252942|valV|tRNA|-
STM1425_823_857	0.02	-2.46	1252943|ydhE|multidrug efflux protein|-
STM1426_529_563	0.68	1.08	1252944|ribE|riboflavin synthase subunit alpha|+
STM1427_1030_1064	0.04	-1.68	1252945|cfa|cyclopropane fatty acyl phospholipid synthase|-
STM1428_335_369	0.15	2.15	1252946|ydhC|inner membrane transport protein YdhC|-
STM1429_769_803	0.01	1.21	1252947|ydhB|putative DNA-binding transcriptional regulator|+
STM1430_699_733	0.06	-1.21	1252948|purR|DNA-binding transcriptional repressor PurR|-
STM1431_61_95	0.25	1.31	1252949|sodB|superoxide dismutase|-
STM1432_713_747	0.20	-1.19	1252950|ydhO|putative cell wall-associated hydrolase|-

STM1433_165_199	0.55	1.16	1252951|ydhD|hypothetical protein|+
STM1434_225_259	0.44	-1.10	1252952|rnt|ribonuclease T|-
STM1435_321_355	0.06	1.47	1252953|gloA|glyoxalase I|-
STM1436_995_1029	0.24	-1.17	1252954|nemA|N-ethylmaleimide reductase FMN-linked|-
STM1437_561_595	0.13	-1.12	1252955|ydhM|putative transcriptional repressor|-
STM1438_29_63	0.05	1.79	1252956|ydhL|putative oxidoreductase|+
STM1439_593_627	0.01	-2.18	1252957|ydhF|putative aldo/keto reductase|+
STM1440_105_139	0.00	-2.06	1252958|sodC|superoxide dismutase|+
STM1441_1421_1455	0.79	-1.22	1252959|STM1441|putative inner membrane protein|-
STM1442_97_131	0.03	-1.61	1252960|ydhJ|putative multidrug resistance efflux pump|-
STM1443_121_155	0.49	-1.12	1252961|ydhI|putative inner membrane protein|-
STM1444_129_163	0.03	1.49	1252962|slyA|transcriptional regulator SlyA|+
STM1445_389_423	0.05	1.47	1252963|slyB|putative outer membrane lipoprotein|-
STM1446_1083_1117	0.31	-1.16	1252964|anmK|anhydro-N-acetylmuramic acid kinase|+
STM1447_113_147	0.53	1.08	1252965|ydhA|hypothetical protein|+
STM1448_177_211	0.05	-1.35	1252966|pdxH|pyridoxamine 5'-phosphate oxidase|+
STM1449_1204_1238	0.02	-1.21	1252967|tyrS|tyrosyl-tRNA synthetase|+
STM1450_129_163	0.13	-1.37	1252968|pdxY|pyridoxamine kinase|+
STM1451_465_499	0.02	-2.57	1252969|gst|glutathionine S-transferase|-
STM1452_667_701	0.02	-1.75	1252970|tppB|putative tripeptide transporter permease|-
STM1453_537_571	0.05	1.51	1252971|nth|endonuclease III|-
STM1454_257_291	0.02	1.47	1252972|ydgQ|SoxR-reducing system protein RsxE|-
STM1455_49_83	0.01	-2.47	1252973|ydgP|electron transport complex protein RnfG|-
STM1456_524_558	0.00	-2.31	1252974|rnfD|electron transport complex protein RnfD|-
STM1457_1225_1259	0.13	-1.34	1252975|STM1457|electron transport complex protein RnfC|-
STM1458_417_451	0.01	-1.87	1252976|ydgM|electron transport complex protein RnfB|-
STM1459_321_355	0.04	-1.41	1252977|STM1459|Na(+)-translocating NADH-quinone reductase subunit E|-
STM1460_81_115	0.07	-1.33	1252978|ydgK|putative inner membrane protein|-
STM1461.S_161_195	0.01	1.39	1252979|ydgT|oriC-binding nucleoid-associated protein|-
STM1462.S_714_748	0.05	1.41	1252980|ydgJ|putative oxidoreductase|+
STM1463_267_301	0.47	1.18	1252981|add|adenosine deaminase|-
STM1464_37_71	0.00	-1.21	1252982|malY|pseudo|-
STM1465_145_179	0.01	-1.28	1252983|malX|pseudo|-
STM1466_1230_1264	0.02	1.21	1252984|ydgA|putative periplasmic protein|-
STM1467_1073_1107	0.16	-1.19	1252985|manA|mannose-6-phosphate isomerase|-
STM1468_1080_1114	0.00	-8.24	1252986|fumA|fumarase A|+

STM1469_469_503	0.00	-3.45	1252987|fumC|fumarate hydratase|+
STM1471_1007_1041	0.01	-1.92	1252989|rstB|sensor protein RstB|-
STM1473_647_681	0.05	1.28	1252991|ompN|outer membrane protein N precursor|-
STM1474_188_222	0.27	1.14	1252992|STM1474|pseudo|+
STM1475_131_167	0.56	1.07	1252993|rstA|DNA-binding response regulator in two-component regulatory system with RstB|-
STM1476_171_205	0.05	-1.72	1252994|ydgC|putative inner membrane protein|+
STM1477_1280_1314	0.06	1.37	1252995|ydgI|putative amino acid transporter|-
STM1478_865_899	0.22	-1.29	1252996|ydgH|putative periplasmic protein|-
STM1479_739_773	0.52	1.11	1252997|pntA|NAD(P) transhydrogenase subunit alpha|+
STM1480_1126_1160	0.09	-1.26	1252998|pntB|pyridine nucleotide transhydrogenase|+
STM1481_292_326	0.40	1.09	1252999|tqsA|putative transport protein|-
STM1483_285_319	0.25	1.13	1253001|ydgE|multidrug efflux system protein MdtI|+
STM1484_432_466	0.01	1.45	1253002|STM1484|putative protease|-
STM1486_1155_1189	0.03	1.92	1253004|ynfM|putative transport protein|-
STM1487_417_451	0.02	-1.23	1253005|ynfL|putative transcriptional regulator|+
STM1488_830_864	0.30	1.10	1253006|mlc|pts operon transcriptional repressor|+
STM1489_65_99	0.02	-1.96	1253007|bioD|putative dithiobiotin synthetase|+
STM1490_575_609	0.95	-1.02	1253008|STM1490|putative voltage-gated ClC-type chloride channel ClcB|-
STM1491_966_1000	0.09	-1.19	1253009|STM1491|proline/glycine betaine transport systems|-
STM1492_289_323	0.31	1.07	1253010|STM1492|putative ABC transporter permease component|-
STM1494_97_131	0.40	1.11	1253012|STM1494|putative transport system permease component|-
STM1495_65_99	0.37	1.05	1253013|ynfI|twin-argninine leader-binding protein DmsD|-
STM1496_577_611	0.18	1.15	1253014|STM1496|putative dimethylsulfoxide reductase|-
STM1497_92_126	0.47	1.56	1253015|STM1497|putative dimethyl sulphoxide reductase|-
STM1498_1597_1631	0.03	2.10	1253016|STM1498|putative dimethyl sulphoxide reductase|-
STM1499_2211_2245	0.27	1.52	1253017|STM1499|putative dimethyl sulphoxide reductase chain A1|-
STM1500_100_134	0.03	1.46	1253018|ynfD|putative outer membrane protein|-
STM1501_33_67	0.06	1.22	1253019|ynfC|hypothetical protein|+
STM1502_409_443	0.80	1.04	1253020|speG|spermidine N1-acetyltransferase|-
STM1503_97_131	0.02	1.35	1253021|ynfB|putative periplasmic protein|-
STM1504_273_308	0.07	-1.12	1253022|ynfA|hypothetical protein|+
STM1505_1144_1178	0.05	2.67	1253023|rspA|putative dehydratase|+
STM1506_789_823	0.23	-1.13	1253024|rspB|putative dehydrogenase|+
STM1509_145_179	0.06	-1.62	1253027|ydfZ|putative cytoplasmic protein|-
STM1510_65_99	0.29	1.19	1253028|ydfH|putative regulatory protein|-

STM1511_65_99	0.33	-1.11	1253029|ydfG|L-allo-threonine dehydrogenase NAD(P)-binding|-
STM1512_1828_1862	0.04	-1.24	1253030|dcp|dipeptidyl carboxypeptidase III|+
STM1513_145_179	0.09	1.24	1253031|STM1513|putative cytoplasmic protein|+
STM1514_4_41	0.05	2.69	1253032|ydeJ|competence damage-inducible protein A|-
STM1515_193_227	0.01	1.30	1253033|ydeI|hypothetical protein|+
STM1516_797_831	0.43	1.19	1253034|ydeE|putative MFS-type transporter YdeE|-
STM1517_401_435	0.69	1.12	1253035|ydeD|O-acetylserine/cysteine export protein|+
STM1519.S_225_259	0.01	-2.10	1253037|marA|DNA-binding transcriptional activator MarA|-
STM1520_257_291	0.01	1.92	1253038|marR|DNA-binding transcriptional repressor MarR|-
STM1521_337_371	0.01	1.63	1253039|marC|multiple drug resistance protein MarC|+
STM1522_1056_1090	0.04	1.49	1253040|ydeA|sugar efflux transporter|-
STM1523_817_851	0.15	1.27	1253041|yneJ|putative transcriptional regulator|-
STM1524_726_760	0.03	1.46	1253042|yneI|putative succinate-semialdehyde dehydrogenase|+
STM1525_81_115	0.29	1.11	1253043|yneH|glutaminase|+
STM1527_601_635	0.01	1.56	1253045|STM1527|putative inner membrane protein|+
STM1528_401_435	0.02	2.44	1253046|STM1528|putative outer membrane protein|-
STM1531_289_323	0.07	1.69	1253049|STM1531|putative hydrogenase|-
STM1532_545_579	0.08	1.14	1253050|STM1532|putative dehydrogenase protein|-
STM1533_575_609	0.12	-1.27	1253051|STM1533|putative hydrogenase|-
STM1534_369_403	0.62	-1.03	1253052|STM1534|putative hydrogenase|-
STM1535_65_99	0.01	1.14	1253053|STM1535|putative hydrogenase protein|-
STM1536_321_355	0.00	-1.52	1253054|STM1536|putative hydrogenase maturation protease|-
STM1537_33_67	0.06	2.35	1253055|STM1537|putative Ni/Fe hydrogenase 1 b-type cytochrome subunit|-
STM1539_515_549	0.00	2.14	1253057|STM1539|putative hydrogenase-1 small subunit|-
STM1540_221_255	0.00	5.67	1253058|STM1540|putative hydrolase|+
STM1541_385_419	0.02	1.48	1253059|STM1541|putative regulatory protein|+
STM1542_899_933	0.83	-1.03	1253060|STM1542|putative zinc-binding dehydrogenase|-
STM1543_1192_1226	0.17	1.28	1253061|STM1543|putative transport protein|-
STM1544_1486_1520	0.01	3.53	1253062|pqaA|PhoPQ-regulated protein|-
STM1545_979_1013	0.23	-1.12	1253063|STM1545|putative multidrug efflux protein|-
STM1548.s_809_843	0.01	3.06	1253066|STM1548.s|putative S-adenosylmethionine/tRNA-ribosyltransferase-isomerase|+
STM1549_52_86	0.03	-1.32	1253067|STM1549|putative translation initiation inhibitor|-
STM1550_105_139	0.06	1.25	1253068|STM1550|putative cytoplasmic protein|-
STM1551_177_211	0.05	1.50	1253069|STM1551|putative cytoplasmic protein|-
STM1551.1n_273_307	0.72	-1.03	2673754|STM1551.1n|hypothetical protein|+

STM1552_729_763	0.52	1.07	1253070|STM1552|putative cytoplasmic protein|+
STM1553_561_595	0.04	1.34	1253071|STM1553|pseudo|-
STM1554_788_822	0.62	1.11	1253072|STM1554|putative coiled-coil protein|-
STM1557_620_654	0.33	-1.30	1253075|STM1557|putative aminotransferase|+
STM1558_1845_1879	0.02	-1.44	1253076|STM1558|putative glycosyl hydrolase|-
STM1559_1690_1724	0.02	-1.56	1253077|STM1559|putative glycosyl hydrolase|-
STM1560_850_884	0.10	1.11	1253078|STM1560|putative alpha amylase|-
STM1561_249_283	0.05	1.77	1253079|STM1561|putative lipoprotein|-
STM1562_45_79	0.03	3.31	1253080|hdeB|acid-resistance protein|-
STM1563_225_259	0.03	1.67	1253081|osmC|putative envelope protein|-
STM1564_121_155	0.01	1.74	1253082|yddX|biofilm-dependent modulation protein|+
STM1565_5_39	0.73	1.05	1253083|rpsV|30S ribosomal subunit S22|+
STM1566_1499_1533	0.08	-1.51	1253084|sfcA|NAD-linked malate dehydrogenase|+
STM1567_332_366	0.10	1.43	1253085|adhP|alcohol dehydrogenase|+
STM1568_113_147	0.07	1.63	1253086|fdnI|formate dehydrogenase-N subunit gamma|-
STM1569_705_739	0.31	1.11	1253087|fdnH|formate dehydrogenase-N beta subunit|-
STM1571_225_259	0.08	1.41	1253089|yddG|hypothetical protein|+
STM1572_730_764	0.01	-2.26	1253090|nmpC|putative outer membrane porin precursor|+
STM1573.Sc_289_323	0.02	-1.54	1253091|STM1573.Sc|putative cytoplasmic protein|+
STM1574_649_683	0.04	1.28	1253092|smvA|methyl viologen resistance|-
STM1575_377_411	0.02	1.79	1253093|STM1575|putative transcriptional regulator|+
STM1576_982_1016	0.07	-1.42	1253094|narU|nitrate extrusion protein|+
STM1577_3606_3640	0.11	1.50	1253095|narZ|nitrate reductase 2 alpha subunit|+
STM1578_1282_1316	0.01	-2.67	1253096|narY|nitrate reductase 2 beta subunit|+
STM1579_65_99	0.01	-2.03	1253097|narW|nitrate reductase 2 delta subunit|+
STM1580_129_163	0.00	-3.40	1253098|narV|nitrate reductase 2 gamma subunit|+
STM1581_321_355	0.61	1.06	1253099|yddE|hypothetical protein|+
STM1582_681_715	0.54	1.07	1253100|nhoA|putative arylamine N-acetyltransferase|-
STM1583_129_163	0.00	2.60	1253101|STM1583|putative cytoplasmic protein|-
STM1584_1311_1345	0.08	1.17	1253102|ansP|L-asparagine transport protein|+
STM1585_65_99	0.02	1.99	1253103|STM1585|putative outer membrane lipoprotein|-
STM1586_575_609	0.05	-1.52	1253104|STM1586|putative periplasmic protein|-
STM1587_1506_1540	0.01	1.28	1253105|yncD|putative outer membrane receptor|+
STM1588_449_483	0.60	-1.09	1253106|yncC|putative DNA-binding transcriptional regulator|-
STM1589_296_330	0.02	-1.14	1253107|yncB|putative NADP-dependent oxidoreductase|-
STM1590_385_419	0.80	1.04	1253108|yncA|putative acyltransferase|+

STM1591_86_121	0.04	-1.14	1253109|ydcZ|putative inner membrane protein|+
STM1592_149_183	0.07	1.33	1253110|ydcY|putative cytoplasmic protein|-
STM1593_321_355	0.03	-1.18	1253111|srfA|putative virulence protein|+
STM1594_2047_2081	0.11	-1.23	1253112|srfB|putative virulence protein|+
STM1595_1418_1452	0.22	-1.14	1253113|srfC|putative virulence protein|+
STM1596_67_102	0.25	-1.11	1253114|ydcX|putative inner membrane protein|-
STM1597_874_908	0.00	-2.11	1253115|ydcW|putative aldehyde dehydrogenase|-
STM1598_530_564	0.02	1.33	1253116|ydcR|putative regulatory protein|-
STM1599_289_323	0.03	2.49	1253117|pdgL|periplasmic dipeptidase precursor|-
STM1601_70_107	0.05	1.68	1253119|ugtL|hypothetical protein|-
STM1602_461_495	0.05	1.65	1253120|sifB|secreted effector protein|+
STM1603_115_149	0.02	-1.85	1253121|yncJ|putative periplasmic protein|+
STM1604_1798_1832	0.07	1.63	1253122|ydcP|putative collagenase|-
STM1605_242_276	0.01	1.68	1253123|ydcN|putative repressor|-
STM1606_452_486	0.11	-1.27	1253124|STM1606|putative benzoate membrane transport protein|+
STM1607_617_651	0.30	-1.11	1253125|STM1607|putative outer membrane lipoprotein|-
STM1608_129_163	0.19	-1.24	1253126|tehB|tellurite resistance protein TehB|-
STM1609_55_89	0.15	-1.13	1253127|tehA|potassium-tellurite ethidium and proflavin transporter|-
STM1611_337_371	0.04	1.64	1253129|rimL|ribosomal-protein-L7/L12-serine acetyltransferase|-
STM1613_17_51	0.02	-2.43	1253131|STM1613|putative PTS system enzymeIIB component|+
STM1614_667_701	0.01	-1.97	1253132|STM1614|putative PTS system enzyme IIC component|+
STM1615_385_419	0.05	-1.41	1253133|STM1615|putative nucleoside triphosphatase|+
STM1617_577_611	0.01	-1.83	1253135|STM1617|ribulose-phosphate 3-epimerase|+
STM1618_129_163	0.01	-1.47	1253136|STM1618|putative transcriptional repressor of sgc operon|+
STM1619_401_435	0.44	-1.13	1253137|STM1619|cryptic aminoglycoside resistance gene|+
STM1620_1036_1070	0.60	-1.04	1253138|STM1620|putative oxidase|-
STM1621_137_171	0.52	-1.08	1253139|STM1621|putative periplasmic protein|-
STM1622_1617_1651	0.02	-1.63	1253140|mdoD|glucan biosynthesis protein D|-
STM1623_1294_1328	0.04	-2.02	1253141|STM1623|putative carboxylesterase|-
STM1624_665_699	0.00	-5.65	1253142|STM1624|putative cytoplasmic protein|-
STM1625_833_867	0.00	-11.25	1253143|ydcI|putative transcriptional regulator|+
STM1626_1427_1461	0.00	-2.50	1253144|trg|methyl-accepting chemotaxis protein III|-
STM1627_248_282	0.03	1.34	1253145|STM1627|alcohol dehydrogenase class III|-
STM1628_85_119	0.39	1.13	1253146|STM1628|putative cytoplasmic protein|-
STM1630_145_179	0.01	3.85	1253148|STM1630|putative inner membrane protein|-
STM1631_1124_1158	0.01	3.76	1253149|sseJ|secreted effector protein|+

STM1632_209_243	0.01	1.94	1253150|STM1632|putative inner membrane protein|-
STM1633_417_451	0.01	1.82	1253151|STM1633|putative periplasmic binding protein|+
STM1634_273_307	0.51	1.08	1253152|STM1634|putative ABC transporter permease component|+
STM1635_513_547	0.66	1.04	1253153|STM1635|putative ABC-type polar amino acid transport system ATPase component|+
STM1636_281_315	0.09	-1.32	1253154|STM1636|putative ABC-type transport system membrane component|+
STM1637_1192_1226	0.20	-1.30	1253155|STM1637|putative inner membrane protein|+
STM1638_321_355	0.18	-1.28	1253156|STM1638|putative SAM-dependent methyltransferase|+
STM1639_301_335	0.01	-2.18	1253157|cybB|cytochrome b561|-
STM1640_545_579	0.99	-1.00	1253158|ydcF|putative inner membrane protein|-
STM1641_3295_3329	0.05	1.14	1253159|hrpA|ATP-dependent RNA helicase HrpA|-
STM1642_31_65	0.02	1.23	1253160|acpD|azoreductase|+
STM1643_33_67	0.07	1.35	1253161|STM1643|putative inner membrane protein|-
STM1644_185_219	0.04	1.23	1253162|ydbL|putative periplasmic protein|-
STM1645_81_115	0.00	1.43	1253163|ynbE|putative outer membrane lipoprotein|-
STM1646_1958_1992	0.05	1.72	1253164|ydbH|hypothetical protein|-
STM1647_497_531	0.04	1.47	1253165|ldhA|D-lactate dehydrogenase|+
STM1648_9_43	0.54	1.07	1253166|hslJ|heat-inducible protein|+
STM1649_65_99	0.06	-1.38	1253167|STM1649|putative cytoplasmic protein|-
STM1651_2910_2944	0.04	1.54	1253169|nifJ|putative pyruvate-flavodoxin oxidoreductase|+
STM1652_337_371	0.00	-3.45	1253170|ynaF|putative universal stress protein|+
STM1653_273_307	0.05	1.22	1253171|STM1653|putative membrane transporter of cations|-
STM1654_897_931	0.02	-1.44	1253172|ydaO|C32 tRNA thiolase|+
STM1656_289_323	0.05	-1.14	1253174|zntB|zinc transporter|-
STM1657_1068_1102	0.16	-1.20	1253175|STM1657|putative methyl-accepting chemotaxis protein|-
STM1658_513_547	0.03	1.69	1253176|ydaL|hypothetical protein|-
STM1659_129_163	0.03	1.65	1253177|ogt|O-6-alkylguanine-DNA:cysteine-protein methyltransferase|+
STM1660.S_577_611	0.11	-1.20	1253178|fnr|fumarate/nitrate reduction transcriptional regulator|+
STM1661_897_931	0.01	1.64	1253179|ydaA|universal stress protein UspE|+
STM1662_137_171	0.39	-1.11	1253180|ynaJ|putative inner membrane protein|-
STM1663_49_83	0.83	-1.05	1253181|ynaI|putative integral membrane protein|+
STM1664_513_547	0.36	-1.08	1253182|STM1664|putative transcriptional regulator|-
STM1665_513_547	0.03	2.09	1253183|STM1665|putative cytoplasmic protein|+
STM1666_161_195	0.01	-1.37	1253184|STM1666|pseudo|+
STM1667_105_139	0.04	1.89	1253185|STM1667|putative thiol peroxidase|-

STM1668_145_179	0.82	-1.03	1253186|STM1668|hypothetical protein|-
STM1670_273_307	0.09	1.53	1253188|STM1670|putative lipoprotein|-
STM1671_291_325	0.02	2.38	1253189|STM1671|putative regulatory protein|+
STM1672_564_598	0.03	1.70	2673745|STM1672|-|+
STM1673_65_99	0.16	-1.14	1253191|STM1673|putative outer membrane lipoprotein|-
STM1675_213_247	0.12	1.27	1253193|STM1675|oxidoreductase|+
STM1676_417_451	0.03	1.37	1253194|STM1676|putative aldo/keto reductase|-
STM1677_481_515	0.11	1.43	1253195|STM1677|putative transcriptional regulator|-
STM1678_369_403	0.07	2.18	1253196|STM1678|putative 2'-hydroxyisoflavone reductase|+
STM1679_671_705	0.15	1.23	1253197|mppA|periplasmic murein tripeptide transport protein|-
STM1680_193_227	0.78	-1.05	1253198|ycjI|murein peptide amidase A|+
STM1681_65_99	0.04	-1.24	1253199|ycjG|putative chloromuconate cycloisomerase|-
STM1682_21_55	0.62	1.04	1253200|tpx|thiol peroxidase|+
STM1683_1119_1153	0.11	1.30	1253201|tyrR|DNA-binding transcriptional dual regulator tyrosine-binding|-
STM1685_469_503	0.02	-2.04	1253203|ycjX|putative ATPase|-
STM1686_33_67	0.00	-3.00	1253204|pspE|thiosulfate:cyanide sulfurtransferase (rhodanese)|-
STM1687_37_71	0.57	1.06	1253205|pspD|peripheral inner membrane phage-shock protein|-
STM1688_81_115	0.45	-1.16	1253206|pspC|DNA-binding transcriptional activator|-
STM1689_125_159	0.06	1.38	1253207|pspB|phage shock protein B|-
STM1690_15_49	0.13	1.34	1253208|pspA|phage shock protein|-
STM1691_897_931	0.08	1.34	1253209|pspF|phage shock protein operon transcriptional activator|+
STM1692_907_941	0.03	1.33	1253210|sapA|peptide transport protein|+
STM1693_801_835	0.02	-1.73	1253211|sapB|peptide transport protein|+
STM1694_769_803	0.20	-1.11	1253212|sapC|peptide transport protein|+
STM1695_385_419	0.64	-1.08	1253213|sapD|peptide transport protein|+
STM1696_417_451	0.03	-1.40	1253214|sapF|peptide transport protein|+
STM1697_513_547	0.04	-1.41	1253215|STM1697|hypothetical protein|-
STM1699_89_123	0.01	2.27	1253218|ycjE|putative cytoplasmic protein|+
STM1700_585_619	0.12	1.52	1253219|fabI|enoyl-(acyl carrier protein) reductase|+
STM1701_465_499	0.23	-2.33	1253220|yciW|putative cytoplasmic protein|+
STM1702_1016_1050	0.10	-1.49	1253221|rnb|exoribonuclease III|+
STM1704_33_67	0.16	-1.22	1253223|yciT|putative regulatory protein|+
STM1705_133_167	0.11	1.83	1253224|osmB|lipoprotein|+
STM1706_121_155	0.03	1.97	1253225|yciH|translation initiation factor Sui1|-
STM1707_641_675	0.91	-1.02	1253226|pyrF|OMP decarboxylase; OMPDCase; OMPdecase|-
STM1708_1131_1165	0.03	1.99	1253227|yciM|hypothetical protein|-

STM1709_61_95	0.01	-1.12	1253228|yciS|putative inner membrane protein|-
STM1710_41_75	0.18	1.24	1253229|pgpB|phosphatidylglycerophosphatase B|-
STM1711_481_515	0.43	-1.14	1253230|ribA|GTP cyclohydrolase III|+
STM1712_1885_1919	0.02	-2.00	1253231|acnA|aconitate hydratase|-
STM1713_641_675	0.77	1.09	1253232|cysB|transcriptional regulator CysB|-
STM1714_1599_1633	0.12	-1.41	1253233|topA|DNA topoisomerase I|-
STM1715_5_39	0.99	1.00	1253234|yciN|hypothetical protein|+
STM1716_880_914	0.08	1.12	1253235|sohB|predicted inner membrane peptidase|-
STM1717_545_579	0.24	-1.26	1253236|yciK|short chain dehydrogenase|+
STM1718_489_523	0.00	-3.21	1253237|btuR|cob(I)yrinic acid a c-diamide adenosyltransferase|+
STM1719_385_419	0.10	-1.32	1253238|yciL|23S rRNA pseudouridylate synthase B|-
STM1720_529_563	0.04	1.44	1253239|yciO|hypothetical protein|-
STM1721_529_563	0.67	1.09	1253240|trpH|hypothetical protein|-
STM1722_9_43	0.21	-1.28	1253241|trpL|trp operon leader peptide|+
STM1723_1468_1502	0.18	-1.24	1253242|trpE|anthranilate synthase component II|+
STM1724_853_887	0.06	1.18	1253243|trpD|bifunctional indole-3-glycerol-phosphate synthase/anthranilate phosphoribosyltransferase|+
STM1725_360_394	0.14	1.19	1253244|trpC|bifunctional indole-3-glycerol phosphate synthase/phosphoribosylanthranilate isomerase|+
STM1726_387_421	0.74	-1.07	1253245|trpB|tryptophan synthase subunit beta|+
STM1727_289_323	0.53	-1.12	1253246|trpA|tryptophan synthase subunit alpha|+
STM1728_9_43	0.02	2.76	1253247|yciG|putative cytoplasmic protein|+
STM1729_151_185	0.02	1.78	1253248|yciF|putative cytoplasmic protein|+
STM1730_65_99	0.03	2.10	1253249|yciE|putative cytoplasmic protein|+
STM1731_385_419	0.36	1.13	1253250|STM1731|putative catalase|+
STM1732_161_195	0.00	-9.02	1253251|ompW|outer membrane protein W|-
STM1733_225_259	0.24	1.36	1253252|STM1733|putative ferredoxin|+
STM1734_577_611	0.08	1.20	1253253|yciC|hypothetical protein|+
STM1735_385_419	0.04	1.34	1253254|yciB|intracellular septation protein A|+
STM1736_101_135	0.71	1.09	1253255|yciA|predicted hydrolase|+
STM1737_49_83	0.07	-1.51	1253256|tonB|membrane spanning protein in TonB-ExbB-ExbD complex; transduces proton motive force of the cytoplasmic membrane to outer membrane transporters; involved in the transport of ron-siderophore complexes vitamin B12 and colicins|-
STM1738_190_224	0.05	-1.29	1253257|yciI|YciI-like protein|+
STM1739_590_624	0.11	-1.19	1253258|cls|cardiolipin synthetase|+

STM1740_308_342	0.16	-1.27	2673771|yciU|-|+
STM1741_545_579	0.51	-1.03	1253260|STM1741|putative voltage-gated potassium channel|-
STM1742_710_744	0.01	-2.48	1253261|oppF|oligopeptide transport protein|-
STM1743_777_811	0.00	-3.08	1253262|oppD|oligopeptide transporter ATP-binding component|-
STM1744_625_659	0.01	-2.10	1253263|oppC|oligopeptide transport protein|-
STM1745_641_675	0.01	-2.61	1253264|oppB|oligopeptide transporter permease|-
STM1746.S_745_779	0.00	-3.83	1253265|oppA|oligopeptide transport protein|-
STM1748_259_293	0.08	2.53	1253267|ychE|hypothetical protein|-
STM1749_1680_1714	0.00	-6.81	1253268|adhE|iron-dependent alcohol dehydrogenase|+
STM1750_17_51	0.01	-1.37	1253269|tdk|thymidine kinase|-
STM1751_17_51	0.14	-1.39	1253270|hns|global DNA-binding transcriptional dual regulator H-NS|+
STM1752_641_675	0.79	-1.01	1253271|galU|UTP--glucose-1-phosphate uridylyltransferase subunit GalU|-
STM1753_911_945	0.31	1.11	1253272|hnr|response regulator of RpoS|-
STM1754_641_675	0.11	1.21	1253273|ychK|hypothetical protein|-
STM1755_65_99	0.12	1.17	1253274|ychJ|hypothetical protein|+
STM1756_385_419	0.77	-1.04	1253275|purU|formyltetrahydrofolate deformylase|+
STM1758_49_83	0.67	-1.07	1253277|rrtT|misc_RNA|+
STM1760_563_597	0.13	-1.30	1253279|STM1760|tetratricopeptide repeat protein|-
STM1761_641_675	0.95	-1.01	1253280|narI|nitrate reductase 1 gamma subunit|-
STM1762_337_371	0.85	-1.02	1253281|narJ|nitrate reductase 1 delta subunit|-
STM1763_1121_1155	0.02	-1.46	1253282|narH|nitrate reductase 1 beta subunit|-
STM1764_3689_3723	0.08	1.85	1253283|narG|nitrate reductase 1 alpha subunit|-
STM1766_830_864	0.03	-1.30	1253285|narX|nitrate/nitrite sensor protein NarX|+
STM1767_241_275	0.04	-1.44	1253286|narL|DNA-binding response regulator in two-component regulatory system with NarX (or NarQ)|+
STM1768_1018_1052	0.91	-1.01	1253287|ychP|predicted invasin|-
STM1769_275_309	0.54	1.07	1253288|ychN|putative sulfur reduction protein|+
STM1770_3_40	0.07	-1.25	1253289|chaB|cation transport regulator|-
STM1771_1006_1040	0.10	1.55	1253290|chaA|calcium/sodium:proton antiporter|+
STM1772_97_131	0.37	-1.18	1253291|kdsA|2-dehydro-3-deoxyphosphooctonate aldolase|-
STM1773_641_675	0.03	1.65	1253292|ychA|putative transcriptional regulator|-
STM1774_129_163	0.97	1.02	1253293|sirC|putative transcriptional regulator|-
STM1775_481_515	0.05	-1.39	1253294|hemK|N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase|-
STM1776_980_1014	0.03	-1.43	1253295|prfA|peptide chain release factor 1|-
STM1777_1058_1092	0.05	-1.33	1253296|hemA|glutamyl-tRNA reductase|-

STM1778_17_51	0.24	1.10	1253297|lolB|outer membrane lipoprotein LolB|+
STM1779_265_299	0.10	-1.39	1253298|ipk|4-diphosphocytidyl-2-C-methyl-D-erythritol kinase|+
STM1780_897_931	0.06	-1.69	1253299|prsA|ribose-phosphate pyrophosphokinase|+
STM1781_1511_1545	0.05	-2.12	1253300|ychM|putative sulfate transporter YchM|+
STM1782_201_235	0.00	-9.98	1253301|ychH|predicted inner membrane protein|-
STM1783.S_385_419	0.04	2.09	1253302|pth|peptidyl-tRNA hydrolase|+
STM1784_861_895	0.79	-1.03	1253303|ychF|translation-associated GTPase|+
STM1785_779_813	0.02	1.77	1253304|STM1785|putative cytoplasmic protein|-
STM1787_795_829	0.91	-1.04	1253306|STM1787|hydrogenase 1 large subunit|+
STM1788_545_579	0.12	-1.23	1253307|STM1788|hydrogenase 1 b-type cytochrome subunit|+
STM1789_377_411	0.04	-1.38	1253308|STM1789|hydrogenase 1 maturation protease|+
STM1791_65_99	0.27	1.41	1253310|STM1791|putative hydrogenase-1 protein|+
STM1792_594_628	0.02	1.24	1253311|STM1792|putative cytochrome oxidase subunit II|+
STM1793_522_556	0.79	-1.02	1253312|STM1793|putative cytochrome oxidase subunit III|+
STM1794_22_56	0.07	1.47	1253313|STM1794|putative periplasmic protein|+
STM1795_1111_1145	0.00	-8.53	1253314|STM1795|putative glutamic dehyrogenase-like protein|+
STM1796_1386_1420	0.54	1.09	1253315|treA|trehalase|+
STM1797_145_179	0.20	1.35	1253316|ymgE|putative transglycosylase-associated protein|-
STM1798_249_283	0.94	-1.02	1253317|ycgR|putative inner membrane protein|+
STM1799_209_243	0.12	1.14	1253318|emtA|membrane-bound lytic murein transglycosylase E|-
STM1800_289_323	0.14	1.12	1253319|ldcA|L D-carboxypeptidase A|+
STM1801_1031_1065	0.02	-1.40	1253320|ycgO|potassium/proton antiporter|+
STM1803_940_974	0.00	-12.53	1253322|dadA|D-amino acid dehydrogenase small subunit|-
STM1804.S_1232_1266	0.51	1.14	1253323|ycgB|hypothetical protein|+
STM1805_513_547	0.01	-1.46	1253324|fadR|fatty acid metabolism regulator|-
STM1806_1442_1476	0.01	-1.26	1253325|nhaB|sodium/proton antiporter|+
STM1807_209_243	0.44	-1.10	1253326|dsbB|disulfide bond formation protein B|+
STM1808_137_171	0.03	2.11	1253327|STM1808|putative cytoplasmic protein|+
STM1809_119_154	0.01	1.93	1253328|STM1809|putative cytoplasmic protein|-
STM1810_6_41	0.02	2.51	1253329|STM1810|putative cytoplasmic protein|-
STM1811_129_163	0.01	1.67	1253330|ycgN|hypothetical protein|-
STM1812_257_291	0.12	1.37	1253331|ycgM|predicted isomerase/hydrolase|-
STM1813_45_81	0.02	1.88	1253332|ycgL|putative cytoplasmic protein|-
STM1814_177_211	0.03	-1.67	1253333|minC|septum formation inhibitor|+
STM1815_705_739	0.02	-2.17	1253334|minD|cell division inhibitor MinD|+
STM1816_161_195	0.78	1.01	1253335|minE|cell division topological specificity factor MinE|+

STM1817_897_931	0.03	1.45	1253336|rnd|ribonuclease D|-
STM1818_879_913	0.00	-6.82	1253337|fadD|long-chain-fatty-acid--CoA ligase|-
STM1819_65_99	0.03	-1.33	1253338|slp|putative outer membrane protein|-
STM1820_198_232	0.01	-2.14	1253339|yeaZ|putative molecular chaperone|-
STM1821_1072_1106	0.07	-1.16	1253340|yoaA|putative DNA helicase|-
STM1822_17_51	0.09	-1.40	1253341|yoaB|putative translation initiation inhibitor|+
STM1823_65_99	0.07	1.38	1253342|yoaH|hypothetical protein|-
STM1824_558_592	0.09	-1.32	1253343|pabB|para-aminobenzoate synthase component II|+
STM1825_49_83	0.21	-1.37	1253344|yeaB|hypothetical protein|+
STM1826_910_944	0.05	1.26	1253345|sdaA|L-serine deaminase I/L-threonine deaminase II|+
STM1827.S_739_773	0.41	1.13	1253346|STM1827.S|putative diguanylate cyclase/phosphodiesterase|+
STM1828_1358_1392	0.07	-1.41	1253347|yoaE|putative inner membrane protein|-
STM1829_157_191	0.10	2.44	1253348|STM1829|putative cytoplasmic protein|-
STM1830_257_291	0.01	-2.83	1253349|manX|mannose-specific enzyme IIAB|+
STM1831_321_355	0.01	-2.46	1253350|manY|mannose-specific enzyme IIC|+
STM1832_481_515	0.01	-2.73	1253351|manZ|mannose-specific PTS system protein IID|+
STM1833_353_387	0.12	1.69	1253352|STM1833|hypothetical protein|+
STM1834_289_323	0.05	-1.36	1253353|yebN|hypothetical protein|+
STM1835_433_467	0.02	-1.80	1253354|rrmA|23S rRNA methyltransferase A|-
STM1836_875_909	0.01	1.15	1253355|STM1836|putative penicillin-binding protein 3|-
STM1837_145_179	0.12	-1.53	1253356|cspC|cold shock-like protein cspC|-
STM1838_25_59	0.01	-2.16	1253357|yobF|putative cytoplasmic protein|-
STM1839_123_160	0.01	3.78	1253358|STM1839|hypothetical protein|-
STM1840_57_91	0.01	1.70	1253359|yobG|hypothetical protein|-
STM1841_153_187	0.02	2.96	1253360|STM1841|hypothetical protein|+
STM1842_385_419	0.38	1.13	1253361|kdgR|putative transcriptional repressor|-
STM1843_967_1001	0.04	-1.30	1253362|STM1843|putative transport protein|+
STM1844_641_675	0.27	1.38	1253363|htpX|heat shock protein HtpX|-
STM1845_1242_1276	0.03	-1.66	1253364|prc|carboxy-terminal protease|-
STM1846_624_658	0.01	-2.17	1253365|proQ|putative solute/DNA competence effector|-
STM1847_173_207	0.04	-1.23	1253366|yebR|putative nucleotide-binding protein|-
STM1848_493_527	0.29	-1.17	1253367|yebS|putative inner membrane protein|+
STM1849_2281_2315	0.77	1.23	1253368|STM1849|putative inner membrane protein|+
STM1850_1097_1131	0.47	-1.13	1253369|yebU|rRNA (cytosine-C(5)-)-methyltransferase RsmF|+
STM1851_30_65	0.03	2.36	1253370|STM1851|putative cytoplasmic protein|+
STM1852_89_123	0.34	-1.19	1253371|yebW|putative inner membrane lipoprotein|+

STM1853_417_451	0.13	2.01	1253372|pphA|serine/threonine protein phosphatase 1|-
STM1854_77_111	0.01	2.55	1253373|STM1854|putative inner membrane protein|-
STM1856.1N_321_355	0.03	2.75	2673765|STM1856.1N|hypothetical protein|+
STM1857_129_163	0.00	-4.54	1253376|STM1857|putative acetyltransferase|-
STM1859_81_115	0.01	1.37	1253378|STM1859|putative cytoplasmic protein|+
STM1861_73_107	0.02	2.76	1253380|STM1861|-|+
STM1862_65_99	0.01	3.18	1253381|pagO|integral membrane protein|+
STM1863_73_107	0.00	2.61	1253382|STM1863|putative inner membrane protein|+
STM1864_225_259	0.00	2.93	1253383|STM1864|putative inner membrane protein|+
STM1865_37_71	0.01	5.28	1253384|STM1865|-|-
STM1866_119_153	0.02	3.63	1253385|STM1866|pseudo|-
STM1867_44_82	0.03	4.40	1253386|pagK|PagK|+
STM1868_553_587	0.02	2.54	1253387|mig-3|phage-tail assembly-like protein|-
STM1868.1N_38_72	0.05	2.55	2673772|STM1868.1N|hypothetical protein|-
STM1868A_75_109	0.79	-1.06	1253388|STM1868A|lytic enzyme|+
STM1869_385_419	0.07	1.21	1253389|STM1869|phage-tail assembly-like protein|-
STM1869A_17_51	0.25	1.15	1253390|STM1869A|hypothetical protein|-
STM1870_217_251	0.02	2.53	1253391|STM1870|RecE-like protein|+
STM1871_593_627	0.03	1.30	1253392|STM1871|-|+
STM1872_51_85	0.10	1.26	1253393|STM1872|putative cytoplasmic protein|-
STM1873_241_275	0.02	1.35	1253394|STM1873|hypothetical protein|-
STM1874_641_675	0.04	1.62	1253395|STM1874|putative inner membrane protein|-
STM1875_289_323	0.02	1.81	1253396|yobA|hypothetical protein|-
STM1876_179_213	0.54	-1.07	1253397|holE|DNA polymerase III subunit theta|+
STM1877_617_651	0.35	-1.18	1253398|STM1877|putative amidohydrolase|+
STM1878_257_291	0.08	-1.24	1253399|exoX|exodeoxyribonuclease X|+
STM1879_1341_1375	0.02	1.51	1253400|ptrB|protease 2|-
STM1880_121_155	0.01	2.22	1253401|yebE|putative inner membrane protein|-
STM1881_49_83	0.01	1.63	1253402|yebF|putative periplasmic protein|-
STM1882_90_124	0.01	2.43	1253403|yebG|DNA damage-inducible protein YebG|-
STM1884_497_531	0.40	1.09	1253405|eda|keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase|-
STM1885_1517_1551	0.76	1.04	1253406|edd|phosphogluconate dehydratase|-
STM1886_1213_1247	0.48	1.10	1253407|zwf|glucose-6-phosphate 1-dehydrogenase|-
STM1887_513_547	0.04	1.46	1253408|yebK|DNA-binding transcriptional regulator HexR|+
STM1888_1340_1374	0.09	-1.53	1253409|pykA|pyruvate kinase|+

STM1889_545_579	0.07	-1.25	1253410|msbB|lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase|-
STM1890_1025_1059	0.00	-2.87	1253411|yebA|hypothetical protein|-
STM1891_81_115	0.02	-10.53	1253412|znuA|high-affinity zinc transporter periplasmic component|-
STM1892.S_225_259	0.02	-2.25	1253413|znuC|high-affinity zinc transporter ATPase|+
STM1893_513_547	0.04	-3.65	1253414|znuB|high-affinity zinc transporter membrane component|+
STM1895_523_557	0.07	1.37	1253416|ruvA|Holliday junction DNA helicase motor protein|-
STM1896_410_444	0.03	2.62	1253417|STM1896|putative cytoplasmic protein|+
STM1897_397_431	0.37	1.14	1253418|yebB|hypothetical protein|+
STM1898_105_139	0.04	-1.21	1253419|ruvC|Holliday junction resolvase|-
STM1900_209_243	0.02	-1.56	1253421|ntpA|dATP pyrophosphohydrolase|-
STM1901_854_888	0.01	-2.41	1253422|aspS|aspartyl-tRNA synthetase|-
STM1902_385_419	0.01	2.44	1253423|yecD|hypothetical protein|+
STM1903_753_787	0.01	1.79	1253424|yecE|hypothetical protein|+
STM1904_209_243	0.09	-1.07	1253425|yecN|putative inner membrane protein|+
STM1905_513_547	0.16	-1.35	1253426|yecO|putative SAM-dependent methyltransferase|+
STM1906_641_675	0.80	-1.04	1253427|yecP|putative enzyme|+
STM1907_137_171	0.01	1.46	1253428|cutC|copper homeostasis protein CutC|-
STM1908_97_131	0.02	-1.65	1253429|yecM|hypothetical protein|-
STM1909_991_1025	0.57	-1.14	1253430|argS|arginyl-tRNA synthetase|+
STM1910_1225_1259	0.05	1.98	1253431|STM1910|putative penicillin-binding protein|+
STM1911_845_879	0.69	1.03	1253432|STM1911|putative cytoplasmic protein|-
STM1912_357_391	0.90	1.01	1253433|flhE|flagellar protein|-
STM1913_1208_1242	0.71	-1.11	1253434|flhA|flagellar biosynthesis protein A|-
STM1914_793_827	0.08	2.17	1253435|flhB|flagellar biosynthesis protein FlhB|-
STM1915_353_387	0.08	-1.47	1253436|cheZ|chemotaxis regulator CheZ|-
STM1916_317_351	0.05	-1.35	1253437|cheY|chemotaxis regulator transmitting signal to flagellar motor component|-
STM1917_539_573	0.02	-1.45	1253438|cheB|chemotaxis-specific methylesterase|-
STM1919_663_697	0.02	-1.77	1253440|cheM|methyl accepting chemotaxis protein III|-
STM1920_225_259	0.01	-2.39	1253441|cheW|purine-binding chemotaxis protein|-
STM1921_1401_1435	0.01	-2.16	1253442|cheA|chemotaxis protein CheA|-
STM1922_537_571	0.02	-1.86	1253443|motB|flagellar motor protein MotB|-
STM1923_21_55	0.15	-1.33	1253444|motA|flagellar motor protein MotA|-
STM1924.S_41_75	0.00	-3.13	1253445|flhC|transcriptional activator FlhC|-
STM1925_209_243	0.00	-3.34	1253446|flhD|transcriptional activator FlhD|-
STM1927_97_131	0.03	-1.80	1253448|yecG|universal stress protein UspC|+

STM1928_903_937	0.45	-1.13	1253449|otsA|trehalose-6-phosphate synthase|-
STM1929_257_291	0.18	1.38	1253450|otsB|trehalose-6-phosphate phosphatase|-
STM1930_81_115	0.41	-1.26	1253451|STM1930|pseudo|-
STM1932_457_491	0.00	2.09	1253453|ftnB|ferritin-like protein|+
STM1933_153_187	0.28	-1.17	1253454|STM1933|hypothetical protein|-
STM1934_225_259	0.06	1.26	1253455|STM1934|putative outer membrane lipoprotein|+
STM1935_161_195	0.06	1.51	1253456|ftn|ferritin|+
STM1936_102_137	0.09	-1.36	1253457|yecH|putative cytoplasmic protein|-
STM1937_1149_1183	0.55	-1.11	1253458|tyrP|tyrosine-specific transport protein|+
STM1938_97_131	0.00	-2.98	1253459|yecA|hypothetical protein|-
STM1939_26_60	0.02	3.40	1253460|STM1939|putative glucose-6-phosphate dehydrogenase|-
STM1940_1049_1083	0.02	1.48	1253461|STM1940|putative cell wall-associated hydrolase|-
STM1941_141_175	0.00	2.33	1253462|STM1941|putative inner membrane protein|-
STM1942_5_40	0.01	-2.11	1253463|leuZ|tRNA|-
STM1943_5_39	0.02	-2.12	1253464|cysT|tRNA|-
STM1945_417_451	0.70	-1.03	1253466|pgsA|phosphatidylglycerophosphate synthetase|-
STM1946_1090_1124	0.14	-1.14	1253467|uvrC|excinuclease ABC subunit C|-
STM1947_337_371	0.13	1.07	1253468|uvrY|response regulator|-
STM1949_35_70	0.02	1.53	1253470|yecF|hypothetical protein|+
STM1950_81_115	0.20	-1.24	1253471|sdiA|DNA-binding transcriptional activator|-
STM1951_529_563	0.48	-1.14	1253472|yecC|putative amino-acid ABC transporter ATP-binding protein YecC|-
STM1952_33_67	0.34	-1.12	1253473|yecS|putative ABC-type amino acid transporter permease
STM1953_65_99	0.76	-1.05	1253474|yedO|D-cysteine desulfhydrase|-
STM1954_357_391	0.09	2.04	1253475|fliY|cystine transporter subunit|-
STM1955_337_371	0.70	1.02	1253476|fliZ|protein FliZ|-
STM1956_161_195	0.07	-1.18	1253477|fliA|flagellar biosynthesis sigma factor|-
STM1957_251_285	0.03	-1.43	1253478|tnpA_2|transposase for IS200|-
STM1958_847_881	0.51	-1.10	1253479|fliB|lysine-N-methylase|-
STM1959_545_579	0.03	-2.40	1253480|fliC|flagellin|-
STM1960_949_983	0.01	-2.49	1253481|fliD|flagellar capping protein|+
STM1961_273_307	0.01	-1.67	1253482|fliS|flagellar protein FliS|+
STM1962_65_99	0.04	-1.54	1253483|fliT|flagellar biosynthesis protein FliT|+
STM1963_1154_1188	0.53	-1.02	1253484|amyA|cytoplasmic alpha-amylase|+
STM1964_241_275	0.27	1.25	1253485|yedD|hypothetical protein|-
STM1965_555_589	0.01	-1.72	1253486|yedE|predicted inner membrane protein|+
STM1966_161_195	0.28	-1.13	1253487|yedF|hypothetical protein|+

STM1968_279_313	0.01	-1.45	1253489|fliE|flagellar hook-basal body protein FliE|-
STM1969_748_782	0.11	1.16	1253490|fliF|flagellar MS-ring protein|+
STM1970_97_131	0.86	-1.01	1253491|fliG|flagellar motor switch protein G|+
STM1971_69_103	0.37	-1.10	1253492|fliH|flagellar assembly protein H|+
STM1974_283_317	0.12	-1.21	1253495|fliK|flagellar hook-length control protein|+
STM1975_177_211	0.02	1.64	1253496|fliL|flagellar basal body-associated protein FliL|+
STM1977_281_315	0.23	1.12	1253498|fliN|flagellar motor switch protein FliN|+
STM1978_209_243	0.03	1.32	1253499|fliO|flagellar biosynthesis protein FliO|+
STM1979_321_355	0.00	1.62	1253500|fliP|flagellar biosynthesis protein FliP|+
STM1980_137_171	0.02	3.35	1253501|fliQ|flagellar biosynthesis protein FliQ|+
STM1981_241_275	0.70	1.03	1253502|fliR|flagellar biosynthesis protein FliR|+
STM1982_313_347	0.01	2.26	1253503|rcsA|colanic acid capsular biosynthesis activation protein A|+
STM1983_123_157	0.04	1.78	1253504|dsrB|hypothetical protein|-
STM1984_129_163	0.91	-1.07	1253505|yodD|putative cytoplasmic protein|+
STM1986_209_243	0.02	1.53	1253507|yedP|mannosyl-3-phosphoglycerate phosphatase|+
STM1987_746_780	0.39	-1.10	1253508|STM1987|putative inner membrane protein|-
STM1988.S_89_123	0.25	-1.29	1253509|STM1988.S|putative cytoplasmic protein|-
STM1989_641_675	0.04	-1.69	1253510|yedI|hypothetical protein|-
STM1990_641_675	0.27	-1.11	1253511|yedA|hypothetical protein|+
STM1991_113_147	0.06	1.19	1253512|vsr|DNA mismatch endonuclease|-
STM1992_1264_1298	0.03	-1.37	1253513|dcm|DNA cytosine methylase|-
STM1993_481_515	0.02	-1.54	1253514|yedJ|hypothetical protein|-
STM1994_263_297	0.39	1.30	1253515|STM1994|putative inner membrane protein|-
STM1995_558_592	0.28	1.20	1253516|ompS|putative porin|+
STM1996_178_212	0.07	1.67	1253517|cspB|putative cold-shock protein|-
STM1997_398_432	0.00	1.44	1253518|umuC|DNA polymerase V subunit UmuC|-
STM1998_225_259	0.02	1.87	1253519|umuD|DNA polymerase V subunit UmuD|-
STM1999_106_140	0.05	1.88	1253520|STM1999|putative cytoplasmic protein|-
STM2000_31_65	0.05	1.39	1253521|serU|tRNA|-
STM2001_402_437	0.00	-4.61	1253522|yeeI|putative inner membrane protein|+
STM2003_57_91	0.27	1.28	1253524|STM2003|pseudo|+
STM2006_685_719	0.37	1.06	2673718|STM2006|-|+
STM2007_1048_1082	0.43	-1.05	1253528|STM2007|tetratricopeptide repeat protein|+
STM2008_1324_1358	0.09	1.68	1253529|STM2008|putative periplasmic protein|+
STM2011_17_51	0.01	-1.16	1253532|STM2011|putative cytoplasmic protein|-
STM2011.1n_133_167	0.15	1.82	2673719|STM2011.1n|hypothetical protein|+

STM2013_971_1005	0.13	-1.17	1253534|yeeO|predicted multidrug efflux system|-
STM2015_705_739	0.03	1.78	1253536|erfK|hypothetical protein|-
STM2016_840_874	0.03	-1.37	1253537|cobT|nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase|-
STM2018_449_483	0.05	-1.28	1253539|cobU|adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase|-
STM2019_1418_1452	0.01	-2.01	1253540|cbiP|cobyric acid synthase|-
STM2020_17_51	0.05	-1.44	1253541|cbiO|vitamin B12 biosynthetic protein|-
STM2021_329_363	0.01	-2.71	1253542|cbiQ|vitamin B12 biosynthetic protein|-
STM2022_61_95	0.01	-2.95	1253543|cbiN|cobalt transport protein CbiN|-
STM2024_289_323	0.00	-2.70	1253545|cbiL|cobalt-precorrin-2 C(20)-methyltransferase|-
STM2025_289_323	0.54	-1.27	1253546|cbiK|vitamin B12 biosynthetic protein|-
STM2026_193_227	0.06	-1.74	1253547|cbiJ|cobalt-precorrin-6x reductase|-
STM2027_685_719	0.00	-2.62	1253548|cbiH|precorrin-3B C17-methyltransferase|-
STM2028_1021_1055	0.00	-3.78	1253549|cbiG|cobalamin biosynthesis protein CbiG|-
STM2029_97_131	0.00	-6.63	1253550|cbiF|vitamin B12 biosynthetic protein|-
STM2030_437_471	0.00	-3.87	1253551|cbiT|cobalt-precorrin-6Y C(15)-methyltransferase|-
STM2032_813_847	0.00	-2.03	1253553|cbiD|cobalt-precorrin-6A synthase|-
STM2033_593_627	0.01	-3.18	1253554|cbiC|precorrin-8X methylmutase|-
STM2034_705_739	0.05	-1.40	1253555|cobD|cobalamin biosynthesis protein|-
STM2035_381_415	0.06	1.84	1253556|cbiA|cobyrinic acid a c-diamide synthase|-
STM2036_313_347	0.97	1.01	1253557|pocR|transcriptional regulator|-
STM2037_397_431	0.06	-1.22	1253558|pduF|propanediol diffusion facilitator|-
STM2038_69_103	0.09	1.29	1253559|pduA|polyhedral body protein|+
STM2042_17_51	0.15	1.14	1253563|pduE|propanediol dehydratase small subunit|+
STM2043_1314_1348	0.04	2.19	1253564|pduG|propanediol dehydratase reactivation protein|+
STM2045_61_95	0.01	4.03	1253566|pduJ|polyhedral body protein|+
STM2047_17_51	0.02	2.33	1253568|pduL|propanediol utilization protein|+
STM2048_9_43	0.04	1.55	1253569|pduM|propanediol utilization protein|+
STM2049_23_57	0.25	-1.33	1253570|pduN|polyhedral body protein|+
STM2051_1164_1198	0.15	1.35	1253572|pduP|CoA-dependent propionaldehyde dehydrogenase|+
STM2055_141_175	0.90	-1.02	1253576|pduU|polyhedral body protein|+
STM2056_401_435	0.94	-1.01	1253577|pduV|propanediol utilization protein|+
STM2057_216_250	0.91	-1.01	1253578|pduW|propionate kinase|+
STM2058_785_819	0.05	2.13	1253579|pduX|propanediol utilization protein|+
STM2059_161_195	0.73	1.06	1253580|yeeX|hypothetical protein|-

STM2060_604_638	0.37	1.11	1253581|yeeA|putative inner membrane protein|-
STM2061_225_259	0.01	-2.68	1253582|sbmC|DNA gyrase inhibitor|-
STM2062_1118_1152	0.01	2.41	1253583|dacD|D-alanyl-D-alanine carboxypeptidase|-
STM2063_265_299	0.37	1.07	1253584|phsC|thiosulfate reductase cytochrome B subunit|-
STM2064_97_131	0.14	1.21	1253585|phsB|thiosulfate reductase electron transport protein|-
STM2066_2198_2232	0.03	1.40	1253587|sopA|secreted effector protein|+
STM2067_768_802	0.12	-1.25	1253588|sbcB|exonuclease II|+
STM2069_129_163	0.01	1.48	1253590|yeeY|putative transcriptional regulator|-
STM2070_9_43	0.29	-1.09	1253591|yeeZ|putative dehydratase|-
STM2071_129_163	0.27	-1.15	1253592|hisG|ATP phosphoribosyltransferase|+
STM2072_946_980	0.27	1.08	1253593|hisD|histidinol dehydrogenase|+
STM2073_861_895	0.14	-1.36	1253594|hisC|histidinol-phosphate aminotransferase|+
STM2074_453_487	0.27	-1.11	1253595|hisB|imidazole glycerol-phosphate dehydratase/histidinol phosphatase|+
STM2075_161_195	0.93	1.01	1253596|hisH|imidazole glycerol phosphate synthase subunit HisH|+
STM2076_497_531	0.33	1.17	1253597|hisA|1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase|+
STM2077_65_99	0.44	1.14	1253598|hisF|imidazole glycerol phosphate synthase subunit HisF|+
STM2078_129_163	0.68	1.04	1253599|hisI|bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase protein|+
STM2080_696_730	0.01	2.48	1253601|ludg|UDP-glucose/GDP-mannose dehydrogenase|-
STM2081_824_858	0.21	-1.25	1253602|gnd|6-phosphogluconate dehydrogenase|-
STM2082_928_962	0.01	-1.45	1253603|rfbP|undecaprenol-phosphate galactosephosphotransferase/O-antigen transferase|-
STM2083_1023_1057	0.98	-1.00	1253604|rfbK|phosphomannomutase|-
STM2084_1193_1227	0.03	-1.54	1253605|rfbM|mannose-1-phosphate guanylyltransferase|-
STM2085_321_355	0.09	1.29	1253606|rfbN|rhamnosyl transferase|-
STM2086_71_105	0.73	1.08	1253607|rfbU|mannosyl transferase|-
STM2087_363_399	0.15	1.31	1253608|rfbV|abequosyltransferase|-
STM2088_845_881	0.04	2.22	1253609|rfbX|putative O-antigen transferase|-
STM2089_556_590	0.26	-1.16	1253610|rfbJ|CDP-abequose synthase|-
STM2090_779_813	0.11	-1.19	1253611|rfbH|CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase|-
STM2091_593_627	0.01	-1.68	1253612|rfbG|CDP glucose 4 6-dehydratase|-
STM2092_385_419	0.03	-1.86	1253613|rfbF|glucose-1-phosphate cytidylyltransferase|-
STM2093_81_115	0.02	-1.87	1253614|rfbI|CDP-6-deoxy-delta-3 4-glucoseen reductase|-
STM2094_513_547	0.03	-1.55	1253615|rfbC|dTDP-4 deoxyrhamnose 3 5 epimerase|-

STM2095_145_179	0.04	-1.27	1253616|rfbA|dTDP-glucose pyrophosphorylase|-
STM2096_129_163	0.09	-1.23	1253617|rfbD|dTDP-4-dehydrorhamnose reductase|-
STM2097_247_281	0.04	1.63	1253618|rfbB|dTDP-glucose 4 6 dehydratase|-
STM2098_17_51	0.02	-1.94	1253619|galF|UTP--glucose-1-phosphate uridylyltransferase subunit GalF|-
STM2099_693_727	0.01	1.99	1253620|wcaM|putative colanic acid biosynthetic protein|-
STM2100_478_512	0.08	1.91	1253621|wcaL|putative glycosyl transferase|-
STM2101_634_668	0.09	-1.18	1253622|wcaK|putative pyruvyl transferase|-
STM2102_792_826	0.22	1.22	1253623|wzx|colanic acid exporter|-
STM2103_780_814	0.39	1.10	1253624|wcaJ|putative UDP-glucose lipid carrier transferase|-
STM2104_932_966	0.02	-1.48	1253625|cpsG|phosphomannomutase|-
STM2106_513_547	0.03	2.41	1253627|wcaI|predicted glycosyl transferase|-
STM2107_326_360	0.63	1.03	1253628|wcaH|GDP-mannose mannosyl hydrolase|-
STM2108_481_515	0.18	1.15	1253629|wcaG|GDP-fucose synthetase|-
STM2109_283_317	0.06	1.85	1253630|gmd|GDP-D-mannose dehydratase|-
STM2111_153_187	0.21	1.22	1253632|wcaE|predicted glycosyl transferase|-
STM2112_936_970	0.01	1.31	1253633|wcaD|putative colanic acid polymerase|-
STM2113_219_253	0.91	-1.02	1253634|wcaC|predicted glycosyl transferase|-
STM2114_193_227	0.17	1.47	1253635|wcaB|putative colanic acid biosynthesis acetyltransferase WcaB|-
STM2115_249_283	0.15	1.18	1253636|wcaA|predicted glycosyl transferase|-
STM2116_1673_1707	0.01	1.31	1253637|wzc|tyrosine kinase|-
STM2117_209_243	0.29	1.61	1253638|wzb|tyrosine phosphatase|-
STM2118_429_463	0.13	1.41	1253639|wza|putative outer membrane polysaccharide export protein|-
STM2119_886_920	0.86	1.02	1253640|yegH|putative inner membrane protein|+
STM2120_1498_1532	0.01	-1.86	1253641|asmA|putative assembly protein|-
STM2121_145_179	0.03	-1.94	1253642|dcd|deoxycytidine triphosphate deaminase|-
STM2122_257_291	0.04	-1.41	1253643|udk|uridine kinase|-
STM2123_2600_2634	0.07	-1.21	1253644|yegE|putative diguanylate cyclase/phosphodiesterase|+
STM2127_2252_2286	0.02	2.58	1253648|yegN|multidrug efflux system subunit MdtB|+
STM2128_2146_2180	0.12	-1.21	1253649|yegO|multidrug efflux system subunit MdtC|+
STM2129_958_992	0.40	1.09	1253650|yegB|multidrug efflux system protein MdtE|+
STM2130_661_695	0.04	1.53	1253651|baeS|signal transduction histidine-protein kinase BaeS|+
STM2131_113_147	0.34	1.08	1253652|baeR|DNA-binding response regulator in two-component regulatory system with BaeS|+
STM2133_705_739	0.07	1.72	1253654|STM2133|putative cytoplasmic protein|+
STM2134_185_219	0.05	2.44	1253655|STM2134|putative inner membrane protein|+
STM2135_1481_1515	0.04	1.29	1253656|STM2135|putative inner membrane protein|+

STM2136_747_781	0.01	-1.63	1253657|yegQ|putative protease|+
STM2137_884_918	0.68	-1.07	1253658|STM2137|putative cytoplasmic protein|+
STM2138_104_142	0.47	-1.13	1253659|STM2138|putative cytoplasmic protein|-
STM2139_189_223	0.02	1.52	1253660|STM2139|putative inner membrane protein|-
STM2139.2n_49_83	0.69	1.05	2673733|STM2139.2n|hypothetical protein|-
STM2140_49_83	0.93	-1.02	1253661|yegS|lipid kinase|+
STM2141_118_152	0.77	-1.05	1253662|fbaB|fructose-bisphosphate aldolase|-
STM2142_433_467	0.03	1.41	1253663|yegT|putative transport protein|+
STM2143_6_40	0.14	1.42	1253664|yegU|putative glycohydrolase|+
STM2144_529_563	0.20	1.16	1253665|yegV|putative sugar kinase|+
STM2145_537_571	0.01	1.69	1253666|yegW|putative regulatory protein|-
STM2146_385_419	0.00	1.89	1253667|thiD|phosphomethylpyrimidine kinase|-
STM2148_137_171	0.01	2.49	1253669|STM2148|putative periplasmic protein|+
STM2149_289_323	0.07	-1.24	1253670|stcD|putative outer membrane lipoprotein|-
STM2150_1891_1925	0.02	1.44	1253671|stcC|putative outer membrane protein|-
STM2151_105_139	0.02	2.33	1253672|stcB|putative periplasmic chaperone protein|-
STM2152_345_379	0.04	1.80	1253673|stcA|putative fimbrial-like protein|-
STM2153_201_235	0.00	6.82	1253674|yehE|putative outer membrane protein|-
STM2154_639_673	0.32	-1.14	1253675|mrp|putative ATPase|-
STM2155_1467_1501	0.00	-2.19	1253676|metG|methionyl-tRNA synthetase|+
STM2156_213_247	0.06	2.13	1253677|yehR|putative lipoprotein|+
STM2156A_321_355	0.15	1.38	1253678|STM2156A|hypothetical protein|+
STM2157_321_355	0.03	-1.42	1253679|yehS|putative cytoplasmic protein|-
STM2158_121_155	0.01	-2.24	1253680|yehT|putative two-component response-regulatory protein YehT|-
STM2159_1327_1361	0.04	-1.74	1253681|yehU|putative sensor kinase|-
STM2160_209_243	0.03	-1.61	1253682|yehV|putative transcriptional repressor|+
STM2161_25_59	0.44	-1.09	1253683|STM2161|putative inner membrane protein|+
STM2162_601_635	0.02	1.80	1253684|yehW|putative ABC-type proline/glycine betaine transport system permease component|-
STM2163_321_355	0.02	-2.03	1253685|yehX|putative ABC-type proline/glycine betaine transport system ATPase component|-
STM2164_1067_1101	0.02	-1.23	1253686|yehY|putative ABC-type proline/glycine betaine transport system permease component|-
STM2165_81_115	0.26	-1.13	1253687|yehZ|putative transport protein|-
STM2166_2227_2261	0.48	1.05	1253688|bglX|periplasmic beta-D-glucoside glucohydrolase|-
STM2167_876_910	0.26	1.14	1253689|ldld|D-lactate dehydrogenase|+

STM2168_817_851	0.02	1.59	1253690|pbpG|D-alanyl-D-alanine endopeptidase|-
STM2169_161_195	0.04	1.70	1253691|yohC|putative transport protein|-
STM2170_201_235	0.75	-1.04	1253692|yohD|hypothetical protein|+
STM2171_273_307	0.08	-1.34	1253693|yohF|acetoin dehydrogenase|-
STM2172_646_680	0.02	1.43	1253694|yohG|multidrug resistance outer membrane protein MdtQ|-
STM2174_785_819	0.76	-1.03	1253696|yohI|tRNA-dihydrouridine synthase C|-
STM2176_529_563	0.31	-1.19	1253698|STM2176|putative glutathione S-transferase|-
STM2177_649_683	0.02	-1.67	1253699|STM2177|putative flutathione S-transferase|-
STM2178_327_361	0.05	1.95	1253700|STM2178|putative 1 2-dioxygenase|-
STM2179_824_858	0.10	-1.42	1253701|STM2179|putative sugar transporter|-
STM2181_337_371	0.00	3.65	1253703|yohJ|hypothetical protein|+
STM2182_289_323	0.07	1.54	1253704|yohK|predicted inner membrane protein|+
STM2183_849_883	0.01	2.58	1253705|cdd|cytidine deaminase|+
STM2184_465_499	0.05	1.53	1253706|sanA|hypothetical protein|+
STM2185_121_155	0.35	-1.04	1253707|b2145|putative inner membrane protein|+
STM2186_507_541	0.02	-1.86	1253708|STM2186|putative oxidoreductase|+
STM2187_1037_1071	0.02	-1.59	1253709|yeiA|dihydropyrimidine dehydrogenase|+
STM2188_524_558	0.01	-2.53	1253710|mglC|beta-methylgalactoside transporter inner membrane component|-
STM2189_1034_1068	0.03	-2.03	1253711|mglA|galactose/methyl galaxtoside transporter ATP-binding protein|-
STM2190_817_851	0.00	-10.12	1253712|mglB|galactose transport protein|-
STM2191_856_890	0.00	-4.75	1253713|galS|DNA-binding transcriptional repressor|-
STM2192_400_434	0.65	1.04	1253714|yeiB|hypothetical protein|-
STM2193_513_547	0.03	-1.52	1253715|folE|GTP cyclohydrolase II|-
STM2194_643_677	0.18	1.24	1253716|yeiG|putative esterase|+
STM2195_25_59	0.05	1.44	1253717|STM2195|putative transcriptional regulator|-
STM2196_1265_1299	0.03	1.65	1253718|STM2196|putative L-serine dehydratase|-
STM2197_633_667	0.04	2.68	1253719|STM2197|putative phosphoserine phosphatase|+
STM2198_356_390	0.49	1.13	1253720|STM2198|putative regulatory protein|+
STM2199_1185_1219	0.08	-1.29	1253721|cirA|ferric iron-catecholate outer membrane transporter|-
STM2200_1119_1153	0.01	-1.73	1253722|lysP|lysine transporter|-
STM2201_257_291	0.50	-1.21	1253723|yeiE|putative DNA-binding transcriptional regulator|-
STM2202_307_341	0.38	-1.17	1253724|yeiH|putative inner membrane protein|+
STM2203_785_819	0.02	1.58	1253725|nfo|endonuclease IV|+
STM2204_1246_1280	0.03	1.29	1253726|fruA|fructose-specific PTS system IIBC component|-
STM2205_385_419	0.37	-1.09	1253727|fruK|1-phosphofructokinase|-

STM2206_692_726	0.03	-1.63	1253728|fruF|fructose-specific PTS IIA/HPr components|-
STM2208_536_570	0.50	-1.07	1253730|STM2208|putative inner membrane protein|-
STM2209.1c_93_127	0.04	1.29	2673743|STM2209.1c|hypothetical protein|-
STM2212_513_547	0.04	-1.54	1253734|yeiR|putative cobalamin biosynthetic protein|+
STM2213_289_323	0.01	-1.61	1253735|yeiU|putative permease|+
STM2214_457_491	0.00	-2.98	1253736|spr|putative lipoprotein|+
STM2215_942_976	0.01	1.90	1253737|rtn|hypothetical protein|+
STM2216_1655_1689	0.02	-1.71	1253738|yejA|putative ABC transporter periplasmic binding protein|+
STM2217_752_786	0.02	2.73	1253739|yejB|putative ABC-type dipeptide/oligopeptide/nickel transport system permease|+
STM2218_731_765	0.03	1.24	1253740|yejE|putative ABC-type dipeptide/oligopeptide/nickel transport system permease component|+
STM2219_1359_1393	0.01	1.75	1253741|yejF|putative ABC-type transport system ATPase component|+
STM2220_17_51	0.04	-1.46	1253742|yejG|hypothetical protein|-
STM2221_960_994	0.09	1.49	1253743|bcr|bicyclomycin/multidrug efflux system|-
STM2222_193_227	0.83	1.02	1253744|rsuA|16S rRNA pseudouridylate synthase A|-
STM2223_954_988	0.16	1.07	1253745|yejH|putative ATP-dependent helicase|+
STM2224_69_103	0.03	-1.92	1253746|rplY|50S ribosomal protein L25|+
STM2225_273_307	0.01	-2.03	1253747|STM2225|putative inner membrane protein|-
STM2226_265_299	0.02	-2.18	1253748|yejK|nucleoid-associated protein NdpA|-
STM2227_117_151	0.04	-1.27	1253749|yejL|putative cytoplasmic protein|+
STM2228_794_828	0.04	-1.26	1253750|yejM|putative hydrolase|+
STM2230.1c_121_155	0.82	-1.04	1253752|STM2230.1c|DNA polymerase V subunit|-
STM2232_1399_1433	0.02	2.02	1253754|oafA|O-antigen acetylase|+
STM2233_53_87	0.01	4.10	1253755|STM2233|putative cytoplasmic protein|-
STM2235_339_373	0.00	4.46	1253757|STM2235|hypothetical protein|-
STM2236_65_99	0.01	3.42	1253758|STM2236|hypothetical protein|-
STM2237_65_99	0.02	2.64	1253759|STM2237|putative inner membrane protein|-
STM2238_369_403	0.23	1.30	1253760|STM2238|hypothetical protein|+
STM2239_113_147	0.02	2.52	1253761|STM2239|putative phage antiterminator|-
STM2240_457_491	0.02	2.38	1253762|STM2240|putative cytoplasmic protein|-
STM2241_1920_1954	0.32	2.25	1253763|sspH2|leucine-rich repeat protein|-
STM2242_13_47	0.06	1.79	1253764|STM2242|putative phage tail fiber protein|-
STM2243_673_707	0.25	1.81	1253765|STM2243|putative tail fiber protein of phage|-
STM2244_87_122	0.03	3.07	1253766|STM2244|virulence protein|+
STM2245_289_323	0.00	3.00	1253767|STM2245|putative outer membrane protein|-

STM2246_305_339	0.37	-1.15	1253768|narP|DNA-binding response regulator in two-component regulatory system with NarQ or NarX|+
STM2247_884_918	0.63	1.03	1253769|ccmH|putative heme lyase subunit|-
STM2248/STM3813_355_38	0.00	1.22	1253770/1255340|ccmG/ccmG|heme lyase/disulfide oxidoreductase|-
STM2249/STM3814_1805_1	0.11	-1.23	1253771/1255341|ccmF/ccmF|cytochrome c-type biogenesis protein|-
STM2252/STM3817_497_53	0.92	-1.01	1253774/1255344|ccmC/ccmC|heme exporter protein|-
STM2253/STM3818_543_57	0.01	-1.71	1253775/1255345|ccmB/ccmB|heme exporter protein|-
STM2255_9_43	0.58	1.07	1253777|napC|cytochrome c-type protein NapC|-
STM2256_389_423	0.83	-1.07	1253778|napB|diheme cytochrome c550|-
STM2257_73_107	0.35	-1.15	1253779|napH|quinol dehydrogenase membrane component|-
STM2258_445_479	0.02	1.44	1253780|napG|quinol dehydrogenase periplasmic component|-
STM2259_2368_2402	0.05	-1.26	1253781|napA|periplasmic nitrate reductase|-
STM2261_353_387	0.73	-1.11	1253783|napF|ferredoxin-type protein|-
STM2262_193_227	0.00	2.67	1253784|ecolecotin precursor|+
STM2263_693_727	0.13	-1.29	1253785|yojI|multidrug transporter membrane component/ATP-binding component|-
STM2264_281_315	0.22	1.09	1253786|alkB|DNA repair system protein|-
STM2266_846_880	0.05	-1.16	1253788|apbE|thiamine biosynthesis lipoprotein ApbE|-
STM2267_746_780	0.02	-2.67	1253789|ompC|outer membrane porin protein C|-
STM2268_17_51	0.90	-1.01	1253790|micF|misc_RNA|-
STM2269_2567_2601	0.22	-1.28	1253791|yojN|phosphotransfer intermediate protein in two-component regulatory system with RcsB|C|+
STM2270_129_163	0.06	-1.48	1253792|rcsB|DNA-binding response regulator in two-component regulatory system with RcsC and YojN|+
STM2271_2288_2322	0.09	1.39	1253793|rcsC|hybrid sensory kinase in two-component regulatory system with RcsB and YojN|-
STM2272_2350_2384	0.02	-2.41	1253794|gyrA|DNA gyrase subunit A|-
STM2273_468_502	0.26	1.32	1253795|STM2273|putative dehydratase|-
STM2274_1087_1121	0.17	2.01	1253796|STM2274|putative permease|-
STM2275_497_531	0.00	2.38	1253797|STM2275|putative regulatory protein|+
STM2276_673_707	0.03	2.05	1253798|ubiG|3-demethylubiquinone-9 3-methyltransferase|+
STM2277_2087_2121	0.35	-1.23	1253799|nrdA|ribonucleotide-diphosphate reductase subunit alpha|+
STM2278_452_486	0.03	1.40	1253800|nrdB|ribonucleotide-diphosphate reductase subunit beta|+
STM2279_145_179	0.09	-1.61	1253801|yfaE|2Fe-2S ferredoxin YfaE|+
STM2280_272_306	0.03	1.15	1253802|STM2280|putative permease|-
STM2281_129_163	0.22	1.44	1253803|STM2281|putative transcriptional regulator|+

STM2282_840_874	0.01	-11.80	1253804|glpQ|glycerophosphodiester phosphodiesterase|-
STM2283_1080_1114	0.21	-1.43	1253805|glpT|sn-glycerol-3-phosphate transporter|-
STM2284_758_792	0.00	-14.13	1253806|glpA|sn-glycerol-3-phosphate dehydrogenase subunit A|+
STM2285_517_551	0.00	-8.86	1253807|glpB|anaerobic glycerol-3-phosphate dehydrogenase subunit B|+
STM2286_368_402	0.00	-6.04	1253808|glpC|sn-glycerol-3-phosphate dehydrogenase subunit C|+
STM2287_817_851	0.14	3.14	1253809|sseL|deubiquitinase|+
STM2288_34_68	0.01	-1.68	1253810|STM2288|putative cytoplasmic protein|-
STM2289_577_611	0.02	-1.94	1253811|STM2289|putative aldolase|-
STM2290_867_901	0.05	-1.41	1253812|yfaV|putative transport protein|-
STM2291_347_381	0.02	-2.36	1253813|yfaW|putative galactonate dehydratase|-
STM2292_193_227	0.00	-2.30	1253814|yfaX|putative transcriptional regulator|-
STM2293_806_840	0.28	1.10	1253815|STM2293|competence damage-inducible protein A|-
STM2294_17_51	0.03	2.31	1253816|yfaZ|putative inner membrane protein|-
STM2295_205_239	0.13	-1.21	1253817|yfaO|putative NTP pyrophosphohydrolase|+
STM2296_513_547	0.19	1.43	1253818|ais|aluminum-inducible protein|-
STM2297_533_567	0.03	1.52	1253819|yfbE|UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase|+
STM2298_833_867	0.02	1.49	1253820|pmrF|undecaprenyl phosphate 4-deoxy-4-formamido-L-arabinose transferase|+
STM2299_1816_1850	0.02	1.86	1253821|yfbG|bifunctional UDP-glucuronic acid decarboxylase/UDP-4-amino-4-deoxy-L-arabinose formyltransferase|+
STM2300_577_611	0.13	1.14	1253822|STM2300|putative cytoplasmic protein|+
STM2301_1416_1450	0.02	-1.54	1253823|arnT|4-amino-4-deoxy-L-arabinose transferase|+
STM2302_181_215	0.87	-1.02	1253824|STM2302|putative inner membrane protein|+
STM2303_269_303	0.00	1.43	1253825|STM2303|hypothetical protein|+
STM2304_105_139	0.01	4.17	1253826|pmrD|polymyxin resistance protein B|-
STM2305_1081_1115	0.01	-1.65	1253827|menE|O-succinylbenzoic acid--CoA ligase|-
STM2306_561_595	0.10	1.14	1253828|menC|O-succinylbenzoate synthase|-
STM2307_129_163	0.05	-1.19	1253829|menB|naphthoate synthase|-
STM2308_113_147	0.03	-2.26	1253830|yfbB|acyl-CoA thioester hydrolase YfbB|-
STM2309_896_930	0.03	-1.64	1253831|menD|2-succinyl-6-hydroxy-2 4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase|-
STM2311_169_203	0.81	-1.03	1253833|elaB|hypothetical protein|-
STM2312_81_115	0.62	-1.04	1253834|elaA|hypothetical protein|-
STM2313_433_467	0.01	-1.49	1253835|elaC|ribonuclease Z|+
STM2314_67_101	0.43	-1.08	1253836|STM2314|putative chemotaxis signal transduction protein|+

STM2315_1263_1297	0.01	1.62	1253837|yfbK|hypothetical protein|-
STM2316.S_971_1005	0.01	-2.18	1253838|nuoN|NADH dehydrogenase subunit N|-
STM2317_915_949	0.01	-1.41	1253839|nuoM|NADH dehydrogenase subunit M|-
STM2318_1639_1673	0.01	-1.73	1253840|nuoL|NADH dehydrogenase subunit L|-
STM2319_163_197	0.01	-2.01	1253841|nuoK|NADH dehydrogenase subunit K|-
STM2320_65_99	0.00	-2.24	1253842|nuoJ|NADH dehydrogenase subunit J|-
STM2321_441_475	0.06	-1.45	1253843|nuoI|NADH dehydrogenase subunit I|-
STM2322_929_963	0.01	-1.57	1253844|nuoH|NADH dehydrogenase subunit H|-
STM2323.S_2568_2602	0.00	-2.06	1253845|nuoG|NADH dehydrogenase subunit G|-
STM2324_1155_1189	0.67	1.03	1253846|nuoF|NADH dehydrogenase I subunit F|-
STM2325_213_247	0.98	-1.00	1253847|nuoE|NADH dehydrogenase subunit E|-
STM2326_820_854	0.60	-1.08	1253848|nuoC|bifunctional NADH:ubiquinone oxidoreductase subunit C/D|-
STM2327_417_451	0.11	-1.25	1253849|nuoB|NADH dehydrogenase subunit B|-
STM2328_129_163	0.05	-1.26	1253850|nuoA|NADH dehydrogenase subunit A|-
STM2329_41_75	0.13	2.53	1253851|STM2329|putative cytoplasmic protein|-
STM2330_385_419	0.01	2.23	1253852|lrhA|NADH dehydrogenase transcriptional repressor|-
STM2331_232_266	0.29	1.12	1253853|yfbQ|aminotransferase AlaT|+
STM2332_193_227	0.06	1.98	1253854|STM2332|hypothetical protein|+
STM2333_988_1022	0.77	-1.03	1253855|yfbS|putative response regulator|-
STM2334_33_67	0.27	1.24	1253856|yfbT|putative phosphatase|-
STM2335_297_331	0.03	1.54	1253857|yfbU|hypothetical protein|-
STM2336_257_291	0.43	1.05	1253858|STM2336|hypothetical protein|-
STM2337_460_494	0.02	1.47	1253859|ackA|acetate kinase|+
STM2338_1626_1660	0.37	1.24	1253860|pta|phosphate acetyltransferase|+
STM2340_673_707	0.02	-2.02	1253862|STM2340|putative transketolase|-
STM2341_225_259	0.00	-4.17	1253863|STM2341|putative transketolase|-
STM2342_527_561	0.01	-3.77	1253864|ulaA|ascorbate-specific PTS system enzyme IIC|-
STM2344_265_299	0.02	-1.85	1253866|STM2344|putative phosphotransferase system enzyme II A component|-
STM2345_21_55	0.05	1.32	1253867|STM2345|putative transcriptional regulator|+
STM2346_9_43	0.01	-1.51	1253868|STM2346|putative NTP pyrophosphohydrolase|-
STM2347_97_131	0.08	-1.33	1253869|yfcE|phosphodiesterase|-
STM2348_345_379	0.02	2.95	1253870|yfcF|putative glutathione S-transferase|-
STM2349_385_419	0.17	1.24	1253871|yfcG|putative glutathione S-transferase|+
STM2350_385_419	0.07	1.23	1253872|yfcH|putative sugar nucleotide epimerase|+
STM2351_353_387	0.00	-1.28	1253873|hisP|histidine/lysine/arginine/ornithine transporter subunit|-

STM2352_577_611	0.30	1.20	1253874|hisM|histidine/lysine/arginine/ornithine transport protein|-
STM2353_209_243	0.01	-1.51	1253875|hisQ|histidine/lysine/arginine/ornithine transport protein|-
STM2354_81_115	0.00	-3.61	1253876|hisJ|histidine transport protein|-
STM2355_269_303	0.03	-2.08	1253877|argT|lysine/arginine/ornithine transport protein|-
STM2356_377_411	0.79	1.03	1253878|ubiX|3-octaprenyl-4-hydroxybenzoate carboxy-lyase|-
STM2357_870_904	0.00	-1.41	1253879|STM2357|putative amino acid transporter|-
STM2358_617_651	0.90	1.02	1253880|STM2358|putative cytoplasmic protein|-
STM2359_1079_1113	0.02	1.70	1253881|STM2359|putative amino acid transporter|-
STM2360_871_905	0.02	1.60	1253882|STM2360|putative diaminopimelate decarboxylase|-
STM2361_629_663	0.48	-1.32	1253883|STM2361|putative regulatory protein|+
STM2362_1031_1065	0.01	-3.34	1253884|purF|amidophosphoribosyltransferase|-
STM2363_133_167	0.03	-2.25	1253885|cvpA|colicin V production protein|-
STM2364_273_307	0.19	1.14	1253886|dedD|hypothetical protein|-
STM2365_1038_1072	0.04	-1.66	1253887|folC|bifunctional folylpolyglutamate synthase/ dihydrofolate synthase|-
STM2366_129_163	0.04	-1.32	1253888|accD|acetyl-CoA carboxylase subunit beta|-
STM2367_257_291	0.09	1.28	1253889|dedA|hypothetical protein|-
STM2368_561_595	0.59	-1.04	1253890|truA|tRNA pseudouridine synthase A|-
STM2369_527_561	0.17	-1.28	1253891|usg|hypothetical protein|-
STM2371_723_757	0.01	-1.80	1253893|flk|predicted flagella assembly protein|+
STM2372_332_366	0.01	-1.96	1253894|STM2372|hypothetical protein|-
STM2373_65_99	0.40	1.44	1253895|STM2373|putative cytoplasmic protein|-
STM2374_65_99	0.02	2.92	1253896|STM2374|putative regulatory protein|+
STM2376_177_211	0.60	-1.02	1253898|STM2376|putative periplasmic protein|+
STM2377_257_291	0.02	2.01	1253899|STM2377|putative inner membrane protein|-
STM2378_504_538	0.12	-1.14	1253900|fabB|3-oxoacyl-(acyl carrier protein) synthase II|-
STM2379_1610_1644	0.01	1.66	1253901|mnmC|5-methylaminomethyl-2-thiouridine methyltransferase|+
STM2380_33_67	0.29	-1.29	1253902|yfcL|putative cytoplasmic protein|-
STM2381_129_163	0.46	-1.09	1253903|yfcM|putative cytoplasmic protein|-
STM2382_513_547	0.40	-1.09	1253904|yfcA|hypothetical protein|-
STM2383_417_451	0.10	-1.13	1253905|mepA|penicillin-insensitive murein endopeptidase|-
STM2384_487_521	0.02	1.74	1253906|aroC|chorismate synthase|-
STM2385_129_163	0.07	-1.51	1253907|yfcB|N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase|-
STM2386_193_227	0.04	1.95	1253908|yfcN|hypothetical protein|+
STM2387_321_355	0.02	1.90	1253909|sixA|phosphohistidine phosphatase|-

STM2388_1853_1887	0.63	1.06	1253910|fadJ|multifunctional fatty acid oxidation complex subunit alpha|-
STM2390_177_211	0.00	3.95	1253912|yfcZ|putative cytoplasmic protein|-
STM2391_1051_1085	0.00	-26.78	1253913|fadL|long-chain fatty acid outer membrane transporter|+
STM2392_641_675	0.28	-1.14	1253914|vacJ|lipoprotein precursor|-
STM2393_593_627	0.28	1.18	1253915|yfdC|hypothetical protein|+
STM2394_31_65	0.43	1.52	1253916|argW|tRNA|+
STM2395_353_387	0.01	2.81	1253917|pgtE|outer membrane protease|-
STM2396_569_603	0.00	-2.53	1253918|pgtA|activator|-
STM2397_1968_2002	0.00	-2.50	1253919|pgtB|phosphoglycerate transport system sensor protein|-
STM2398_915_949	0.05	-1.34	1253920|pgtC|phosphoglycerate transport regulatory protein precursor|-
STM2399_1065_1099	0.00	-2.72	1253921|pgtP|transporter|+
STM2400_189_223	0.69	1.04	1253922|STM2400|putative inner membrane protein|-
STM2401_699_733	0.03	1.71	1253923|ddg|lipid A biosynthesis palmitoleoyl acyltransferase|+
STM2402_720_754	0.10	-1.49	1253924|yfdZ|aminotransferase|-
STM2403_129_163	0.78	-1.03	1253925|glk|glucokinase|-
STM2404_1101_1135	0.01	-1.11	1253926|STM2404|hypothetical protein|+
STM2405_862_896	0.04	1.44	1253927|STM2405|indolepyruvate decarboxylase|-
STM2406_881_915	0.01	1.74	1253928|STM2406|putative oxidoreductase|+
STM2407_97_131	0.31	1.09	1253929|ypeC|putative periplasmic protein|+
STM2408_691_725	0.07	-1.39	1253930|mntH|manganese transport protein MntH|-
STM2409_908_942	0.00	-4.12	1253931|nupC|nucleoside transport|+
STM2410_1575_1609	0.16	-1.13	1253932|yfeA|hypothetical protein|-
STM2413_33_67	0.04	-2.50	1253935|yfeC|putative negative regulator|+
STM2414_137_171	0.00	-1.87	1253936|yfeD|putative negative regulator|+
STM2415_593_627	0.71	-1.06	1253937|gltX|glutamyl-tRNA synthetase|-
STM2420_161_195	0.51	1.12	1253942|xapR|DNA-binding transcriptional activator|-
STM2420.1n_8_46	0.69	1.48	2673749|STM2420.1n|hypothetical protein|-
STM2421_514_548	0.11	1.59	1253943|xapB|xanthosine permease|-
STM2423_321_355	0.08	1.56	1253945|yfeN|hypothetical protein|+
STM2424_577_611	0.13	1.73	1253946|yfeR|putative transcriptional regulator|-
STM2425_17_51	0.61	1.07	1253947|yfeH|putative Na+-dependent transporter|+
STM2426_24_58	0.03	-1.23	1253948|STM2426|putative cytoplasmic protein|-
STM2427_1753_1787	0.79	-1.07	1253949|ligA|NAD-dependent DNA ligase LigA|-
STM2428_97_131	0.05	1.25	1253950|zipA|cell division protein ZipA|-
STM2429_649_683	0.94	1.01	1253951|cysZ|putative sulfate transport protein CysZ|+
STM2430_265_299	0.28	1.59	1253952|cysK|cysteine synthase A|+

STM2431_209_243	0.34	1.21	1253953|ptsH|phosphohistidinoprotein-hexose phosphotransferase component of PTS system (Hpr)|+
STM2432_1657_1691	0.01	1.53	1253954|ptsI|phosphoenolpyruvate-protein phosphotransferase|+
STM2433_241_275	0.27	1.27	1253955|crr|glucose-specific PTS system component|+
STM2434_123_157	0.02	1.90	1253956|STM2434|putative cytoplasmic protein|-
STM2435_321_355	0.24	1.45	1253957|pdxK|pyridoxal kinase|-
STM2436_422_456	0.94	1.02	1253958|ptsJ|putative regulatory protein|+
STM2437_129_163	0.01	1.62	1253959|yfeJ|glutamine amidotransferase|+
STM2438_141_175	0.02	2.15	1253960|yfeK|hypothetical protein|+
STM2439_89_123	0.64	1.15	1253961|yfeL|putative membrane carboxypeptidase|+
STM2440_849_883	0.06	-1.84	1253962|cysM|cysteine synthase B|-
STM2441_163_197	0.91	-1.05	1253963|cysA|sulfate/thiosulfate transporter subunit|-
STM2442_105_139	0.59	1.27	1253964|cysW|sulfate/thiosulfate transporter permease subunit|-
STM2443_425_459	0.15	1.93	1253965|cysU|sulfate/thiosulfate transporter subunit|-
STM2444_338_372	0.18	1.93	1253966|cysP|thiosulfate transporter subunit|-
STM2445_513_547	0.00	-8.21	1253967|ucpA|short chain dehydrogenase|-
STM2446_113_147	0.16	-1.28	1253968|STM2446|putative iron-dependent peroxidase|-
STM2447_417_451	0.02	1.85	1253969|STM2447|hypothetical protein|-
STM2448_385_419	0.04	1.34	1253970|yfeZ|putative inner membrane protein|-
STM2449.S_105_139	0.09	1.46	1253971|STM2449.S|putative acetyltransferase|-
STM2450_705_739	0.13	1.45	1253972|amiA|N-acetylmuramoyl-l-alanine amidase II|+
STM2451_617_651	0.10	1.78	1253973|hemF|coproporphyrinogen III oxidase|+
STM2453_983_1017	0.72	1.03	1253975|STM2453|putative cytoplasmic protein|+
STM2454_118_152	0.01	-1.97	1253976|eutR|transcriptional regulator EutR|-
STM2455_81_115	0.01	-1.76	1253977|eutK|putative carboxysome structural protein|-
STM2456_545_579	0.01	-1.80	1253978|eutL|putative carboxysome structural protein|-
STM2457_301_335	0.69	1.14	1253979|eutC|ethanolamine ammonia-lyase small subunit|-
STM2458_1067_1101	0.18	-1.09	1253980|eutB|ethanolamine ammonia-lyase heavy chain|-
STM2459_597_631	0.61	1.07	1253981|eutA|reactivating factor for ethanolamine ammonia lyase|-
STM2460_1092_1126	0.40	1.11	1253982|eutH|putative transport protein|-
STM2461_933_967	0.19	1.12	1253983|eutG|putative transport protein|-
STM2462_345_379	0.05	-1.35	1253984|eutJ|ethanolamine utilization protein|-
STM2464_233_267	0.06	-1.10	1253986|eutN|putative detox protein|-
STM2465_37_71	0.03	-1.44	1253987|eutM|putative detox protein|-
STM2466_346_380	0.06	-1.68	1253988|eutD|phosphotransacetylase|-
STM2468_497_531	0.17	-1.42	1253990|eutQ|putative ethanolamine utilization protein|-

STM2469_233_267	0.02	1.85	1253991|eutP|putative ethanolamine utilization protein|-
STM2470_177_211	0.11	1.19	1253992|eutS|putative carboxysome structural protein|-
STM2472_2177_2211	0.00	-3.24	1253994|maeB|malic enzyme|-
STM2473_321_355	0.04	1.57	1253995|talA|transaldolase A|+
STM2474_1642_1676	0.14	-1.22	1253996|tktB|transketolase|+
STM2475_161_195	0.01	1.98	1253997|STM2475|putative cytoplasmic protein|-
STM2476_557_591	0.13	2.04	1253998|ypfG|putative periplasmic protein|-
STM2477_257_291	0.56	1.12	1253999|yffH|putative pyrophosphohydrolase|-
STM2478_588_622	0.09	-1.26	1254000|STM2478|hypothetical protein|+
STM2479_1379_1413	0.08	1.88	1254001|aegA|putative oxidoreductase Fe-S binding subunit|-
STM2480_846_880	0.14	-1.52	1254002|narQ|nitrate/nitrite sensor protein NarQ|+
STM2481_2307_2341	0.03	-1.49	1254003|acrD|aminoglycoside/multidrug efflux system|+
STM2482_241_275	0.50	1.03	1254004|yffB|hypothetical protein|+
STM2483_721_755	0.06	-1.41	1254005|dapE|succinyl-diaminopimelate desuccinylase|+
STM2484_41_76	0.05	-1.48	1254006|STM2484|putative inner membrane protein|+
STM2485_1256_1290	0.04	-1.24	1254007|ypfF|putative acetyltransferase|-
STM2486_529_563	0.12	1.28	1254008|STM2486|putative inner membrane protein|-
STM2487_65_99	0.02	-4.24	1254009|purC|phosphoribosylaminoimidazole-succinocarboxamide synthase|-
STM2488_692_726	0.24	-1.12	1254010|nlpB|lipoprotein|-
STM2489_257_291	0.66	-1.02	1254011|dapA|dihydrodipicolinate synthase|-
STM2490_161_195	0.04	-1.21	1254012|gcvR|glycine cleavage system transcriptional repressor|+
STM2491_21_55	0.03	1.80	1254013|bcp|thioredoxin-dependent thiol peroxidase|+
STM2492_161_195	0.00	-1.46	1254014|STM2492|putative glycerate kinase|-
STM2493_997_1031	0.01	-1.51	1254015|perM|putative permease|-
STM2494_849_883	0.21	1.28	1254016|STM2494|hypothetical protein|+
STM2495_249_283	0.62	-1.08	1254017|yfgD|putative arsenate reductase|+
STM2496_257_291	0.63	-1.05	1254018|yfgE|DNA replication initiation factor|-
STM2497_803_837	0.95	-1.01	1254019|uraA|uracil transporter|-
STM2498_65_99	0.01	1.71	1254020|upp|uracil phosphoribosyltransferase|-
STM2499.S_790_824	0.00	-4.88	1254021|purM|phosphoribosylaminoimidazole synthetase|+
STM2500_481_515	0.01	-2.41	1254022|purN|phosphoribosylglycinamide formyltransferase|+
STM2501_1132_1166	0.04	1.39	1254023|ppk|polyphosphate kinase|+
STM2502_607_641	0.54	-1.05	1254024|ppx|exopolyphosphatase|+
STM2506_34_68	0.01	2.03	1254028|STM2506|putative inner membrane protein|+
STM2508_257_291	0.05	1.21	1254030|STM2508|putative cytoplasmic protein|+
STM2509_25_59	0.01	1.95	1254031|STM2509|putative transposase|-

STM2510_1379_1413	0.17	-1.36	1254032|guaA|bifunctional GMP synthase/glutamine amidotransferase protein|-
STM2511_1236_1270	0.05	-4.01	1254033|guaB|inositol-5-monophosphate dehydrogenase|-
STM2512_959_993	0.04	2.21	1254034|xseA|exodeoxyribonuclease VII large subunit|+
STM2513_5569_5603	0.08	-1.23	1254035|shdA|AIDA autotransporter-like protein|-
STM2514_6885_6919	0.51	-1.20	1254036|ratB|putative outer membrane protein|-
STM2515_4983_5017	0.10	1.23	1254037|ratA|putative outer membrane protein|-
STM2518_65_99	0.09	1.23	1254040|yfgJ|putative cytoplasmic protein|-
STM2519_1306_1340	0.93	-1.02	1254041|engA|GTP-binding protein EngA|-
STM2520_780_814	0.06	-1.63	1254042|yfgL|outer membrane protein assembly complex subunit YfgL|-
STM2521_553_587	0.90	-1.02	1254043|yfgM|putative inner membrane protein|-
STM2522_404_438	0.21	-1.23	1254044|hisS|histidyl-tRNA synthetase|-
STM2523_120_154	0.81	-1.05	1254045|ispG|4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase|-
STM2524_934_968	0.07	-1.25	1254046|yfgA|hypothetical protein|-
STM2525_1096_1130	0.03	-2.09	1254047|yfgB|hypothetical protein|-
STM2526_321_355	0.00	-7.48	1254048|ndk|nucleoside diphosphate kinase|-
STM2527_177_211	0.83	-1.03	1254049|STM2527|putative polyferredoxin|-
STM2528_577_611	0.03	-1.44	1254050|STM2528|putative dimethylsulfoxide reductase|-
STM2529_489_523	0.03	1.32	1254051|STM2529|putative anaerobic dimethylsulfoxide reductase|-
STM2530_2079_2113	0.11	-1.21	1254052|STM2530|putative anaerobic dimethylsulfoxide reductase|-
STM2531_1445_1479	0.02	-1.62	1254053|pbpC|penicillin-binding protein 1C|-
STM2532_4096_4130	0.00	-2.75	1254054|STM2532|putative inner membrane lipoprotein|-
STM2533_609_643	0.17	-1.46	1254055|sseA|3-mercaptopyruvate sulfurtransferase|+
STM2534_513_547	0.05	2.77	1254056|STM2534|putative cytoplasmic protein|+
STM2535_385_419	0.38	-1.22	1254057|sseB|enhanced serine sensitivity protein|-
STM2536_301_335	0.71	-1.05	1254058|pepB|aminopeptidase B|-
STM2537_65_99	0.03	3.31	1254059|yfhJ|hypothetical protein|-
STM2538_297_331	0.04	4.09	1254060|fdx|electron carrer protein|-
STM2539_1060_1094	0.03	3.82	1254061|hscA|chaperone protein HscA|-
STM2540_273_307	0.04	4.00	1254062|hscB|co-chaperone HscB|-
STM2541_169_203	0.04	3.10	1254063|iscA|iron-sulfur cluster assembly protein|-
STM2542_57_91	0.02	7.57	1254064|nifU|scaffold protein|-
STM2543_1112_1146	0.04	4.25	1254065|nifS|cysteine desulfurase|-
STM2544_17_51	0.01	5.74	1254066|yfhP|DNA-binding transcriptional repressor|-
STM2545_385_419	0.06	1.55	1254067|STM2545|putative rRNA methylase|-
STM2546_673_707	0.04	-1.63	1254068|suhB|inositol monophosphatase|+
STM2547_385_419	0.10	1.15	1254069|STM2547|putative hydrolase|+

STM2548_717_751	0.02	1.70	1254070|asrA|anaerobic sulfide reductase|+
STM2549_577_611	0.47	1.12	1254071|asrB|anaerobic sulfite reductase subunit B|+
STM2550_271_305	0.06	1.41	1254072|asrC|anaerobic sulfide reductase|+
STM2551_689_723	0.06	-1.57	1254073|STM2551|putative inner membrane protein|-
STM2552_353_387	0.49	-1.08	1254074|STM2552|hypothetical protein|-
STM2553_855_889	0.00	-4.52	1254075|csiE|stationary phase inducible protein CsiE|+
STM2554_157_191	0.02	-1.35	1254076|hcaT|putative 3-phenylpropionic acid transporter|-
STM2555_1063_1097	0.02	-1.67	1254077|glyA|serine hydroxymethyltransferase|-
STM2556_264_298	0.00	-3.03	1254078|hmpA|nitric oxide dioxygenase|+
STM2557_1458_1492	0.17	1.36	1254079|cadC|DNA-binding transcriptional activator|+
STM2558_1117_1151	0.92	1.01	1254080|cadB|predicted lysine/cadaverine transporter|+
STM2559_1498_1532	0.00	2.84	1254081|cadA|lysine decarboxylase 1|+
STM2561_209_243	0.67	-1.09	1254083|glnB|regulatory protein P-III|-
STM2562_467_501	0.36	-1.14	1254084|yfhA|putative transcriptional regulator|-
STM2563_689_723	0.91	-1.03	1254085|yfhG|hypothetical protein|-
STM2564_1196_1230	0.01	1.30	1254086|yfhK|putative sensor kinase|-
STM2566_97_131	0.03	1.73	1254088|STM2566|putative periplasmic protein|+
STM2567_802_836	0.01	1.57	1254089|yfhD|putative transglycosylase|+
STM2568_257_291	0.50	-1.08	1254090|yfhC|tRNA-specific adenosine deaminase|-
STM2569_289_323	0.03	1.59	1254091|yfhB|hypothetical protein|-
STM2570_877_911	0.02	1.51	1254092|STM2570|putative phosphotransferase system IIB component|-
STM2571_17_51	0.12	-1.23	1254093|murQ|N-acetylmuramic acid-6-phosphate etherase|-
STM2572_225_259	0.02	1.80	1254094|yfhH|putative DNA-binding transcriptional regulator|+
STM2573_577_611	0.11	-1.25	1254095|STM2573|2-dehydropantoate 2-reductase|-
STM2574_582_616	0.14	1.32	1254096|STM2574|putative permease|-
STM2575_641_675	0.37	1.07	1254097|STM2575|putative transcriptional regulator|+
STM2576_97_131	0.01	-1.74	1254098|yfhL|putative ferredoxin|+
STM2577_17_51	0.70	1.07	1254099|acpS|4'-phosphopantetheinyl transferase|-
STM2578_385_419	0.36	1.16	1254100|pdxJ|pyridoxal phosphate biosynthetic protein PdxJ|-
STM2579_521_555	0.13	1.07	1254101|recO|DNA repair protein RecO|-
STM2580_17_51	0.24	-1.14	1254102|eraA|GTP-binding protein Era|-
STM2581_337_371	0.57	-1.07	1254103|rnc|ribonuclease III|-
STM2582_545_579	0.01	1.34	1254104|lepB|signal peptidase I|-
STM2583_1249_1283	0.27	-1.17	1254105|lepA|GTP-binding protein LepA|-
STM2584_1339_1374	0.01	2.66	1254106|gogB|leucine-rich repeat protein|+
STM2585_489_523	0.01	5.76	1254107|STM2585|transposase-like protein|+

STM2585A_148_183	0.00	3.72	1254108|STM2585A|PagK-like protein|+
STM2586_436_471	0.07	2.39	1254109|STM2586|phage tail assembly-like protein|-
STM2587_105_139	0.08	1.59	1254110|STM2587|phage tail assembly-like protein|-
STM2589_2890_2924	0.04	1.41	1254112|STM2589|host specificity protein-J-like|-
STM2590_177_211	0.06	1.69	1254113|STM2590|tail assembly protein I-like|-
STM2591_293_327	0.10	1.42	1254114|STM2591|tail assembly protein K-like|-
STM2592_385_419	0.05	1.78	1254115|STM2592|phage tail component L-like protein|-
STM2593_113_147	0.06	1.52	1254116|STM2593|phage tail component M-like protein|-
STM2594_2615_2649	0.09	1.79	1254117|STM2594|phage tail component H-like protein|-
STM2595_161_195	0.02	2.87	1254118|STM2595|minor tail-like protein|-
STM2596_92_126	0.26	1.55	1254119|STM2596|minor tail-like protein|-
STM2597_375_409	0.02	2.37	1254120|STM2597|major tail-like protein|-
STM2598_129_163	0.02	2.37	1254121|STM2598|hypothetical protein|-
STM2599_612_646	0.03	1.85	1254122|STM2599|putative virulence protein|+
STM2600_321_355	0.02	2.39	1254123|STM2600|minor tail protein Z-like|-
STM2601_220_254	0.02	2.21	1254124|STM2601|minor capsid protein FIII|-
STM2602_193_227	0.05	2.21	1254125|STM2602|DNA packaging-like protein|-
STM2603_606_640	0.03	2.39	1254126|STM2603|phage head-like protein|-
STM2604_7_41	0.07	1.82	1254127|STM2604|phage head-like protein|-
STM2605_674_708	0.27	1.47	1254128|STM2605|head-tail preconnector-like protein|-
STM2606_1446_1480	0.05	1.82	1254129|STM2606|head-tail preconnector-like protein|-
STM2607_81_115	0.01	1.55	1254130|STM2607|head-to-tail joining-like protein|-
STM2608_1749_1783	0.05	2.01	1254131|STM2608|terminase-like large protein|-
STM2610_201_235	0.54	1.12	1254133|STM2610|hypothetical protein|+
STM2611.S_78_113	0.02	2.01	1254134|STM2611.S|endopeptidase-like protein|-
STM2612_357_391	0.16	1.35	1254135|STM2612|morphogenesis-like protein|-
STM2613_88_122	0.02	2.82	1254136|STM2613|hypothetical protein|-
STM2614_99_133	0.08	1.30	1254137|STM2614|hypothetical protein|+
STM2615_25_59	0.01	2.47	1254138|STM2615|tRNA|-
STM2616_441_475	0.33	-1.15	1254139|STM2616|antirepressor-like protein|-
STM2617_289_323	0.07	1.79	1254140|STM2617|antiterminator-like protein|-
STM2618_73_107	0.11	1.61	1254141|STM2618|hypothetical protein|-
STM2619_439_473	0.03	2.61	1254142|STM2619|hypothetical protein|-
STM2620_532_566	0.69	1.07	1254143|STM2620|hypothetical protein|-
STM2622_56_95	0.04	1.43	1254145|STM2622|hypothetical protein|-
STM2629_148_183	0.02	2.00	1254152|STM2629|hypothetical protein|+

STM2630_108_142	0.12	1.30	1254153|STM2630|hypothetical protein|+
STM2631_180_214	0.03	1.26	1254154|STM2631|hypothetical protein|+
STM2635_81_115	0.05	1.86	1254158|STM2635|excisionase-like protein|+
STM2636_1031_1065	0.40	-1.03	1254159|STM2636|integrase-like protein|-
STM2637_121_155	0.01	2.36	1254160|rseC|SoxR reducing system protein RseC|-
STM2638_769_803	0.55	1.06	1254161|rseB|periplasmic negative regulator of sigmaE|-
STM2639_193_227	0.08	1.28	1254162|rseA|anti-RNA polymerase sigma factor SigE|-
STM2640_417_451	0.05	1.24	1254163|rpoE|RNA polymerase sigma factor RpoE|-
STM2641_912_946	0.78	-1.06	1254164|nadB|L-aspartate oxidase|+
STM2642_449_483	0.07	-1.37	1254165|yfiC|putative transferase|-
STM2643_504_538	0.02	-1.47	1254166|srmB|ATP-dependent RNA helicase SrmB|+
STM2644_529_563	0.00	2.10	1254167|yfiE|putative transcriptional regulator|-
STM2645_97_131	0.17	-1.58	1254168|yfiK|neutral amino-acid efflux protein|+
STM2647_353_387	0.45	1.09	1254170|ung|uracil-DNA glycosylase|+
STM2648_839_873	0.86	-1.02	1254171|yfiF|predicted methyltransferase|-
STM2649_129_163	0.03	1.53	1254172|trxC|thioredoxin 2|+
STM2650_529_563	0.00	-1.62	1254173|yfiP|putative cytoplasmic protein|+
STM2651_2494_2528	0.05	-1.57	1254174|yfiQ|putative acetyl-CoA synthetase|+
STM2652_421_455	0.00	-2.25	1254175|pssA|phosphatidylserine synthase|+
STM2653_101_135	0.00	-1.66	1254176|yfiM|hypothetical protein|+
STM2654_815_849	0.02	-1.64	1254177|kgtP|alpha-ketoglutarate transporter|-
STM2655_401_435	0.16	1.58	1254178|STM2655|putative cytoplasmic protein|-
STM2660_1719_1753	0.05	1.65	1254183|clpB|protein disaggregation chaperone|-
STM2661_251_285	0.02	1.66	1254184|yfiH|hypothetical protein|-
STM2662_129_163	0.73	1.08	1254185|rluD|23S rRNA pseudouridine synthase D|-
STM2663_465_499	0.90	1.01	1254186|yfiO|predicted lipoprotein|+
STM2664_45_79	0.04	3.08	1254187|STM2664|pseudo|+
STM2665_33_67	0.01	-1.78	1254188|yfiA|translation inhibitor protein RaiA|+
STM2667_482_516	0.01	1.14	1254190|pheA|bifunctional chorismate mutase/prephenate dehydratase|+
STM2669_507_541	0.86	-1.10	1254192|tyrA|bifunctional chorismate mutase/prephenate dehydrogenase|-
STM2670_968_1002	0.61	-1.36	1254193|aroF|phospho-2-dehydro-3-deoxyheptonate aldolase|-
STM2671_97_131	0.04	-1.44	1254194|yfiR|putative periplasmic protein|+
STM2672_926_960	0.06	1.23	1254195|yfiN|putative diguanylate cyclase/phosphodiesterase|+
STM2673_289_323	0.02	-2.03	1254196|rplS|50S ribosomal protein L19|-
STM2674_385_419	0.02	-2.95	1254197|trmD|tRNA (guanine-N(1)-)-methyltransferase|-
STM2675_353_387	0.02	-2.62	1254198|rimM|16S rRNA-processing protein|-

STM2676_49_83	0.02	-1.42	1254199|rpsP|30S ribosomal protein S16|-
STM2677_971_1005	0.09	1.32	1254200|ffh|signal recognition particle protein|-
STM2678_561_595	0.34	-1.27	1254201|corE|hypothetical protein|+
STM2679_454_488	0.31	1.40	1254202|yfjD|hypothetical protein|+
STM2680_177_211	0.01	1.33	1254203|STM2680|putative cytoplasmic protein|+
STM2681_257_291	0.49	1.26	1254204|grpE|heat shock protein GrpE|-
STM2682_7_41	0.03	1.94	2673728|STM2682|-|-
STM2683_641_675	0.02	1.91	1254206|ppnK|inorganic polyphosphate/ATP-NAD kinase|+
STM2684_1159_1193	0.03	2.10	1254207|recN|recombination and repair protein|+
STM2685_169_203	0.06	1.32	1254208|smpA|hypothetical protein|+
STM2686_216_251	0.02	1.62	1254209|yfjF|hypothetical protein|-
STM2687_193_227	0.01	2.42	1254210|yfjG|hypothetical protein|-
STM2688_305_339	0.01	1.68	1254211|smpB|SsrA-binding protein|+
STM2689_7512_7546	0.02	-3.37	1254212|STM2689|pseudo|+
STM2690_1371_1405	0.04	-2.76	1254213|STM2690|putative outer membrane efflux protein|+
STM2691_1346_1380	0.07	-1.67	1254214|STM2691|putative ABC transporter transmembrane region|+
STM2694_181_215	0.01	2.11	1254217|STM2694|late control-like protein|-
STM2695_934_968	0.36	1.19	1254218|STM2695|late control-like protein|-
STM2696_25_59	0.46	1.05	1254219|STM2696|putative phage tail protein|-
STM2697_2577_2611	0.68	1.08	1254220|STM2697|phage tail-like protein|-
STM2698_33_67	0.67	1.22	1254221|STM2698|gpE-like protein|-
STM2700_417_451	0.23	1.11	1254223|STM2700|phage tail fiber-like protein|-
STM2702_205_239	0.24	1.19	1254225|STM2702|DNA invertase-like protein|-
STM2705_369_403	0.80	-1.03	1254228|STM2705|hypothetical protein|-
STM2707_417_451	0.82	-1.05	1254230|STM2707|phage tail-like protein|-
STM2711_182_216	0.23	-1.31	1254234|STM2711|phage tail-like protein|-
STM2712_113_147	0.07	-1.64	1254235|STM2712|phage tail-like protein|-
STM2713_193_227	0.86	1.03	1254236|STM2713|hypothetical protein|-
STM2714_153_187	0.20	1.44	1254237|STM2714|lysis-like protein|-
STM2715.S_27_61	0.48	1.21	1254238|STM2715.S|probable prophage lysozyme|-
STM2717_67_101	0.00	-1.41	1254240|STM2717|phage tail-like protein|-
STM2718_161_195	0.04	-1.28	1254241|STM2718|head completion-like protein|-
STM2719_457_491	0.07	1.91	1254242|STM2719|terminase-like protein|-
STM2720_532_566	0.17	1.41	1254243|STM2720|major capsid-like protein|-
STM2722_1472_1506	0.01	2.12	1254245|STM2722|terminase-like protein|+
STM2725_47_81	0.03	-1.57	1254248|STM2725|pseudo|-

STM2726_241_275	0.07	-1.54	1254249|STM2726|hypothetical protein|-
STM2728_105_139	0.07	-1.61	1254251|STM2728|hypothetical protein|-
STM2729_2367_2401	0.16	-1.26	1254252|STM2729|hypothetical protein|-
STM2730_513_547	0.48	-1.05	1254253|STM2730|DNA adenine methylase-like protein|-
STM2732_133_167	0.01	-1.66	1254255|STM2732|hypothetical protein|-
STM2734_145_179	0.58	-1.08	1254257|STM2734|hypothetical protein|+
STM2737_153_187	0.25	-1.27	1254260|STM2737|hypothetical protein|-
STM2738_33_67	0.24	-1.37	1254261|STM2738|hypothetical protein|+
STM2740_226_260	0.00	-3.52	1254263|STM2740|integrase-like protein|+
STM2740.1N_37_71	0.00	-18.32	2673740|STM2740.1N|hypothetical protein|+
STM2741_465_499	0.00	-5.60	1254264|STM2741|putative periplasmic protein|+
STM2742_675_709	0.03	-1.30	1254265|STM2742|putative cytoplasmic protein|+
STM2743_57_91	0.02	1.55	1254266|STM2743|putative cytoplasmic protein|-
STM2745_1515_1549	0.15	-1.29	1254268|STM2745|putative inner membrane protein|+
STM2746_794_830	0.34	1.18	1254269|STM2746|putative ATPase|+
STM2747_637_674	0.02	2.17	1254270|STM2747|putative cytoplasmic protein|+
STM2748_193_227	0.51	1.16	1254271|STM2748|putative transcriptional regulator|-
STM2749_97_131	0.05	1.15	1254272|STM2749|putative cytoplasmic protein|+
STM2750_443_477	0.50	1.11	1254273|STM2750|putative PTS system glucitol/sorbitol-specific enzyme III|+
STM2751_97_131	0.84	-1.03	1254274|STM2751|putative glucitol-specific PTS enzyme IIII|+
STM2752_97_131	0.27	-1.18	1254275|STM2752|putative glucitol-specific PTS enzyme IIII|+
STM2753_751_785	0.94	1.01	1254276|STM2753|putative dehydrogenase|+
STM2754_686_720	0.02	2.41	1254277|STM2754|putative hexulose 6 phosphate synthase|+
STM2755_161_195	0.23	-1.21	1254278|STM2755|putative hexulose 6 phosphate synthase|-
STM2756_497_531	0.02	1.54	1254279|STM2756|putative sugar phosphate aminotransferase|-
STM2759_1417_1451	0.03	-1.91	1254282|STM2759|putative dipeptide/oligopeptide/nickel ABC-type transport system periplasmic component|+
STM2760_353_387	0.02	1.29	1254283|STM2760|putative integrase|+
STM2761_1252_1286	0.05	1.30	1254284|STM2761|putative inner membrane protein|+
STM2762_685_723	0.01	2.41	1254285|STM2762|putative inner membrane protein|-
STM2763_417_451	0.02	1.63	2673753|STM2763|-|+
STM2764_239_274	0.01	1.57	2673748|STM2764|-|-
STM2766_89_127	0.05	1.58	1254289|STM2766|putative cytoplasmic protein|-
STM2767_1688_1722	0.12	1.48	1254290|STM2767|putative DNA/RNA helicase|-
STM2768_195_229	0.02	1.59	1254291|STM2768|putative transposase|+
STM2769_435_469	0.75	-1.08	1254292|STM2769|putative transposase|+

STM2770_49_83	0.03	1.55	1254293|fljA|phase-1 flagellin repressor|-
STM2771_1354_1388	0.58	-1.08	1254294|fljB|flagellin|-
STM2772_221_257	0.28	-1.16	1254295|hin|DNA-invertase Hin|+
STM2773_341_375	0.23	-1.13	1254296|iroB|putative glycosyl transferase|+
STM2774_2943_2977	0.94	1.02	1254297|iroC|putative ABC transporter protein|+
STM2775_630_664	0.02	-1.72	1254298|iroD|enterochelin esterase=-like protein|+
STM2776_321_355	0.25	1.21	1254299|iroE|putative hydrolase|+
STM2777_2014_2048	0.20	1.46	1254300|iroN|TonB-dependent siderophore receptor protein|-
STM2778_39_73	0.35	1.17	1254301|STM2778|pseudo|+
STM2780_470_504	0.00	2.33	1254303|pipB2|secreted effector protein|-
STM2781_561_595	0.01	4.13	1254304|virK|virulence protein|+
STM2782_729_763	0.03	2.23	1254305|mig-14|putative transcriptional activator|+
STM2783_175_209	0.04	-1.59	1254306|nixA|putative nickel transporter|-
STM2784_609_643	0.00	-2.54	1254307|tctE|regulatory protein|-
STM2785_465_499	0.01	-2.66	1254308|tctD|regulatory protein|-
STM2786_113_147	0.00	-3.64	1254309|STM2786|tricarboxylic transport|+
STM2787_3_37	0.00	-6.24	1254310|STM2787|tricarboxylic transport|+
STM2788_1124_1158	0.01	-2.19	1254311|STM2788|tricarboxylic transport|+
STM2789_713_747	0.01	-5.05	1254312|STM2789|hypothetical protein|+
STM2790_494_528	0.00	-5.64	1254313|ygaF|hypothetical protein|+
STM2791_866_900	0.01	-2.12	1254314|gabD|succinate-semialdehyde dehydrogenase II|+
STM2792_765_799	0.00	-7.17	1254315|gabT|4-aminobutyrate aminotransferase|+
STM2793_786_820	0.04	-1.52	1254316|gabP|gamma-aminobutyrate transporter|+
STM2794_505_539	0.00	-2.81	1254317|ygaE|DNA-binding transcriptional regulator CsiR|+
STM2795_233_267	0.28	1.18	1254318|ygaU|hypothetical protein|-
STM2796_63_97	0.17	1.53	1254319|yqaE|putative transport protein|-
STM2797_191_225	0.50	1.05	1254320|STM2797|putative regulatory protein|+
STM2798_75_109	0.23	-1.15	1254321|ygaP|putative rhodanese-like sulfurtransferase|+
STM2799_49_83	0.02	1.77	1254322|stpA|DNA binding protein nucleoid-associated|-
STM2801_241_275	0.02	2.03	1254324|ygaC|hypothetical protein|-
STM2802_17_52	0.05	1.35	1254325|ygaM|hypothetical protein|+
STM2803_544_578	0.76	-1.04	1254326|STM2803|putative regulatory protein|-
STM2804.1n_27_61	0.02	1.40	2673735|STM2804.1n|hypothetical protein|+
STM2806_97_131	0.49	-1.31	1254329|nrdI|ribonucleotide reductase stimulatory protein|+
STM2807_1338_1372	0.16	-1.54	1254330|nrdE|ribonucleotide-diphosphate reductase subunit alpha|+
STM2808_721_755	0.35	-1.18	1254331|nrdF|ribonucleotide-diphosphate reductase subunit beta|+

STM2809_940_974	0.62	1.07	1254332|proV|glycine betaine transporter ATP-binding subunit|+
STM2810_162_196	0.39	1.11	1254333|proW|glycine betaine transporter membrane protein|+
STM2811_641_675	0.17	1.36	1254334|proX|glycine betaine transporter periplasmic subunit|+
STM2812_890_924	0.01	-2.41	1254335|STM2812|putative inner membrane protein|+
STM2813_81_115	0.04	-1.38	1254336|emrR|transcriptional repressor MprA|+
STM2814_430_464	0.04	1.30	1254337|emrA|multidrug resistance secretion protein|+
STM2815_828_862	0.16	-1.18	1254338|emrB|putative multidrug transport protein|+
STM2816_372_406	0.02	1.44	1254339|STM2816|putative glycoporin|-
STM2817_9_43	0.15	1.15	1254340|luxS|S-ribosylhomocysteinase|-
STM2818_846_880	0.09	-1.30	1254341|gshA|glutamate--cysteine ligase|-
STM2819_257_291	0.05	-1.52	1254342|yqaA|putative inner membrane protein|-
STM2820_161_195	0.00	1.96	1254343|yqaB|predicted hydrolase|-
STM2821/STM2822/STM282	0.11	-1.52	1254344/1254345/1254346/1254347|STM2821/STM2822/STM2823/STM2824|tRNA|-
STM2826_9_43	0.47	1.06	1254349|csrA|carbon storage regulator|-
STM2827_2032_2066	0.03	-1.74	1254350|alaS|alanyl-tRNA synthetase|-
STM2828_29_63	0.08	1.81	1254351|recX|recombination regulator RecX|-
STM2829_799_833	0.12	1.56	1254352|recA|recombinase A|-
STM2830_139_173	0.25	-1.13	1254353|ygaD|competence damage-inducible protein A|-
STM2831_225_259	0.09	-1.36	1254354|mltB|membrane-bound lytic murein transglycosylase B; catalyzes the cleavage of the glycosidic bonds between N-acetylmuramic acid and N-acetylglucosamine in peptidoglycan|-
STM2832_257_291	0.26	-1.24	1254355|srlA|glucitol/sorbitol-specific enzyme IIC component|+
STM2833_263_297	0.06	2.19	1254356|srlE|glucitol/sorbitol-specific enzyme IIB component|+
STM2834_169_203	0.04	1.71	1254357|slrB|glucitol/sorbitol-specific PTS system component IIA|+
STM2835_705_739	0.31	1.11	1254358|srlD|sorbitol-6-phosphate dehydrogenase|+
STM2836_305_339	0.02	1.45	1254359|gutM|DNA-binding transcriptional activator of glucitol operon|+
STM2837_545_579	0.15	-1.18	1254360|srlR|DNA-bindng transcriptional repressor|+
STM2838.S_401_435	0.04	-1.48	1254361|gutQ|D-arabinose 5-phosphate isomerase|+
STM2839_810_844	0.44	-1.10	1254362|ygaA|anaerobic nitric oxide reductase transcription regulator|-
STM2840_1105_1139	0.37	1.07	1254363|STM2840|anaerobic nitric oxide reductase flavorubredoxin|+
STM2841_663_697	0.07	-1.36	1254364|ygbD|nitric oxide reductase|+
STM2842_1250_1284	0.28	1.18	1254365|hypF|hydrogenase maturation protein|-
STM2843_257_291	0.67	1.07	1254366|hydN|electron transport protein HydN|-
STM2844_545_579	0.01	1.12	1254367|STM2844|hypothetical protein|-
STM2845_265_299	0.06	1.15	1254368|hycI|hydrogenase 3 maturation protease|-

STM2846_81_115	0.02	1.28	1254369|hycH|hydrogenase 3 large subunit processing protein|-
STM2848_209_243	0.03	1.48	1254371|hycF|formate hydrogenlyase complex iron-sulfur subunit|-
STM2849_967_1001	0.59	-1.06	1254372|hycE|hydrogenase 3 large subunit|-
STM2850_257_291	0.20	1.36	1254373|hycD|hydrogenase 3 membrane subunit|-
STM2851_1532_1566	0.99	1.00	1254374|hycC|formate hydrogenlyase subunit 3|-
STM2853_385_419	0.88	1.01	1254376|hycA|transcriptional repressor|-
STM2854_145_179	0.04	1.39	1254377|hypA|hydrogenase nickel incorporation protein|+
STM2855_209_243	0.13	1.24	1254378|hypB|hydrogenase nickel incorporation protein HypB|+
STM2856_73_107	0.13	-1.09	1254379|hypC|hydrogenase isoenzymes formation protein|+
STM2857_152_186	0.03	1.39	1254380|hypD|putative hydrogenase formation protein|+
STM2858_716_750	0.06	-1.17	1254381|hypE|putative hydrogenase formation protein|+
STM2859_1848_1882	0.18	-1.18	1254382|fhlA|formate hydrogen-lyase transcriptional activator|+
STM2860_187_221	0.01	1.62	1254383|ygbA|hypothetical protein|-
STM2861_441_475	0.91	1.02	1254384|sitA|putative periplasmic binding protein|+
STM2862_257_291	0.02	1.58	1254385|sitB|putative ATP-binding protein|+
STM2863_129_163	0.67	1.09	1254386|sitC|putative permease|+
STM2864_513_547	0.99	-1.00	1254387|sitD|putative permease|+
STM2865_113_147	0.02	2.16	1254388|avrA|secreted effector protein|-
STM2866_705_739	0.03	1.44	1254389|sprB|transcriptional regulator|-
STM2868_115_149	0.18	-1.35	1254391|orgC|putative cytoplasmic protein|-
STM2869_545_579	0.32	-1.17	1254392|orgB|needle complex export protein|-
STM2871_33_67	0.45	1.07	1254394|prgK|needle complex inner membrane lipoprotein|-
STM2873_129_163	0.01	-1.54	1254396|prgI|needle complex major subunit|-
STM2874_308_342	0.03	2.67	1254397|prgH|needle complex inner membrane protein|-
STM2875_577_611	0.02	1.60	1254398|hilD|invasion protein regulatory protein|+
STM2876_1455_1489	0.02	2.93	1254399|hilA|invasion protein regulator|+
STM2877_145_179	0.08	2.03	1254400|iagB|invasion protein precursor|+
STM2878_1337_1371	0.13	1.31	1254401|sptP|protein tyrosine phosphatase/GTPase activating protein|-
STM2879_253_287	0.17	1.28	1254402|sicP|secretion chaperone|-
STM2881_81_115	0.02	1.51	1254404|iacP|acyl carrier protein|-
STM2882_1699_1733	0.31	1.15	1254405|sipA|secreted effector protein|-
STM2883_425_459	0.01	2.20	1254406|sipD|translocation machinery component|-
STM2884_423_457	0.12	-1.18	1254407|sipC|translocation machinery component|-
STM2885_927_961	0.01	-1.42	1254408|sipB|translocation machinery component|-
STM2886_409_443	0.07	1.82	1254409|sicA|secretion chaperone|-
STM2887_936_970	0.14	1.13	1254410|spaS|surface presentation of antigens protein SpaS|-

STM2888_481_515	0.41	-1.11	1254411|spaR|needle complex export protein|-
STM2889_193_227	0.90	1.02	1254412|spaQ|needle complex export protein|-
STM2890_422_459	0.34	1.45	1254413|spaP|surface presentation of antigens protein SpaP|-
STM2891_769_803	0.57	-1.15	1254414|spaO|surface presentation of antigens protein SpaO|-
STM2892_876_910	0.65	-1.04	1254415|invJ|needle length control protein|-
STM2895_9_43	0.98	1.00	1254418|invB|secretion chaperone|-
STM2896_1795_1829	0.95	1.01	1254419|invA|needle complex export protein|-
STM2897_376_410	0.19	1.13	1254420|invE|invasion protein|-
STM2898_1346_1380	0.20	-1.26	1254421|invG|outer membrane secretin precursor|-
STM2899_513_547	0.36	1.22	1254422|invF|invasion regulatory protein|-
STM2900_114_148	0.03	2.30	1254423|invH|needle complex outer membrane lipoprotein precursor|+
STM2901_321_355	0.63	-1.05	1254424|STM2901|putative cytoplasmic protein|+
STM2902_261_297	0.33	1.14	1254425|STM2902|putative cytoplasmic protein|+
STM2903_281_315	0.76	1.08	1254426|STM2903|putative cytoplasmic protein|-
STM2904_169_203	0.61	-1.06	1254427|STM2904|putative ABC-type transporter|+
STM2905_145_179	0.34	1.17	1254428|STM2905|putative acetyltransferase|+
STM2906_129_163	0.02	1.42	1254429|STM2906|-|-
STM2907_401_435	0.18	1.22	1254430|pphB|serine/threonine-specific protein phosphatase 2|+
STM2908_193_227	0.01	1.85	1254431|STM2908|putative cytoplasmic protein|-
STM2909_1697_1731	0.07	1.29	1254432|mutS|DNA mismatch repair protein|+
STM2910_193_227	0.89	1.05	1254433|STM2910|putative cytoplasmic protein|-
STM2911_514_548	0.59	-1.27	1254434|STM2911|putative permease|-
STM2912_321_355	0.78	-1.03	1254435|STM2912|putative transcriptional regulator|+
STM2913_946_980	0.00	1.53	1254436|STM2913|putative permease|-
STM2915_705_739	0.37	-1.22	1254438|ygbM|hypothetical protein|-
STM2916_161_195	0.03	-1.65	1254439|ygbL|putative aldolase|-
STM2917_360_394	0.03	-1.48	1254440|ygbK|putative tRNA synthase|-
STM2918_193_227	0.07	-1.21	1254441|ygbJ|3-hydroxyisobutyrate dehydrogenase|-
STM2919_193_227	0.03	1.19	1254442|ygbI|putative regulatory protein|+
STM2920_113_147	0.02	1.34	1254443|STM2920|putative transcriptional regulator|-
STM2921_65_99	0.17	-1.15	1254444|STM2921|putative flavoprotein|+
STM2922_1197_1231	0.39	1.06	1254445|STM2922|putative 3-polyprenyl-4-hydroxybenzoate decarboxylase|+
STM2923_81_115	0.03	2.38	1254446|STM2923|putative cytoplasmic protein|+
STM2924_257_291	0.00	-2.52	1254447|rpoS|RNA polymerase sigma factor RpoS|-
STM2925_327_361	0.36	-1.16	1254448|nlpD|predicted outer membrane lipoprotein|-
STM2926_273_307	0.44	-1.10	1254449|pcm|protein-L-isoaspartate O-methyltransferase|-

STM2927_481_515	0.03	-1.47	1254450|surE|stationary phase survival protein SurE|-
STM2928_643_677	0.00	-1.35	1254451|truD|tRNA pseudouridine synthase D|-
STM2929_353_387	0.40	-1.19	1254452|ispF|2-C-methyl-D-erythritol 2 4-cyclodiphosphate synthase|-
STM2930_513_547	0.93	-1.02	1254453|ispD|2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase|-
STM2931_49_83	0.01	-1.60	1254454|ftsB|cell divison protein FtsB|-
STM2932_229_263	0.12	1.77	1254455|ygbE|hypothetical protein|-
STM2933_161_195	0.43	-1.45	1254456|cysC|adenylylsulfate kinase|-
STM2934_697_731	0.48	-1.39	1254457|cysN|sulfate adenylyltransferase subunit 1|-
STM2935_161_195	0.99	1.01	1254458|cysD|sulfate adenylyltransferase subunit 2|-
STM2936_336_370	0.51	1.13	1254459|iaa|aminopeptidase in alkaline phosphatase isozyme conversion|+
STM2937_146_180	0.03	-1.22	1254460|ygbF|hypothetical protein|-
STM2938_769_803	0.05	-1.21	1254461|STM2938|putative cytoplasmic protein|-
STM2939_481_515	0.02	-1.55	1254462|ygcH|putative cytoplasmic protein|-
STM2940_513_547	0.08	-1.30	1254463|STM2940|putative cytoplasmic protein|-
STM2941_988_1022	0.01	-2.11	1254464|yghJ|putative cytoplasmic protein|-
STM2943_622_656	0.01	-2.18	1254466|STM2943|putative cytoplasmic protein|-
STM2944_1857_1891	0.00	-1.68	1254467|ygcB|putative helicase|-
STM2945_713_747	0.04	1.64	1254468|sopD|secreted effector protein|+
STM2946_553_587	0.44	-1.22	1254469|cysH|phosphoadenosine phosphosulfate reductase|-
STM2947_1146_1180	0.39	-1.34	1254470|cysI|sulfite reductase alpha subunit|-
STM2948_1201_1235	0.39	-1.35	1254471|cysJ|sulfite reductase subunit alpha|-
STM2949_129_163	0.86	1.03	1254472|ptpS|putative 6-pyruvoyl tetrahydrobiopterin synthase|+
STM2950_193_227	0.31	1.25	1254473|STM2950|putative metal-dependent hydrolase|-
STM2951_129_163	0.01	2.11	1254474|ygcF|hypothetical protein|-
STM2952_684_718	0.07	1.41	1254475|eno|phosphopyruvate hydratase|-
STM2953_895_929	0.02	2.07	1254476|pyrG|CTP synthase|-
STM2954_609_643	0.01	1.44	1254477|mazG|nucleoside triphosphate pyrophosphohydrolase|-
STM2954.1n_217_254	0.01	2.45	2673739|STM2954.1n|hypothetical protein|-
STM2955.S_77_111	0.01	1.44	1254478|STM2955.S|putative transcriptional regulator|-
STM2956_2176_2210	0.09	1.44	1254479|relA|GDP/GTP pyrophosphokinase|-
STM2957_1225_1259	0.03	1.29	1254480|rumA|23S rRNA 5-methyluridine methyltransferase|-
STM2958_1790_1824	0.11	-1.16	1254481|barA|hybrid sensory histidine kinase BarA|+
STM2959_800_834	0.04	1.22	1254482|STM2959|putative glycerate kinase 2|-
STM2960_1190_1224	0.07	-1.50	1254483|gudD|d-glucarate dehydratase|-
STM2961_374_408	0.46	1.26	1254484|ygcY|putative D-glucarate dehydratase|-
STM2962_748_782	0.64	-1.10	1254485|gudT|putative D-glucarate permease|-

STM2963_137_171	0.92	1.01	1254486|STM2963|flavodoxin|-
STM2964_513_547	0.02	-1.84	1254487|yqcB|tRNA pseudouridine synthase C|-
STM2965_169_203	0.02	-1.47	1254488|yqcC|putative cytoplasmic protein|-
STM2966_210_244	0.04	-2.45	1254489|csrB|misc_RNA|-
STM2967_417_451	0.15	-1.17	1254490|sydl|SecY interacting protein Sydl|-
STM2968_785_819	0.59	1.07	1254491|queF|7-cyano-7-deazaguanine reductase|+
STM2969_638_672	0.05	1.17	1254492|ygdH|putative nucleotide binding|+
STM2970_1187_1221	0.03	-2.09	1254493|sdaC|putative serine transport protein|+
STM2971_497_531	0.14	-1.43	1254494|sdaB|L-serine dehydratase/L-threonine deaminase 2|+
STM2972_417_451	0.01	1.50	1254495|xni|exonuclease IX|+
STM2973_182_216	0.24	-1.27	1254496|fucO|L-1 2-propanediol oxidoreductase|-
STM2974_545_579	0.08	-1.35	1254497|fucA|L-fuculose phosphate aldolase|-
STM2975_831_865	0.00	-2.39	1254498|fucP|pseudo|+
STM2977_708_742	0.09	-1.49	1254500|fucK|L-fuculokinase|+
STM2978_137_171	0.00	-1.45	1254501|fucU|putative L-fucose-binding protein|+
STM2979_225_259	0.00	-7.83	1254502|fucR|DNA-binding transcriptional activator|+
STM2980_1014_1048	0.33	1.13	1254503|ygdE|putative SAM-dependent methyltransferase|-
STM2981_345_379	0.37	1.07	1254504|ygdD|hypothetical protein|-
STM2982_833_867	0.08	1.80	1254505|gcvA|DNA-binding transcriptional activator GcvA|-
STM2983_49_83	0.92	-1.01	1254506|ygdI|putative lipoprotein|-
STM2984_741_775	0.32	1.07	1254507|csdA|cysteine sulfinate desulfinase|+
STM2985_199_233	0.05	1.78	1254508|ygdK|putative FeS center assembly protein|+
STM2986.Sc_705_739	0.05	1.23	1254509|STM2986.Sc|putative integral membrane protein|+
STM2987_193_227	0.94	-1.01	1254510|ygdL|putative enzyme|-
STM2988_867_901	0.11	-1.37	1254511|mltA|murein transglycosylase A|-
STM2991_1087_1121	0.11	1.57	1254514|amiC|N-acetylmuramoyl-L-alanine amidase|-
STM2992_333_367	0.09	1.21	1254515|argA|N-acetylglutamate synthase|+
STM2993_1581_1615	0.06	-1.66	1254516|RecD|exonuclease V subunit alpha|-
STM2994_2739_2773	0.17	-1.19	1254517|RecB|exonuclease V subunit beta|-
STM2995_2370_2404	0.43	1.07	1254518|ptr|protease III|-
STM2996_3301_3335	0.16	1.28	1254519|recC|exonuclease V subunit gamma|-
STM2997_65_99	0.83	-1.02	1254520|ppdC|hypothetical protein|-
STM2998_286_320	0.41	-1.06	1254521|ygdB|hypothetical protein|-
STM2999_321_355	0.04	2.31	1254522|ppdB|hypothetical protein|-
STM3000_17_51	0.07	1.37	1254523|ppdA|hypothetical protein|-
STM3001_321_355	0.05	-1.28	1254524|thyA|thymidylate synthase|-

STM3002_593_627	0.21	-1.16	1254525|lgt|prolipoprotein diacylglyceryl transferase|-
STM3003_1344_1378	0.25	-1.14	1254526|ptsP|fused phosphoenolpyruvate-protein phosphotransferase PtsP/GAF domain|-
STM3004_449_483	0.06	1.18	1254527|ygdP|dinucleoside polyphosphate hydrolase|-
STM3004.1n_21_55	0.07	1.66	2673726|STM3004.1n|hypothetical protein|-
STM3005_233_267	0.12	1.44	1254528|mutH|DNA mismatch repair protein|+
STM3006_417_451	0.01	-1.23	1254529|ygdQ|putative transport protein|+
STM3007_57_91	0.00	-1.89	1254530|ygdR|putative peptide transport protein|+
STM3008_266_300	0.02	-2.30	1254531|tas|putative aldo/keto reductase|+
STM3009_356_390	0.03	-1.36	1254532|ygeD|hypothetical protein|-
STM3010_2009_2043	0.03	-1.33	1254533|aas|bifunctional acyl-[acyl carrier protein] synthetase/2-acylglycerophosphoethanolamine acyltransferase|-
STM3011_318_352	0.37	-1.08	1254534|galR|DNA-binding transcriptional repressor|+
STM3012_392_426	0.03	1.62	1254535|STM3012|putative transcriptional regulator|+
STM3013_776_810	0.76	1.04	1254536|lysA|diaminopimelate decarboxylase|-
STM3014_193_227	0.02	1.43	1254537|lysR|DNA-binding transcriptional regulator LysR|+
STM3015_353_387	0.05	-1.42	1254538|ygeA|putative racemase|-
STM3016_1188_1222	0.80	1.04	1254539|araE|L-arabinose/proton symport protein|-
STM3017_193_227	0.63	1.03	1254540|kduD|2-deoxy-D-gluconate 3-dehydrogenase|-
STM3019_692_726	0.01	-6.30	1254542|yqeF|acetyl-CoA acetyltransferase|-
STM3020_337_371	0.29	1.13	1254543|STM3020|putative transcriptional regulator|-
STM3021_321_355	0.17	1.09	1254544|STM3021|putative inner membrane protein|+
STM3022_615_649	0.03	1.76	1254545|STM3022|putative transport protein|+
STM3023_149_183	0.01	1.47	1254546|yohL|putative cytoplasmic protein|-
STM3024_449_483	0.11	-1.07	1254547|yohM|nickel/cobalt efflux protein RcnA|+
STM3025_145_179	0.01	1.31	1254548|STM3025|putative cytoplasmic protein|-
STM3025.1N_181_215	0.14	1.45	2673750|STM3025.1N|hypothetical protein|-
STM3026_174_209	0.05	-1.33	1254549|STM3026|putative outer membrane protein|-
STM3028_1779_1813	0.03	-1.67	1254551|stdB|putative outer membrane usher protein|-
STM3031_473_507	0.00	3.41	1254554|STM3031|Ail/OmpX-like protein|-
STM3033_225_259	0.01	1.45	1254556|STM3033|putative nucleic acid-binding protein|-
STM3034_37_72	0.01	1.58	1254557|STM3034|putative cytoplasmic protein|-
STM3036_257_291	0.01	-1.53	1254559|STM3036|putative inner membrane protein|+
STM3037_2_36	0.55	-1.08	1254560|glyU|tRNA|-
STM3038_101_135	0.12	1.66	1254561|STM3038|putative metalloendopeptidase|-
STM3039_305_339	0.01	1.52	1254562|idi|isopentenyl-diphosphate delta-isomerase|+

STM3040_775_809	0.04	-1.70	1254563|lysS|lysyl-tRNA synthetase|-
STM3041c_638_672	0.53	-1.13	1254564|prfB|peptide chain release factor 2|-
STM3042_1407_1441	0.92	1.01	1254565|recJ|ssDNA exonuclease RecJ|-
STM3043_553_587	0.04	1.37	1254566|dsbC|thiol:disulfide interchange protein DsbC|-
STM3044_321_355	0.15	-1.30	1254567|xerD|site-specific tyrosine recombinase XerD|-
STM3045_361_395	0.92	-1.03	1254568|fldB|flavodoxin FldB|+
STM3046_193_227	0.02	-1.40	1254569|ygfX|putative inner membrane protein|-
STM3047_169_203	0.95	-1.01	1254570|ygfY|hypothetical protein|-
STM3048_513_547	0.05	1.57	1254571|ygfZ|putative global regulator|+
STM3049_257_291	0.06	-1.28	1254572|yqfA|putative hemolysin|-
STM3050_68_102	0.07	1.16	1254573|yqfB|hypothetical protein|-
STM3051_827_861	0.09	1.21	1254574|bglA|6-phospho-beta-glucosidase A|+
STM3052_561_595	0.02	2.69	1254575|STM3052|putative outer membrane protein|-
STM3053_2483_2517	0.01	-1.94	1254576|gcvP|glycine dehydrogenase|-
STM3054_49_83	0.01	-3.26	1254577|gcvH|glycine cleavage system protein H|-
STM3055_864_898	0.01	-3.23	1254578|gcvT|glycine cleavage system aminomethyltransferase T|-
STM3056_268_302	0.07	1.41	1254579|visC|hypothetical protein|-
STM3057_884_918	0.34	1.18	1254580|ubiH|2-octaprenyl-6-methoxyphenyl hydroxylase|-
STM3058_990_1024	0.71	1.05	1254581|pepP|proline aminopeptidase P III|-
STM3059.S_385_419	0.02	1.38	1254582|ygfB|hypothetical protein|-
STM3060_265_299	0.02	1.55	1254583|ygfE|Z-ring-associated protein|+
STM3061_445_479	0.02	1.62	1254584|ygfA|predicted ligase|+
STM3062_298_332	0.81	-1.03	1254585|serA|D-3-phosphoglycerate dehydrogenase|-
STM3063_241_275	0.00	-3.26	1254586|rpiA|ribose-5-phosphate isomerase A|-
STM3064_641_675	0.03	1.23	1254587|iciA|chromosome replication initiation inhibitor protein|+
STM3065_273_307	0.05	-1.54	1254588|yggE|hypothetical protein|-
STM3066_377_411	1.00	-1.00	1254589|yggA|arginine exporter protein|-
STM3067_769_803	0.02	-1.48	1254590|yggB|mechanosensitive channel MscS|-
STM3068_593_627	0.28	-1.22	1254591|fba|fructose-bisphosphate aldolase|-
STM3069_677_711	0.62	-1.05	1254592|pgk|phosphoglycerate kinase|-
STM3070_432_466	0.01	-1.77	1254593|epdD|D-erythrose 4-phosphate dehydrogenase|-
STM3071_193_227	0.06	-1.44	1254594|STM3071|putative DNA-binding protein|+
STM3072_453_487	0.03	-1.64	1254595|STM3072|putative inner membrane protein|+
STM3073_289_323	0.01	-1.97	1254596|STM3073|putative ABC-type cobalt transport system permease component|+

STM3074_385_419	0.09	1.34	1254597|STM3074|putative ABC-type cobalt transport system ATP-binding component|+
STM3075_9_43	0.44	-1.10	1254598|STM3075|putative ABC-type cobalt transport system ATP-binding component|+
STM3076_1201_1235	0.60	-1.13	1254599|tktA|transketolase|-
STM3077_257_291	0.01	1.38	1254600|yggG|putative Zn-dependent protease|+
STM3078_97_131	0.74	-1.06	1254601|speB|agmatinase|-
STM3079.S_129_163	0.54	-1.11	1254602|STM3079.S|putative hydrolase/acyltransferase|-
STM3081_809_843	0.05	2.09	1254604|STM3081|putative malate/L-lactate dehydrogenase|-
STM3082_770_804	0.04	2.25	1254605|STM3082|putative zinc-binding dehydrogenase|-
STM3083_922_956	0.37	-1.13	1254606|STM3083|putative mannitol dehydrogenase|-
STM3084.S_297_331	0.25	1.17	1254607|STM3084.S|putative regulatory protein|-
STM3086_1106_1140	0.04	1.11	1254609|speA|arginine decarboxylase|-
STM3087_49_83	0.96	1.01	1254610|yqgB|putative inner membrane protein|-
STM3088_10_44	0.04	1.80	2673737|yqgC|-|+
STM3089_77_111	0.02	1.21	1254612|yqgD|putative inner membrane protein|-
STM3090_284_318	0.01	9.64	1254613|metK|methionine adenosyltransferase|+
STM3091_460_494	0.77	-1.08	1254614|galP|galactose/proton symporter|+
STM3093_177_211	0.03	2.10	1254616|endA|DNA-specific endonuclease II|+
STM3094_65_99	0.02	-1.51	1254617|yggJ|hypothetical protein|+
STM3095_217_251	0.18	-1.20	1254618|gshB|glutathione synthetase|+
STM3096_43_77	0.18	1.42	1254619|yqgE|hypothetical protein|+
STM3097_177_211	0.01	-2.03	1254620|yqgF|Holliday junction resolvase-like protein|+
STM3100_9_43	0.06	1.45	1254623|yggS|hypothetical protein|+
STM3101_257_291	0.04	-1.16	1254624|yggT|putative integral membrane protein|+
STM3102_65_99	0.03	-1.54	1254625|yggU|hypothetical protein|+
STM3103_305_339	0.13	1.41	1254626|yggV|putative deoxyribonucleotide triphosphate pyrophosphatase|+
STM3104_490_524	0.03	-1.68	1254627|yggW|coproporphyrinogen III oxidase|+
STM3105_299_333	0.00	1.78	1254628|yggM|putative periplasmic protein|-
STM3106_592_626	0.02	-1.82	1254629|ansB|L-asparaginase II|-
STM3107_577_611	0.36	1.13	1254630|yggN|hypothetical protein|-
STM3108_289_323	0.02	1.81	1254631|yggL|hypothetical protein|-
STM3109_673_707	0.03	1.38	1254632|trmB|tRNA (guanine-N(7))-methyltransferase|-
STM3110_118_152	0.15	-1.36	1254633|mutY|adenine DNA glycosylase|+
STM3111_85_119	0.68	-1.05	1254634|yggX|hypothetical protein|+
STM3112_407_441	0.02	-1.50	1254635|mltC|murein transglycosylase C|+

STM3113_514_548	0.35	1.20	1254636|nupG|nucleoside transport|+
STM3114_1457_1491	0.47	-1.09	1254637|speC|ornithine decarboxylase isozyme|-
STM3115_481_515	0.14	1.24	1254638|yqgA|putative inner membrane protein|+
STM3117_361_395	0.04	1.37	1254640|STM3117|putative lactoylglutathione lyase|-
STM3118_1063_1097	0.05	1.62	1254641|STM3118|putative acetyl-CoA hydrolase|-
STM3119_449_483	0.08	1.20	1254642|STM3119|putative monoamine oxidase|-
STM3120_753_787	0.39	-1.07	1254643|STM3120|putative transcriptional regulator|-
STM3121_673_707	0.01	1.80	1254644|STM3121|putative transcriptional regulator|+
STM3122_1637_1671	0.18	1.33	1254645|STM3122|putative arylsulfatase|-
STM3123_1146_1180	0.03	2.04	1254646|STM3123|putative arylsulfatase regulator|-
STM3124_17_51	0.01	-8.38	1254647|STM3124|putative response regulator|+
STM3125_277_313	0.05	1.30	1254648|STM3125|putative cytoplasmic protein|-
STM3126_501_535	0.09	2.29	1254649|STM3126|putative amino acid transporter|-
STM3127_173_207	0.31	-1.19	1254650|STM3127|putative cytoplasmic protein|-
STM3128_495_529	0.13	1.06	1254651|STM3128|putative oxidoreductase|-
STM3129_646_680	0.12	1.18	1254652|STM3129|putative NAD-dependent aldehyde dehydrogenase|+
STM3130_345_379	0.04	3.01	1254653|STM3130|putative cytoplasmic protein|-
STM3131_273_307	0.13	-1.11	1254654|STM3131|putative cytoplasmic protein|-
STM3132_65_99	0.68	1.11	1254655|STM3132|putative xylanase/chitin deacetylase|-
STM3133_354_388	0.02	-1.45	1254656|STM3133|putative amidohydrolase|-
STM3134_354_388	0.60	1.12	1254657|STM3134|putative permease|-
STM3135_954_988	0.01	-3.58	1254658|STM3135|mannonate dehydratase|+
STM3137_1342_1376	0.00	-4.09	1254660|STM3137|glucuronate isomerase|+
STM3138_636_670	0.04	1.67	1254661|STM3138|putative methyl-accepting chemotaxis protein|-
STM3139_1002_1036	0.01	1.60	1254662|gsp|bifunctional glutathionylspermidine amidase/glutathionylspermidine synthetase|-
STM3140_769_803	0.21	1.10	1254663|yghU|putative glutathione S-transferase YghU|+
STM3141_545_579	0.00	2.01	1254664|STM3141|hypothetical protein|-
STM3142_846_880	0.02	3.20	1254665|STM3142|putative periplasmic ferrichrome-binding protein|-
STM3143_113_147	0.01	-1.50	1254666|hybG|hydrogenase 2 accessory protein HypG|-
STM3144_12_46	0.02	-1.28	1254667|hypA|hydrogenase nickel incorporation protein HybF|-
STM3145_265_299	0.23	-1.16	1254668|hybE|hydrogenase 2-specific chaperone|-
STM3146_449_483	0.13	-1.30	1254669|hybD|predicted maturation element for hydrogenase 2|-
STM3147_1249_1283	0.73	-1.03	1254670|hybC|hydrogenase 2 large subunit|-
STM3148_228_262	0.16	-1.28	1254671|hybB|predicted hydrogenase 2 cytochrome b type component|-
STM3149_673_707	0.04	1.19	1254672|hybA|hydrogenase 2 protein HybA|-

STM3150_120_154	0.42	1.18	1254673|hypO|hydrogenase 2 small subunit|-
STM3151_113_147	0.20	-1.10	1254674|yghW|putative cytoplasmic protein|-
STM3152_1061_1095	0.05	-1.34	1254675|STM3152|putative methyl-accepting chemotaxis protein|-
STM3153_201_235	0.18	1.17	1254676|yqhA|hypothetical protein|-
STM3154_41_75	0.07	1.82	1254677|STM3154|putative ATP-dependent RNA helicase-like protein|-
STM3155_177_213	0.03	1.52	1254678|STM3155|putative cytoplasmic protein|+
STM3156_177_211	0.10	1.51	1254679|STM3156|putative cytoplasmic protein|+
STM3157_545_579	0.72	1.06	1254680|yghA|oxidoreductase|+
STM3158_129_163	0.34	1.08	1254681|exbD|biopolymer transport protein ExbD|-
STM3159_81_115	0.06	-1.20	1254682|exbB|biopolymer transport protein ExbB|-
STM3160_41_80	0.01	-2.20	1254683|STM3160|putative inner membrane protein|-
STM3161_1101_1135	0.17	-1.23	1254684|metC|cystathionine beta-lyase|+
STM3162_513_547	0.02	1.90	1254685|yghB|hypothetical protein|+
STM3163_577_611	0.73	-1.02	1254686|yqhC|putative transcriptional regulator|-
STM3164_229_263	0.04	1.99	1254687|yqhD|putative alcohol dehydrogenase|+
STM3165_117_151	0.43	1.10	1254688|dkgA|2 5-diketo-D-gluconate reductase A|+
STM3167_377_411	0.14	-1.21	1254690|STM3167|putative diadenosine tetraphosphatehydrolase|+
STM3168_1301_1335	0.03	-1.61	1254691|ygiR|hypothetical protein|-
STM3170_53_87	0.03	1.46	1254693|STM3170|putative inner membrane protein|+
STM3171_1237_1271	0.50	1.11	1254694|ygiK|putative transporter|+
STM3172_494_528	0.04	-1.38	1254695|sufI|repressor protein for FtsI|-
STM3173_337_371	0.62	-1.02	1254696|plsC|1-acyl-sn-glycerol-3-phosphate acyltransferase|-
STM3174_1644_1678	0.02	-1.74	1254697|parC|DNA topoisomerase IV subunit A|-
STM3175_801_835	0.15	-1.05	1254698|STM3175|putative regulatory protein|-
STM3176_203_237	0.23	-1.26	1254699|ygiW|putative outer membrane protein|-
STM3177_25_59	0.15	1.18	1254700|ygiX|DNA-binding response regulator in two-component regulatory system with QseC|+
STM3179_49_83	0.03	1.36	1254702|mdaB|NADPH-specific quinone oxidoreductase|+
STM3180_161_195	0.72	-1.08	1254703|ygiN|putative cytoplasmic protein|+
STM3181_1406_1440	0.02	-1.43	1254704|parE|DNA topoisomerase IV subunit B|-
STM3182_425_459	0.01	-1.96	1254705|yqiA|esterase YqiA|-
STM3183_135_169	0.00	-3.11	1254706|icc|cyclic 3' 5'-adenosine monophosphate phosphodiesterase|-
STM3184_385_419	0.02	-1.55	1254707|yqiB|putative cytoplasmic protein|-
STM3185_489_523	0.03	1.48	1254708|nudF|ADP-ribose pyrophosphatase NudF|-
STM3186_535_569	0.14	-1.13	1254709|tolC|outer membrane channel protein|+
STM3187_123_157	0.00	2.84	1254710|ygiB|hypothetical protein|+

STM3188_1029_1063	0.29	1.09	1254711|ygiC|putative glutathionylspermidine synthase|+
STM3189_529_563	0.17	-1.07	1254712|ygiD|putative cytoplasmic protein|-
STM3190_585_619	0.02	-1.21	1254713|ygiE|zinc transporter ZupT|+
STM3191_833_867	0.78	1.04	1254714|STM3191|putative arylsulfate sulfotransferase|+
STM3192_641_675	0.43	1.08	1254715|STM3192|putative arylsulfate sulfotransferase|+
STM3193_625_659	0.06	2.75	1254716|STM3193|putative disulfide bond formation protein|+
STM3194_141_175	0.24	1.10	1254717|STM3194|putative disulfide oxidoreductase|+
STM3195_505_539	0.01	-3.93	1254718|ribB|3 4-dihydroxy-2-butanone 4-phosphate synthase|-
STM3196.S_33_67	0.01	1.78	1254719|yqiC|putative cytoplasmic protein|+
STM3197_113_147	0.02	-1.73	1254720|glgS|glycogen synthesis protein GlgS|-
STM3198_321_355	0.23	1.49	1254721|STM3198|putative inner membrane protein|+
STM3199_1561_1595	0.94	-1.00	1254722|yqiK|hypothetical protein|+
STM3200_659_693	0.02	-1.84	1254723|rfaE|bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase|-
STM3201_2549_2583	0.00	-2.82	1254724|glnE|bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase|-
STM3202_1199_1233	0.02	1.26	1254725|ygiF|putative cytoplasmic protein|-
STM3203_113_147	0.02	-1.35	1254726|ygiM|putative signal transduction protein|+
STM3204_1139_1173	0.33	1.18	1254727|cca|multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase|+
STM3205_161_195	0.03	-1.29	1254728|uppP|undecaprenyl pyrophosphate phosphatase|-
STM3206_257_291	0.09	1.84	1254729|folB|bifunctional dihydroneopterin aldolase/dihydroneopterin triphosphate 2'-epimerase|-
STM3207_389_423	0.67	-1.07	1254730|ygiH|hypothetical protein|+
STM3208_307_341	0.05	1.23	1254731|gcp|O-sialoglycoprotein endopeptidase|-
STM3209_11_45	0.03	-2.18	1254732|rpsU|30S ribosomal protein S21|+
STM3210_875_909	0.00	-1.58	1254733|dnaG|DNA primase|+
STM3211.S_1185_1219	0.03	-1.44	1254734|rpoD|RNA polymerase sigma factor RpoD|+
STM3212_241_275	0.02	1.87	1254735|mug|G/U mismatch-specific DNA glycosylase|-
STM3213_29_63	0.45	-1.18	1254736|ileX|tRNA|+
STM3214_425_459	0.45	1.08	1254737|yqjH|putative transporter|-
STM3215_297_331	0.06	1.41	1254738|yqjI|putative transcriptional regulator|+
STM3216_567_601	0.05	-1.24	1254739|STM3216|putative methyl-accepting chemotaxis protein|-
STM3217_1042_1076	0.01	-1.45	1254740|aer|aerotaxis sensor receptor|-
STM3218_1144_1178	0.01	-3.65	1254741|oat|putrescine--2-oxoglutarate aminotransferase|+
STM3220_786_820	0.76	-1.05	1254743|ygjO|putative methyltransferase|-

STM3221_337_371	0.11	1.39	1254744|ygjP|putative metal-dependent hydrolase|+
STM3223_641_675	0.00	-2.94	1254746|ygjR|putative dehydrogenase|+
STM3224_225_259	0.07	1.40	1254747|ygjT|putative tellurite resistance protein|+
STM3225_1142_1176	0.00	-4.52	1254748|ygjU|putative dicarboxylate permease|+
STM3226_353_387	0.18	-1.28	1254749|yqjA|hypothetical protein|+
STM3227_273_307	0.05	1.20	1254750|yqjB|hypothetical protein|+
STM3228_297_331	0.01	1.88	1254751|yqjC|putative periplasmic protein|+
STM3229_9_43	0.49	-1.09	1254752|yqjD|putative inner membrane protein|+
STM3230_257_291	0.02	-1.42	1254753|yqjE|putative inner membrane protein|+
STM3231_113_147	0.04	-1.37	1254754|yqjK|putative inner membrane protein|+
STM3232_193_227	0.89	1.03	1254755|yqjF|hypothetical protein|+
STM3233_769_803	0.51	1.14	1254756|yqjG|putative glutathione S-transferase|+
STM3234_277_311	0.13	-1.15	1254757|yhaH|putative inner membrane protein|+
STM3235_137_171	0.04	-1.16	1254758|yhaJ|putative transcriptional regulator|-
STM3236_449_483	0.02	1.60	1254759|yhaK|putative cytoplasmic protein|+
STM3237_20_54	0.00	-3.02	1254760|yhaL|putative cytoplasmic protein|+
STM3239_397_431	0.07	-1.11	1254762|yhaO|putative transport protein|-
STM3240_918_952	0.78	1.13	1254763|tdcG|L-serine deaminase|-
STM3241_1664_1698	0.06	1.65	1254764|tdcE|pyruvate formate-lyase 4/2-ketobutyrate formate-lyase|-
STM3242_258_292	0.01	-1.45	1254765|tdcD|propionate/acetate kinase|-
STM3243_333_367	0.02	-1.61	1254766|tdcC|L-threonine/L-serine permease|-
STM3244_641_675	0.40	-1.14	1254767|tdcB|threonine dehydratase|-
STM3245_65_99	0.03	-1.83	1254768|tdcA|DNA-binding transcriptional activator|-
STM3246_9_43	0.99	-1.00	1254769|rnpB|misc_RNA|+
STM3247_571_605	0.03	1.87	1254770|garK|glycerate kinase II|-
STM3248_185_219	0.00	-1.66	1254771|garR|tartronate semialdehyde reductase|-
STM3249_385_419	0.05	1.53	1254772|garL|alpha-dehydro-beta-deoxy-D-glucarate aldolase|-
STM3250_1277_1311	0.02	-1.79	1254773|garD|galactarate dehydrogenase|+
STM3251_649_683	0.80	-1.03	1254774|STM3251|putative sugar kinase|-
STM3252_401_435	0.03	1.43	1254775|agaR|Aga operon transcriptional repressor|-
STM3253_289_323	0.14	-1.26	1254776|gatY|tagatose-bisphosphate aldolase|+
STM3254_833_867	0.03	2.15	1254777|STM3254|putative fructose-1-phosphate kinase|+
STM3255_701_735	0.56	-1.07	1254778|STM3255|putative phosphotransferase system fructose-specific component IIB|+
STM3256_97_131	0.03	-1.37	1254779|STM3256|putative phosphotransferase system mannitol/fructose-specific IIA domain|+

STM3258_81_115	0.13	-1.30	1254781|STM3258|galactitol-specific PTS system component IIA|+
STM3260_599_633	0.15	-1.15	1254783|STM3260|PTS family galactitol-specific enzyme IIC|+
STM3262_561_595	0.12	-1.32	1254785|STM3262|galactitol utilization operon transcriptional repressor|+
STM3263_689_723	0.03	1.82	1254786|yraL|putative methyltransferase|-
STM3264_1236_1270	0.00	1.41	1254787|yraM|putative transglycosylase|+
STM3265_321_355	0.13	1.26	1254788|yraN|hypothetical protein|+
STM3266_401_435	0.00	1.74	1254789|yraO|DnaA initiator-associating protein DiaA|+
STM3267_321_355	0.09	1.44	1254790|yraP|hypothetical protein|+
STM3268_449_483	0.03	1.17	1254791|yraR|putative nucleoside-diphosphate-sugar epimerase|-
STM3269_193_227	0.02	-1.78	1254792|yhbO|putative intracellular proteinase|+
STM3271_47_81	0.88	1.02	1254794|yhbQ|hypothetical protein|+
STM3272_49_83	0.13	-1.28	1254795|yhbS|putative transport protein|-
STM3273_45_79	0.49	1.08	1254796|yhbT|putative lipid carrier protein|-
STM3274_337_371	0.08	-1.29	1254797|yhbU|putative protease|+
STM3276_289_323	0.09	-1.28	1254799|yhbW|hypothetical protein|+
STM3277_609_643	0.03	3.11	1254800|STM3277|putative inner membrane protein|-
STM3278_405_439	0.73	1.03	1254801|STM3278|putative cytoplasmic protein|+
STM3279_694_728	0.10	-1.34	1254802|mtr|tryptophan permease|-
STM3280.S_1563_1597	0.95	-1.01	1254803|deaD|ATP-dependent RNA helicase DeaD|-
STM3281_449_483	0.01	1.59	1254804|nlpI|lipoprotein NlpI|-
STM3282_1841_1875	0.36	-1.16	1254805|pnp|polynucleotide phosphorylase/polyadenylase|-
STM3283_201_235	0.34	-1.28	1254806|rpsO|30S ribosomal protein S15|-
STM3284_609_643	0.08	-1.57	1254807|truB|tRNA pseudouridine synthase B|-
STM3285_321_355	0.34	1.11	1254808|rbfA|ribosome-binding factor A|-
STM3286_2256_2290	0.04	-1.24	1254809|infB|translation initiation factor IF-2|-
STM3287_1400_1434	0.26	1.08	1254810|nusA|transcription elongation factor NusA|-
STM3288_241_275	0.46	1.21	1254811|yhbC|hypothetical protein|-
STM3291_434_468	0.78	1.06	1254814|STM3291|putative cytoplasmic protein|-
STM3292_9_43	0.35	-1.19	1254815|leuU|tRNA|-
STM3293_137_171	0.03	-1.26	1254816|secG|preprotein translocase subunit SecG|-
STM3294_339_373	0.60	1.18	1254817|glmM|phosphoglucosamine mutase|-
STM3295_673_707	0.15	-1.29	1254818|folP|dihydropteroate synthase|-
STM3296_1416_1450	0.04	-1.41	1254819|hflB|ATP-dependent metalloprotease|-
STM3297_289_323	0.64	1.02	1254820|rrmJ|23S rRNA methyltransferase J|-
STM3298.S_33_67	0.06	-1.20	1254821|yhbY|RNA-binding protein YhbY|+
STM3299_203_237	0.11	-1.31	1254822|greA|transcription elongation factor GreA|-

STM3300_563_597	0.35	1.09	1254823|dacB|D-alanyl-D-alanine carboxypeptidase/endopeptidase|+
STM3301_510_544	0.01	1.60	1254824|obgE|GTPase ObgE|-
STM3302_217_251	0.24	-1.09	1254825|yhbE|pseudo|-
STM3303_37_71	0.01	-3.11	1254826|rpmA|50S ribosomal protein L27|-
STM3304_225_259	0.02	-2.43	1254827|rplU|50S ribosomal protein L21|-
STM3305_497_531	0.13	1.09	1254828|ispB|octaprenyl diphosphate synthase|+
STM3306_65_99	0.01	2.07	1254829|nlp|DNA-binding transcriptional activator of maltose metabolism|+
STM3307_517_551	0.11	-1.38	1254830|murA|UDP-N-acetylglucosamine 1-carboxyvinyltransferase|-
STM3308_209_243	0.03	-1.69	1254831|yrbA|putative transcriptional regulator|-
STM3309_97_131	0.01	1.57	1254832|yrbB|hypothetical protein|-
STM3310_145_179	0.03	1.28	1254833|yrbC|putative transport protein|-
STM3311_97_131	0.13	-1.50	1254834|yrbD|putative transport protein|-
STM3312_229_263	0.03	-1.24	1254835|yrbE|putative transport protein|-
STM3313_617_651	0.08	2.04	1254836|yrbF|putative ABC transporter ATP-binding protein YrbF|-
STM3314_273_307	0.10	1.12	1254837|yrbG|putative calcium/sodium:proton antiporter|+
STM3315_929_963	0.04	-1.31	1254838|yrbH|D-arabinose 5-phosphate isomerase|+
STM3316_161_195	0.18	-1.15	1254839|yrbI|3-deoxy-D-manno-octulosonate 8-phosphate phosphatase|+
STM3317_385_419	0.06	1.14	1254840|yrbK|hypothetical protein|+
STM3318_129_163	0.65	-1.03	1254841|yhbN|hypothetical protein|+
STM3319_565_599	0.14	-1.27	1254842|yhbG|putative ABC transporter ATP-binding protein YhbG|+
STM3320_643_677	0.00	-1.52	1254843|rpoN|RNA polymerase factor sigma-54|+
STM3321_217_251	0.09	-1.58	1254844|yhbH|putative sigma(54) modulation protein|+
STM3323_457_491	0.02	-1.69	1254846|yhbJ|hypothetical protein|+
STM3324_233_267	0.01	2.12	1254847|ptsO|phosphohistidinoprotein-hexose phosphotransferase component of N-regulated PTS system (Npr)|+
STM3325_369_403	0.94	1.01	1254848|yrbL|hypothetical protein|+
STM3326_465_499	0.49	-1.17	1254849|mtgA|monofunctional biosynthetic peptidoglycan transglycosylase|-
STM3327_129_163	0.16	1.22	1254850|yhbL|isoprenoid biosynthesis protein with amidotransferase-like domain|-
STM3328_2026_2060	0.07	1.68	1254851|arcB|aerobic respiration control sensor protein ArcB|-
STM3329_283_317	0.17	-1.30	1254852|yhcC|putative FeS oxidoreductase|-
STM3330_4230_4264	0.39	1.14	1254853|gltB|glutamate synthase subunit alpha|+
STM3331_1380_1414	0.39	1.58	1254854|gltD|glutamate synthase subunit beta|+
STM3334_1114_1148	0.79	1.04	1254857|STM3334|cytosine deaminase|+
STM3335_209_243	0.01	-2.05	1254858|yhcH|putative cytoplasmic protein|-
STM3336_129_163	0.00	-3.13	1254859|nanK|N-acetylmannosamine kinase|-

STM3337_193_227	0.03	-1.48	1254860|nanE|N-acetylmannosamine-6-phosphate 2-epimerase|-
STM3340_545_579	0.09	1.69	1254863|yhcK|transcriptional regulator NanR|-
STM3341_409_443	0.86	1.03	1254864|sspB|ClpXP protease specificity-enhancing factor|-
STM3342_145_179	0.08	1.25	1254865|sspA|stringent starvation protein A|-
STM3343_33_67	0.06	-1.88	1254866|STM3343|putative cytoplasmic protein|-
STM3344_321_355	0.13	1.34	1254867|rpsI|30S ribosomal protein S9|-
STM3345_129_163	0.01	-2.90	1254868|rplM|50S ribosomal protein L13|-
STM3346_1086_1120	0.02	-1.91	1254869|yhcM|putative ATPase|-
STM3347_33_67	0.13	1.31	1254870|yhcB|cytochrome d ubiquinol oxidase subunit III|+
STM3348_1153_1187	0.01	2.26	1254871|degQ|serine endoprotease|+
STM3349_456_490	0.16	-1.09	1254872|degS|serine endoprotease|+
STM3350_417_451	0.07	1.35	1254873|STM3350|putative inner membrane protein|-
STM3353_2_37	0.03	1.26	1254876|oadG|oxaloacetate decarboxylase subunit gamma|-
STM3354_97_131	0.26	1.29	1254877|STM3354|L(+)-tartrate dehydratase subunit beta|-
STM3355_129_163	0.81	-1.02	1254878|STM3355|tartrate dehydratase subunit alpha|-
STM3356_302_336	0.13	-1.32	1254879|STM3356|putative cation transporter|-
STM3357_65_99	0.22	1.22	1254880|STM3357|putative regulatory protein|-
STM3358_105_139	0.09	-1.20	1254881|STM3358|putative regulatory protein|-
STM3359_833_867	0.00	-5.18	1254882|mdh|malate dehydrogenase|-
STM3360_129_163	0.02	-1.51	1254883|argR|arginine repressor|+
STM3361_129_163	0.88	-1.02	1254884|yhcN|putative outer membrane protein|+
STM3362_97_131	0.00	3.30	1254885|STM3362|putative periplasmic protein|+
STM3363_95_133	0.03	1.77	1254886|yhcO|putative cytoplasmic protein|-
STM3364_1673_1707	0.82	1.04	1254887|yhcP|p-hydroxybenzoic acid efflux subunit AaeB|-
STM3365_161_195	0.12	1.30	1254888|yhcQ|p-hydroxybenzoic acid efflux subunit AaeA|-
STM3366_132_166	0.03	2.37	1254889|yhcR|hypothetical protein|-
STM3367_193_227	0.65	1.07	1254890|yhcS|putative DNA-binding transcriptional regulator|+
STM3368_1215_1249	0.03	-1.54	1254891|tldD|microcin B17-processing protein|-
STM3369_3314_3348	0.01	-1.59	1254892|yhdP|hypothetical protein|-
STM3370_727_761	0.21	1.20	1254893|cafA|ribonuclease G|-
STM3371_513_547	0.00	-1.80	1254894|maf|Maf-like protein|-
STM3372_241_275	0.03	-1.70	1254895|mreD|rod shape-determining protein MreD|-
STM3373_374_408	0.03	-1.42	1254896|mreC|cell wall structural complex MreBCD transmembrane component MreC|-
STM3374_637_671	0.08	-1.58	1254897|mreB|rod shape-determining protein|-
STM3374.1n_61_95	0.05	1.93	2673730|STM3374.1n|hypothetical protein|+

STM3375_1438_1472	0.04	-1.32	1254898|yhdA|regulatory protein CsrD|-
STM3376_929_963	0.01	2.06	1254899|yhdH|putative oxidoreductase|+
STM3377_870_904	0.02	-1.43	1254900|STM3377|putative sulfite oxidase subunit YedY|+
STM3378_449_483	0.04	-1.36	1254901|STM3378|putative sulfite oxidase subunit YedZ|+
STM3379_401_435	0.04	-1.81	1254902|accB|acetyl-CoA carboxylase biotin carboxyl carrier protein subunit|+
STM3380_863_897	0.83	-1.06	1254903|accC|acetyl-CoA carboxylase biotin carboxylase subunit|+
STM3381_65_99	0.06	-1.27	1254904|yhdT|hypothetical protein|+
STM3382_1093_1127	0.06	-1.41	1254905|panF|sodium/panthothenate symporter|+
STM3383_237_271	0.83	-1.05	1254906|prmA|ribosomal protein L11 methyltransferase|+
STM3385_25_59	0.06	-1.30	1254908|fis|DNA-binding protein Fis|+
STM3386_697_731	0.11	1.85	1254909|yhdJ|putative methyltransferase|+
STM3387_81_115	0.28	1.13	1254910|yhdU|putative periplasmic protein|+
STM3388_1101_1135	0.05	2.51	1254911|STM3388|putative signal transduction protein|+
STM3389_81_115	0.12	1.13	1254912|envR|DNA-binding transcriptional regulator|-
STM3390_255_289	0.36	1.09	1254913|acrE|acriflavine resistance protein E precursor|+
STM3391_2563_2597	0.30	1.11	1254914|acrF|multidrug transport protein|+
STM3392_73_107	0.00	12.55	1254915|yhdV|putative outer membrane lipoprotein|+
STM3399_225_259	0.01	-2.00	1254922|yrdA|putative ferripyochelin-binding protein|+
STM3400_17_51	0.15	1.35	1254923|yrdB|putative periplasmic protein|-
STM3401_433_467	0.03	-1.44	1254924|aroE|shikimate 5-dehydrogenase|-
STM3402_446_480	0.09	-1.47	1254925|yrdC|putative ribosome maturation factor|-
STM3403_113_147	0.07	-1.19	1254926|yrdD|putative DNA topoisomerase|-
STM3404_97_131	0.01	-1.59	1254927|smg|hypothetical protein|-
STM3405_846_880	0.03	-1.47	1254928|smf|hypothetical protein|-
STM3406_161_195	0.06	1.14	1254929|def|peptide deformylase|+
STM3407_393_427	0.26	1.12	1254930|fmt|methionyl-tRNA formyltransferase|+
STM3409_1082_1116	0.07	1.25	1254932|trkA|potassium transporter peripheral membrane component|+
STM3410_193_227	0.00	1.30	1254933|mscL|large-conductance mechanosensitive channel|+
STM3411_117_152	0.04	1.65	1254934|STM3411|putative cytoplasmic protein|-
STM3412_81_115	0.07	1.39	1254935|zntR|zinc-responsive transcriptional regulator|-
STM3413_241_275	0.01	2.01	1254936|yhdN|hypothetical protein|-
STM3414_9_43	0.02	-1.87	1254937|rplQ|50S ribosomal protein L17|-
STM3415_769_803	0.00	-1.91	1254938|rpoA|DNA-directed RNA polymerase subunit alpha|-
STM3416_545_579	0.02	-2.46	1254939|rpsD|30S ribosomal protein S4|-
STM3417_329_363	0.10	1.84	1254940|rpsK|30S ribosomal protein S11|-
STM3418_233_267	0.01	-1.81	1254941|rpsM|30S ribosomal protein S13|-

STM3419_33_67	0.80	-1.05	1254942|rpmJ|50S ribosomal protein L36|-
STM3420_333_367	0.01	-2.48	1254943|secY|preprotein translocase subunit SecY|-
STM3422_17_51	0.01	-3.25	1254945|rpmD|50S ribosomal protein L30|-
STM3423_209_243	0.01	-2.99	1254946|rpsE|30S ribosomal protein S5|-
STM3424_97_131	0.04	-2.39	1254947|rplR|50S ribosomal protein L18|-
STM3425_137_171	0.01	-3.17	1254948|rplF|50S ribosomal protein L6|-
STM3426_357_391	0.02	-1.88	1254949|rpsH|30S ribosomal protein S8|-
STM3427.S_97_131	0.02	-3.29	1254950|rpsN|30S ribosomal subunit protein S14|-
STM3428_353_387	0.01	-4.21	1254951|rplE|50S ribosomal protein L5|-
STM3429_233_267	0.01	-1.63	1254952|rplX|50S ribosomal protein L24|-
STM3430_33_67	0.00	-3.80	1254953|rplN|50S ribosomal protein L14|-
STM3431_129_163	0.03	-2.74	1254954|rpsQ|30S ribosomal protein S17|-
STM3432_143_177	0.02	-3.00	1254955|rpmC|50S ribosomal protein L29|-
STM3433_257_291	0.01	-2.95	1254956|rplP|50S ribosomal protein L16|-
STM3434_385_419	0.03	-2.58	1254957|rpsC|30S ribosomal protein S3|-
STM3435_177_211	0.00	-8.12	1254958|rplV|50S ribosomal protein L22|-
STM3436_121_155	0.01	-2.85	1254959|rpsS|30S ribosomal protein S19|-
STM3437_225_259	0.01	-5.23	1254960|rplB|50S ribosomal protein L2|-
STM3438_153_187	0.02	-1.66	1254961|rplW|50S ribosomal protein L23|-
STM3439_529_563	0.01	-2.44	1254962|rplD|50S ribosomal protein L4|-
STM3440_385_419	0.00	-4.72	1254963|rplC|50S ribosomal protein L3|-
STM3441_225_259	0.01	-2.58	1254964|rpsJ|30S ribosomal protein S10|-
STM3443_315_349	0.16	-1.29	1254966|bfr|bacterioferritin iron storage and detoxification protein|-
STM3444_105_139	0.36	1.17	1254967|bfd|bacterioferritin-associated ferredoxin|-
STM3445_972_1006	0.04	-1.84	1254968|tuf|elongation factor Tu|-
STM3446_1628_1662	0.04	-1.97	1254969|fusA|elongation factor G|-
STM3447_193_227	0.03	-1.89	1254970|rpsG|30S ribosomal protein S7|-
STM3448_321_355	0.05	-1.81	1254971|rpsL|30S ribosomal protein S12|-
STM3449_217_252	0.66	1.05	1254972|yheL|hypothetical protein|-
STM3450_165_199	0.04	-1.56	1254973|yheM|hypothetical protein|-
STM3451_117_151	0.09	-1.59	1254974|yheN|hypothetical protein|-
STM3452_105_139	0.09	-1.51	1254975|yheO|putative regulatory protein|-
STM3453_697_731	0.58	1.09	1254976|fkpA|FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)|-
STM3454_156_190	0.05	2.14	1254977|slyX|hypothetical protein|+
STM3455_257_291	0.23	1.32	1254978|slyD|FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)|-
STM3456_105_139	0.74	-1.09	1254979|yheV|putative cytoplasmic protein|-

STM3457_1639_1673	0.03	-1.21	1254980|kefB|glutathione-regulated potassium-efflux system protein KefB|-
STM3458_97_131	0.08	-1.27	1254981|yheR|glutathione-regulated potassium-efflux system ancillary protein KefG|-
STM3459_1261_1295	0.04	-1.73	1254982|yheS|putative ABC transporter ATP-binding protein|+
STM3460_97_131	0.00	-2.50	1254983|STM3460|pseudo|-
STM3461_161_195	0.06	1.45	1254984|STM3461|hypothetical protein|-
STM3462_389_423	0.01	2.03	1254985|yheT|predicted hydrolase|+
STM3463_137_171	0.07	-1.21	1254986|yheU|hypothetical protein|+
STM3464_545_579	0.11	1.23	1254987|prkB|putative phosphoribulokinase|+
STM3465_173_207	0.00	-2.69	1254988|yhfA|hypothetical protein|-
STM3466_25_59	0.36	1.08	1254989|crp|cAMP-regulatory protein|+
STM3468_515_549	0.05	1.61	1254991|argD|bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein|-
STM3469_289_323	0.98	-1.00	1254992|pabA|para-aminobenzoate synthase component III|-
STM3470_329_363	0.39	1.12	1254993|fic|cell filamentation protein Fic|-
STM3471_129_163	0.54	-1.11	1254994|yhfG|hypothetical protein|-
STM3472_533_567	0.00	4.65	1254995|ppiA|peptidyl-prolyl cis-trans isomerase A (rotamase A)|-
STM3473_463_497	0.67	1.10	1254996|yhfC|hypothetical protein|+
STM3474_1753_1787	0.04	1.39	1254997|nirB|nitrite reductase large subunit|+
STM3475_81_115	0.02	-1.28	1254998|nirD|nitrite reductase small subunit|+
STM3476_197_231	0.40	1.06	1254999|nirC|nitrite transporter NirC|+
STM3477_1271_1305	0.01	-1.90	1255000|cysG|siroheme synthase|+
STM3478_5535_5569	0.27	1.08	1255001|bigA|putative surface-exposed virulence protein|+
STM3480_38_72	0.17	1.90	1255003|yhfL|putative outer membrane lipoprotein|+
STM3481_278_312	0.21	-1.38	1255004|trpS|tryptophanyl-tRNA synthetase|-
STM3482_385_419	0.71	1.04	1255005|gph|phosphoglycolate phosphatase|-
STM3483_105_139	0.21	-1.17	1255006|rpe|ribulose-phosphate 3-epimerase|-
STM3484_417_451	0.07	1.39	1255007|dam|DNA adenine methylase|-
STM3485_631_665	0.08	-1.73	1255008|damX|hypothetical protein|-
STM3486_642_676	0.01	-2.43	1255009|aroB|3-dehydroquinate synthase|-
STM3487_449_483	0.02	-2.20	1255010|aroK|shikimate kinase II|-
STM3488_1000_1034	0.19	1.08	1255011|hofQ|predicted fimbrial transporter|-
STM3489_129_163	0.84	-1.05	1255012|yrfA|putative inner membrane protein|-
STM3490_363_397	0.80	-1.03	1255013|yrfB|putative inner membrane protein|-
STM3491_481_515	0.65	-1.18	1255014|yrfC|putative inner membrane protein|-
STM3492_325_359	0.73	1.07	1255015|yrfD|putative periplasmic protein|-

STM3493_2190_2224	0.15	-1.34	1255016|mrcA|peptidoglycan synthetase|+
STM3494.S_145_179	0.86	1.02	1255017|nudE|ADP-ribose diphosphatase NudE|-
STM3495_1246_1280	0.87	-1.03	1255018|yrfF|putative inner membrane protein|+
STM3496_177_211	0.76	-1.02	1255019|yrfG|putative hydrolase|+
STM3497_353_387	0.38	-1.07	1255020|yrfH|ribosome-associated heat shock protein Hsp15|+
STM3498_65_99	0.04	1.40	1255021|hslO|Hsp33-like chaperonin|+
STM3499_1111_1145	0.03	-1.60	1255022|yhgE|putative inner membrane protein|-
STM3500_954_988	0.00	-3.82	1255023|pckA|phosphoenolpyruvate carboxykinase|+
STM3501_930_964	0.02	-1.21	1255024|envZ|osmolarity sensor protein|-
STM3502_193_227	0.01	1.70	1255025|ompR|osmolarity response regulator|-
STM3503_429_463	0.01	1.55	1255026|greB|transcription elongation factor GreB|+
STM3504_1969_2003	0.16	-1.22	1255027|yhgF|putative RNase R|+
STM3505_145_179	0.01	2.45	1255028|feoA|ferrous iron transport protein A|+
STM3506_1896_1930	0.64	1.15	1255029|feoB|ferrous iron transport protein B|+
STM3507_89_123	0.33	1.13	1255030|yhgG|putative cytoplasmic protein|+
STM3508_841_875	0.02	1.67	1255031|STM3508|putative cytoplasmic protein|+
STM3509_649_683	0.13	1.39	1255032|bioH|carboxylesterase BioH|-
STM3510_17_51	0.12	1.17	1255033|yhgH|gluconate periplasmic binding protein|+
STM3511_449_483	0.02	5.17	1255034|yhgI|predicted gluconate transport-associated protein|+
STM3512_846_880	0.04	-1.58	1255035|gntT|high-affinity gluconate permease|+
STM3513_1856_1890	0.01	1.45	1255036|malQ|4-alpha-glucanotransferase|-
STM3514_1427_1461	0.06	1.54	1255037|malP|maltodextrin phosphorylase|-
STM3515_1707_1741	0.01	-3.18	1255038|malT|transcriptional regulator MalT|+
STM3516_153_187	0.70	1.06	1255039|STM3516|putative cytoplasmic protein|-
STM3517_149_183	0.44	-1.09	1255040|STM3517|putative DNA-damage-inducibile protein|-
STM3518_981_1015	0.06	1.42	1255041|rtcA|RNA 3'-terminal-phosphate cyclase|-
STM3519_1099_1133	0.64	1.08	1255042|rtcB|putative cytoplasmic protein|-
STM3520_17_51	0.01	2.10	1255043|STM3520|pseudo|-
STM3519.1N_124_158	0.48	1.10	2673723|STM3519.1N|-|-
STM3521_1291_1325	0.02	1.59	1255044|STM3521|putative ribonucleoprotein related-protein|-
STM3523_513_547	0.02	-1.84	1255046|glpR|DNA-binding transcriptional repressor|-
STM3524_305_339	0.21	-1.12	1255047|glpG|predicted intramembrane serine protease|-
STM3525_65_99	0.03	-1.41	1255048|glpE|thiosulfate sulfurtransferase|-
STM3526_1318_1352	0.26	1.13	1255049|glpD|glycerol-3-phosphate dehydrogenase|+
STM3527_65_99	0.10	-1.11	1255050|STM3527|hypothetical protein|-
STM3528_1265_1299	0.03	1.40	1255051|STM3528|putative periplasmic phosphate-binding protein|-

STM3529_367_401	0.04	-1.74	1255052|gldA|glycerol dehydrogenase|-
STM3530_975_1009	0.33	1.26	1255053|STM3530|pseudo|+
STM3533_201_235	0.06	1.41	1255056|STM3533|putative transcriptional regulator|-
STM3534_2345_2379	0.14	-1.17	1255057|glgP|glycogen phosphorylase|-
STM3535_1043_1077	0.02	-1.62	1255058|glgA|glycogen synthase|-
STM3536_905_939	0.17	-1.12	1255059|glgC|glucose-1-phosphate adenylyltransferase|-
STM3537_1074_1108	0.02	1.50	1255060|glgX|glycogen debranching enzyme|-
STM3538_1484_1518	0.81	-1.02	1255061|glgB|glycogen branching enzyme|-
STM3539_1020_1054	0.97	1.01	1255062|asd|aspartate-semialdehyde dehydrogenase|-
STM3540_73_107	0.04	2.37	2673721|STM3540|-|+
STM3541_598_632	0.43	-1.05	1255064|gntU|gluconate transporter low affinity GNT 1 system|-
STM3542_175_209	0.03	2.35	1255065|gntK|gluconate kinase 1|-
STM3543_209_243	0.01	1.94	1255066|gntR|gluconate operon transcriptional repressor|-
STM3544_641_675	0.14	1.39	1255067|yhhW|putative cytoplasmic protein|-
STM3545_871_905	0.05	-1.43	1255068|yhhX|putative oxidoreductase|-
STM3546_321_355	0.53	1.06	1255069|yhhY|putative acetyltransferase YhhY|+
STM3547.Sc_113_147	0.01	1.55	1255070|STM3547.Sc|putative transcriptional regulator|+
STM3548_609_643	0.06	2.06	1255071|STM3548|putative cytoplasmic protein|+
STM3549_97_131	0.08	2.04	1255072|STM3549|putative inner membrane protein|+
STM3550_836_870	0.09	1.16	1255073|STM3550|putative phosphotriesterase|+
STM3551_880_914	0.33	-1.09	1255074|ggt|gamma-glutamyltranspeptidase periplasmic precursor|-
STM3552_201_235	0.12	1.32	1255075|yhhA|hypothetical protein|+
STM3553_93_127	0.03	-1.64	1255076|ugpQ|cytoplasmic glycerophosphodiester phosphodiesterase|-
STM3554_552_586	0.18	-1.13	1255077|ugpC|glycerol-3-phosphate transporter ATP-binding subunit|-
STM3555_641_675	0.01	-1.41	1255078|ugpE|glycerol-3-phosphate transporter membrane protein|-
STM3557_1118_1152	0.01	-2.39	1255080|ugpB|glycerol-3-phosphate transporter periplasmic binding protein|-
STM3558_273_307	0.46	1.07	1255081|STM3558|death-on-curing protein|-
STM3559_3_37	0.21	-1.31	1255082|yhhV|putative cytoplasmic protein|-
STM3560_521_555	0.12	-1.23	1255083|livF|leucine/isoleucine/valine transporter ATP-binding subunit|-
STM3561_49_83	0.41	1.07	1255084|livG|leucine/isoleucine/valine transporter ATP-binding subunit|-
STM3562_663_697	0.85	1.02	1255085|livM|leucine/isoleucine/valine transporter permease subunit|-
STM3563_657_691	0.06	-1.41	1255086|livH|branched-chain amino acid transporter permease subunit LivH|-
STM3564_191_225	0.72	1.03	1255087|livK|high-affinity branched-chain amino acid transporter|-
STM3565_25_59	0.01	1.64	1255088|yhhK|putative acetyltransferase|+
STM3566_85_120	0.00	1.64	1255089|STM3566|putative cytoplasmic protein|+
STM3567_259_293	0.82	1.03	1255090|livJ|high-affinity branched-chain amino acid transporter|-

STM3568_353_387	0.14	1.29	1255091|rpoH|RNA polymerase factor sigma-32|-
STM3569_281_315	0.01	2.40	1255092|ftsX|cell division protein FtsX|-
STM3570_577_611	0.04	1.84	1255093|ftsE|cell division protein FtsE|-
STM3571_1357_1391	0.04	-1.13	1255094|ftsY|cell division protein FtsY|-
STM3572_529_563	0.96	1.01	1255095|yhhF|predicted methyltransferase|+
STM3573_13_47	0.03	1.27	1255096|yhhL|hypothetical protein|+
STM3574_129_163	0.21	-1.18	1255097|yhhM|putative inner membrane protein|-
STM3575_385_419	0.58	1.03	1255098|yhhN|putative inner membrane protein|+
STM3576_1712_1746	0.27	-1.09	1255099|zntA|zinc/cadmium/mercury/lead-transporting ATPase|+
STM3577_813_847	0.25	1.14	1255100|tcp|methyl-accepting transmembrane citrate/phenol chemoreceptor|+
STM3578_89_123	0.00	1.86	1255101|yhhP|cell developmental protein SirA|-
STM3579_249_283	0.35	-1.14	1255102|yhhQ|hypothetical protein|+
STM3580_345_379	0.01	2.46	1255103|STM3580|hypothetical protein|+
STM3581.S_1021_1055	0.01	1.97	1255104|yhhS|hypothetical protein|-
STM3582_83_117	0.90	-1.03	1255105|yhhT|putative permease|+
STM3583_33_67	0.03	1.67	1255106|acpT|holo-(acyl carrier protein) synthase 2|+
STM3584_17_51	0.13	1.16	1255107|nikR|nickel responsive regulator|+
STM3586.S_1791_1825	0.18	-1.11	1255109|yhiH|putative ABC-type multidrug transport system ATPase component|-
STM3587_165_199	0.03	1.37	1255110|yhiI|hypothetical protein|-
STM3588_774_808	0.04	-1.44	1255111|yhiN|putative periplasmic protein|-
STM3589_914_948	0.03	-1.34	1255112|pitA|low-affinity phosphate transporter|+
STM3590_65_99	0.02	1.74	1255113|uspB|universal stress protein UspB|-
STM3591_161_195	0.11	1.34	1255114|uspA|universal stress protein A|+
STM3592_1111_1145	0.04	-1.14	1255115|yhiP|inner membrane transporter YhiP|+
STM3593_233_267	0.40	-1.12	1255116|yhiQ|putative methyltransferase|-
STM3594_1908_1942	0.12	1.34	1255117|prlC|oligopeptidase A|-
STM3595_601_635	0.00	2.33	1255118|STM3595|putative phosphatase|-
STM3596_33_67	0.11	2.14	1255119|yhiR|putative cytoplasmic protein|+
STM3597_386_420	0.83	1.05	1255120|gor|glutathione reductase|+
STM3598_573_607	0.05	2.14	1255121|STM3598|putative L-asparaginase|-
STM3599_705_739	0.10	-1.29	1255122|STM3599|anaerobic C4-dicarboxylate transporter|-
STM3600_33_67	0.81	1.03	1255123|STM3600|putative sugar kinase|-
STM3601_289_323	0.10	-1.21	1255124|STM3601|putative phosphosugar isomerase|-
STM3602_257_291	0.48	-1.08	1255125|STM3602|putative regulatory protein|-

STM3603_1195_1229	0.00	2.43	1255126|treF|trehalase|+
STM3604_1071_1105	0.09	1.22	1255127|STM3604|putative inner membrane protein|-
STM3605_97_131	0.17	1.22	1255128|STM3605|putative phage endolysin|+
STM3606_273_307	0.01	2.48	1255129|yhjB|putative transcriptional regulator|-
STM3607_705_739	0.07	1.43	1255130|yhjC|putative transcriptional regulator|+
STM3608_606_640	0.27	1.56	1255131|yhjD|putative tRNA-processing ribonuclease|+
STM3609_1140_1174	0.00	-2.55	1255132|yhjE|putative transport protein|+
STM3610_1114_1148	0.22	-1.12	1255133|yhjG|putative inner membrane protein|-
STM3611_385_419	0.51	-1.10	1255134|yhjH|EAL domain containing protein involved in flagellar function|-
STM3612_289_323	0.01	-3.55	1255135|kdgK|ketodeoxygluconokinase|+
STM3613_809_843	0.03	-1.96	1255136|yhjJ|putative Zn-dependent peptidase|-
STM3614_896_930	0.01	-8.22	1255137|dctA|C4-dicarboxylate transporter DctA|-
STM3615_1743_1777	0.97	1.01	1255138|yhjK|putative diguanylate cyclase/phosphodiesterase|-
STM3616_2768_2802	0.18	-1.21	1255139|yhjL|cellulose synthase subunit BcsC|-
STM3617_511_545	0.07	-1.34	1255140|STM3617|endo-1 4-D-glucanase|-
STM3618_1750_1784	0.39	-1.13	1255141|yhjN|cellulose synthase regulator protein|-
STM3619_1882_1916	0.39	-1.15	1255142|bcsA|cellulose synthase catalytic subunit|-
STM3620_433_467	0.09	1.11	1255143|yhjQ|cell division protein|-
STM3621_5_39	0.69	1.03	1255144|yhjR|putative cytoplasmic protein|-
STM3622_717_751	0.03	1.59	1255145|yhjS|putative cytoplasmic protein|+
STM3623_125_159	0.01	2.62	1255146|yhjT|putative inner membrane protein|+
STM3624_1449_1483	0.30	1.11	1255147|yhjU|putative inner membrane protein|+
STM3624.1N_239_273	0.74	1.10	2673734|STM3624.1N|-|-
STM3624A_97_131	0.05	-1.66	1255148|STM3624A|cystathionine gamma-synthase|+
STM3625_1140_1174	0.06	1.42	1255149|yhjV|putative transport protein|+
STM3626_919_953	0.02	-2.04	1255150|dppF|dipeptide transporter ATP-binding subunit|-
STM3627_401_435	0.00	-1.70	1255151|dppD|dipeptide transporter ATP-binding subunit|-
STM3628_369_403	0.02	-1.53	1255152|dppC|dipeptide transporter|-
STM3629_533_567	0.00	-3.54	1255153|dppB|dipeptide transporter permease DppB|-
STM3630_777_811	0.88	1.03	1255154|dppA|dipeptide transport protein|-
STM3631_727_761	0.05	1.23	1255155|STM3631|putative xanthine permease|-
STM3632_926_960	0.17	-1.35	1255156|STM3632|hypothetical protein|-
STM3635_1149_1183	0.40	1.18	1255159|yhjW|phosphoethanolamine transferase|-
STM3636_145_179	0.01	2.00	1255160|lpfE|long polar fimbrial minor protein|-
STM3638_2106_2140	0.05	-1.30	1255162|lpfC|long polar fimbrial outer membrane usher protein|-
STM3640_353_387	0.04	1.23	1255164|lpfA|long polar fimbrial protein A precursor|-

STM3641_385_419	0.79	1.04	1255165|yhjY|putative lipase|-
STM3642_97_131	0.96	1.00	1255166|tag|3-methyl-adenine DNA glycosylase II|+
STM3643_81_115	0.01	-1.90	1255167|yiaC|hypothetical protein|+
STM3644_1399_1433	0.06	-1.40	1255168|bisC|biotin sulfoxide reductase|-
STM3645_625_659	0.01	3.07	1255169|yiaD|predicted outer membrane lipoprotein|+
STM3646_209_243	0.00	-1.60	1255170|yiaE|2-hydroxyacid dehydrogenase|+
STM3647_513_547	0.37	1.09	1255171|yiaF|putative outer membrane lipoprotein|-
STM3648_221_255	0.57	1.14	1255172|yiaG|putative transcriptional regulator|+
STM3649_66_100	0.01	2.16	1255173|cspA|major cold shock protein|+
STM3650_161_195	0.06	1.99	1255174|STM3650|hypothetical protein|+
STM3651_193_227	0.01	2.20	1255175|STM3651|putative acetyltransferase|-
STM3652_215_249	0.01	1.94	1255176|STM3652|putative cytoplasmic protein|-
STM3653_129_163	0.07	1.22	1255177|STM3653|putative acetyltransferase|-
STM3654_53_87	0.78	-1.02	1255178|STM3654|pseudo|-
STM3655_1615_1649	0.03	-1.95	1255179|glyS|glycyl-tRNA synthetase subunit beta|-
STM3656_785_819	0.01	-1.49	1255180|glyQ|glycyl-tRNA synthetase subunit alpha|-
STM3657_25_59	0.04	-1.47	1255181|STM3657|putative outer membrane lipoprotein|-
STM3658_693_727	0.88	-1.01	1255182|yiaH|putative inner membrane protein|+
STM3659_153_187	0.02	1.41	1255183|yiaB|putative inner membrane protein|-
STM3660_1384_1418	0.04	1.28	1255184|xylB|xylulokinase|-
STM3662_1140_1174	0.01	-1.66	1255186|xylR|xylose operon regulatory protein|+
STM3663_769_803	0.05	1.47	1255187|bax|hypothetical protein|-
STM3664_1157_1191	0.00	1.29	1255188|malS|periplasmic alpha-amylase precursor|+
STM3666_241_275	0.02	1.95	1255190|lysaA|putative oxidoreductase|-
STM3667_465_499	0.39	-1.15	1255191|yiaJ|transcriptional repressor|-
STM3668_489_523	0.88	-1.03	1255192|yiaK|2 3-diketo-L-gulonate reductase|+
STM3669_173_207	0.03	1.38	1255193|yiaL|putative cytoplasmic protein|+
STM3670_273_307	0.10	1.64	1255194|STM3670|putative chemotaxis protein|+
STM3672_1175_1209	0.11	2.10	1255196|yiaN|hypothetical protein|+
STM3673_577_611	0.02	1.73	1255197|yiaO|putative periplasmic dicarboxylate-binding protein|+
STM3675_481_515	0.45	-1.09	1255199|sgbH|3-keto-L-gulonate-6-phosphate decarboxylase|+
STM3676_513_547	0.49	1.15	1255200|sgbU|putative L-xylulose 5-phosphate 3-epimerase|+
STM3677_417_451	0.67	-1.05	1255201|sgbE|L-ribulose-5-phosphate 4-epimerase|+
STM3680_732_766	0.00	-15.10	1255204|aldB|aldehyde dehydrogenase B|-
STM3681_609_643	0.01	1.86	1255205|STM3681|putative transcriptional regulator|+
STM3682_1428_1462	0.12	-1.13	1255206|selB|selenocysteinyl-tRNA-specific translation factor|-

STM3683_1001_1035	0.13	-1.11	1255207|selA|selenocysteine synthase|-
STM3684_87_121	0.13	-1.15	1255208|yibF|predicted glutathione S-transferase|-
STM3685_1574_1608	0.01	-4.19	1255209|mtlA|mannitol-specific enzyme IIABC component|+
STM3686_694_728	0.00	-4.60	1255210|mtlD|mannitol-1-phosphate 5-dehydrogenase|+
STM3687_193_227	0.00	-4.38	1255211|mtlR|mannitol repressor protein|+
STM3688_33_67	0.04	1.81	1255212|STM3688|putative cytoplasmic protein|-
STM3689_141_175	0.01	2.10	1255213|yibL|hypothetical protein|+
STM3690_513_547	0.04	2.62	1255214|STM3690|putative inner membrane lipoprotein|+
STM3692_1009_1043	0.02	-2.02	1255216|lldP|L-lactate permease|+
STM3693_545_579	0.75	-1.16	1255217|lldR|DNA-binding transcriptional repressor|+
STM3694_592_626	0.01	-2.65	1255218|lldD|L-lactate dehydrogenase|+
STM3695_417_451	0.01	-1.44	1255219|yibK|putative tRNA/rRNA methyltransferase YibK|+
STM3696_70_104	0.98	-1.00	1255220|STM3696|putative transcriptional regulator|-
STM3697_838_872	0.18	1.18	1255221|STM3697|putative mandelate racemase|+
STM3698_888_922	0.27	1.33	1255222|STM3698|putative permease|+
STM3699_513_547	0.03	1.51	1255223|cysE|serine acetyltransferase|-
STM3700_533_567	0.00	-2.76	1255224|gpsA|NAD(P)H-dependent glycerol-3-phosphate dehydrogenase|-
STM3701_169_203	0.00	-2.30	1255225|secB|preprotein translocase subunit SecB|-
STM3702_129_163	0.02	-2.36	1255226|grxC|glutaredoxin 3|-
STM3703_25_59	0.02	-2.18	1255227|yibN|putative rhodanese-like sulfurtransferase|-
STM3704_826_860	0.00	1.41	1255228|pmgI|phosphoglyceromutase|+
STM3705_1082_1116	0.01	-1.65	1255229|yibP|hypothetical protein|+
STM3706_513_547	0.23	1.25	1255230|yigQ|putative periplasmic protein|+
STM3707_740_774	0.01	1.27	1255231|yibD|predicted glycosyl transferase|-
STM3708_59_93	0.02	1.50	1255232|tdh|L-threonine 3-dehydrogenase|-
STM3709_582_616	0.01	-2.33	1255233|kbl|2-amino-3-ketobutyrate coenzyme A ligase|-
STM3710_305_339	0.05	1.33	1255234|rfaD|ADP-L-glycero-D-mannoheptose-6-epimerase|+
STM3711_48_82	0.45	1.06	1255235|rfaF|ADP-heptose:LPS heptosyltransferase III|+
STM3712_817_851	0.14	1.21	1255236|rfaC|ADP-heptose:LPS heptosyl transferase II|+
STM3713_856_890	0.28	1.34	1255237|rfaL|O-antigen ligase|+
STM3714_947_981	0.02	2.23	1255238|rfaK|putative hexose transferase|-
STM3715_593_627	0.07	1.36	1255239|rfaZ|lipopolysaccharide core biosynthesis protein|-
STM3716_445_479	0.05	1.52	1255240|rfaY|lipopolysaccharide core biosynthesis protein|-
STM3717_784_818	0.06	1.64	1255241|rfaJ|lipopolysaccharide glucosyltransferase|-
STM3718_480_514	0.03	-1.60	1255242|rfaI|lipopolysaccharide-alpha-1 3-D-galactosyltransferase|-

STM3719_865_899	0.21	1.16	1255243|rfaB|UDP-D-galactose:(glucosyl)lipopolysaccharide-1 6-D-galactosyltransferase|-
STM3720_111_147	0.02	1.63	1255244|yibR|putative inner membrane protein|-
STM3721_649_683	0.05	1.60	1255245|rfaP|lipopolysaccharide core biosynthetic protein|-
STM3722_254_288	0.11	1.17	1255246|rfaG|glucosyltransferase II|-
STM3723_740_774	0.27	1.20	1255247|rfaQ|lipopolysaccharide core biosynthesis protein|-
STM3724_1175_1209	0.00	-1.32	1255248|kdtA|3-deoxy-D-manno-octulosonic-acid transferase|+
STM3725_433_467	0.02	-1.80	1255249|coaD|phosphopantetheine adenylyltransferase|+
STM3726_129_163	0.06	1.30	1255250|mutM|formamidopyrimidine-DNA glycosylase|-
STM3727_117_151	0.01	-2.37	1255251|rpmG|50S ribosomal protein L33|-
STM3728_113_147	0.01	-2.23	1255252|rpmB|50S ribosomal protein L28|-
STM3729_577_611	0.01	-1.77	1255253|radC|DNA repair protein RadC|-
STM3730_686_720	0.10	1.59	1255254|dfp|bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase|+
STM3731_145_179	0.17	-1.28	1255255|dut|deoxyuridine 5'-triphosphate nucleotidohydrolase|+
STM3732_161_195	0.05	2.36	1255256|slmA|nucleoid occlusion protein|+
STM3733_509_543	0.56	-1.07	1255257|pyrE|orotate phosphoribosyltransferase|-
STM3734_65_99	0.04	1.16	1255258|rph|ribonuclease PH|-
STM3735_177_211	0.04	1.54	1255259|yicC|hypothetical protein|+
STM3736_105_139	0.05	-1.31	1255260|STM3736|putative transcriptional regulator|-
STM3737_577_611	0.01	2.07	1255261|STM3737|putative Zn-dependent hydrolase|+
STM3738_393_427	0.94	-1.02	1255262|yigC|putative inner membrane protein|+
STM3739_1023_1057	0.00	-2.17	1255263|ligB|NAD-dependent DNA ligase LigB|-
STM3740_81_115	0.45	1.13	1255264|gmk|guanylate kinase|+
STM3741_225_259	0.21	-1.25	1255265|rpoZ|DNA-directed RNA polymerase subunit omega|+
STM3742_2073_2107	0.60	1.05	1255266|spoT|bifunctional (p)ppGpp synthetase II/ guanosine-3' 5'-bis pyrophosphate 3'-pyrophosphohydrolase|+
STM3743_513_547	0.40	-1.23	1255267|spoU|tRNA guanosine-2'-O-methyltransferase|+
STM3744_1979_2013	0.05	1.15	1255268|recG|ATP-dependent DNA helicase RecG|+
STM3745_273_307	0.96	-1.01	1255269|STM3745|putative cytoplasmic protein|-
STM3746_655_689	0.02	1.40	1255270|gltS|glutamate transport protein|-
STM3747_993_1027	0.01	-3.32	1255271|yicE|putative purine/xanthine transport protein|+
STM3748_919_953	0.01	1.48	1255272|yicH|putative inner membrane protein|+
STM3749_2104_2138	0.36	1.08	1255273|yicI|alpha-xylosidase YicI|-
STM3750_992_1026	0.29	1.09	1255274|yicJ|putative transporter|-
STM3752_305_340	0.01	1.45	1255276|STM3752|putative cytoplasmic protein|-

STM3753_512_546	0.18	1.09	1255277|sugR|ATP binding protein|+
STM3754_257_291	0.03	1.32	1255278|STM3754|putative cytoplasmic protein|+
STM3755_871_905	0.02	1.72	1255279|rhuM|putative cytoplasmic protein|+
STM3755.1N_80_115	0.01	1.55	2673725|STM3755.1N|-|-
STM3757_2349_2383	0.44	-1.11	1255281|misL|putative autotransporter|+
STM3758_305_339	0.04	1.45	1255282|fidL|putative inner membrane protein|-
STM3759.S_705_739	0.01	2.72	1255283|marT|putative transcriptional regulator|-
STM3760_65_99	0.24	1.34	1255284|STM3760|-|-
STM3761_417_451	0.01	3.86	1255285|slsA|putative inner membrane protein|+
STM3762_193_227	0.02	1.83	1255286|cigR|putative inner membrane protein|-
STM3763_2000_2034	0.33	1.16	1255287|mgtB|Mg2+ transporter|-
STM3764_577_611	0.31	1.31	1255288|mgtC|Mg2+ transport protein|-
STM3765_337_371	0.01	2.28	1255289|yicL|putative permease|+
STM3766_561_595	0.20	-1.20	1255290|STM3766|putative cytoplasmic protein|-
STM3767_657_691	0.07	-1.09	1255291|STM3767|putative cytoplasmic protein|-
STM3768_655_689	0.35	1.18	1255292|STM3768|putative selenocysteine synthase|-
STM3769.S_321_355	0.90	-1.03	1255293|STM3769.S|putative phosphotransferase system enzyme III|-
STM3770_641_675	0.05	1.24	1255294|STM3770|putative phosphotransferase system enzyme IIC|-
STM3771_81_115	0.15	1.21	1255295|STM3771|putative phosphotransferase system enzyme IIB|-
STM3772_385_419	0.12	1.19	1255296|STM3772|putative phosphotransferase system enzyme IIA|-
STM3773_2376_2410	0.01	-1.57	1255297|STM3773|putative transcriptional regulator|-
STM3774_229_263	0.15	1.32	1255298|STM3774|putative inner membrane protein|+
STM3775_640_674	0.02	-1.94	1255299|STM3775|putative glycosyl hydrolase|+
STM3776_723_757	0.10	-1.29	1255300|nepI|ribonucleoside transporter|-
STM3777_273_307	0.02	2.75	1255301|STM3777|putative cytoplasmic protein|+
STM3778_193_227	0.01	1.61	1255302|STM3778|putative DNA-binding protein|+
STM3779_16_50	0.28	1.36	1255303|STM3779|putative phosphotransferase system HPr protein|-
STM3780_549_583	0.52	1.08	1255304|gatY|putative fructose-1 6-bisphosphate aldolase|-
STM3781_694_728	0.11	1.36	1255305|STM3781|putative sugar kinase|-
STM3782_1096_1130	0.03	-1.49	1255306|STM3782|putative PTS system galactitol-specific enzyme IIC component|-
STM3783_185_219	0.04	2.15	1255307|STM3783|putative periplasmic protein|-
STM3784_209_243	0.01	-2.25	1255308|STM3784|putative phosphotransferase system mannitol/fructose-specific IIA domain|-
STM3785_17_52	0.01	-1.38	1255309|STM3785|putative regulatory protein|-
STM3786_175_209	0.00	-2.32	1255310|yicN|putative inner membrane protein|-

STM3787_593_627	0.09	1.34	1255311|uhpT|sugar phosphate antiporter|-
STM3788_854_888	0.03	1.33	1255312|uhpC|regulatory protein UhpC|-
STM3789_744_778	0.44	1.13	1255313|uhpB|sensory histidine kinase UhpB|-
STM3790_137_171	0.78	-1.05	1255314|uhpA|DNA-binding response regulator in two-component regulatory system wtih UhpB|-
STM3791_175_209	0.04	-1.93	1255315|STM3791|putative cytoplasmic protein|-
STM3794_161_195	0.48	1.07	1255318|STM3794|putative regulatory protein|+
STM3795_89_123	0.07	-1.72	1255319|ilvN|acetolactate synthase 1 regulatory subunit|-
STM3796_962_996	0.02	-1.91	1255320|ilvB|acetolactate synthase catalytic subunit|-
STM3797_9_43	0.52	-1.42	1255321|ivbL|ilvB operon leader peptide|-
STM3797A_3_37	0.49	1.22	1255322|lysdA|-|+
STM3796B_20_55	0.12	1.67	1255323|lysdB|-|+
STM3798_378_412	0.02	1.61	1255325|emrD|multidrug resistance protein D|+
STM3799_279_313	0.01	1.70	1255326|STM3799|putative periplasmic protein|-
STM3800_17_51	0.67	1.06	1255327|dsdC|DNA-binding transcriptional dual regulator|-
STM3801_851_885	0.37	1.09	1255328|dsdX|DsdX permease|+
STM3802_516_550	0.04	2.22	1255329|dsdA|D-serine dehydratase|+
STM3803_97_131	0.00	-4.73	1255330|yidF|putative cytoplasmic protein|-
STM3804_148_182	0.27	-1.12	1255331|yidG|putative inner membrane protein|-
STM3805_257_291	0.25	1.13	1255332|yidH|putative inner membrane protein|-
STM3806_16_50	0.03	1.93	1255333|STM3806|pseudo|+
STM3807_1575_1609	0.18	1.16	1255334|yidE|hypothetical protein|-
STM3808.S_137_171	0.18	1.46	1255335|ibpB|heat shock chaperone IbpB|-
STM3809.S_257_291	0.04	1.90	1255336|ibpA|heat shock protein IbpA|-
STM3810_121_155	0.00	-2.53	1255337|yidQ|hypothetical protein|+
STM3811_804_838	0.05	1.31	1255338|yidR|putative cytoplasmic protein|-
STM3812_882_916	0.31	1.10	1255339|ccmH|putative heme lyase subunit|-
STM3820_690_724	0.05	2.68	1255347|STM3820|putative cytochrome c peroxidase|-
STM3821_383_417	0.10	1.55	1255348|torD|chaperone protein TorD|-
STM3822_2066_2100	0.33	-1.20	1255349|torA|trimethylamine N-oxide reductase subunit|-
STM3823_970_1004	0.90	1.08	1255350|torC|trimethylamine N-oxide reductase cytochrome c-like subunit|-
STM3824_569_603	0.13	-1.09	1255351|torR|DNA-binding response regulator in two-component regulatory system with TorS|+
STM3825_570_604	0.20	-1.12	1255352|torT|periplasmic sensory protein associated with the TorRS two-component regulatory system|-
STM3827_1043_1077	0.17	-1.30	1255354|dgoT|D-galactonate transport protein|-

STM3828_446_480	0.02	-1.72	1255355|dgoA|2-oxo-3-deoxygalactonate 6-phosphate aldolase/galactonate dehydratase|-
STM3828.1N_734_768	0.04	-1.33	2673742|STM3828.1N|-|-
STM3829_113_147	0.80	1.02	1255356|dgoK|2-oxo-3-deoxygalactonate kinase|-
STM3830_385_419	0.03	-1.59	1255357|dgoR|galactonate operon transcriptional repressor|-
STM3831_353_387	0.09	1.24	1255358|yidA|predicted hydrolase|-
STM3832_680_714	0.01	1.38	1255359|STM3832|putative permease|+
STM3833_931_965	0.07	1.36	1255360|STM3833|putative mandelate racemase|+
STM3834_485_519	0.04	2.70	1255361|STM3834|putative transcriptional regulator|+
STM3835_2056_2090	0.39	-1.14	1255362|gyrB|DNA gyrase subunit B|-
STM3837_1062_1096	0.01	-2.23	1255364|dnaN|DNA polymerase III subunit beta|-
STM3838_658_692	0.27	1.21	1255365|dnaA|chromosomal replication initiation protein|-
STM3839_13_47	0.01	-3.04	1255366|rpmH|50S ribosomal protein L34|+
STM3840_177_211	0.05	-1.58	1255367|rnpA|ribonuclease P|+
STM3842_1128_1162	0.00	-2.21	1255369|yidC|putative inner membrane protein translocase component YidC|+
STM3843_1006_1040	0.04	1.12	1255370|trmE|tRNA modification GTPase TrmE|+
STM3844_478_512	0.31	1.14	1255371|STM3844|pseudo|+
STM3845_369_403	0.01	2.33	1255372|STM3845|putative inner membrane protein|+
STM3847_477_511	0.00	1.38	1255374|yidY|multidrug efflux system protein MdtL|+
STM3848_521_555	0.09	1.23	1255375|yidZ|DNA-binding transcriptional regulator YidZ|+
STM3849_561_595	0.43	1.23	1255376|yieE|putative cytoplasmic protein|+
STM3850_489_523	0.13	-1.23	1255377|yieF|putative oxidoreductase|+
STM3851.S_1147_1181	0.05	-1.27	1255378|yieG|hypothetical protein|-
STM3852_97_131	0.00	-2.16	1255379|yieH|predicted hydrolase|+
STM3853_53_87	0.05	-1.48	1255380|phoU|transcriptional regulator PhoU|-
STM3854_673_707	0.02	-1.51	1255381|pstB|phosphate transporter subunit|-
STM3855_73_107	0.11	-1.27	1255382|pstA|phosphate transporter permease subunit|-
STM3856_897_931	0.03	-1.39	1255383|pstC|phosphate transporter permease subunit|-
STM3857_634_668	0.11	-1.34	1255384|pstS|phosphate transporter subunit|-
STM3858_923_957	0.63	1.02	1255385|STM3858|putative phosphotransferase system fructose-specific component IIB|-
STM3859_481_515	0.48	1.12	1255386|aroE|shikimate 5-dehydrogenase|-
STM3860_999_1033	0.11	1.25	1255387|STM3860|putative dipeptide/oligopeptide/nickel ABC-type transport system periplasmic component|+
STM3861_895_929	0.14	-1.11	1255388|glmS|D-fructose-6-phosphate amidotransferase|-

STM3862_1268_1302	0.02	1.69	1255389|glmU|bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase|-
STM3863_177_211	0.11	1.29	1255390|STM3863|putative permease|-
STM3864_129_163	0.11	-1.31	1255391|atpC|F0F1 ATP synthase subunit epsilon|-
STM3865_480_514	0.22	-1.33	1255392|atpD|F0F1 ATP synthase subunit beta|-
STM3866_641_675	0.01	-1.83	1255393|atpG|F0F1 ATP synthase subunit gamma|-
STM3867_1343_1377	0.20	-1.34	1255394|atpA|F0F1 ATP synthase subunit alpha|-
STM3868_321_355	0.07	-1.27	1255395|atpH|F0F1 ATP synthase subunit delta|-
STM3869_57_91	0.51	1.07	1255396|atpF|F0F1 ATP synthase subunit B|-
STM3870_177_211	0.07	-1.38	1255397|atpE|F0F1 ATP synthase subunit C|-
STM3871_769_803	0.01	-1.68	1255398|atpB|F0F1 ATP synthase subunit A|-
STM3872_9_43	0.04	-1.43	1255399|atpI|F0F1 ATP synthase subunit I|-
STM3873.S_65_99	0.01	-1.68	1255400|gidB|glucose-inhibited division protein B|-
STM3874_1275_1309	0.02	-1.73	1255401|gidA|tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA|-
STM3875_105_139	0.01	-2.21	1255402|mioC|flavodoxin|-
STM3876_337_371	0.04	1.41	1255403|asnC|DNA-binding transcriptional regulator AsnC|-
STM3877_745_779	0.02	1.73	1255404|asnA|asparagine synthetase AsnA|+
STM3878.S_1381_1415	0.13	-1.22	1255405|yieM|hypothetical protein|-
STM3879_538_572	0.01	1.98	1255406|yieN|putative regulatory protein|-
STM3880_1510_1544	0.01	-1.51	1255407|trkD|potassium transport protein Kup|+
STM3881_225_259	0.98	1.01	1255408|rbsD|high-affinity D-ribose transport protein|+
STM3882_763_797	0.00	-2.10	1255409|rbsA|D-ribose transporter ATP binding protein|+
STM3883_561_595	0.02	-2.11	1255410|rbsC|ribose ABC transporter permease protein|+
STM3884_361_395	0.04	-1.47	1255411|rbsB|D-ribose transporter subunit RbsB|+
STM3885_193_227	0.01	-3.96	1255412|rbsK|ribokinase|+
STM3886_161_195	0.01	-1.62	1255413|rbsR|transcriptional repressor RbsR|+
STM3887_1197_1231	0.41	-1.09	1255414|yieO|putative tranport protein|-
STM3888_481_515	0.20	1.13	1255415|yieP|putative regulatory protein|-
STM3893_11_48	0.02	-2.09	1255419|9S|misc_RNA|+
STM3896_6_40	0.02	-2.23	1255422|trpT|tRNA|+
STM3897_97_131	0.01	1.18	1255423|yifA|transcriptional regulator HdfR|-
STM3898_97_131	0.01	-2.29	1255424|yifE|hypothetical protein|+
STM3899_522_556	0.03	1.36	1255425|yifB|putative ATP-dependent protease|-
STM3900_9_43	0.88	-1.10	1255426|ilvL|ilvG operon leader peptide|+
STM3901_776_810	0.00	-13.21	1255427|ilvG|acetolactate synthase 2 catalytic subunit|+

STM3902_9_43	0.00	-11.02	1255428|ilvM|acetolactate synthase 2 regulatory subunit|+
STM3903_833_867	0.00	-9.87	1255429|ilvE|branched-chain amino acid aminotransferase|+
STM3904_1236_1270	0.00	-13.51	1255430|ilvD|dihydroxy-acid dehydratase|+
STM3905_1202_1236	0.00	-13.42	1255431|ilvA|threonine dehydratase|+
STM3906_33_67	0.31	-1.18	1255432|STM3906|putative cytoplasmic protein|+
STM3907_13_47	0.03	-1.33	1255433|STM3907|putative cytoplasmic protein|+
STM3908_609_643	0.03	2.52	1255434|ilvY|DNA-binding transcriptional regulator IlvY|-
STM3910_165_199	0.13	1.22	1255436|ppiC|peptidyl-prolyl cis-trans isomerase C|-
STM3911_89_123	0.01	1.51	1255437|STM3911|putative inner membrane protein|+
STM3912_1330_1364	0.03	-1.55	1255438|rep|ATP-dependent DNA helicase Rep|+
STM3913_1059_1093	0.26	1.21	1255439|gppA|guanosine pentaphosphate phosphohydrolase|-
STM3914_1099_1133	0.03	-1.22	1255440|rhlB|ATP-dependent RNA helicase RhlB|-
STM3915_205_239	0.63	1.09	1255441|trxA|thioredoxin|+
STM3916_3_37	0.12	1.61	1255442|rhoL|pseudo|+
STM3917_421_455	0.92	1.02	1255443|rho|transcription termination factor Rho|+
STM3918_649_683	0.96	1.00	1255444|rfe|undecaprenyl-phosphate N-acetylglucosaminyltransferase|+
STM3919_368_402	0.05	-1.26	1255445|wzzE|lipopolysaccharide biosynthesis protein WzzE|+
STM3920_708_742	0.10	1.20	1255446|wecB|UDP-N-acetyl glucosamine-2-epimerase|+
STM3921_984_1018	0.09	1.23	1255447|wecC|UDP-N-acetyl-D-mannosamine dehydrogenase|+
STM3922_389_423	0.23	1.09	1255448|rffG|dTDP-glucose 4 6-dehydratase|+
STM3923_177_211	0.01	1.61	1255449|rffH|glucose-1-phosphate thymidyl transferase|+
STM3924_473_507	0.34	1.42	1255450|wecD|TDP-fucosamine acetyltransferase|+
STM3925_420_454	0.09	1.18	1255451|wecE|TDP-4-oxo-6-deoxy-D-glucose transaminase|+
STM3926_556_590	0.60	1.10	1255452|wzxE|O-antigen translocase|+
STM3927_929_963	0.28	1.08	1255453|STM3927|4-alpha-L-fucosyltransferase|+
STM3928_1288_1322	0.23	1.35	1255454|wecF|putative enterobacterial common antigen polymerase|+
STM3929_65_99	0.02	1.41	1255455|wecG|putative UDP-N-acetyl-D-mannosaminuronic acid transferase|+
STM3930_1203_1237	0.27	-1.28	1255456|yifK|putative transport protein YifK|+
STM3931_33_67	0.85	1.16	1255457|argX|tRNA|+
STM3935_841_875	0.19	-1.21	1255461|hemY|putative protoheme IX biogenesis protein|-
STM3936_659_693	0.68	-1.05	1255462|hemX|putative uroporphyrinogen III C-methyltransferase|-
STM3937_321_355	0.01	-1.44	1255463|hemD|uroporphyrinogen-III synthase|-
STM3938_241_275	0.03	-1.58	1255464|hemC|porphobilinogen deaminase|-
STM3939_1964_1998	0.00	3.19	1255465|cyaA|adenylate cyclase|+
STM3940_313_347	0.60	1.05	1255466|STM3940|putative inner membrane protein|+
STM3941_297_331	0.96	-1.00	1255467|STM3941|putative inner membrane protein|+

STM3942_315_349	0.76	1.01	1255468|STM3942|putative cytoplasmic protein|+
STM3943_141_175	0.07	1.53	1255469|cyaY|frataxin-like protein|-
STM3944_305_339	0.29	1.39	1255470|STM3944|putative inner membrane protein|-
STM3945_145_179	0.04	1.70	1255471|STM3945|pseudo|-
STM3946_9_45	0.02	1.69	1255472|yifL|putative outer membrane lipoprotein|+
STM3947_769_803	0.48	-1.08	1255473|dapF|diaminopimelate epimerase|+
STM3948_409_443	0.86	-1.02	1255474|yigA|hypothetical protein|+
STM3949_97_131	0.02	1.26	1255475|xerC|site-specific tyrosine recombinase XerC|+
STM3950_65_99	0.02	-1.28	1255476|yigB|predicted hydrolase|+
STM3951_1836_1870	0.06	1.43	1255477|uvrD|DNA-dependent helicase II|+
STM3952_273_307	0.51	1.09	1255478|corA|magnesium/nickel/cobalt transporter CorA|+
STM3953_273_307	0.01	1.79	1255479|yigF|putative inner membrane protein|-
STM3955_577_611	0.14	1.14	1255481|rarD|chloramphenicol resistance|-
STM3956_49_83	0.00	-3.44	1255482|yigI|hypothetical protein|-
STM3957_769_803	0.00	-1.68	1255483|pldA|phospholipase A|+
STM3958_1361_1395	0.08	-1.29	1255484|recQ|ATP-dependent DNA helicase RecQ|+
STM3959_533_567	0.03	-1.41	1255485|rhtC|threonine efflux system|+
STM3960_65_99	0.08	-1.27	1255486|rhtB|homoserine/homoserine lactone efflux protein|-
STM3961_482_516	0.13	1.16	1255487|pldB|lysophospholipase L2|+
STM3962_129_163	0.07	1.08	1255488|yigL|predicted hydrolase|+
STM3963_273_307	0.22	1.21	1255489|yigM|putative transport protein|+
STM3964_529_563	0.01	11.23	1255490|metR|metE/metH regulator|-
STM3965_1930_1964	0.26	1.81	1255491|metE|5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase|+
STM3966_521_555	0.40	-1.11	1255492|STM3966|putative arylsulfatase regulator|+
STM3967_705_739	0.03	-1.33	1255493|dlhH|putative dienelactone hydrolase|-
STM3968_481_515	1.00	1.00	1255494|udp|uridine phosphorylase|+
STM3969_1152_1186	0.04	1.86	1255495|yigN|DNA recombination protein RmuC|+
STM3970_321_355	0.30	1.17	1255496|ubiE|ubiquinone/menaquinone biosynthesis methyltransferase|+
STM3971_193_227	0.10	-1.23	1255497|yigP|putative inner membrane protein|+
STM3972_1122_1156	0.10	1.33	1255498|ubiB|putative ubiquinone biosynthesis protein UbiB|+
STM3973_29_63	0.09	1.19	1255499|tatA|twin arginine translocase protein A|+
STM3974_433_467	0.03	1.49	1255500|tatB|sec-independent translocase|+
STM3975_297_331	0.22	1.20	1255501|tatC|TatABCE protein translocation system subunit|+
STM3977_289_323	0.28	1.18	1255503|rfaH|transcriptional activator RfaH|-
STM3978_1232_1266	0.00	-1.44	1255504|yigC|3-octaprenyl-4-hydroxybenzoate decarboxylase|+

STM3979_529_563	0.04	-1.38	1255505|frel|FMN reductase|+
STM3980_193_227	0.01	2.73	1255506|STM3980|putative outer membrane protein|+
STM3981_60_94	0.03	2.02	1255507|STM3981|putative cytoplasmic protein|+
STM3982_287_321	0.00	-12.42	1255508|fadA|3-ketoacyl-CoA thiolase|-
STM3983_1447_1481	0.03	-2.05	1255509|fadB|multifunctional fatty acid oxidation complex subunit alpha|-
STM3984_1005_1039	0.03	-1.48	1255510|pepQ|proline dipeptidase|+
STM3985_289_323	0.02	-1.77	1255511|yigZ|hypothetical protein|+
STM3986_869_903	0.19	-1.40	1255512|trkH|potassium transporter|+
STM3987_153_187	0.06	-1.21	1255513|hemG|protoporphyrinogen oxidase|+
STM3989/STM4133_4_38	0.03	-1.58	1255515/1255659|ileT/ileU|tRNA|+
STM3993_417_451	0.04	2.14	1255519|mobB|molybdopterin-guanine dinucleotide biosynthesis protein B|-
STM3994_129_163	0.04	1.33	1255520|mobA|molybdopterin-guanine dinucleotide biosynthesis protein A|-
STM3995_97_131	0.94	1.02	1255521|yihD|putative cytoplasmic protein|+
STM3996_641_675	0.04	1.59	1255522|yihE|predicted kinase|+
STM3997_353_387	0.01	2.42	1255523|dsbA|periplasmic protein disulfide isomerase II|+
STM3998_193_227	0.08	2.88	1255524|yihG|putative endonuclease|-
STM3999_2300_2334	0.29	-1.06	1255525|polA|DNA polymerase I|+
STM4000_27_65	0.05	4.19	2673732|spf|misc_RNA|+
STM4001_465_499	0.12	1.19	1255527|yihA|GTPase EngB|-
STM4002_48_82	0.80	-1.09	1255528|STM4002|putative cytoplasmic protein|+
STM4003_289_323	0.06	-1.63	1255529|yihI|hypothetical protein|+
STM4004_1079_1113	0.19	1.19	1255530|hemN|coproporphyrinogen III oxidase|+
STM4005_475_509	0.29	-1.10	1255531|glnG|nitrogen regulation protein NR(I)|-
STM4006_307_341	0.02	2.68	1255532|glnL|nitrogen regulation protein NR(II)|-
STM4007_475_509	0.04	1.85	1255533|glnA|glutamine synthetase|-
STM4009_1145_1179	0.94	1.04	1255535|typA|GTP-binding protein|+
STM4010_129_163	0.17	1.42	1255536|STM4010|putative hydrolase|-
STM4011_833_867	0.08	1.66	1255537|STM4011|putative inner membrane protein|-
STM4013.S_737_771	0.24	1.37	1255539|STM4013.S|putative membrane-associated metal-dependent hydrolase|-
STM4014_289_323	0.63	-1.06	1255540|STM4014|putative periplasmic protein|-
STM4015_625_659	0.01	1.52	1255541|STM4015|putative cytoplasmic protein|-
STM4016_307_341	1.00	-1.00	1255542|yshA|predicted outer membrane porin L|-
STM4017_1095_1129	0.10	1.59	1255543|yihO|putative GPH family transport protein|-
STM4018_1120_1154	0.01	1.63	1255544|yihP|putative GPH family transport protein|-
STM4020.S_353_387	0.11	1.19	1255546|yihR|putative aldose-1-epimerase|-

STM4021_979_1013	0.91	-1.09	1255547|yihS|putative isomerase|-
STM4022_801_835	0.71	-1.03	1255548|yihT|putative aldolase|-
STM4023_257_291	0.16	-1.29	1255549|yihU|putative oxidoreductase|-
STM4024.S_33_67	0.37	-1.16	1255550|yihV|putative sugar kinase|+
STM4025_33_67	0.02	-1.57	1255551|yihW|putative glycerol-3-phosphate regulon repressor|+
STM4026_257_291	0.01	1.72	1255552|yihX|phosphatase|+
STM4027_593_627	0.18	1.14	1255553|rbn|ribonuclease BN|+
STM4028_2_36	0.10	1.72	1255554|yihZ|D-tyrosyl-tRNA deacylase|+
STM4029_929_963	0.41	-1.10	1255555|yiiD|putative acetyltransferase|+
STM4030.S_253_287	0.03	2.25	1255556|STM4030.S|putative cytoplasmic protein|-
STM4031_257_291	0.00	2.32	1255557|STM4031|putative cytoplasmic protein|-
STM4032_257_291	0.07	1.14	1255558|STM4032|putative acetyl esterase|-
STM4032.2N_97_131	0.48	1.21	2673731|STM4032.2N|hypothetical protein|+
STM4033_161_195	0.23	-1.21	1255559|STM4033|putative regulatory protein|+
STM4034_321_355	0.35	1.11	1255560|fdhE|formate dehydrogenase accessory protein FdhE|-
STM4035_421_455	0.87	-1.03	1255561|fdoI|formate dehydrogenase-O subunit gamma|-
STM4036_681_715	0.04	-1.25	1255562|fdoH|formate dehydrogenase-O beta subunit|-
STM4037_2884_2918	0.07	1.86	1255563|fdoG|formate dehydrogenase alpha subunit|-
STM4038_425_459	0.01	1.92	1255564|fdhD|formate dehydrogenase accessory protein|+
STM4039_929_963	0.33	1.26	1255565|STM4039|putative inner membrane lipoprotein|-
STM4040_548_582	0.45	1.06	1255566|yiiG|putative cytoplasmic protein|+
STM4041_249_283	0.05	1.54	1255567|STM4041|putative inner membrane protein|-
STM4042_493_527	0.02	1.95	1255568|STM4042|putative branched-chain amino acid permease|-
STM4042A_105_139	0.00	2.93	1255569|STM4042A|hypothetical protein|+
STM4043_49_83	0.01	-2.60	1255570|yiiL|putative cytoplasmic protein|-
STM4044_438_472	0.00	-5.55	1255571|STM4044|putative alcohol dehydrogenase|-
STM4046_709_743	0.53	1.19	1255573|rhaA|L-rhamnose isomerase|-
STM4047_983_1017	0.70	1.08	1255574|rhaB|rhamnulokinase|-
STM4048_449_483	0.24	-1.06	1255575|rhaS|L-rhamnose operon regulatory protein|+
STM4049_289_323	0.01	-2.58	1255576|rhaR|rhaRS operon regulatory protein|+
STM4050_740_774	0.80	-1.12	1255577|rhaT|L-rhamnose/H+ symporter protein|-
STM4052_741_775	0.02	-1.17	1255579|STM4052|putative C4-dicarboxylate transport system|-
STM4053_209_243	0.01	1.49	1255580|STM4053|putative C4-dicarboxylate transport system|-
STM4054_321_355	0.51	1.25	1255581|STM4054|putative periplasmic dicarboxylate-binding protein|-
STM4055_49_83	0.11	-1.13	1255582|sodA|superoxide dismutase|+
STM4056.S_545_579	0.03	-1.83	1255583|yiiM|hypothetical protein|+

STM4057_327_361	0.02	-1.06	1255584|STM4057|putative inner membrane protein|+
STM4058_1079_1113	0.25	1.15	1255585|cpxA|two-component sensor protein|-
STM4059_399_433	0.12	1.55	1255586|cpxR|DNA-binding response regulator in two-component regulatory system with CpxA|-
STM4060_137_171	0.00	13.88	1255587|cpxP|periplasmic repressor CpxP|+
STM4061_385_419	0.04	1.28	1255588|fieF|ferrous iron efflux protein F|+
STM4062_129_163	0.06	1.37	1255589|pfkA|6-phosphofructokinase|+
STM4063_769_803	0.76	1.29	1255590|sbp|sulfate transporter subunit|+
STM4064_161_195	0.13	1.60	1255591|ushB|CDP-diacylglycerol pyrophosphatase|+
STM4066_625_659	0.14	-1.62	1255593|STM4066|aminoimidazole riboside kinase|+
STM4067_778_812	0.14	-1.12	1255594|STM4067|putative ADP-ribosylglycohydrolase|+
STM4068_161_195	0.14	1.30	1255595|STM4068|putative regulatory protein|+
STM4069_33_67	0.13	1.42	1255596|STM4069|putative periplasmic protein|+
STM4070_53_87	0.75	-1.05	1255597|STM4070|putative cytoplasmic protein|+
STM4071_25_59	0.05	-12.37	1255598|STM4071|putative mannose-6-phosphate isomerase|-
STM4072_1330_1364	0.15	-4.36	1255599|lydeV|autoinducer-2 (AI-2) kinase|-
STM4074_1257_1291	0.06	-8.53	1255601|lego|putative ABC-type aldose transport system ATPase component|+
STM4075_333_367	0.06	-9.36	1255602|lydeY|putative sugar transport protein|+
STM4076_139_173	0.15	-4.14	1255603|lydeZ|putative sugar transport protein|+
STM4078_289_323	0.02	-22.30	1255605|lyneB|aldolase|+
STM4079.S_97_131	0.19	-3.71	1255606|lyneC|autoinducer-2 (AI-2) modifying protein LsrG|+
STM4080_673_707	0.03	-11.48	1255607|STM4080|ribulose-phosphate 3-epimerase|+
STM4081_193_227	0.10	1.28	1255608|tpiA|triosephosphate isomerase|-
STM4082_457_491	0.40	-1.15	1255609|yiiQ|putative periplasmic protein|-
STM4083_333_367	0.36	1.12	1255610|yiiR|putative inner membrane protein|+
STM4084_37_71	0.01	1.73	1255611|fpr|ferredoxin-NADP reductase|-
STM4085_940_974	0.04	-2.05	1255612|glpX|fructose 1 6-bisphosphatase III|-
STM4086_678_712	0.00	-51.35	1255613|glpK|glycerol kinase|-
STM4087_545_579	0.00	-32.58	1255614|glpF|glycerol diffusion|-
STM4088_199_233	0.07	-1.33	1255615|yiiU|putative cytoplasmic protein|+
STM4089_441_475	0.00	3.21	1255616|menG|ribonuclease activity regulator protein RraA|-
STM4090_289_323	0.26	1.15	1255617|menA|1 4-dihydroxy-2-naphthoate octaprenyltransferase|-
STM4091_365_399	0.08	1.38	1255618|hslU|ATP-dependent protease ATP-binding subunit|-
STM4092_233_267	0.05	1.77	1255619|hslV|ATP-dependent protease peptidase subunit|-
STM4093_897_931	0.02	1.37	1255620|ftsN|essential cell division protein|-
STM4094_603_637	0.92	1.02	1255621|cytR|DNA-binding transcriptional regulator CytR|-

STM4095_1912_1946	0.70	-1.06	1255622|priA|primosome assembly protein PriA|-
STM4096_127_161	0.17	1.33	1255623|rpmE|50S ribosomal protein L31|+
STM4097_321_355	0.08	1.79	1255624|STM4097|putative outer membrane lipoprotein|-
STM4098_1144_1178	0.07	1.92	1255625|STM4098|putative arylsulfate sulfotransferase|-
STM4099_205_239	0.01	3.02	1255626|metJ|transcriptional repressor protein MetJ|-
STM4100_290_324	0.02	10.64	1255627|metB|cystathionine gamma-synthase|+
STM4101_1658_1692	0.02	4.25	1255628|metL|bifunctional aspartate kinase II/homoserine dehydrogenase III|+
STM4102_245_279	0.01	2.09	1255629|STM4102|putative inner membrane protein|-
STM4103_926_960	0.01	-2.88	1255630|STM4103|putative cytoplasmic protein|-
STM4104_1198_1232	0.18	1.28	1255631|STM4104|putative 5'-nucleotidase/2' 3'-cyclic phosphodiesterase|+
STM4105_385_419	0.01	6.11	1255632|metF|5 10-methylenetetrahydrofolate reductase|+
STM4106_1726_1760	0.01	-3.63	1255633|katG|hydroperoxidase|+
STM4107_65_99	0.16	1.65	1255634|yijF|putative periplasmic protein|-
STM4108_605_639	0.98	-1.01	1255635|gldA|glycerol dehydrogenase|-
STM4109_577_611	0.01	1.69	1255636|talC|fructose-6-phosphate aldolase|-
STM4110_1631_1665	0.01	-2.13	1255637|ptsA|PEP-protein phosphotransferase|-
STM4112_363_397	0.03	1.24	1255639|frwC|PTS system fructose-like IIC component|+
STM4113_193_227	0.12	-1.32	1255640|frwB|PTS system fructose-like IIB component 1|+
STM4114_2003_2037	0.07	1.27	1255641|pflD|predicted formate acetyltransferase 2 (pyruvate formate lyase II)|+
STM4115_161_195	0.12	1.44	1255642|pflC|pyruvate formate lyase II activase|+
STM4116_177_211	0.09	1.20	1255643|frwD|PTS system fructose-like IIB component 2|+
STM4117_417_451	0.40	-1.10	1255644|yijO|putative regulatory protein|-
STM4119_2517_2551	0.42	1.23	1255646|ppc|phosphoenolpyruvate carboxylase|-
STM4120_793_827	0.01	2.49	1255647|argE|acetylornithine deacetylase|-
STM4122_321_355	0.46	1.14	1255649|argB|acetylglutamate kinase|+
STM4123_1154_1188	0.04	1.54	1255650|argH|argininosuccinate lyase|+
STM4125_321_355	0.11	1.35	1255651|oxyR|DNA-binding transcriptional regulator OxyR|+
STM4126_1330_1364	0.00	-2.04	1255652|udhA|soluble pyridine nucleotide transhydrogenase|-
STM4127_401_435	0.02	1.42	1255653|yijC|DNA-binding transcriptional repressor FabR|+
STM4128_97_131	0.20	1.29	1255654|yijD|hypothetical protein|+
STM4129_102_136	0.04	-1.26	1255655|trmA|tRNA (uracil-5-)-methyltransferase|-
STM4130_1486_1520	0.02	-1.76	1255656|btuB|vitamin B12/cobalamin outer membrane transporter|+
STM4131_449_483	0.01	1.58	1255657|murI|glutamate racemase|+
STM4137_862_896	0.02	1.70	1255663|murB|UDP-N-acetylenolpyruvoylglucosamine reductase|+
STM4138_513_547	0.05	1.14	1255664|birA|biotin--protein ligase|+

STM4139_609_643	0.83	-1.05	1255665|coaA|pantothenate kinase|-
STM4140_65_100	0.65	1.20	1255666|STM4140|pseudo|-
STM4141_117_151	0.59	-1.04	1255667|STM4141|putative cytoplasmic protein|-
STM4146_980_1014	0.01	-2.78	1255672|tuf|elongation factor Tu|+
STM4147_225_259	0.06	-1.25	1255673|secE|preprotein translocase subunit SecE|+
STM4148_193_227	0.01	-1.76	1255674|nusG|transcription antitermination protein NusG|+
STM4149_385_419	0.01	-3.39	1255675|rplK|50S ribosomal protein L11|+
STM4150_137_171	0.01	-4.70	1255676|rplA|50S ribosomal protein L1|+
STM4151_225_259	0.01	-2.25	1255677|rplJ|50S ribosomal protein L10|+
STM4153_3350_3384	0.05	-2.26	1255679|rpoB|DNA-directed RNA polymerase subunit beta|+
STM4154_3225_3259	0.01	-3.86	1255680|rpoC|DNA-directed RNA polymerase subunit beta'|+
STM4155_3_37	0.01	-1.89	1255681|STM4155|putative inner membrane protein|+
STM4156_127_164	0.01	2.38	1255682|STM4156|putative cytoplasmic protein|-
STM4157_780_814	0.89	-1.02	1255683|STM4157|putative cytoplasmic protein|+
STM4157.1N_55_89	0.28	1.96	2673736|STM4157.1N|-|-
STM4158_93_127	0.01	3.28	1255684|STM4158|putative cytoplasmic protein|+
STM4159_647_681	0.15	-1.64	1255685|thiH|thiamine biosynthesis protein ThiH|-
STM4160_122_156	0.05	-2.12	1255686|thiG|thiazole synthase|-
STM4162_353_387	0.06	-1.80	1255688|thiF|thiamine biosynthesis protein ThiF|-
STM4163_193_227	0.04	-2.35	1255689|thiE|thiamine-phosphate pyrophosphorylase|-
STM4164_1313_1347	0.98	1.01	1255690|thiC|thiamine biosynthesis protein ThiC|-
STM4165_81_115	0.06	-1.48	1255691|rsd|anti-RNA polymerase sigma 70 factor|-
STM4166_737_771	0.02	1.69	1255692|nudC|NADH pyrophosphatase|+
STM4167_402_436	0.03	1.32	1255693|hemE|uroporphyrinogen decarboxylase|+
STM4168_161_195	0.02	1.23	1255694|nfi|endonuclease V|+
STM4169_481_515	0.10	1.52	1255695|yjaG|putative cytoplasmic protein|+
STM4170_113_147	0.01	-1.80	1255696|hupA|transcriptional regulator HU subunit alpha|+
STM4171_577_611	0.13	-1.32	1255697|yjaH|putative inner membrane protein|+
STM4172_305_339	0.09	1.45	1255698|zraP|zinc resistance protein|-
STM4173_895_929	0.45	-1.20	1255699|hydH|sensor protein ZraS|+
STM4174_471_505	0.15	-1.28	1255700|hydG|transcriptional regulatory protein ZraR|+
STM4175_803_837	0.00	-3.78	1255701|purD|phosphoribosylamine--glycine ligase|-
STM4176_1503_1537	0.00	-4.97	1255702|purH|bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase|-
STM4181_289_323	0.94	-1.01	1255707|yjaB|hypothetical protein|-
STM4182_385_419	0.01	13.69	1255708|metA|homoserine O-succinyltransferase|+

STM4183_1115_1149	0.91	1.02	1255709|aceB|malate synthase|+
STM4184_434_468	0.07	-1.62	1255710|aceA|isocitrate lyase|+
STM4185_1137_1171	0.05	-1.39	1255711|aceK|bifunctional isocitrate dehydrogenase kinase/phosphatase protein|+
STM4186_345_379	0.19	1.29	1255712|STM4186|putative cytoplasmic protein|-
STM4187_65_99	0.08	-1.31	1255713|iclR|acetate operon transcriptional repressor IclR|-
STM4188.S_2813_2847	0.10	-1.44	1255714|metH|B12-dependent methionine synthase|+
STM4189_1113_1147	0.19	1.28	1255715|yjbB|putative transport protein|+
STM4190_133_167	0.02	-2.20	1255716|pepE|peptidase E|-
STM4191_41_75	0.05	1.73	1255717|STM4191|putative cytoplasmic protein|+
STM4192_353_387	0.01	-2.39	1255718|STM4192|putative cytoplasmic protein|+
STM4193_545_579	0.21	-1.21	1255719|yjbC|23S rRNA pseudouridine synthase F|+
STM4194_132_166	0.02	1.48	1255720|yjbD|hypothetical protein|-
STM4195_417_451	0.01	-1.34	1255721|STM4195|putative Na+-dependent transporter|-
STM4196_549_587	0.02	2.83	1255722|STM4196|putative cytoplasmic protein|-
STM4197_109_144	0.07	2.18	1255723|STM4197|putative inner membrane protein|-
STM4198_321_355	0.50	1.10	1255724|STM4198|putative cytoplasmic protein|-
STM4199_481_515	0.19	-1.13	1255725|STM4199|putative cytoplasmic protein|-
STM4202_1077_1111	0.23	-1.23	1255728|STM4202|putative phage baseplate protein|-
STM4204_869_903	0.12	1.97	1255730|STM4204|putative inner membrane protein|-
STM4205_841_875	0.09	2.10	1255731|STM4205|putative phage glycosyltransferase|-
STM4206_200_234	0.02	1.26	1255732|STM4206|putative phage glucose translocase|-
STM4207_369_403	0.04	2.00	1255733|STM4207|putative phage baseplate component|-
STM4208_237_271	0.01	1.70	1255734|STM4208|putative cytoplasmic protein|-
STM4209_33_67	0.11	-1.18	1255735|STM4209|putative inner membrane protein|-
STM4210_481_515	0.02	2.59	1255736|STM4210|putative methyl-accepting chemotaxis protein|-
STM4211.1N_193_227	0.20	-1.13	2673741|STM4211.1N|-|-
STM4213_957_991	0.36	1.08	1255739|STM4213|putative phage tail sheath protein|-
STM4216_205_239	0.10	1.55	1255742|STM4216|putative inner membrane protein|-
STM4217_312_346	0.08	2.18	1255743|STM4217|putative soluble lytic murein transglycosylase|-
STM4218_45_79	0.03	1.48	1255744|STM4218|putative inner membrane protein|-
STM4219.S_209_243	0.10	1.38	1255745|STM4219.S|putative cytoplasmic protein|+
STM4220_1231_1265	0.44	-1.13	1255746|lysC|aspartate kinase III|-
STM4221_1323_1357	0.25	1.23	1255747|pgi|glucose-6-phosphate isomerase|+
STM4222.S_120_154	0.13	1.75	1255748|yjbE|putative outer membrane protein|+
STM4223_321_355	0.64	-1.05	1255749|yjbF|putative outer membrane lipoprotein|+

STM4224_321_355	0.37	-1.11	1255750|yjbG|putative periplasmic protein|+
STM4225_1274_1308	0.49	1.14	1255751|yjbH|putative outer membrane lipoprotein|+
STM4226_321_355	0.04	2.36	1255752|yjbA|phosphate-starvation-inducible protein PsiE|+
STM4227_737_771	0.39	1.16	1255753|malG|maltose transporter permease|-
STM4229_1064_1098	0.09	-1.34	1255755|malE|maltose ABC transporter periplasmic protein|-
STM4230_975_1009	0.05	2.48	1255756|malK|maltose/maltodextrin transporter ATP-binding protein|+
STM4231_760_794	0.08	-1.24	1255757|lamB|maltoporin|+
STM4232_545_579	0.05	1.10	1255758|malM|maltose regulon periplasmic protein|+
STM4233_193_227	0.01	1.91	1255759|ubiC|chorismate pyruvate lyase|+
STM4234_33_67	0.02	1.25	1255760|ubiA|4-hydroxybenzoate octaprenyltransferase|+
STM4235_2254_2288	0.00	-1.98	1255761|plsB|glycerol-3-phosphate acyltransferase|-
STM4236_278_312	0.05	-1.51	1255762|dgkA|diacylglycerol kinase|+
STM4237_283_317	0.10	1.26	1255763|lexA|LexA repressor|+
STM4238_1031_1065	0.95	1.01	1255764|dinF|DNA-damage-inducible SOS response protein|+
STM4239_73_107	0.03	1.43	1255765|STM4239|putative cytoplasmic protein|+
STM4240_129_163	0.10	1.49	1255766|yjbJ|putative stress-response protein|+
STM4241_113_147	0.03	1.43	1255767|zur|zinc uptake transcriptional repressor|-
STM4243_705_739	0.24	-1.22	1255769|yjbN|tRNA-dihydrouridine synthase A|+
STM4244_121_155	0.01	1.76	1255770|pspG|phage shock protein G|+
STM4245_265_299	0.12	-1.07	1255771|qor|quinone oxidoreductase NADPH-dependent|-
STM4246_1313_1347	0.03	-1.81	1255772|dnaB|replicative DNA helicase|+
STM4247_849_883	0.02	-2.07	1255773|alr|alanine racemase|+
STM4248_611_645	0.05	-2.22	1255774|tyrB|aromatic amino acid aminotransferase|+
STM4249_577_611	0.01	-1.72	1255775|aphA|acid phosphatase/phosphotransferase|+
STM4250_369_403	0.03	1.45	1255776|yjbQ|putative cytoplasmic protein|+
STM4251_257_291	0.30	1.19	1255777|yjbR|putative cytoplasmic protein|+
STM4252_281_315	0.15	1.26	1255778|STM4252|putative inner membrane protein|-
STM4254_2659_2693	0.98	1.01	1255780|uvrA|excinuclease ABC subunit A|-
STM4255_33_67	0.78	-1.08	1255781|STM4255|putative cytoplasmic protein|+
STM4256_226_260	0.23	1.24	1255782|ssb|single-strand DNA-binding protein|+
STM4257_273_307	0.06	3.22	1255783|STM4257|hypothetical protein|+
STM4258_506_540	0.06	2.50	1255784|STM4258|putative methyl-accepting chemotaxis protein|+
STM4259_753_787	0.02	3.05	1255785|STM4259|putative ABC exporter outer membrane component|+
STM4260_1199_1233	0.82	1.15	1255786|STM4260|predicted cation efflux pump|+
STM4261_7001_7035	0.16	-1.29	1255787|STM4261|putative inner membrane protein|+
STM4262_1948_1982	0.01	2.20	1255788|STM4262|putative ABC-type bacteriocin/lantibiotic exporter|+

STM4263_177_211	0.00	12.42	1255789|yjcB|putative inner membrane protein|-
STM4264_1467_1501	0.30	-1.09	1255790|yjcC|putative diguanylate cyclase/phosphodiesterase|+
STM4265_113_147	0.16	1.47	1255791|soxS|DNA-binding transcriptional dual regulator|-
STM4266_289_323	0.02	3.22	1255792|soxR|redox-sensing transcriptional activator|+
STM4267_145_179	0.50	-1.11	1255793|STM4267|putative glutathione S-transferase|+
STM4268_735_769	0.01	-3.26	1255794|yjcD|hypothetical protein|+
STM4269_1416_1450	0.02	1.34	1255795|yjcE|Na/H transport protein|+
STM4270_161_195	0.20	1.16	1255796|STM4270|putative transcriptional regulator|-
STM4271_297_331	0.05	-1.37	1255797|STM4271|putative inner membrane protein|+
STM4273_763_797	0.01	-7.54	1255799|actP|acetate permease|-
STM4274_73_107	0.00	-8.67	1255800|yjcH|putative inner membrane protein|-
STM4275_1376_1410	0.00	-46.59	1255801|acs|acetyl-CoA synthetase|-
STM4276_45_83	0.17	1.27	1255802|STM4276|putative cytoplasmic protein|+
STM4277_1142_1176	0.23	1.10	1255803|nrfA|cytochrome c nitrite reductase|+
STM4279_545_579	0.33	1.15	1255805|nrfC|putative formate-dependent nitrite reductase|+
STM4280_441_475	0.29	-1.14	1255806|nrfD|putative formate-dependent nitrate reductase|+
STM4281_2008_2042	0.10	1.17	1255807|nrfE|formate-dependent nitrite reductase|+
STM4282_369_403	0.47	1.14	1255808|nrfG|formate-dependent nitrite reductase complex subunit NrfG|+
STM4284_513_547	0.33	1.53	1255810|yjcO|tetratricopeptide repeat protein|-
STM4285_1597_1631	0.05	1.28	1255811|fdhF|formate dehydrogenase|-
STM4286_129_163	0.05	1.20	1255812|lpxO|putative dioxygenase|-
STM4287.S_9_43	0.01	2.65	1255813|phnO|aminoalkylphosphonic acid N-acetyltransferase|-
STM4288_129_163	0.94	-1.01	1255814|phnB|hypothetical protein|-
STM4289_119_153	0.42	1.10	1255815|phnA|hypothetical protein|-
STM4290_840_874	0.06	1.69	1255816|proP|proline/glycine betaine transporter|+
STM4291_376_410	0.00	1.59	1255817|basS|sensor protein BasS/PmrB|-
STM4292_385_419	0.01	1.96	1255818|basR|DNA-binding response regulator in two-component regulatory system with BasS|-
STM4293_1349_1383	0.04	1.93	1255819|yjdB|predicted metal dependent hydrolase|-
STM4294_531_565	0.09	1.14	1255820|yjdE|arginine:agmatin antiporter|-
STM4295_257_291	0.01	3.10	1255821|adiY|transcriptional activator|-
STM4297_577_611	0.91	1.04	1255823|melR|DNA-binding transcriptional dual regulator|-
STM4299_568_602	0.03	1.35	1255825|melB|melibiose:sodium symporter|+
STM4300_1072_1106	0.02	-1.85	1255826|fumB|fumarase B|-
STM4301_1142_1176	0.01	-1.54	1255827|dcuB|anaerobic C4-dicarboxylate transporter|-
STM4302_9_43	0.27	-1.30	1255828|STM4302|putative cytoplasmic protein|-

STM4304_1369_1403	0.00	-3.70	1255830|dcuS|sensory histidine kinase DcuS|-
STM4305.S_2055_2089	0.01	-3.00	1255831|STM4305.S|putative anaerobic dimethylsulfoxide reductase subunit A|+
STM4306_513_547	0.25	-1.36	1255832|STM4306|putative anaerobic dimethylsulfoxide reductase subunit B|+
STM4307_105_139	0.06	-1.24	1255833|STM4307|putative anaerobic dimethylsulfoxide reductase subunit C|+
STM4308_390_424	0.03	-1.61	1255834|STM4308|putative anaerobic dehydrogenase component|+
STM4309_850_884	0.02	1.29	1255835|STM4309|hypothetical protein|-
STM4310_641_675	0.06	-2.09	1255836|STM4310|putative inner membrane protein|+
STM4312_49_83	0.02	2.12	1255838|STM4312|hypothetical protein|-
STM4313_81_115	0.03	1.41	1255839|STM4313|putative cytoplasmic protein|-
STM4314_119_153	0.08	1.90	1255840|STM4314|putative regulatory protein|-
STM4316_51_85	0.16	1.24	1255842|STM4316|putative cytoplasmic protein|-
STM4317_153_187	0.07	1.25	1255843|STM4317|hypothetical protein|+
STM4318_145_179	0.01	1.67	1255844|STM4318|putative acetyltransferase|+
STM4319_457_491	0.00	4.54	1255845|phoN|non-specific acid phosphatase|-
STM4320_41_75	0.73	1.03	1255846|STM4320|putative regulatory protein|+
STM4322_513_547	0.48	1.09	1255848|yjdC|putative transcriptional regulator|-
STM4324_247_281	0.03	1.27	1255850|cutA|divalent-cation tolerance protein CutA|-
STM4325_911_945	0.13	-1.71	1255851|dcuA|anaerobic C4-dicarboxylate transporter|-
STM4326_1078_1112	0.00	-4.14	1255852|aspA|aspartate ammonia-lyase|-
STM4327_49_83	0.26	1.24	1255853|fxsA|FxsA|+
STM4328_883_917	0.03	3.34	1255854|yjeH|inner membrane protein YjeH|-
STM4329_49_83	0.17	1.24	1255855|groES|co-chaperonin GroES|+
STM4330_760_794	0.29	1.42	1255856|groEL|chaperonin GroEL|+
STM4331_146_180	0.22	-1.11	1255857|yjeI|putative outer membrane lipoprotein|+
STM4332_353_387	0.78	-1.02	1255858|yjeJ|putative inner membrane protein|-
STM4333_366_400	0.01	1.24	1255859|yjeK|putative aminomutase|-
STM4334_513_547	0.01	-2.19	1255860|efp|elongation factor P|+
STM4335_41_75	0.02	-1.63	1255861|ecnA|putative entericidin A precursor|+
STM4337_257_291	0.02	1.41	1255863|ecnR|putative regulatory protein|-
STM4338_257_291	0.07	1.28	1255864|sugE|quaternary ammonium compound-resistance protein SugE|+
STM4339_401_435	0.08	1.49	1255865|blc|outer membrane lipoprotein Blc|-
STM4340_291_325	0.00	-3.79	1255866|frdD|fumarate reductase subunit D|-
STM4341_359_393	0.00	-11.56	1255867|frdC|fumarate reductase subunit C|-
STM4342_193_227	0.00	-6.59	1255868|frdB|fumarate reductase iron-sulfur subunit|-
STM4343_984_1018	0.00	-3.99	1255869|frdA|fumarate reductase flavoprotein subunit|-

STM4344_417_451	0.01	-2.37	1255870|yjeA|lysyl-tRNA synthetase|+
STM4345_672_706	0.07	1.31	1255871|yjeM|putative amino-acid transport protein|+
STM4346_87_121	0.07	-1.27	1255872|yjeO|putative inner membrane protein|+
STM4347_2584_2618	0.45	-1.07	1255873|yjeP|predicted mechanosensitive channel|-
STM4348_449_483	0.01	-1.28	1255874|psd|phosphatidylserine decarboxylase|-
STM4349_182_216	0.05	-1.35	1255875|yjeQ|ribosome-associated GTPase|-
STM4350_209_243	0.10	-1.59	1255876|orn|oligoribonuclease|+
STM4351_257_291	0.02	1.49	1255877|STM4351|putative arginine-binding periplasmic protein|-
STM4355.S_461_495	0.17	1.18	1255881|yjeS|putative FeS protein|-
STM4356_1061_1095	0.01	-1.20	1255882|yjeF|hypothetical protein|+
STM4357_417_451	0.00	-1.35	1255883|yjeE|putative ATPase|+
STM4358_1121_1155	0.05	-1.64	1255884|amiB|N-acetylmuramoyl-l-alanine amidase III|+
STM4359_1306_1340	0.43	1.05	1255885|mutL|DNA mismatch repair protein|+
STM4360_801_835	0.27	-1.12	1255886|miaA|tRNA delta(2)-isopentenylpyrophosphate transferase|+
STM4361_165_199	0.18	1.10	1255887|hfq|RNA-binding protein Hfq|+
STM4362_474_508	0.13	-1.09	1255888|hflX|putative GTPase HflX|+
STM4363_581_615	0.04	-1.44	1255889|hflK|FtsH protease regulator HflK|+
STM4364_934_968	0.18	1.26	1255890|hflC|FtsH protease regulator HflC|+
STM4365_153_187	0.08	1.87	1255891|yjeT|putative inner membrane protein|+
STM4366_876_910	0.40	-1.15	1255892|purA|adenylosuccinate synthetase|+
STM4367_353_387	0.02	1.33	1255893|yjeB|transcriptional repressor NsrR|+
STM4368_2144_2178	0.01	1.83	1255894|vacB|exoribonuclease R|+
STM4369_193_227	0.02	1.53	1255895|yjfH|23S rRNA (guanosine-2'-O-)-methyltransferase|+
STM4370_241_275	0.17	1.25	1255896|yjfI|putative cytoplasmic protein|+
STM4372_936_970	0.20	1.11	1255898|STM4372|putative potassium channels|+
STM4374_184_218	0.04	2.22	1255900|yjfL|putative inner membrane protein|+
STM4375_209_243	0.37	1.34	1255901|yjfM|putative inner membrane protein|+
STM4376_357_391	0.08	-1.26	1255902|yjfC|putative glutathionylspermidine synthase|+
STM4377_1426_1460	0.00	-4.74	1255903|aidB|isovaleryl CoA dehydrogenase|+
STM4378_153_187	0.00	-3.80	1255904|yjfN|putative inner membrane protein|-
STM4379_9_43	0.05	-1.77	1255905|yjfO|putative lipoprotein|-
STM4380_641_675	0.04	1.74	1255906|yjfP|predicted hydrolase|+
STM4381_273_307	0.09	1.24	1255907|yjfQ|putative transcriptional repressor|-
STM4382_930_964	0.37	-1.10	1255908|yjfR|putative L-ascorbate 6-phosphate lactonase|-
STM4384_161_195	0.98	1.01	1255910|sgaB|L-ascorbate-specific enzyme IIB component of PTS|+
STM4386_321_355	0.44	1.08	1255912|ulaD|3-keto-L-gulonate-6-phosphate decarboxylase|+

STM4387_609_643	0.30	1.13	1255913|sgaU|L-xylulose 5-phosphate 3-epimerase|+
STM4388_593_627	0.02	1.90	1255914|sgaE|L-ribulose-5-phosphate 4-epimerase|+
STM4389_115_149	0.01	1.87	1255915|yjfY|putative outer membrane protein|-
STM4391_41_75	0.01	-2.89	1255917|rpsF|30S ribosomal protein S6|+
STM4392_65_99	0.01	-3.55	1255918|priB|primosomal replication protein N|+
STM4393_105_139	0.01	-3.43	1255919|rpsR|30S ribosomal protein S18|+
STM4394_129_163	0.02	-2.89	1255920|rplI|50S ribosomal protein L9|+
STM4395_337_371	0.22	-1.38	1255921|yifZ|putative permease|+
STM4396_41_75	0.77	1.02	1255922|ytfB|putative cell envelope opacity-associated protein A|-
STM4397_17_51	0.05	-1.65	1255923|fklB|peptidyl-prolyl cis-trans isomerase|+
STM4398_667_701	0.06	-1.57	1255924|cycA|D-alanine/D-serine/glycine permease|+
STM4401_389_423	0.12	1.91	1255927|ytfG|putative reductase|-
STM4402_225_259	0.44	-1.26	1255928|ytfH|putative transcriptional regulator|+
STM4403_1297_1331	0.07	-1.17	1255929|cpdB|bifunctional 2' 3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase periplasmic precursor protein|-
STM4404_513_547	0.01	1.87	1255930|cysQ|PAPS (adenosine 3'-phosphate 5'-phosphosulfate) 3'(2') 5'-bisphosphate nucleotidase|+
STM4405_321_355	0.45	-1.20	1255931|ytfJ|putative transcriptional regulator|-
STM4406.S_57_91	0.00	-1.63	1255932|ytfK|putative cytoplasmic protein|+
STM4407_665_699	0.04	1.83	1255933|ytfL|putative hemolysin-like protein|-
STM4408_225_259	0.01	2.72	1255934|msrA|methionine sulfoxide reductase A|-
STM4409_1295_1329	0.36	1.07	1255935|ytfM|putative outer membrane protein|+
STM4410_3549_3583	0.16	-1.13	1255936|ytfN|putative periplasmic protein|+
STM4411_257_291	0.41	-1.09	1255937|ytfP|putative cytoplasmic protein|+
STM4412_770_804	0.02	1.49	1255938|STM4412|putative permease|-
STM4413_421_455	0.00	3.10	1255939|STM4413|putative metallo-dependent hydrolase|-
STM4414_65_99	0.19	-1.33	1255940|ppa|inorganic pyrophosphatase|-
STM4415_689_723	0.41	-1.13	1255941|fbp|fructose-1 6-bisphosphatase|-
STM4416_829_863	0.64	1.08	1255942|mpl|UDP-N-acetylmuramate/L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase|+
STM4417_417_451	0.30	1.08	1255943|STM4417|putative transcriptional regulator|+
STM4418_835_869	0.19	-1.19	1255944|STM4418|sugar transporter|-
STM4419_1014_1048	0.62	-1.10	1255945|STM4419|sugar transporter|+
STM4421_1405_1439	0.01	-2.12	1255947|STM4421|putative NAD-dependent aldehyde dehydrogenase|-
STM4425_12_46	0.05	1.24	1255951|STM4425|putative dehydrogenase|+
STM4426_505_539	0.01	2.72	1255952|srfJ|lysosomal glucosyl ceramidase-like protein|+

STM4427_513_547	0.02	1.41	1255953|STM4427|putative endonuclease|+
STM4429_754_788	0.29	1.30	1255955|STM4429|-|-
STM4431_1396_1430	0.15	1.09	2673766|STM4431|-|+
STM4433_760_794	0.00	1.98	1255959|STM4433|myo-inositol 2-dehydrogenase|+
STM4434_900_934	0.63	-1.07	1255960|STM4434|putative permease|+
STM4435_317_351	0.28	1.18	1255961|STM4435|putative cytoplasmic protein|+
STM4436_289_323	0.01	-1.38	1255962|STM4436|putative endonuclease|+
STM4437_425_459	0.02	1.73	1255963|yjgA|hypothetical protein|-
STM4438_386_420	0.02	1.67	1255964|pmbA|peptidase PmbA|+
STM4439_249_283	0.04	-1.34	1255965|cybC|cytochrome b562|+
STM4440_33_67	0.02	-1.41	1255966|STM4440|putative cytoplasmic protein|+
STM4441_225_259	0.69	-1.04	1255967|STM4441|putative cytoplasmic protein|+
STM4442_241_275	0.24	1.24	1255968|STM4442|putative cytoplasmic protein|+
STM4444_97_131	0.10	-1.25	1255970|STM4444|putative inner membrane protein|+
STM4445_839_873	0.14	-1.16	1255971|STM4445|dihydroorotase|+
STM4446_684_718	0.13	1.30	1255972|STM4446|putative selenocysteine synthase|+
STM4447_497_531	0.02	-1.30	1255973|STM4447|putative periplasmic protein|+
STM4448_1619_1653	0.30	1.11	1255974|STM4448|putative phosphotransferase system mannitol/fructose-specific IIA domain|+
STM4449_88_122	0.00	-1.44	1255975|STM4449|bifunctional antitoxin/transcriptional repressor RelB|+
STM4450_160_194	0.00	-1.31	1255976|STM4450|putative inner membrane protein|+
STM4451_429_463	0.41	1.15	1255977|nrdG|anaerobic ribonucleotide reductase-activating protein|-
STM4452_1908_1942	0.06	-1.58	1255978|nrdD|anaerobic ribonucleoside triphosphate reductase|-
STM4452.1N_60_94	0.08	2.45	2673768|STM4452.1N|hypothetical protein|+
STM4454_739_773	0.02	-2.64	1255980|treB|pseudo|-
STM4455_481_515	0.12	1.28	1255981|treR|trehalose repressor|-
STM4457_281_315	0.03	1.79	1255983|STM4457|putative transposase|-
STM4458_65_99	0.09	-1.75	1255984|yjgF|putative translation initiation inhibitor|-
STM4459_33_67	0.01	2.00	1255985|pyrI|aspartate carbamoyltransferase regulatory subunit|-
STM4460_586_620	0.48	-1.20	1255986|pyrB|aspartate carbamoyltransferase catalytic subunit|-
STM4461_50_84	0.01	2.14	1255987|pyrL|pyrBI operon leader peptide|-
STM4464_533_567	0.78	-1.07	1255990|STM4464|putative arginine repressor|-
STM4465_54_88	0.04	2.69	1255991|STM4465|ornithine carbamoyltransferase|-
STM4468_89_123	0.01	-1.64	1255994|yjgK|putative cytoplasmic protein|+
STM4469_438_472	0.34	-1.07	1255995|argI|ornithine carbamoyltransferase subunit II|-
STM4470_81_115	0.02	1.35	1255996|yjgD|hypothetical protein|+

STM4471_513_547	0.44	-1.10	1255997|miaE|hydroxylase|+
STM4472_267_306	0.00	2.18	1255998|ytgA|putative inner membrane protein|-
STM4473_55_89	0.00	2.15	1255999|yjgM|putative acetyltransferase|-
STM4474_717_751	0.04	1.39	1256000|yjgN|putative inner membrane protein|+
STM4475_2273_2307	0.35	-1.14	1256001|valS|valyl-tRNA synthetase|-
STM4476.S_9_43	0.32	1.09	1256002|holC|DNA polymerase III subunit chi|-
STM4477_545_579	0.02	-1.26	1256003|pepA|leucyl aminopeptidase|-
STM4478_85_119	0.34	-1.15	1256004|STM4478|putative cytoplasmic protein|-
STM4479_998_1032	0.29	1.20	1256005|yjgP|putative permease|+
STM4480_516_550	0.04	-1.32	1256006|yjgQ|putative permease|+
STM4482_977_1011	0.01	-2.95	1256008|idnT|L-idonate transport protein|-
STM4483_289_323	0.45	-1.08	1256009|idnO|gluconate 5-dehydrogenase|-
STM4484_241_275	0.01	-1.61	1256010|idnD|L-idonate 5-dehydrogenase NAD-binding|-
STM4486_853_887	0.01	-2.68	1256012|yjgB|putative alcohol dehydrogenase|-
STM4487_21_55	0.46	-1.41	1256013|leuX|tRNA|+
STM4488_97_131	0.01	2.43	1256014|STM4488|putative integrase|+
STM4489_3381_3415	0.07	-1.51	1256015|STM4489|putative DNA helicases|+
STM4490_321_355	0.08	-1.36	1256016|STM4490|putative restriction endonuclease|+
STM4491_2046_2080	0.65	-1.05	1256017|STM4491|putative ATP-dependent Lon protease|-
STM4492_2319_2353	0.63	1.04	1256018|STM4492|putative cytoplasmic protein|-
STM4493_273_307	0.09	-1.18	1256019|STM4493|putative cytoplasmic protein|-
STM4494_797_831	0.04	-1.54	1256020|STM4494|putative ABC-type sugar/spermidine/putrescine transport system ATPase component|-
STM4495_2951_2985	0.52	-1.28	1256021|STM4495|putative type II restriction enzyme methylase subunit|-
STM4496_2675_2709	0.03	-1.66	1256022|STM4496|putative DNA repair ATPase|-
STM4497_228_262	0.05	2.01	1256023|STM4497|putative cytoplasmic protein|-
STM4498_161_195	0.48	-1.11	1256024|STM4498|putative inner membrane protein|-
STM4498.1N_2_36	0.83	-1.01	2673776|STM4498.1N|-|+
STM4499_257_291	0.05	1.15	1256025|yeeN|hypothetical protein|-
STM4500_1049_1083	0.87	-1.02	1256026|yjhP|putative SAM-dependent methyltransferase|-
STM4502_569_603	0.02	2.55	1256028|STM4502|putative cytoplasmic protein|+
STM4503_249_283	0.02	1.34	1256029|STM4503|putative inner membrane protein|+
STM4504_353_387	0.00	3.26	1256030|STM4504|putative cytoplasmic protein|+
STM4505_385_419	0.03	2.09	1256031|STM4505|hypothetical protein|+
STM4506_257_291	0.27	1.30	1256032|STM4506|putative dienelactone hydrolase|-
STM4507_209_243	0.00	-1.73	1256033|luxuR|DNA-binding transcriptional repressor|+

STM4509.S_229_263	0.36	-1.10	1256035|STM4509.S|putative cytoplasmic protein|+
STM4510_177_211	0.00	-1.74	1256036|STM4510|putative aspartate racemase|+
STM4511_833_867	0.09	-1.42	1256037|yjiE|putative DNA-binding transcriptional regulator|-
STM4512_750_784	0.01	-1.62	1256038|iadA|isoaspartyl dipeptidase|-
STM4513_129_163	0.09	1.35	1256039|yjiG|hypothetical protein|-
STM4514.S_547_581	0.13	-1.25	1256040|yjiH|putative inner membrane protein|-
STM4517_1171_1205	0.45	1.23	1256043|yjiO|putative transport protein|-
STM4518_257_291	0.17	1.18	1256044|STM4518|putative inner membrane protein|+
STM4519_1028_1062	0.01	-2.25	1256045|STM4519|putative NAD-dependent aldehyde dehydrogenase|+
STM4520_15_49	0.29	1.31	1256046|STM4520|putative cytoplasmic protein|-
STM4521_97_131	0.12	1.73	1256047|yjiS|putative cytoplasmic protein|+
STM4522_91_128	0.01	2.86	1256048|STM4522|putative inner membrane protein|-
STM4523_65_99	0.00	1.94	1256049|yjiW|putative SOS response protein|-
STM4524_563_597	0.05	1.99	1256050|hsdS|type I restriction enzyme specificity protein|-
STM4525_1207_1241	0.01	1.61	1256051|hsdM|DNA methylase M|-
STM4527_593_627	0.03	-1.26	1256053|mrr|restriction endonuclease|+
STM4528_217_251	0.02	2.13	1256054|STM4528|putative inner membrane protein|+
STM4529_233_267	0.58	1.08	1256055|STM4529|putative cytoplasmic protein|+
STM4530_337_371	0.17	1.20	1256056|yjiA|putative GTP-binding protein YjiA|-
STM4531_103_137	0.79	1.11	1256057|yjiX|putative cytoplasmic protein|-
STM4532_1152_1186	1.00	-1.00	1256058|yjiY|putative carbon starvation protein|-
STM4533_1263_1297	0.01	-2.31	1256059|tsr|methyl-accepting chemotaxis protein II|+
STM4534_2223_2257	0.00	-3.84	1256060|STM4534|putative transcriptional regulator|+
STM4535_309_343	0.16	1.87	1256061|STM4535|putative PTS permease|+
STM4538_705_739	0.05	2.01	1256064|STM4538|putative PTS permease|+
STM4539_575_609	0.01	-3.09	1256065|STM4539|putative glucosamine-fructose-6-phosphate aminotransferase|+
STM4540.S_460_494	0.79	1.04	1256066|STM4540.S|putative glucosamine-fructose-6-phosphate aminotransferase|+
STM4541_1741_1775	0.75	-1.04	1256067|mdoB|phosphoglycerol transferase II|-
STM4542_357_391	0.01	2.07	1256068|yjjA|hypothetical protein|-
STM4543_257_291	0.54	1.09	1256069|dnaC|DNA replication protein DnaC|-
STM4544_177_211	0.02	1.54	1256070|dnaT|primosomal protein I|-
STM4545_225_259	0.19	-1.16	1256071|STM4545|hypothetical protein|-
STM4546_385_419	0.01	1.48	1256072|yjjP|hypothetical protein|-
STM4547_577_611	0.31	1.18	1256073|yjjQ|putative transcriptional regulator|+

STM4549_409_443	0.52	1.11	1256075|STM4549|putative cytoplasmic protein|-
STM4550_17_51	0.48	-1.18	1256076|fhuF|ferric iron reductase involved in ferric hydroximate transport|-
STM4551_898_932	0.27	1.06	1256077|STM4551|hypothetical protein|-
STM4552_43_77	0.33	1.06	1256078|STM4552|putative inner membrane protein|+
STM4556_742_776	0.26	-1.15	1256082|rsmC|16S ribosomal RNA m2G1207 methyltransferase|-
STM4557_249_283	0.05	1.44	1256083|holD|DNA polymerase III subunit psi|+
STM4558_193_227	0.00	-1.46	1256084|rimI|ribosomal-protein-alanine N-acetyltransferase|+
STM4559.S_129_163	0.01	-1.74	1256085|yjjG|nucleotidase|+
STM4560_1103_1137	0.13	-1.29	1256086|prfC|peptide chain release factor 3|+
STM4561_385_419	0.05	1.71	1256087|osmY|periplasmic protein|+
STM4562_43_77	0.04	1.59	1256088|STM4562|putative inner membrane protein|+
STM4563_523_557	0.12	1.26	1256089|yjjU|putative phosphoesterase|+
STM4564_737_771	0.57	1.07	1256090|yjjV|putative deoxyribonuclease YjjV|+
STM4565_649_683	0.02	-1.54	1256091|yjjW|pyruvate formate lyase-activating enzyme|-
STM4566_1020_1054	0.02	-1.56	1256092|yjjI|hypothetical protein|-
STM4567_225_259	0.01	1.31	1256093|deoC|deoxyribose-phosphate aldolase|+
STM4568_580_614	0.08	-1.23	1256094|deoA|thymidine phosphorylase|+
STM4569_1089_1123	0.51	-1.13	1256095|deoB|phosphopentomutase|+
STM4570_129_163	0.70	1.08	1256096|deoD|purine nucleoside phosphorylase|+
STM4572_2170_2204	0.07	3.04	1256098|stjB|putative fimbrial usher protein|-
STM4573_321_355	0.02	3.01	1256099|stjC|putative periplasmic chaperone protein|-
STM4575_173_207	1.00	-1.00	1256101|STM4575|putative outer membrane protein|-
STM4576_562_596	0.01	1.88	1256102|lplA|lipoate-protein ligase A|-
STM4577_265_299	0.03	2.26	1256103|smp|hypothetical protein|-
STM4579_704_738	0.48	1.08	1256105|radA|DNA repair protein RadA|+
STM4580.S_538_572	0.01	-1.46	1256106|nadR|nicotinamide-nucleotide adenylyltransferase|+
STM4581_1629_1663	0.33	-1.30	1256107|yjjK|putative ABC transporter ATP-binding protein|-
STM4582_1851_1885	0.06	-1.35	1256108|slt|lytic murein transglycosylase|+
STM4583_277_311	0.02	-1.90	1256109|trpR|Trp operon repressor|+
STM4584_209_243	0.01	-1.93	1256110|yjjX|NTPase|-
STM4585_513_547	0.01	-1.69	1256111|gpmB|phosphoglycerate mutase|+
STM4586_801_835	0.00	2.07	1256112|rob|transcriptional regulator|-
STM4587_215_249	0.18	1.10	1256113|creA|hypothetical protein|+
STM4588_145_179	0.61	-1.06	1256114|creB|DNA-binding response regulator CreB|+
STM4589_1210_1244	0.63	1.11	1256115|creC|sensory histidine kinase CreC|+
STM4590_863_897	0.13	-1.19	1256116|creD|hypothetical protein|+

STM4591_631_665	0.51	1.11	1256117|sthE|putative major fimbrial subunit|-
STM4592_33_67	0.19	1.16	1256118|sthD|putative fimbrial subunit|-
STM4593_1731_1765	0.08	1.60	1256119|sthB|putative fimbrial usher protein|-
STM4594_641_675	0.09	1.71	1256120|sthA|putative fimbrial chaparone|-
STM4595_97_131	0.03	1.43	1256121|STM4595|putative fimbrial chaparone|-
STM4596_209_243	0.03	-1.25	1256122|STM4596|putative inner membrane protein|-
STM4597_197_231	0.01	3.09	1256123|STM4597|putative periplasmic protein|-
STM4598_65_99	0.02	-2.17	1256124|arcA|DNA-binding response regulator in two-component regulatory system with ArcB or CpxA|-
STM4599_49_83	0.47	1.16	1256125|yjjY|putative inner membrane protein|+
STM4600_257_291	0.09	1.33	1256126|lasT|putative tRNA/tRNA methyltransferase|+
PSLT001_2_36	0.25	1.14	1256238|PSLT001|putative cytoplasmic protein|+
PSLT002_100_134	0.69	1.06	1256237|PSLT002|putative phospholipase D|+
PSLT003_22_59	0.48	1.07	1256235|repC|DNA replication protein|+
PSLT004_56_90	0.24	1.21	1256236|repA3|DNA replication protein|+
PSLT005_20_55	0.24	-1.11	1256234|tap|plasmid replication control protein|+
PSLT006_627_661	0.01	-1.47	1256233|repA|DNA replication protein|+
PSLT007_72_106	0.09	1.45	1256232|PSLT007|putative outer membrane protein|+
PSLT008_338_372	0.11	1.45	1256231|srgC|putative regulatory protein|-
PSLT009_477_511	0.24	1.41	1256230|rcK|resistance to complement killing|-
PSLT011_527_561	0.10	1.20	1256229|srgA|putative thiol-disulfide isomerase or thioredoxin|-
PSLT012_54_88	0.80	1.04	1256227|orf7|putative bacterial regulatory protein|-
PSLT013_178_212	0.35	-1.18	1256226|pefI|regulator|-
PSLT014_525_559	0.14	1.16	1256224|orf6|putative outer membrane protein|-
PSLT017_1655_1689	0.18	-1.23	1256222|pefC|usher protein|-
PSLT018_51_85	0.11	-1.41	1256221|pefA|major fimbrial subunit|-
PSLT020_73_107	0.02	3.44	1256220|PSLT020|-|+
PSLT020.1N_129_163	0.71	-1.12	1256218|PSLT020.1N|-|+
PSLT023_813_847	0.03	1.28	1256216|repA2|DNA replication protein|-
PSLT024_208_246	0.51	1.26	1256217|PSLT024|hypothetical protein|+
PSLT025_152_189	0.06	1.27	1256215|PSLT025|putative cytoplasmic protein|-
PSLT026_408_443	0.02	2.35	1256213|PSLT026|putative periplasmic protein|-
PSLT027_56_90	0.20	-1.22	1256214|ccdA|antidote|+
PSLT028_14_48	0.05	1.55	1256209|ccdB|toxin|+
PSLT029_154_188	0.04	-1.36	1256212|PSLT029|putative cytoplasmic protein|+
PSLT030_451_485	0.16	1.18	1256211|PSLT030|putative cytoplasmic protein|+

PSLT031_371_405	0.05	-1.30	1256210|rsdB|resolvase|+
PSLT032_38_73	0.17	1.25	1256207|PSLT032|putative diguanylate cyclase/phosphodiesterase|+
PSLT032.1N_209_243	0.02	1.41	1256208|PSLT032.1N|hypothetical protein|+
PSLT033_4_38	0.07	1.51	1256205|PSLT033|putative inner membrane protein|+
PSLT034_956_991	0.42	1.14	1256206|PSLT034|-|+
PSLT035_239_273	0.14	1.32	1256204|PSLT035|-|-
PSLT036_202_236	0.01	1.92	1256203|PSLT036|putative transposase|+
PSLT037_292_327	0.10	1.50	1256202|spvD|hydrophilic protein|-
PSLT039_1860_1894	0.02	1.57	1256199|spvB|hydrophilic protein|-
PSLT040_3_37	0.02	3.02	1256200|spvA|outer membrane protein|-
PSLT040.1N_117_151	0.02	1.72	1256198|PSLT040.1N|-|-
PSLT041_831_865	0.01	1.95	1256197|spvR|regulator of spv operon|-
PSLT042_857_891	0.57	1.12	1256195|PSLT042|putative integrase protein|+
PSLT043_161_195	0.02	1.36	1256196|PSLT043|type II secretion system protein|-
PSLT044_848_882	0.01	1.53	1256194|rlgA|putative integrase protein|-
PSLT045_312_346	0.10	1.33	1256192|PSLT045|putative resolvase|-
PSLT046_413_447	0.01	2.36	1256193|PSLT046|putative carbonic anhydrase|-
PSLT047_335_369	0.07	-1.25	1256191|PSLT047|putative cytoplasmic protein|-
PSLT048_687_721	0.73	-1.05	1256190|tlpA|alpha-helical coiled-coil protein|+
PSLT049_53_87	0.29	1.32	1256189|PSLT049|-|+
PSLT050.1N_39_73	0.05	-1.66	1256187|PSLT050.1N|hypothetical protein|+
PSLT050.2N_361_395	0.48	-1.17	1256188|PSLT050.2N|hypothetical protein|+
PSLT051_107_141	0.71	1.03	1256185|PSLT051|putative cytoplasmic protein|-
PSLT052_577_611	0.20	-1.12	1256186|parA|plasmid partition protein A|+
PSLT053_310_344	0.08	-1.72	1256184|parB|plasmid partition protein B|+
PSLT054_456_490	0.04	2.05	1256183|umuC|DNA polymerase V subunit UmuC|-
PSLT055_259_293	0.01	1.72	1256182|samA|SamA|-
PSLT056_403_437	0.18	-1.32	1256180|PSLT056|putative cytoplasmic protein|+
PSLT057_247_281	0.81	-1.06	1256181|PSLT057|putative cytoplasmic protein|+
PSLT058_145_179	0.58	1.09	1256179|PSLT058|-|+
PSLT059_470_504	0.67	-1.06	1256178|PSLT059|putative adenine-specific DNA methylase|+
PSLT060_98_132	0.14	-1.33	1256177|PSLT060|putative cytoplasmic protein|+
PSLT060.1N_93_127	0.01	-1.60	1256175|PSLT060.1N|hypothetical protein|+
PSLT062_207_241	0.02	1.32	1256173|PSLT062|putative cytoplasmic protein|+
PSLT063_304_338	0.13	1.41	1256174|PSLT063|putative cytoplasmic protein|+
PSLT064_42_76	0.20	-1.08	1256172|PSLT064|putative inner membrane protein|+

PSLT065_493_527	0.09	1.63	1256171|PSLT065|-|-
PSLT066_151_185	0.31	1.12	1256170|ssbB|single-strand DNA binding protein|+
PSLT067_7_41	0.57	-1.06	1256168|PSLT067|putative cytoplasmic protein|+
PSLT069_372_407	0.10	1.15	1256167|psiB|PsiB|+
PSLT070_608_643	0.04	1.44	1256166|psiA|PsiA|+
PSLT071_321_355	0.01	1.54	1256165|PSLT071|-|+
PSLT072_23_57	0.28	-1.20	1256164|PSLT072|putative transglycosylase|-
PSLT073_111_145	0.92	-1.01	1256163|traM|mating signal protein|+
PSLT075_180_214	0.64	-1.32	1256127|traJ|regulatory protein|+
PSLT074_58_92	0.14	-1.18	1256162|finP|misc_RNA|-
PSLT077_208_242	0.06	1.28	1256159|traA|pilus subunit|+
PSLT078_218_252	0.19	-1.26	1256160|traL|pilus assembly protein|+
PSLT079_447_481	0.01	2.57	1256158|traE|pilus assembly protein|+
PSLT080_550_584	0.61	1.13	1256157|traK|pilus assembly protein|+
PSLT082_388_422	0.05	1.56	1256156|traP|conjugative transfer protein|+
PSLT083_104_139	0.52	-1.05	1256154|trbD|conjugative transfer protein|+
PSLT084_226_260	0.03	1.40	1256153|traV|pilus assembly protein|+
PSLT085_34_68	0.27	1.20	1256151|traR|conjugative transfer protein|+
PSLT087_96_134	0.16	-1.31	1256152|PSLT087|OrfG2|+
PSLT088_2183_2217	0.11	1.48	1256150|traC|ATP-binding protein|+
PSLT089_84_118	0.01	1.46	1256149|trbI|pilus assembly protein|+
PSLT091_285_319	0.02	-1.25	1256147|traW|pilus assembly protein|+
PSLT092_415_449	0.97	1.01	1256148|traU|pilus assembly protein|+
PSLT093_64_99	0.61	-1.10	1256146|PSLT093|OrfF|+
PSLT094_451_485	0.02	-1.86	1256145|trbC|pilus assembly protein|+
PSLT094.1N_317_351	0.31	1.09	1256143|PSLT094.1N|hypothetical protein|+
PSLT095_1553_1587	0.40	1.10	1256144|traN|mating pair stabilization protein|+
PSLT096_63_97	0.02	-1.46	1256142|trbE|conjugative transfer protein|+
PSLT097_322_356	0.02	-1.25	1256140|traF|pilus assembly protein|+
PSLT098_128_162	0.20	-1.21	1256141|traQ|pilin chaperone|+
PSLT099_59_93	0.06	-1.24	1256139|trbB|conjugative transfer protein|+
PSLT100_422_456	0.58	-1.07	1256138|traH|pilus assembly protein|+
PSLT101_2108_2142	0.11	-1.11	1256136|traG|mating pair stabilization and pilus assembly protein|+
PSLT102_436_470	0.05	-1.44	1256137|traS|entry exclusion protein|+
PSLT103_496_530	0.22	-1.21	1256135|traT|surface exclusion protein|+
PSLT104_1579_1613	0.05	-1.10	1256134|traD|ATP-binding protein/DNA transporter|+

PSLT105_444_478	0.22	1.18	1256132|trbH|conjugative transfer protein|+
PSLT106_88_122	0.03	1.74	1256133|PSLT106|MvpA-like protein|-
PSLT107_168_202	0.01	1.99	1256131|PSLT107|putative cytoplasmic protein|-
PSLT108_5003_5038	0.56	1.06	1256130|traI|oriT nickase/helicase|+
PSLT110_6_40	0.23	1.14	1256128|traX|pilin subunit acetylation|+
PSLT111_431_465	0.04	1.36	1256129|finO|finP binding-protein|+
SLP1_0001_191_225	0.01	1.58	|||-
SLP1_0002_179_213	0.45	1.07	|||-
SLP1_0003_4387_4422	0.13	-1.18	|||-
SLP1_0004_428_462	0.05	-1.37	|||-
SLP1_0005_168_202	0.06	1.36	|||+
SLP1_0006_188_222	0.03	1.33	|||+
SLP1_0007_1378_1412	0.98	-1.00	|||-
SLP1_0008_496_530	0.06	-1.33	|||-
SLP1_0009_438_472	0.13	-1.20	|||-
SLP1_0010_2530_2564	0.66	1.16	|||-
SLP1_0011_1326_1360	0.33	-1.18	|||-
SLP1_0012_175_209	0.04	1.21	|||-
SLP1_0013_128_162	0.24	-1.25	|||-
SLP1_0014_615_649	0.96	-1.00	|||-
SLP1_0015_63_97	0.01	-1.53	|||-
SLP1_0016_1553_1587	0.37	1.15	|||-
SLP1_0017_451_485	0.01	-1.97	|||-
SLP1_0018_72_107	0.30	1.17	|||-
SLP1_0020_331_365	0.05	-1.18	|||-
SLP1_0022_1765_1799	0.05	1.25	|||-
SLP1_0023_96_134	0.62	1.12	|||-
SLP1_0024_34_68	0.06	1.71	|||-
SLP1_0025_226_260	0.05	1.31	|||-
SLP1_0026_104_139	0.05	1.25	|||-
SLP1_0029_558_592	0.15	2.02	|||-
SLP1_0030_143_177	0.03	-1.59	|||-
SLP1_0031_276_310	0.93	1.05	|||-
SLP1_0032_208_242	0.07	1.25	|||-
SLP1_0033_156_195	0.00	2.81	|||-
SLP1_0034_176_215	0.09	1.26	|||-

SLP1_0035_111_145	0.92	1.02	III-
SLP1_0036_391_425	0.42	1.27	III+
SLP1_0037_612_646	0.07	1.22	III-
SLP1_0038_372_407	0.41	-1.04	III-
SLP1_0040_71_105	0.16	1.13	III-
SLP1_0041_475_509	0.27	-1.15	III-
SLP1_0042_34_68	0.04	1.16	III-
SLP1_0043_306_340	0.07	1.56	III-
SLP1_0050_71_105	0.15	-1.12	III-
SLP1_0051_403_437	0.18	-1.30	III-
SLP1_0052_119_153	0.02	1.52	III+
SLP1_0053_776_810	0.02	1.79	III+
SLP1_0054_434_468	0.23	-1.43	III-
SLP1_0055_579_613	0.31	-1.14	III-
SLP1_0056_107_141	0.67	-1.03	III+
SLP1_0057_52_86	0.07	-1.20	III+
SLP1_0058_40_74	0.38	1.18	III-
SLP1_0059_119_153	0.49	-1.18	III-
SLP1_0060_335_369	0.35	1.08	III+
SLP1_0061_85_119	0.00	3.45	III+
SLP1_0062_312_346	0.09	1.24	III+
SLP1_0063_848_882	0.02	1.64	III+
SLP1_0064_161_195	0.04	1.56	III+
SLP1_0065_79_113	0.01	1.54	III-
SLP1_0066_447_481	0.04	2.17	III+
SLP1_0067_413_447	0.00	5.45	III+
SLP1_0069_295_329	0.04	2.42	III+
SLP1_0070_292_327	0.06	1.68	III+
SLP1_0071_206_240	0.01	1.85	III-
SLP1_0072_231_265	0.70	1.05	III+
SLP1_0073_496_531	0.94	-1.02	III-
SLP1_0074_72_106	0.32	1.13	III-
SLP1_0075_38_73	0.88	1.03	III-
SLP1_0076_371_405	0.01	-1.37	III-
SLP1_0077_455_489	0.06	1.32	III-
SLP1_0078_166_200	0.02	-1.47	III-

SLP1_0079_14_48	0.07	1.52	III-
SLP1_0080_56_90	0.03	-1.58	III-
SLP1_0081_408_443	0.01	2.79	III+
SLP1_0082_240_277	0.04	2.22	III+
SLP1_0083_208_246	0.50	1.20	III-
SLP1_0084_813_847	0.04	1.30	III+
SLP1_0085_8_42	0.12	1.30	III-
SLP1_0086_192_227	0.50	-1.07	III+
SLP1_0087_455_489	0.03	-1.65	III+
SLP1_0088_1908_1942	0.62	1.08	III+
SLP1_0090_75_109	0.25	-1.13	III+
SLP1_0091_693_727	0.70	1.05	III+
SLP1_0092_102_136	0.36	-1.10	III+
SLP1_0093_50_84	0.22	-1.22	III+
SLP1_0094_527_561	0.04	1.29	III+
SLP1_0096_295_329	0.45	1.27	III+
SLP1_0097_418_452	0.16	1.62	III+
SLP1_0098_72_106	0.05	1.75	III-
SLP1_0099_627_661	0.00	-1.40	III-
SLP1_0100_24_59	0.91	-1.01	III-
SLP1_0101_56_90	0.95	-1.01	III-
SLP1_0102_8_47	0.01	1.74	III-
SLP1_0103_100_134	0.92	-1.01	III-
SLP1_0104_239_273	0.34	1.10	III-
SLP2_0001_33_67	0.45	1.10	III+
SLP2_0002_177_211	0.22	1.15	III+
SLP2_0003_2_40	0.26	-1.18	III+
SLP2_0004_81_115	0.72	-1.03	III+
SLP2_0005_53_87	0.28	-1.19	III+
SLP2_0006_225_259	0.02	1.79	III+
SLP2_0007_105_139	0.00	2.79	III+
SLP2_0008_225_259	0.01	2.06	III-
SLP2_0009_243_279	0.01	1.97	III-
SLP2_0010_375_409	0.07	1.30	III-
SLP2_0011_1248_1282	0.79	1.02	III+
SLP2_0012_1106_1140	0.07	1.47	III+

SLP2_0014_101_135	0.79	1.07	III+
SLP2_0016_53_87	0.91	1.02	III+
SLP2_0017_81_115	0.15	1.19	III+
SLP2_0019_213_247	0.19	-1.22	III+
SLP2_0020_69_103	0.15	-1.18	III+
SLP2_0021_161_195	0.06	-1.34	III+
SLP2_0022_205_239	0.03	1.53	III+
SLP2_0023_85_120	0.09	1.43	III-
SLP2_0024_9_43	0.10	1.21	III+
SLP2_0025_577_611	0.60	-1.05	III+
SLP2_0026_180_214	0.09	-1.32	III+
SLP2_0027_17_51	0.06	1.94	III+
SLP2_0028_49_83	0.45	-1.10	III+
SLP2_0029_209_243	0.52	-1.13	III+
SLP2_0031_403_437	0.07	-1.62	III+
SLP2_0032_261_295	0.67	1.14	III+
SLP2_0033_173_207	0.99	1.00	III+
SLP2_0034_14_48	0.03	-1.28	III+
SLP2_0035_3_37	0.26	-1.25	III+
SLP2_0036_1274_1308	0.07	1.21	III+
SLP2_0038_453_488	0.57	-1.07	III+
SLP2_0039_9_43	0.88	1.02	III+
SLP2_0040_372_406	0.73	1.03	III+
SLP2_0041_282_317	0.62	-1.07	III+
SLP2_0042_213_247	0.03	-2.45	III+
SLP2_0043_17_51	0.68	1.03	III+
SLP2_0044_587_621	0.09	-1.29	III+
SLP2_0045_193_227	0.33	-1.11	III+
SLP2_0047_193_227	0.02	1.62	III+
SLP2_oriT_41_75	0.25	-1.15	III+
SLP2_0048_257_291	0.02	2.13	III+
SLP2_0049_1861_1895	0.02	-1.62	III+
SLP2_0050_2061_2095	0.00	3.22	III-
SLP2_0053_89_123	0.37	-1.16	III+
SLP2_0054_92_126	0.08	1.51	III+
SLP2_0055_553_587	0.02	1.84	III-

SLP2_0056_1313_1347	0.02	1.54	III-
SLP2_0058_1020_1054	0.04	2.41	III-
SLP2_0059_321_355	0.06	1.51	III-
SLP2_0060_2558_2592	0.03	1.28	III-
SLP2_0061_337_371	0.47	-1.26	III-
SLP2_0062_137_171	0.10	1.89	III-
SLP2_0063_129_163	0.02	2.28	III-
SLP2_0065_113_147	0.09	2.11	III-
SLP2_0066_451_485	0.01	1.85	III-
SLP2_0067_545_579	0.55	1.17	III-
SLP2_0068_533_567	0.07	1.51	III-
SLP2_0069_97_131	0.05	2.31	III-
SLP2_0072_481_515	0.09	1.70	III-
SLP2_0073_243_277	0.07	2.38	III-
SLP2_0074_246_280	0.73	1.05	III-
SLP2_0076_401_435	0.02	1.91	III-
SLP2_0077_529_563	0.88	-1.02	III-
SLP2_0079_449_483	0.03	3.02	III-
SLP2_0081_113_147	0.14	-1.16	III+
SLP2_0082_145_179	0.17	-1.29	III-
SLP2_0083_129_163	0.93	-1.01	III+
SLP2_0085_1219_1253	0.05	-1.28	III-
SLP2_0086_457_491	0.02	1.99	III-
SLP2_0088_541_575	0.26	-1.20	III-
SLP2_0089_323_357	0.04	3.45	III-
SLP2_0090_555_589	0.00	2.04	III-
SLP2_0091_321_355	0.28	-1.19	III-
SLP2_0094_97_131	0.04	1.49	III-
SLP2_0096_273_307	0.14	1.31	III-
SLP2_0097_331_370	0.03	3.22	III-
SLP2_0098_129_163	0.07	2.31	III-
SLP2_0100_217_252	0.54	1.13	III-
SLP2_0101_385_419	0.04	1.30	III-
SLP2_0102_225_259	0.04	1.43	III-
SLP2_0103_145_179	0.07	2.09	III-
SLP3_0001_257_291	0.33	-1.23	III-

SLP3_0002_129_163	0.06	1.43	III-
SLP3_0003_673_707	0.51	1.08	III-
SLP3_0004_609_643	0.21	-1.18	III-
SLP3_0005_3_37	0.01	2.97	III-
SLP3_0006_137_171	0.02	1.80	III-
SLP3_0008_1459_1493	0.33	1.14	III-
SLP3_0007_840_874	0.05	1.81	III-
SLP3_0009_282_317	0.01	1.34	III-
SLP3_0010_355_389	0.01	1.92	III-
SLP3_0011_48_82	0.30	1.44	III+
SLP3_0012_65_99	0.70	-1.06	III+
SLP3_0013_209_243	0.62	-1.05	III-
SLP3_0014_417_451	0.09	1.14	III-
lytB STM0050_41_75	0.29	1.16	ISTnc30II+
yabN/leuD_161_196	0.09	1.83	IsgrSII+
secA mutT_5_39	0.02	1.95	ISTnc40II+
lpdA STM0155_11_45	0.10	2.12	ISTnc50II-
STM0294.1n / STM0295_204	0.16	-1.34	IisrAII+
ybaK/ybaP_29_63	0.12	1.35	IsroBII+
dsbG ahpC_13_47	0.11	-1.19	ISTnc70II+
gltJ/gltI_33_67	0.07	-1.43	IsroCII-
STM0869/STM0870_5_39	0.95	1.06	IrybBII-
STM0904 STM0905_88_122	0.38	-1.21	ISTnc100II+
serS dmsA_63_101	0.02	2.93	ISTnc130II-
icdA STM1239_158_193	0.24	1.59	ISTnc150II-
envF / msgA_233_267	0.86	1.03	IisrCII+
STM1273 / STM1274_22_56	0.41	-1.75	IisrEII-
STM1273/yeaQ_36_70	0.57	-1.46	IryhB-2II-
ydiL/ydiK_60_94	0.18	1.63	IrprAII-
ydiH/STM1368_10_44	0.01	1.78	IrydBII+
STM1528 STM1530_138_17	0.03	1.82	ISTnc170II-
acnA cysB_145_179	0.04	-1.77	ISTnc180II-
STM1841 kdgR_45_84	0.02	2.40	ISTnc190II+
STM1871/STM1872_21_55	0.62	1.47	IryeBII-
edd zwf_2_36	0.28	-1.12	ISTnc200II-
yecA STM1939_63_97	0.00	2.09	ISTnc210II+

STM1994/ompS_17_54	0.01	3.22	lrseX ll+
ompS cspB_5_39	0.05	2.20	lSTnc220ll-
yegD/STM2126_77_116	0.60	1.26	lryeCll+
yegQ/STM2137_17_51	0.02	-13.14	lcyaRll+
STM2243 / STM2244_213_2	0.02	1.90	lisrGll+
ompC/yojN_40_76	0.29	1.97	lmicF ll+
glpC / STM2287_72_106	0.13	-1.17	lisrH-2 ll-
STM2287 /glpC_200_234	0.33	1.10	lisrH-1ll-
acrD yffB_29_63	0.01	-9.05	lSTnc250ll-
STM2534/sseB_209_243	0.21	1.34	lryfAll+
yfhK/purG_33_67	0.36	1.38	lglmY ll-
STM2614 / STM2616_33_67	0.04	1.89	lisrIll-
STM2616 / STM2614_2_39	0.15	1.57	lisrJll-
smpB / STM2690_178_212	0.07	-1.33	lisrLll-
STM2816 luxS_68_105	0.46	1.22	lSTnc260ll+
invH STM2901_16_54	0.95	1.01	lSTnc270ll+
invH/STM2901_8_46	0.59	1.06	linvRll+
yqcC/syd_311_345	0.03	-4.07	lcsrBll-
gcvA/ygdI_155_189	0.05	-1.50	lgcvBll+
kduI yqeF_9_43	0.94	-1.04	lSTnc280ll+
STM3038 / STM3039_65_99	0.58	-1.09	lisrOll+
ygfE/ygfA_93_127	0.43	1.30	lssrSll+
ygfA/serA_57_91	0.60	1.31	lrygC ll+
STM3123 STM3124_109_14	0.66	1.32	lSTnc300ll-
yqiK/rfaE_98_136	0.73	1.23	lrygD ll-
greA dacB_3_37	0.04	1.84	lSTnc330ll-
yhbL/arcB_17_51	0.06	-1.88	lsraH ll+
tnpA_5 yhfL_64_103	0.02	1.43	lSTnc340ll-
yhhX/yhhY_25_59	0.83	-1.07	lryhB-1ll-
yhjB yhjC_73_107	0.06	2.75	lSTnc360ll+
STM3691 lldP_3_38	0.17	-1.31	lSTnc380ll-
yibD tdh_12_46	0.04	-1.66	lSTnc390ll-
ilvB/emrD_49_83	0.14	1.22	listR ll-
STM3844 STM3845_25_59	0.12	1.59	lSTnc400ll+
glmU STM3863_89_123	0.05	3.24	lSTnc410ll+
yihA/yihI_158_192	1.00	-1.00	lcsrCll+

STM4097 / STM4098_65_99	0.35	1.11	lisrPll+
argH/oxyR_73_107	0.50	1.18	loxySll-
pgi yjbE_87_121	0.03	1.98	lSTnc430ll-
soxR/STM4267_65_99	0.37	2.98	lsraLll-
STM4310 tnpA_6_11_46	0.14	5.19	lSTnc440ll+
STM4503 STM4504_85_119	0.00	1.88	lSTnc460ll-