

Table S1. List of *Dehalobacteriia* genomes used in the analysis (in green rows)Types of the genomes provided in this table are **isolate**, **mixed culture** and **MAG**

Cmpl.: CheckM completion rate

Cntmn: CheckM contamination rate

Order	Genome	Genome Assembly ID	Size (Mb)	Cmpl. (%)	Cntmn (%)	GC (%)	CD (%)	Protein Count	16S	Ref.
o__Dehalobacteriales	<i>D.formicoaceticum</i>	GCF_002224645.1	3.8	95.6	2.6	43.2	86.1	3,620	Yes	9
	<i>Ca F. warabiya</i>	GCF_002777255.1	6.4	98.9	2.7	46.4	87.5	5,804	Yes	11
	DJPU01	GCA_012838175.1	2.4	91.9	2.0	42.1	88.8	2,447	No	38
	HGM13862	GCF_900760825.1	1.7	79.9	2.7	47.6	87.1	1,878	No	N/A
	AS06rmrACSlP_243	GCA_012515255.1	1.3	71.2	2.0	55.4	88.6	1,371	No	38
	UBA5752	GCA_002419055.1	2.1	91.9	0.7	42.7	88.8	1,965	No	36
	UBA4068	GCA_002382665.1	2.0	91.2	0.3	43.2	89.0	1,966	No	36
	UBA5757	GCA_002418965.1	1.9	89.1	0.9	43.8	86.2	1,808	Yes	36
o__UBA4068	Lab28P3bin203	GCA_009783495.1	1.1	59.6	1.8	55.7	87.6	1,315	No	38
	Nt197P3bin103	GCA_009783415.1	2.8	64.2	2.5	46.6	86.8	2,197	No	38
	Nt197P4bin8	GCA_00978255.1	2.2	70.8	1.7	42.9	90.0	2,024	No	38
	Nt197P3bin19	GCA_00978295.1	0.9	57.8	0.9	52.2	90.0	968	No	38
	UBA4997	GCA_002398485.1	1.7	78.5	0.8	40.5	74.9	1,568	Yes	39
	UBA5755	GCA_002419005.1	1.5	90.9	0.5	42.2	89.7	1,456	No	36
	UBA7702	GCA_002482535.1	2.6	93.1	0.9	49.5	88.8	2,402	No	40
o__UBA7702	RUG14212	GCA_902796855.1	2.1	84.8	2.6	57.4	88.8	1,936	No	37
	RUG11176	GCA_902766525.1	1.5	80.5	0.9	49.9	90.4	1,649	No	37

Table S2. List of primer sequences matched against 16S sequences from *Dehalobacteriia*

a. Primer sequences from Engelbrekston et al., ISMEJ 2010, representative of commonly used 16S rRNA gene primers

b. Metacharacters: K=GT, M=AC, R=AG, S=CG, W=AG, Y=CT

c. matches, mismatches

16S rRNA primer (a)	5'-3' sequence (b)	Dehalobacteriia sequence (c)	Variants	Comments
27F	AGAGTTGATC M TGGCTAG	AGAGTTGATC T GGCTAG	f__UBA5755: AGAGTTGAT C GGAT A TCAG	Should amplify, with exception of variant
357F	CTCC T ACGGGAGGCAGCAG	CTCC T ACGGGAGGCAGCAG	none	Should amplify
530F	GTGCCAG C GCCCGG	GTGCCAG C GCCCGG	none	Should amplify
803F	ATTAGATA CC CT G GTAGTC	ATTAGATA CC CCGGTA A TC	none	Probably won't amplify with mismatches near 3' end
926F	AAACT Y AAAK GA ATTGACGG	AAACT CA AA G GAATTGACGG	none	Should amplify
1114F	GCAACGAGCGCAACCC	GCAACGAGCGCAACCC	none	Should amplify
342R	CTGCTGCS Y CCCCTAG	CTGCTG C CCCCTAG	none	Should amplify
519R	GW ATTACCGCGGCKGCTG	G TATTACCGCGG T GCTG	none	Should amplify even with mismatch at 5' end
787R	CT ACCA GG GTATCTAA T	T TAC C GGGTATCTAA T	none	May amplify, noting mismatches closer to 5' end
907R	CCGTCAATT C TTTRAGTTT	CCGTCAATT C TTTGAGTTT	none	Should amplify
1100R	GGGTTCGCTCGTTG	GGGTTCGCTCGTTG	none	Should amplify
1392R	ACGGGCGGTGTG R C	ACGGGCGGTGTG A C	none	Should amplify

Table S3. List of 16S rRNA gene amplicon datasets associated with the identified *Dehalobacteriia* sequences5% raw num: raw number of sequences that share 95% or higher similarity to *Dehalobacteriia* sequences

5% perc: proportion of the "5% raw num" sequences out of total downloaded sequences from each study

Isolation Source	Reference	Total Downloaded Sequences	5% raw num	5% perc
Mouse cecum	41	7223	7	0.10
Cecal contents from <i>Mus musculus</i> strain C57BL/6J; sample lean_donor, leptin genotype +/+	42	4157	6	0.14
Cecum of mother 1 mouse offspring with genotype ob/ob	43	Offspring: 3998	Offspring: 5	0.13
Cecum of mother 1 mouse offspring with genotype ob/ob	43	Mother: 1120	Mother: 2	0.18
Human feces; subj10; 12 weeks; carb-r diet	44	6909	1	0.01
Insect gut	45	623	3	0.48
Push core sediment sample from the vadose zone of a hydrocarbon contaminated aquifer	46	486	3	0.62
Mud volcano	47	185	2	1.08

Table S4. List of KEGG Orthology IDs and their presence/absence in Dehalobacteria genomes based on BlastKOALA search

KO_ID	Description	D. formicoaceticum	Ca. f. warabiya	DUPU01	UBA7702	RUG14212	UBA4997	UBA5755	UBA5757	UBA4068	UBA5752
K00001	E1.1.1.1; adh; alcohol dehydrogenase [EC:1.1.1.1]	0	0	1	0	2	0	0	1	1	1
K00003	hom; homoserine dehydrogenase [EC:1.1.1.3]	1	1	2	1	1	1	1	1	1	1
K00004	BDH; butB; (R,R)-butanediol dehydrogenase / meso-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4 1.1.1.- 1.1.1.303]	0	0	1	0	0	0	0	0	0	0
K00008	SORD; grtB; L-iditol 2-dehydrogenase [EC:1.1.1.14]	0	0	3	1	1	0	0	0	0	0
K00012	UDG14; ggd; UDPglucose 6-dehydrogenase [EC:1.1.1.22]	1	0	2	0	0	0	0	0	0	0
K00013	hisD; histidinol dehydrogenase [EC:1.1.1.23]	1	1	3	1	1	1	0	1	1	1
K00014	arcE; shikimate dehydrogenase [EC:1.1.1.25]	1	1	2	1	1	2	0	1	1	1
K00015	gyrA; GORI; glyoxylate reductase [EC:1.1.1.26]	0	0	0	0	0	0	1	0	0	0
K00016	LDH; ldh; L-lactate dehydrogenase [EC:1.1.1.27]	0	0	0	0	1	0	0	0	0	0
K00018	hprA; glyceraldehyde dehydrogenase [EC:1.1.1.29]	0	0	0	1	0	0	0	0	1	0
K00027	ME2; stca; maaE; malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]	1	1	4	0	0	0	1	1	1	1
K00030	IDH3; isocitrate dehydrogenase (NAD+) [EC:1.1.1.41]	0	0	0	0	0	1	0	0	0	0
K00031	IDH1; IDH2; icd; isocitrate dehydrogenase [EC:1.1.1.42]	1	0	3	0	0	0	0	1	0	0
K00034	gdh; glucose 1-dehydrogenase [EC:1.1.1.47]	0	0	1	0	0	0	0	0	0	0
K00038	E1.1.1.53; Salphalor 20beta-hydroxysteroid dehydrogenase [EC:1.1.1.53]	0	0	0	1	1	0	0	0	0	0
K00046	idnO; glucuronate 5-dehydrogenase [EC:1.1.1.69]	0	0	0	0	0	0	0	2	0	0
K00052	leuB; IMDH; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]	1	1	1	0	1	1	0	2	1	1
K00053	ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]	1	1	1	0	1	1	1	1	1	1
K00057	gpsA; glycerol-3-phosphate dehydrogenase (NAD(P)) [EC:1.1.1.94]	2	1	1	0	1	1	1	1	1	1
K00058	serA; PHGDH; D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase [EC:1.1.1.95 1.1.1.399]	1	1	3	2	1	1	1	1	1	1
K00059	fabG; ORA1; 3-oxacy-[acyl-carrier protein] reductase [EC:1.1.1.100]	3	2	8	0	4	2	1	3	2	1
K00060	tdh; threonine dehydrogenase [EC:1.1.1.103]	0	0	1	0	0	0	0	0	0	0
K00065	kduD; 2-dehydro-3-deoxy-D-glucuronate 5-dehydrogenase [EC:1.1.1.127]	0	0	2	0	0	0	0	0	0	0
K00067	rfdD; rmdD; tDP-4-dehydrorhamose reductase [EC:1.1.1.133]	0	0	0	0	1	0	0	0	0	0
K00073	allD; uridylglycolate dehydrogenase (NAD+) [EC:1.1.1.135]	0	0	1	0	0	0	0	0	0	0
K00074	paAB; hbd; fadB; rnmB; 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]	0	0	5	0	0	0	0	0	1	1
K00075	murB; UDP-N-acetylmuramate dehydrogenase [EC:1.3.1.98]	1	1	1	1	1	1	1	1	1	1
K00077	panE; apBA; 2-dehydropropane 2-reductase [EC:1.1.1.169]	0	0	2	0	1	0	1	1	2	2
K00087	ygeS; xdhA; xanthine dehydrogenase molybdenum-binding subunit [EC:1.17.1.4]	5	2	18	0	0	2	1	2	5	4
K00088	IMPDH; guaB; IMP dehydrogenase [EC:1.1.1.205]	1	2	2	1	1	1	1	2	1	1
K00090	ghrB; glyoxylate hydroxypropanate 2-ketogluconate reductase [EC:1.1.1.79 1.1.1.81 1.1.1.215]	0	0	1	0	0	0	0	0	0	0
K00099	dcr; D-3-deoxy-D-xylulose 5-phosphate reductoisomerase [EC:1.1.1.267]	1	1	1	1	1	1	1	1	1	1
K01000	bhdAB; butanol dehydrogenase [EC:1.1.1.1]	0	0	1	0	0	0	0	0	0	0
K01012	LHDH; lhd; D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]	0	0	0	0	0	0	0	0	1	1
K01040	gldC; glycerol dehydrogenase FAO-linked subunit [EC:1.19.9.14]	1	0	7	0	0	0	0	0	0	0
K01011	gldA; gldD; glycerol 3-phosphate dehydrogenase [EC:1.1.1.53]	0	0	2	1	1	0	0	0	0	0
K01012	gldB; glycerol-3-phosphate dehydrogenase subunit B [EC:1.1.5.3]	0	0	1	0	0	0	0	0	0	0
K01013	gldC; glycerol-3-phosphate dehydrogenase subunit C	0	0	1	0	0	0	0	0	0	0
K01021	frmA; ADH; adhC; S-hydroxymethylglutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	0	0	1	0	0	0	1	0	0	0
K01023	fdoG; fdfH; fdwA; formate dehydrogenase major subunit [Ec:1.17.1.9]	2	2	2	0	0	0	1	0	0	0
K01024	fdoH; fdfB; formate dehydrogenase iron-sulfur subunit	0	1	0	1	0	0	1	0	0	0
K01028	ALD8; aldehyde dehydrogenase (NAD+) [EC:1.2.1.2.3]	0	0	0	2	1	2	0	1	0	0
K01029	betB; gbaB; betaine-aldehyde dehydrogenase [EC:1.2.1.1.8]	0	0	1	0	0	0	0	0	0	0
K01031	gapN; glyceraldehyde 3-phosphate dehydrogenase (NADP) [EC:1.2.1.9]	0	0	0	0	0	0	1	0	0	0
K01032	E1.2.1.10; acetaldehyde dehydrogenase (acetylating) [EC:1.2.1.10]	2	1	1	1	1	0	0	0	0	0
K01033	asdC; aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	1	1	2	1	1	1	0	1	1	1
K01034	GAPDH; gapA; glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]	1	1	1	1	1	1	1	1	1	1
K01035	gapB; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.20]	1	0	2	0	0	0	0	0	0	0
K01040	mmab; acdB; acdB-Coa dehydrogenase/synthase, CODH/ACS complex subunit delta [EC:2.1.1.245]	1	0	1	0	0	0	0	0	0	0
K01046	cofC; anaerobic carbon-monoxide dehydrogenase iron sulfur subunit	1	1	2	1	2	0	1	0	1	1
K01047	proA; glutamate 5-semialdehyde dehydrogenase [EC:2.1.1.41]	1	0	1	1	1	1	0	1	1	1
K01059	porA; pyruvate ferredoxin oxidoreductase alpha subunit [EC:1.2.7.1]	1	1	3	0	0	1	1	1	2	2
K01070	porB; pyruvate ferredoxin oxidoreductase beta subunit [EC:1.2.7.1]	1	1	2	0	0	1	1	1	2	2
K01071	porD; pyruvate ferredoxin oxidoreductase delta subunit [EC:1.2.7.1]	1	1	3	0	0	1	1	0	1	2
K01072	porC; porG; pyruvate ferredoxin oxidoreductase gamma subunit [EC:1.2.7.1]	1	1	3	0	0	1	1	1	2	2
K01074	korA; oorA; oorF; 2-oxacid ferredoxin oxidoreductase subunit alpha [Ec:1.2.7.3 1.2.7.11]	1	1	7	3	3	3	1	2	1	1
K01075	korB; oorB; 2-oxoglutarate 2-oxacid ferredoxin oxidoreductase subunit beta [EC:1.2.7.3 1.2.7.11]	1	1	3	3	3	0	2	1	1	1
K01076	korD; oorD; 2-oxoglutarate ferredoxin oxidoreductase subunit delta [Ec:1.2.7.3]	0	1	6	3	3	0	2	1	1	1
K01077	korC; oorC; 2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]	0	1	7	3	3	1	2	1	1	1
K01079	iorA; indolepyruvate ferredoxin oxidoreductase, alpha subunit [Ec:1.2.7.8]	1	2	4	2	2	1	1	3	2	1
K01080	iorB; indolepyruvate ferredoxin oxidoreductase, beta subunit [Ec:1.2.7.8]	1	2	4	2	2	1	3	2	1	1
K01084	dmsB; dimethyl sulfoxide reductase iron-sulfur subunit	1	1	2	0	0	0	0	0	0	0
K01085	dmsC; dimethyl sulfoxide reductase membrane subunit	1	1	1	0	0	0	0	0	0	0
K01094	cddB; acdB; CoA-dehydrogenase/synthase, CODH/ACS complex subunit delta [EC:2.1.1.245]	1	1	1	1	1	0	0	0	0	0
K01096	cofA; anaerobic carbon-monoxide dehydrogenase iron sulfur subunit	1	1	2	1	1	0	0	0	0	0
K01097	cddH; acydC; acydC-dehydrogenase [EC:2.1.1.245]	1	1	1	1	1	1	0	0	0	0
K01098	co5A; co5A; anaerobic carbon-monoxide dehydrogenase catalytic subunit [EC:1.2.7.4]	3	2	3	2	1	0	0	0	0	0
K02000	fwdA; fwdM; formylmethanofuran dehydrogenase subunit A [EC:1.2.7.12]	0	0	1	0	0	0	0	0	0	0
K02001	fwdB; fwdN; formylmethanofuran dehydrogenase subunit B [EC:1.2.7.12]	0	0	1	0	0	0	0	0	0	0
K02003	fwdD; fwdN; formylmethanofuran dehydrogenase subunit D [EC:1.2.7.12]	0	0	1	0	0	0	0	0	0	0
K02015	dapB; 4-hydroxy-tetrahydropicolinate reductase [EC:1.17.1.8]	1	1	1	2	1	1	1	1	1	1
K02019	fadH; 2,6-dienoyl-CoA reductase (NADPH) [EC:1.3.1.34]	0	0	3	0	0	0	2	1	0	1
K02023	PPOX; hemB; protoporphyrinogen propoxygenase III oxidase [EC:3.3.4.1 3.3.15]	1	1	1	0	0	0	0	0	0	0
K02040	sdhA; fadD; succinate dehydrogenase flavoprotein subunit [EC:3.3.5.1]	0	0	6	1	1	1	1	0	0	0
K02041	sdhB; fadB; succinate dehydrogenase iron-sulfur subunit [EC:3.3.5.1]	0	0	3	1	1	1	1	0	0	0
K02044	frdA; succinate dehydrogenase flavoprotein subunit [EC:3.3.5.1]	0	0	0	0	0	0	0	1	0	0
K02048	ACADS; bcd; butyryl-CoA dehydrogenase [EC:1.3.8.1]	0	0	2	0	0	0	0	1	0	0
K02061	GLUD1_2; gdhA; glutamate dehydrogenase (NADP) [EC:1.4.1.3]	0	0	0	0	0	1	0	0	0	0
K02062	E1.4.1.4; GLUD1_2; gdhA; glutamate dehydrogenase (NADP) [EC:1.4.1.4]	1	2	2	1	1	1	0	1	1	1
K02063	E1.4.1.9; leucine dehydrogenase [EC:1.4.1.9]	0	0	2	0	0	0	0	0	0	0
K02065	gltB; glutamate synthase (NADPH) large chain [EC:1.4.1.13]	0	0	1	0	0	0	0	0	0	0
K02066	gltB; glutamate synthase (NADPH) small chain [EC:1.4.1.13]	0	0	1	0	0	0	0	0	0	0
K02078	nadB; L-spartate oxidase [EC:1.4.3.16]	0	0	1	2	1	0	0	0	0	1
K02082	govPA; glycine dehydrogenase 1 subunit 1 [EC:1.4.4.2]	1	1	2	0	0	0	0	1	1	1
K02083	govPB; glycine dehydrogenase 2 subunit 2 [EC:1.4.4.2]	1	1	2	0	0	0	1	1	1	1
K02084	GLU1_2; gltB; glutamate synthase (ferredoxin) [EC:1.4.7.3]	0	0	1	0	0	0	0	0	0	0
K02086	procN; myrcillin-5-carboxylate reductase [EC:1.5.5.2]	1	1	2	1	1	1	1	1	1	1
K02087	DHF; dihydrofolate reductase [EC:1.5.1.3]	1	0	0	0	0	0	1	0	0	0
K02090	LYS1; saccharopine dehydrogenase (NAD+ -Lysine forming) [EC:1.5.1.7]	1	0	1	0	1	1	0	1	1	1
K02094	E1.2.1.8B; 1-pyrroline 5-carboxylate dehydrogenase [EC:1.2.1.8B]	1	0	3	0	0	0	0	1	0	0
K02097	metF; MTHFR; methenyltetrahydrofolate reductase (NADH) [EC:1.5.1.54]	2	2	1	1	1	1	1	1	1	1
K02098	ceo; NS-1; carboxyethyl-jorithione synthase [Ec:1.5.1.24]	0	0	0	0	0	0	0	0	1	1
K03020	soxA; sarcosine oxidase, subunit alpha [Ec:1.5.3.24 1.5.3.1]	2	2	4	1	1	0	0	0	0	0
K03023	soxB; sarcosine oxidase, subunit beta [Ec:1.5.3.24 1.5.3.1]	1	1	2	0	0	0	0	0	0	0
K03133	txcC; electron transfer flavoprotein-quinone oxidoreductase [Ec:1.5.5.-]	5	1	2	0	0	0	0	2	1	0
K03242	pntA; H+-translocating NADP+ transhydrogenase subunit alpha [Ec:1.6.1.2 7.1.1.1]	2	2	3	2	0	0	0	0	0	0
K03255	pntB; H+-translocating NADP+ transhydrogenase subunit beta [Ec:1.6.1.2 7.1.1.1]	1	1	1	0	0	0	1	0	0	0
K03300	nuoA; NADH-quinone oxidoreductase subunit A [Ec:1.1.2]	1	1	1	0	0	0	1	0	1	1
K03311	nuoB; NADH-quinone oxidoreductase subunit B [Ec:1.1.2]	1	1	1	0	0	0	0	0	0	0
K03322	nuoC; NADH-quinone oxidoreductase subunit C [Ec:1.1.2]	1	0	1	0	0	0	0</			

K00426	cydB; cytochrome bd ubiquinol oxidase subunit II [EC:7.7.1.7]	0	0	1	0	0	0	0	0	0	0	0
K00432	gpx; btb1; bsa1; glutathione peroxidase [EC:1.11.1.9]	0	0	0	1	0	0	0	0	0	0	0
K00433	cpo; non-heme chloroperoxidase [EC:1.11.1.10]	0	0	1	1	0	0	0	1	1	1	1
K00436	hoxH; NAD-reducing hydrogenase large subunit [EC:1.12.1.2]	0	0	0	0	0	0	0	1	1	2	1
K00441	frhB; coenzyme F420 hydrogenase subunit beta [EC:1.12.98.1]	0	0	1	0	0	0	0	0	0	0	0
K00459	ned2; nitrated-nitronate monooxygenase [EC:1.13.12.16]	1	0	1	0	0	0	0	0	0	1	1
K00525	E1.17.4.1A; nrdA; nrdE; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]	1	1	0	1	1	0	1	1	1	1	1
K00528	fpr; ferredoxin/flavodoxin-NADP+ reductase [EC:1.18.1.2.1.19.1.1]	0	0	0	0	0	0	0	0	1	1	1
K00533	E1.12.7.2L; ferredoxin hydrogenase large subunit [EC:1.12.7.2]	0	1	1	0	0	0	0	0	0	0	0
K00537	arsC; arsenite reductase (glutaredoxin) [EC:1.2.2.1]	0	1	1	1	0	0	0	1	1	0	0
K00548	metH; MTR; S-methyltetrahydrofolate--homocysteine methyltransferase [EC:2.1.1.13]	11	6	56	5	9	2	5	2	3	3	3
K00554	trmD; tRNA (guanine-37(N1)-methyltransferase [EC:2.1.1.228]	1	1	1	1	1	1	1	1	1	1	1
K00558	DNMT1; dcm; DNA (cytosine-5)-methyltransferase 1 [EC:2.1.1.37]	1	0	0	0	1	0	0	0	0	1	1
K00560	thyA; IYMS; thymidylate synthase [EC:2.1.1.45]	1	1	1	1	1	1	2	1	1	1	1
K00563	rlnA1; 23S rRNA (guanine-745(N1)-methyltransferase [EC:2.1.1.187]	1	0	1	0	0	0	0	0	0	0	0
K00566	mnmA; tmrM; RNA-uridine 2-sulfurtransferase [EC:2.8.1.13]	1	1	1	1	1	1	1	1	1	2	2
K00567	ogt; MGMT; methylated-DNA-protein--cytidine S-methyltransferase [EC:2.1.1.63]	1	1	2	1	2	1	1	1	1	1	1
K00569	ubG; 2-polymer-6-hydroxypyrimidine methylase / 3-demethylubiquinone-9,3-methyltransferase [EC:2.1.1.222.2.1.1.64]	0	0	0	0	0	0	0	0	0	1	1
K00571	E2.1.1.7Z; site-specific DNA-methyltransferase (adenine-specific) [EC:2.1.1.7Z]	0	0	0	1	0	0	0	0	1	2	1
K00573	E2.1.1.7Z; pcm; protein-1-isoparate(D-aspartate)-O-methyltransferase [EC:2.1.1.7Z]	1	1	1	0	0	0	0	0	0	0	0
K00574	cfa; cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79]	1	1	1	0	0	0	0	0	0	0	0
K00575	cheR; chemotaxis protein methyltransferase CheR [EC:2.1.1.80]	0	2	3	0	1	0	1	0	1	1	1
K00584	mttr; tetrahydromethanopterin S-methyltransferase subunit H [EC:2.1.1.86]	1	0	3	0	0	0	0	0	0	0	0
K00588	E2.1.1.104; coffeeYL-CoA O-methyltransferase [EC:2.1.1.104]	1	1	1	0	0	0	0	0	0	0	0
K00590	E2.1.1.113; site-specific DNA-methyltransferase (cytosine-N4-specific) [EC:2.1.1.113]	0	0	2	0	0	0	0	0	0	0	0
K00595	cobL-cbtE; precorrin-6B C5,15-methyltransferase / cobalt-precorrin-6B C15-methyltransferase [EC:2.1.1.132.2.1.1.289.2.1.1.196]	0	0	1	1	1	0	1	0	1	1	1
K00600	glyA; SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1]	1	1	2	0	1	1	0	1	1	1	1
K00602	purH; phosphoribosylaminodecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.5.3.5.4.10]	1	1	1	1	1	1	1	1	1	2	2
K00603	fcdT; glutamate formiminotransferase / 5-formyltetrahydrofolate cyclo-ligase [EC:2.1.2.5.6.3.3.2]	0	0	0	1	0	0	0	0	1	1	1
K00604	MTFM; fmt; methyl-β-D-ribofuranose formyltransferase [EC:2.1.2.9]	1	1	1	1	1	1	1	1	1	1	1
K00605	govT; AMT; aminomethyltransferase [EC:2.1.2.10]	1	1	1	0	0	0	0	0	1	1	1
K00606	panB; 3-methyl-2-oxobutanate hydroxymethyltransferase [EC:2.1.2.11]	1	0	8	0	0	1	1	1	1	1	1
K00609	pyR; PYR2; aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]	1	1	1	1	1	1	1	1	1	1	1
K00611	OTC; argF; argI; ornithine carbamoyltransferase [EC:2.1.3.3]	1	1	1	1	1	1	1	1	1	1	1
K00615	E2.2.1.1; tkTA; tkTB; transketolase [EC:2.2.1.1]	2	2	2	2	2	2	2	1	2	2	2
K00616	E2.2.1.2; talA; talB; transaldolase [EC:2.2.1.2]	1	1	1	1	1	1	1	0	0	0	0
K00619	argA; amino-acid N-acetyltransferase [EC:2.3.1.1]	1	0	1	0	0	1	1	1	0	0	0
K00620	argJ; glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.35.2.3.1.1]	1	1	1	1	1	1	1	1	1	1	1
K00621	GNPNNAT1; GNA1; glucosamine-phosphate N-acetyltransferase [EC:2.3.1.4]	0	0	1	0	0	0	0	0	0	0	0
K00625	pta; phosphate acyltransferase [EC:2.3.1.8]	0	0	0	0	0	0	0	0	1	0	0
K00626	ACAT; atOB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	0	0	6	0	0	0	0	3	0	0	0
K00634	ptb; phosphate butyryltransferase [EC:2.3.1.19]	0	0	1	0	0	0	0	0	1	0	0
K00638	catB; chloramphenicol O-acetyltransferase type B [EC:2.3.1.28]	0	0	0	0	0	0	0	0	0	0	1
K00639	khB; GATC; glycine C-acetyltransferase [EC:2.3.1.29]	0	0	2	0	0	0	0	0	0	0	0
K00640	cysE; serine O-acetyltransferase [EC:2.3.1.30]	1	1	1	1	1	1	1	1	1	1	1
K00645	fabB; MCAT; MCT1; [acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]	1	1	1	0	1	1	1	1	1	1	1
K00648	fabH; 3-oxoacyl-[acyl-carrier-protein] synthase III [EC:2.3.1.180]	3	2	1	0	0	1	1	1	1	1	1
K00651	metK; homoserine O-succinyltransferase/O-acetyltransferase [EC:2.3.1.46.2.3.1.31]	1	1	1	1	1	1	0	0	1	0	1
K00655	plsC; 1-O-acyl-sn-glycerol-3-phosphate acyltransferase [EC:2.3.1.51]	1	1	1	1	1	1	1	1	1	1	1
K00656	E2.3.1.54; pfld; formate C-acetyltransferase [EC:2.3.1.54]	4	2	2	0	0	1	1	0	0	0	0
K00657	speG; SAT; diaminobutyrate acetyltransferase [EC:2.3.1.57]	0	0	1	0	1	0	0	0	0	0	0
K00661	malA; maltose O-acetyltransferase [EC:2.3.1.79]	2	1	0	0	1	0	0	0	1	0	0
K00666	K00666; fatty acyl-CoA synthase [EC:2.1.1.1]	3	2	4	0	1	1	1	1	1	1	1
K00672	ftr; formylmethanofuran-tetrahydromethanopterin N-formyltransferase [EC:2.3.1.101]	0	0	2	0	0	0	0	0	0	0	0
K00686	tgt; protein-glutamine gamma-glutamyltransferase [EC:2.3.2.13]	0	0	2	0	0	0	0	0	1	1	1
K00688	PVG; PGP; glycogen phosphorylase [EC:2.4.1.1]	3	2	2	0	0	0	0	0	0	0	0
K00700	G8El; g8B; 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	1	1	1	0	0	0	0	0	0	0	0
K00703	glgA; starch synthase [EC:2.4.1.21]	1	1	1	1	0	0	0	0	0	0	0
K00705	malQ; 4-alpha-glucanotransferase [EC:2.4.1.25]	1	0	0	1	1	0	0	0	0	0	0
K00721	DPM1; diolchol-phosphate mannosyltransferase [EC:2.4.1.83]	1	1	1	1	1	1	1	1	1	2	2
K00750	pdP; pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]	1	1	1	1	1	1	1	1	1	1	1
K00759	APRT; apt; adenosine phosphoribosyltransferase [EC:2.4.2.7]	0	0	0	0	0	0	0	0	1	1	1
K00760	hpT; hpt; HPRT1; hypoxanthine phosphoribosyltransferase [EC:2.4.2.8]	2	1	1	1	1	1	1	1	1	1	1
K00761	upT; upR; uracil phosphoribosyltransferase [EC:2.4.2.9]	1	1	1	1	1	0	0	0	0	0	0
K00762	pyE; orotate phosphoribosyltransferase [EC:2.4.2.10]	1	1	2	1	1	1	1	1	1	1	1
K00763	pncB; NAPRT1; nicotinate phosphoribosyltransferase [EC:6.3.4.21]	1	1	1	1	1	0	0	0	0	1	0
K00764	pufP; PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]	2	0	2	1	1	1	2	1	2	1	1
K00765	hisG; ATP phosphoribosyltransferase [EC:2.4.2.17]	1	0	0	1	1	1	0	1	1	1	1
K00766	trpD; anthranilate phosphoribosyltransferase [EC:2.4.2.18]	2	0	2	1	2	1	0	0	1	1	1
K00767	adnC; QPR7; nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19]	0	0	1	0	1	1	0	1	1	2	2
K00768	E2.4.2.21; cobU; cobT; nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase [EC:2.4.2.21]	2	1	1	1	1	0	0	0	0	0	0
K00772	mtaP; MTAP; S'-methyladenosine phosphorylase [EC:2.4.2.28]	1	1	1	1	1	0	1	1	2	2	2
K00773	tgt; quevRNA tRNA phosphoribosyltransferase [EC:2.4.2.29]	1	0	1	1	1	1	1	1	1	1	1
K00782	IldG; L-actate dehydrogenase complex protein IldG	0	0	0	0	0	1	0	0	0	0	0
K00783	rlnM; 23S rRNA (pseudouridine1915(N3)-methyltransferase [EC:2.1.1.177]	1	1	1	1	1	1	1	1	1	1	1
K00784	rnz; ribonuclease Z [EC:3.2.16.11]	2	1	1	1	1	0	1	1	1	1	1
K00785	GALT29A; beta-1,6-galactosyltransferase [EC:2.4.1.1]	1	0	0	0	0	0	0	0	1	2	1
K00788	thiE; thiamine-phosphate pyrophosphorylase [EC:2.5.1.3]	1	0	1	2	1	1	1	0	1	0	0
K00789	metK; MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]	3	1	1	1	1	1	0	1	1	1	1
K00790	murK; UDP-N-aculosamine 1-carboxyvinyltransferase [EC:2.5.1.7]	3	3	3	2	2	2	2	2	2	2	2
K00791	miaA; TRT1; tRNA dimethylallyltransferase [EC:2.5.1.75]	1	1	1	1	1	1	1	1	1	1	1
K00793	ribE; RIBB; riboflavin synthase [EC:2.5.1.9]	1	0	1	1	1	1	1	0	1	1	1
K00794	ribH; RIBB; 6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]	1	0	1	1	1	1	1	0	1	1	1
K00796	folP; dihydropteroate synthase [EC:2.5.1.15]	1	1	2	1	1	1	1	1	1	1	1
K00797	speE; SRP; spermidine synthase [EC:2.5.1.16]	0	1	1	0	0	0	0	0	0	0	0
K00798	MMAB; pduO; colB; laminin adenylyltransferase [EC:2.5.1.17]	0	1	1	0	0	0	0	0	0	0	0
K00800	araO; 3-phosphoshikimate 1-carboxyvinyltransferase [EC:2.5.1.19]	1	1	1	1	1	1	1	1	1	1	1
K00805	hepS; heptaprenyl diphosphate synthase component 1 [EC:2.5.1.30]	3	2	3	1	2	1	1	1	1	0	1
K00806	upP5; undecaprenyl diphosphate synthase [EC:2.5.1.31]	1	1	1	1	1	1	1	2	1	1	1
K00812	aspB; aspartate aminotransferase [EC:2.6.1.1]	0	0	2	0	0	0	0	0	0	0	0
K00817	hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]	1	1	5	2	2	1	1	1	1	1	1
K00819	roG; OAT; ornithine--oxo-acid transaminase [EC:2.6.1.13]	0	0	2	0	0	0	0	0	0	0	0
K00820	glmS; GPT; glutamine--fructose-6-phosphate transaminase (isomerizing) [EC:2.6.1.16]	1	1	1	1	1	1	1	1	1	1	1
K00821	argA; acetylornithine/N-succinylargininephosphate aminotransferase [EC:2.6.1.12.2.6.1.17]	1	1	1	1	1	1	1	1	1	1	1
K00823	pudE; 4-diphosphocytidylyl-2-C-methyl-D-erythritol kinase [EC:2.7.1.148]	0	0	1	0	0	0	0	0	0	0	0
K00825	isPE; 4-diphosphocytidylyl-2-C-methyl-D-erythritol kinase [EC:2.7.1.148]	1	1	1	1	1	1	1	1	1	1	1
K00826	E2.6.1.42; IVc; branched-chain amino acid aminotransferase [EC:2.6.1.42]	1	1	2	1	1	0	0				

K00937	ppk1; polyphosphate kinase [EC:2.7.4.1]	1	0	1	0	0	0	0	1	0	0
K00939	adk; AK; adenylate kinase [EC:2.7.4.3]	1	1	1	1	1	1	1	1	1	1
K00940	ndk; NME; nucleoside-diphosphate kinase [EC:2.7.4.6]	1	1	1	0	1	0	0	0	1	1
K00941	thiD; hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [EC:2.7.1.49 2.7.4.7]	1	0	1	1	1	1	1	0	1	0
K00942	grmk; GUK1; guanylate kinase [EC:2.7.4.8]	1	1	1	1	1	1	1	1	1	1
K00943	tnk; DTMK; cGMP kinase [EC:2.7.4.9]	1	1	1	1	1	1	1	1	1	1
K00945	cmk; CMP/GCMP kinase [EC:2.7.4.25]	1	1	1	2	2	1	1	1	1	1
K00948	PRPS; prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	1	1	1	1	1	1	1	1	1	1
K00949	thin; TPK1; THI80; thiamine pyrophosphokinase [EC:2.7.6.2]	1	1	1	1	1	1	1	1	1	1
K00950	tkf2; 2-amino-4-hydroxy-6-hydroxymethyl/dihydropteridine diphosphokinase [EC:2.7.6.3]	1	0	1	1	1	1	1	0	1	0
K00951	relA; GTP pyrophosphokinase [EC:2.7.6.5]	1	1	1	1	1	1	1	1	1	1
K00954	E2.7.7.3A; cobA; kdtB; pantetheine-phosphate acetyltransferase [EC:2.7.7.3]	1	1	1	1	1	1	1	1	1	1
K00962	ppn; PNP1; polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]	1	1	0	1	1	1	1	1	1	1
K00963	UGP2; galU; galF; UTP-glucosidase 1-phosphate uridylyltransferase [EC:2.7.7.9]	1	0	1	0	0	0	0	0	0	0
K00966	GMPP; mannose-3-phosphate guanylyltransferase [EC:2.7.7.13]	0	0	0	0	0	1	0	0	0	0
K00969	nadD; nicotinate-nucleotide adenyltransferase [EC:2.7.7.18]	1	1	1	1	1	1	1	1	1	1
K00971	manC; cpsB; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]	1	1	2	1	1	1	0	0	0	0
K00973	rfaB; rma1; rffB; glucose-1-phosphate thymidylate transferase [EC:2.7.7.24]	2	0	2	1	2	0	1	0	0	0
K00974	cca; tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.72 3.1.3.- 3.1.4.-]	2	1	2	1	1	1	1	1	1	1
K00975	glgC; glucose-1-phosphate acetyltransferase [EC:2.7.7.27]	3	3	0	0	1	0	0	0	1	1
K00978	rflF; glucose-1-phosphate cytidylyltransferase [EC:2.7.7.33]	0	0	1	0	1	0	0	0	0	0
K00981	E2.7.7.41; C01; CS02; csdS; phosphatidate cytidylyltransferase [EC:2.7.7.41]	1	0	1	1	1	1	0	1	1	1
K00986	ltrA; RNA-directed DNA polymerase [EC:2.7.7.49]	2	0	9	0	0	0	0	0	0	0
K00989	rph; ribonuclease PH [EC:2.7.7.56]	1	1	1	1	1	0	1	0	0	0
K00991	ispD; 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [EC:2.7.7.60]	1	1	0	0	1	0	1	1	1	1
K00995	pgsA; PGSL; CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase [EC:2.7.8.5]	1	1	3	1	1	1	1	1	1	1
K00996	rfpP; undecaprenyl-phosphate galactose phosphotransferase [EC:2.7.8.6]	1	0	0	0	0	0	0	0	0	0
K00997	agsP; halo-[acyl-carrier protein] synthase [EC:2.7.8.7]	1	1	1	1	1	0	1	0	0	0
K01000	mravP; pyrophospho-N-acetylmannosaminylpentapeptide-transferase [EC:2.7.8.13]	1	1	1	1	1	1	0	1	1	1
K01006	ppdk; pyruvate, orthophosphate dikinase [EC:2.7.9.1]	1	1	1	1	1	1	0	1	1	1
K01007	pps; ppsA; pyruvate, water dikinase [EC:2.7.9.2]	1	1	7	0	0	0	0	0	0	0
K01008	selD; SEPHS; selinole, water dikinase [EC:2.7.9.3]	1	1	1	0	0	1	1	1	1	1
K01012	bioB; biotin synthase [EC:2.8.1.6]	0	1	3	2	1	1	0	1	1	1
K01023	asST; arylsulfatase sulfotransferase [EC:2.8.2.22]	3	0	0	0	0	0	0	0	0	0
K01034	atbO; acetate CoA/acetoacetate CoA-transferase beta subunit [EC:2.8.3.8 2.8.3.9]	0	0	2	0	0	0	0	2	0	0
K01035	atoA; acetate CoA/acetoacetate CoA-transferase beta subunit [EC:2.8.3.8 2.8.3.9]	0	0	1	0	0	0	0	2	0	0
K01039	gctA; glutamate CoA-transferase, subunit A [EC:2.8.3.12]	1	0	3	0	0	0	0	0	0	0
K01040	gctB; glutamate CoA-transferase, subunit B [EC:2.8.3.12]	1	0	3	0	0	0	0	0	0	0
K01042	selA; L-seryl-tRNA(Ser) seleniumtransferase [EC:2.9.1.1]	1	1	1	0	0	1	1	1	1	1
K01046	lip; TGL2; triacylglycerol lipase [EC:3.1.1.3]	0	0	2	0	0	0	0	0	1	1
K01048	pldB; lysophospholipase [EC:3.1.1.5]	0	0	0	1	0	0	1	0	0	0
K01055	pcaO; 3-oxoadipate enol-lactonase [EC:3.1.1.24]	0	0	1	0	0	0	0	0	1	1
K01056	PTH1; PTHR1; pth; spoVC; peptidyl-tRNA hydrolase, PTH1 family [EC:3.1.1.29]	1	1	1	1	1	1	1	1	1	1
K01061	E3.1.1.45; carboxymethylbenzenolmildase [EC:3.1.1.45]	0	0	1	0	0	0	0	0	0	0
K01066	aes; acetyl esterase [EC:3.1.1.1-]	1	0	0	0	0	1	0	1	1	1
K01069	glob; gloc; HAGH; hydroxycyclathione hydrolase [EC:3.1.2.6]	2	2	3	1	1	1	1	2	1	1
K01071	MCH; medium-chain acyl-[acyl-carrier-protein] hydrolase [EC:3.1.2.21]	0	0	1	0	0	0	0	0	0	0
K01073	E3.1.2.20; acyl-CoA hydrolase [EC:3.1.2.20]	1	0	0	0	0	0	0	0	0	0
K01077	E3.1.3.1; phoA; phoB; alkaline phosphatase [EC:3.1.3.1]	1	0	2	0	0	0	0	0	0	1
K01081	E3.1.3.5; 5'-nucleotidase [EC:3.1.3.5]	0	0	0	0	0	0	0	0	0	1
K01089	E3.1.3.16; protein phosphatase [EC:3.1.3.16]	0	0	1	0	0	0	0	0	0	0
K01091	gbp; phosphoglycerate phosphatase [EC:3.1.3.18]	0	2	3	3	5	0	0	1	1	1
K01092	E3.1.3.25; IMPA; subB; myo-inositol-(4R)-monophosphate [EC:3.1.3.25]	1	0	1	0	0	0	0	0	0	0
K01096	pgpB; phosphatidylglycerophosphate B [EC:3.1.3.27 3.6.1.75 3.1.3.4.3 3.6.1.27]	0	0	0	1	1	0	0	0	0	0
K01104	E3.1.3.48; protein tyrosine phosphatase [EC:3.1.3.48]	2	2	2	2	4	2	1	1	0	0
K01114	plc; phospholipase C [EC:3.1.4.3]	0	0	1	0	0	0	0	0	0	0
K01118	acpD; azorF; FMN-dependent NADH-azoreductase [EC:1.7.1.17]	0	0	0	0	1	0	1	0	0	0
K01129	E3.1.4.46; pfpA; upgD; glycerocephosphoryl diester phosphodiesterase [EC:3.1.4.46]	1	1	2	1	1	1	1	1	1	1
K01138	K01138; uncharacterized sulfatase [EC:3.1.6.-]	0	0	0	0	0	0	0	1	0	0
K01142	E3.1.11.2; xtbH; exodeoxyribonuclease III [EC:3.1.11.2]	1	1	1	0	0	1	1	1	0	0
K01151	nfd; deoxyribonuclease IV [EC:3.1.21.2]	1	1	1	1	1	0	0	1	2	1
K01153	hsdR; type I restriction enzyme, R subunit [EC:3.1.21.3]	1	0	0	0	2	0	0	1	0	1
K01154	hsdS; type I restriction enzyme, S subunit [EC:3.1.21.3]	1	0	0	0	2	0	0	1	0	1
K01155	E3.1.21.4; type II restriction enzyme [EC:3.1.21.4]	1	0	0	1	0	0	0	0	0	0
K01159	rucC; crossover junction endodeoxyribonuclease RucC [EC:3.1.21.10]	1	1	1	1	1	1	1	1	1	1
K01160	rusA; crossover junction endodeoxyribonuclease RusA [EC:3.1.21.10]	0	0	0	0	0	0	0	0	0	1
K01163	K01163; uncharacterized protein	1	0	0	0	0	1	1	1	1	1
K01200	pulaA; pullulanase [EC:3.2.2.14]	0	0	1	0	0	0	0	0	0	0
K01207	nagZ; beta-N-acetylxosaminidase [EC:3.2.1.25]	0	1	1	0	0	0	0	0	1	1
K01239	E3.2.2.1.2; purine nucleosidase [EC:3.2.2.1]	0	0	1	0	0	0	0	0	0	0
K01246	tag; DNA-3-methylenadenine glycosylase I [EC:3.2.2.20]	0	0	1	0	0	0	0	0	0	0
K01247	alkA; DNA-3-methylenadenine glycosylase II [EC:3.2.2.21]	1	0	0	0	0	0	0	0	0	0
K01251	AHCY; acnC; adenosylhomocysteine [EC:3.13.2.1]	1	1	1	1	1	0	0	0	0	0
K01259	pip; proline iminopeptidase [EC:3.4.11.5]	0	0	0	1	0	0	0	0	0	0
K01262	pepP; Xaa-Pro aminopeptidase [EC:3.4.11.9]	1	1	1	1	1	0	1	0	1	1
K01265	map; methionyl aminopeptidase [EC:3.4.11.18]	2	1	2	1	1	1	1	1	1	1
K01266	dmpD; dpaD; D-aminopeptidase [EC:3.4.11.19]	0	0	0	1	1	0	0	0	0	0
K01269	yhfE; aminopeptidase [EC:3.4.11.-]	0	0	1	0	0	0	0	0	0	0
K01271	pepC; Xaa-Pro dipeptidase [EC:3.4.13.9]	0	1	5	0	1	1	0	2	1	1
K01273	DPEP; membrane dipeptidase [EC:3.4.13.19]	1	1	2	1	1	1	1	1	1	1
K01297	ldcA; muramoyl tetrapeptide carboxypeptidase [EC:3.4.17.13]	0	0	0	0	0	0	0	0	1	0
K01305	iadA; beta-aspartyl-dipeptidase (metallo-type) [EC:3.4.19.-]	1	1	1	0	0	0	0	0	0	0
K01308	vgtT; e-G-glutamyl-meso-diaminopimelate peptidase [EC:3.4.19.11]	0	0	0	0	0	1	0	0	0	0
K01338	Ion; ATP-dependent Lon protease [EC:3.4.21.53]	3	2	2	2	2	2	2	1	1	1
K01356	lexA; repressor LexA [EC:3.4.21.88]	2	0	4	2	2	2	2	1	0	0
K01358	cipP; CLPP; ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]	1	1	2	1	2	1	1	1	1	2
K01409	OSGP; KAE1; QR1; NG-t-hreonylcarbamoyladenine synthase [EC:2.3.2.1.234]	2	2	2	2	2	1	1	2	2	1
K01419	hslV; cipQ; ATP-dependent HslUV protease, peptidase subunit HslV [EC:3.4.25.2]	1	1	1	1	1	1	1	1	1	1
K01420	fnr; CRP/NFR family transcriptional regulator, anaerobic regulatory protein	2	0	0	0	1	0	0	0	1	1
K01421	yhgB; putative membrane protein [EC:3.5.1.20]	0	0	0	2	1	1	2	0	2	2
K01424	E3.5.1.1; ansA; ansB; L-anspiragine [EC:3.5.1.1]	0	1	1	0	0	1	0	0	1	1
K01436	yhaB; N-methylhydantoinase B [EC:3.5.2.14]	1	1	2	0	0	0	0	0	0	0
K01462	PDF; def; peptide deformylase [EC:3.5.1.88]	1	1	2	1	1	1	1	1	1	1
K01464	DY5; dft; hydA; dihydroprymidinase [EC:3.5.2.2]	0	1	3	0	0	0	0	1	0	0
K01465	URA4; prcF; dihydrorotase [EC:3.5.2.3]	1	1	1	1	1	0	0	0	0	0
K01466	allB; allantoinase [EC:3.5.2.5.2]	0	0	1	0	0	0	1	0	1	1
K01468	hutL; AMDHD1; imidazolonepropionatease [EC:3.5.2.7]	1	1	2	0	0	0	0	0	0	0
K01470	E3.5.2.10; creatinine amidohydrolase [EC:3.5.2.10]	0	0	1	0	0	0	0	2	0	0
K01473	hyuA; N-methylhydantoinase A [EC:3.5.2.14]	0	2	4	0	2	0	0	0	0	0
K01474	hyuB; N-methylhydantoinase B [EC:3.5.2.14]	0	2	4	0	2	0	0	0	0	0
K01476	E3.5.3.1; rocF; arg; arginase [EC:3.5.3.1]	1	0	0	0	0	0	0	0	0	0
K01478	arcA; arginase deiminase [EC:3.5.3.6]	0	0	2	0	1	0	0	0	0	0
K01480	speB; agmatinase [EC:3.5.3.11]	1	0	1	0	2	1	0	1	1	1
K01482	DDAH; ddah; dimethylargininase [EC:3.5.3.18]	0	0	1	0	0	0	0	0	0	0
K01483	codA; cytosine/creatinine deaminase [EC:3.5.4.21]	0	0	0	0	0	0	0	0	1	0
K01486	ade; adenine deaminase [EC:										

K01524	ppx-gppA; exopolyphosphatase / guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase [EC:3.6.1.11.3.6.1.40]	2	1	3	1	1	1	1	2	1	1
K01531	mgtA, mgtB; P-type Mg ²⁺ transporter [EC:7.2.2.14]	1	0	0	2	0	0	0	0	0	0
K01532	copB; P-type Cu ²⁺ transporter [EC:7.2.2.29]	1	0	0	1	0	0	0	0	0	0
K01534	zntA; Zn ²⁺ /Cd ²⁺ -exporting ATPase [EC:7.2.12.7.2.2.21]	3	2	3	4	1	0	0	1	1	1
K01537	ATP2C; P-type Ca ²⁺ transporter type 2C [EC:7.2.2.10]	1	1	3	1	3	2	0	2	2	3
K01546	kdpA; potassium-translocating ATPase potassium-binding subunit	1	0	1	0	0	0	0	0	0	0
K01547	kdpB; potassium-translocating ATPase ATP-binding subunit [EC:7.2.2.6]	1	0	1	0	0	0	0	0	0	0
K01551	arsA, ASNA1, GET3; arsenite/tellurite-anchored protein-translocating ATPase [EC:7.3.2.7.7.3.-.]	0	0	0	1	0	0	0	0	0	0
K01560	E3.8.1.2; 2-haloacid dehalogenase [EC:3.8.1.2]	1	0	0	1	0	0	0	0	0	0
K01571	oaaD; oxalacetate decarboxylase (Na ⁺ -extruding) subunit alpha [EC:7.2.4.2]	1	1	1	0	0	1	1	1	1	1
K01575	alsD, budA, aldC; acetolactate decarboxylase [EC:4.1.1.5]	0	0	0	1	0	0	0	0	1	1
K01579	panD; aspartate 1-decarboxylase [EC:4.1.1.11]	1	0	0	1	0	0	1	1	1	1
K01582	E4.1.1.18; lccD, cdaD; lysine decarboxylase [EC:4.1.1.18]	0	0	0	0	0	0	0	1	0	0
K01585	speA; arginine decarboxylase [EC:4.1.1.19]	2	1	2	1	1	2	0	1	2	2
K01586	lysA; diaminopimelate decarboxylase [EC:4.1.1.20]	1	1	1	1	1	1	1	1	1	1
K01588	purE; 5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]	1	1	1	1	1	1	1	1	1	1
K01591	pyfR; 5'-phosphate decarboxylase [EC:4.1.1.23]	1	1	1	1	1	1	1	1	1	1
K01596	E4.1.1.32; pckA, PCK; phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]	0	0	0	0	0	0	0	0	1	1
K01599	hemF, UROD; uroporphyrinogen decarboxylase [EC:4.1.1.37]	6	3	10	0	4	0	1	0	0	0
K01607	pcaC; 4-carboxymuconolactone decarboxylase [EC:4.1.1.44]	1	0	0	1	0	0	0	0	0	0
K01609	trpC; indole-3-glycerol phosphate synthase [EC:4.1.1.48]	1	0	1	0	1	1	0	0	1	1
K01610	E4.1.1.49; pckA; phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	0	0	2	0	0	1	1	1	0	0
K01611	speD, AM1; S-adenosylmethionine decarboxylase [EC:4.1.1.50]	1	1	1	1	1	0	1	1	1	1
K01613	psd, PISD; phosphatidylserine decarboxylase [EC:4.1.1.65]	1	1	0	0	0	0	0	0	0	0
K01615	gdcA; glutamyl-CoA decarboxylase subunit alpha [EC:7.2.4.5]	0	0	1	0	0	0	0	0	0	0
K01619	deoC, DERA; deoxyribose-phosphate aldolase [EC:4.1.2.4]	1	1	1	1	0	0	1	1	1	1
K01620	ItaE; threonine aldolase [EC:4.1.2.48]	0	1	2	1	1	0	0	0	0	0
K01621	xfp, xpk; xylulose 5-phosphate/fructose-6-phosphate phosphoketolase [EC:4.1.2.9.4.1.2.22]	0	0	0	0	0	1	0	0	1	0
K01622	ko1622; fructose-1,6-bisphosphate aldolase/phosphatase [EC:4.1.2.13.3.1.11]	0	1	1	0	0	0	0	0	0	0
K01624	FBA, fbaA; fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	1	1	1	1	1	1	0	1	1	1
K01626	E2.5.1.4, arfO, aroN, aroH; 3-deoxy-7-phosphophenylalanine synthase [EC:2.5.1.54]	1	0	0	1	0	0	0	0	0	0
K01628	fucA; L-fuculose-phosphate aldolase [EC:4.1.2.17]	1	1	3	1	1	0	1	1	1	1
K01633	folB; D,L-hydroxyneopterin aldolase/epimerase/oxygenase [EC:4.1.2.25.5.1.99.8.1.13.11.81]	1	1	1	1	1	1	1	1	1	1
K01640	HMGCL, hmgT; hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]	0	0	1	0	0	0	0	0	0	0
K01643	citF; citrate lyase subunit alpha / citrate CoA-transferase [EC:2.8.3.10]	0	0	3	0	0	0	0	0	0	0
K01644	citE; citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.34]	0	0	4	0	0	0	0	0	0	0
K01646	citD; citrate lyase subunit gamma (acyl carrier protein)	0	0	3	0	0	0	0	0	0	0
K01647	C5, gtaA; citrate synthase [EC:2.3.3.1]	1	0	0	0	0	0	0	0	0	0
K01649	leuA, IM5; 2-isopropylmalate synthase [EC:2.3.3.13]	2	2	3	1	2	3	1	2	1	2
K01652	E2.2.1.6I, ilvB, ilvL, ilvV; acetyl CoA acetyltransferase [EC:2.2.1.6]	2	2	4	1	3	2	1	1	2	2
K01653	E2.2.1.6S, ilvH, ilvV; acetylCoA synthase [ILV small subunit] [EC:2.2.1.6]	2	2	2	1	2	1	2	2	2	2
K01657	trpE; antranilate synthase component I [EC:4.1.3.27]	1	0	1	0	1	1	0	0	0	0
K01658	trpG; antranilate synthase component II [EC:4.1.3.27]	1	0	2	0	1	1	0	0	0	0
K01661	menB; naphthoate synthase [EC:4.1.3.36]	0	0	1	0	0	0	0	0	0	0
K01662	dks; 3-deoxy-D-xylulose 5-phosphate synthase [EC:2.2.1.7]	1	1	1	1	1	1	1	1	1	1
K01664	pabB; para-aminobenzoate synthase component II [EC:2.6.1.85]	1	0	0	1	1	0	0	0	0	0
K01665	pabB; para-aminobenzoate synthase component I [EC:2.6.1.85]	1	0	1	1	0	0	0	0	0	0
K01673	cynT, can; carbonic anhydrase [EC:4.2.1.1]	1	0	0	0	0	0	0	1	0	0
K01677	E4.2.1.2AA, fumA; fumarate hydratase subunit alpha [EC:4.2.1.2]	1	1	5	1	1	2	0	1	1	1
K01678	E4.2.1.2AB, fumB; fumarate hydratase subunit beta [EC:4.2.1.2]	1	1	5	1	1	2	1	1	1	1
K01681	ACO, acoA; ascorbate hydratase [EC:4.2.1.3]	1	1	6	0	0	1	0	1	0	0
K01683	araD; D-arabinonate dehydratase [EC:4.2.4.5]	0	0	1	0	0	0	0	1	0	0
K01684	dgoD; galactonate dehydratase [EC:4.2.1.6]	0	0	0	0	0	0	0	0	0	0
K01687	ivlO; dihydroxy-acid dehydratase [EC:4.2.1.9]	1	1	3	0	1	1	1	1	1	1
K01689	ENO, eno; enolase [EC:4.2.1.11]	1	1	2	1	1	1	0	1	1	1
K01692	paaF, echA; enoyl-CoA hydratase [EC:4.2.1.17]	0	0	1	0	0	0	0	0	0	0
K01693	hisB; imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]	1	1	4	1	1	1	1	1	1	1
K01695	trpA; tryptophan synthase alpha chain [EC:4.2.1.20]	1	1	0	1	1	1	1	1	1	1
K01696	trpB; tryptophan synthase beta chain [EC:4.2.1.20]	1	1	0	1	1	1	1	1	1	2
K01698	hemB; ALAD; porphobilinogen synthase [EC:4.2.1.24]	1	1	1	1	1	1	0	1	0	0
K01699	pdUc; propandiol dehydratase large subunit [EC:4.2.1.28]	0	1	1	0	0	0	0	0	0	0
K01703	leuC, IM1; 3-isopropylmalate/[R]-2-methylmalate dehydratase large subunit [EC:4.2.1.33.4.2.1.35]	1	1	5	0	1	1	1	2	1	1
K01704	leuD, IM5; 3-isopropylmalate/[R]-2-methylmalate dehydratase small subunit [EC:4.2.1.33.4.2.1.35]	1	1	5	0	1	1	1	2	1	1
K01709	rfbG; CDP-glucose 4,6-dehydratase [EC:4.2.1.45]	0	0	1	0	1	0	0	0	0	0
K01710	rfbB, rmbB, ffbG; DTDP-glucose 4,6-dehydratase [EC:4.2.1.46]	2	2	1	4	0	1	0	0	1	0
K01712	hutU, UROC1; uracanate hydrolase [EC:4.2.1.49]	0	0	1	0	0	0	0	0	0	0
K01714	dapA; 4-hydroxy-tetrahydrodipicolinate synthase [EC:4.3.3.7]	2	2	5	1	1	1	0	1	1	1
K01715	crt; enoyl-CoA hydratase [EC:4.2.1.17]	1	0	5	0	0	0	0	0	0	0
K01720	prpD; 2-methylcitrate dehydratase [EC:4.2.1.79]	0	1	2	0	0	0	0	0	0	0
K01733	thrC; threonine synthase [EC:4.2.3.1]	1	1	2	1	1	1	1	0	1	1
K01734	mpgA; methylglyoxal synthase [EC:4.2.3.3]	0	0	0	0	0	0	0	1	0	0
K01735	aroB; 3-dehydroquinate synthase [EC:4.2.3.4]	1	1	1	1	1	1	1	1	1	1
K01736	aroC; chorismate synthase [EC:4.2.3.5]	1	1	2	1	1	1	1	1	1	1
K01737	queD, ptsP, PTS; 6-pyruvoyltetrahydropterin/6-carboxytetrahydropterin synthase [EC:4.2.3.12.4.1.2.50]	2	1	3	1	2	1	0	2	2	2
K01738	cysK; cysteine synthase [EC:2.5.1.47]	0	0	1	0	0	0	0	0	0	0
K01739	metB; cystathione gamma-synthase [EC:2.5.1.48]	1	1	2	1	2	0	0	2	0	1
K01740	metY; acetylhomoserine (thiol)-lyase [EC:2.5.1.49]	1	1	2	0	0	0	1	0	0	0
K01744	aspA; aspartate ammonia-lyase [EC:4.3.1.1]	0	1	2	0	0	0	1	0	0	0
K01745	hutH, HAL; histidine ammonia-lyase [EC:4.3.1.3]	0	0	1	0	0	0	0	0	0	0
K01746	E4.3.1.4; formiminotetrahydrofolate cyclodeaminase [EC:4.3.1.4]	1	1	2	1	1	1	1	1	1	1
K01749	hemC, HMBS; hydroxymethylblanine synthase [EC:2.5.1.61]	1	0	1	1	0	1	0	0	0	0
K01750	E4.3.1.12; ocd; ornithine cyclodeaminase [EC:4.3.1.12]	1	1	1	0	0	0	0	0	0	0
K01752	E4.3.1.17; sdaB, sdaB; L-serine dehydratase [EC:4.3.1.17]	3	2	3	1	0	0	1	0	3	3
K01753	dsdA; D-serine dehydratase [EC:4.3.1.18]	0	0	1	0	0	0	0	0	0	0
K01754	F4.3.1.19; IVa, tdcB; threonine dehydratase [EC:4.3.1.19]	0	1	0	0	1	0	1	1	0	0
K01755	argH, ASL; arginosuccinate lyase [EC:4.3.2.1]	1	1	1	1	1	1	1	1	1	1
K01756	purB, ADSL; adenylosuccinate lyase [EC:4.3.2.2]	1	1	2	1	1	1	2	1	1	1
K01758	CTH; cystathione gamma-lyase [EC:4.4.1.1]	1	1	1	1	1	1	1	1	1	1
K01759	GLO1, gloA; lactoylglutathione lyase [EC:4.4.1.5]	2	0	2	1	1	0	0	1	1	1
K01760	metC; cysteine-S-conjugate beta-lyase [EC:4.4.1.13]	0	0	1	0	0	0	0	0	0	0
K01761	E4.4.1.11; methionine-gamma-lyase [EC:4.4.1.11]	0	0	1	0	0	0	0	0	0	0
K01770	ispF; 2-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:4.6.1.12]	1	1	2	0	1	0	0	0	0	0
K01772	hemH; FECH; protoporphyrin/coprotoporphyrin ferrochelatase [EC:4.9.8.1.4.99.1.9]	1	1	0	0	0	0	0	0	0	0
K01775	ali; alanine racemase [EC:5.1.1.1]	2	2	2	1	1	2	2	2	2	2
K01776	mut; glutamine racemase [EC:5.1.1.13]	0	1	1	1	1	1	1	1	1	1
K01777	prfD; proline racemase [EC:5.1.1.4]	1	1	3	0	0	0	0	0	0	0
K01778	dapF; diisopropylimide epimerase [EC:5.1.1.7]	1	1	1	1	1	1	1	1	1	1
K01783	rpeF; RPE; ribulose-5-phosphate isomerase [EC:5.3.1.6]	1	1	1	1	1	1	1	1	1	1
K01809	manA, MP; mannose-6-phosphate isomerase [EC:5.3.1.8]	0	0	0	1	1	1	1	0	0	0
K01810	GPI, pgI; glucose-6-phosphate isomerase [EC:5.3.1.9]	0	0	0	1	1	1	1	0	0	0
K01814	hisA; phosphoribosylformimino-5-aminimidazole carboxamide ribotide isomerase [EC:5.3.1.16]	1	0	2	1	1	1	0	2	2	2
K01817	trpF; phosphoribosylribanilate isomerase [EC:5.3.1.24]	1	1	1	0	1	1	0	1	1	1
K01821	prcA, xyH; 4-oxalocrotonate tautomerase [EC:5.3.2.6]	1	1	2	1	0	1	1	1	1	1
K01829											

K01872	AARS, alaS; alanyl-tRNA synthetase [EC:6.1.1.7]	0	1	1	1	1	1	0	1	1	1
K01873	VARS, valS; valyl-tRNA synthetase [EC:6.1.1.9]	1	1	1	1	1	1	1	1	1	1
K01874	MARS, metG; methionyl-tRNA synthetase [EC:6.1.1.10]	1	1	1	1	1	1	1	1	1	1
K01875	SARS, serS; seryl-tRNA synthetase [EC:6.1.1.11]	1	1	1	1	1	1	1	1	1	1
K01876	DARS2, epps; aspartyl-tRNA synthetase [EC:6.1.1.12]	1	1	1	1	1	1	0	1	1	1
K01878	glnQ; glycyl-tRNA synthetase alpha chain [EC:6.1.1.14]	1	1	1	1	1	1	1	1	1	1
K01879	glnQ; glycyl-tRNA synthetase beta chain [EC:6.1.1.14]	1	1	1	1	1	1	0	1	1	1
K01881	PARS, proS; prolyl-tRNA synthetase [EC:6.1.1.15]	1	1	1	1	1	1	1	1	1	1
K01883	CARS, cysS; cysteinyl-tRNA synthetase [EC:6.1.1.16]	1	1	1	1	1	1	1	1	1	1
K01885	EARS, glnX; glutamyl-tRNA synthetase [EC:6.1.1.17]	1	0	1	0	0	0	0	0	1	1
K01886	QARS, glnS; glutaminyl-tRNA synthetase [EC:6.1.1.18]	1	1	1	1	1	1	1	1	1	1
K01887	RARS, argS; arginyl-tRNA synthetase [EC:6.1.1.19]	1	2	2	2	2	1	0	1	1	1
K01889	FARSa, phes; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]	2	2	2	2	1	0	1	1	1	1
K01890	NARS, hisS; histidyl-tRNA synthetase [EC:6.1.1.21]	1	1	1	1	1	1	0	1	1	1
K01891	NARS, asnS; asparaginyl-tRNA synthetase [EC:6.1.1.22]	1	1	1	1	0	0	0	0	0	0
K01893	ACCSL_2_acs; acetyl-CoA synthetase [EC:6.2.1.1]	1	0	1	2	2	0	0	0	0	0
K01897	ACSL_fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	0	0	2	2	0	1	0	0	1	2
K01902	sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]	0	0	3	0	0	0	0	0	0	0
K01903	sucC; succinyl-CoA synthetase beta subunit [EC:6.2.1.5]	0	0	2	0	0	0	0	0	0	0
K01905	acdA; acetate—CoA ligase (ADP-forming) subunit alpha [EC:6.2.1.13]	0	0	1	0	0	0	0	0	0	0
K01910	citC; citrate (pro-35)-lyase [EC:6.2.1.22]	0	0	1	0	0	0	0	0	0	0
K01912	paaK; phenylacetate-CoA ligase [EC:6.2.1.30]	2	3	3	3	2	3	3	3	3	3
K01915	glnA; GLU; glutamine synthetase [EC:6.3.1.2]	2	2	5	2	2	3	1	1	1	2
K01916	nadE; NAD+ synthase [EC:6.3.1.5]	0	0	0	1	0	1	0	0	0	0
K01918	panC; pantetheate-alanine ligase [EC:6.3.2.1]	1	0	1	0	0	1	1	1	1	1
K01919	gshA; glutamate-cysteine ligase [EC:6.3.2.2]	0	0	1	1	0	0	0	0	0	0
K01921	ddl; D-alanine-D-alanine ligase [EC:6.3.2.4]	1	1	1	1	1	1	0	1	1	1
K01923	purC; phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2.6]	2	2	1	1	1	1	1	1	1	1
K01924	murC; UDP-N-acetylmuramate-alanine ligase [EC:6.3.2.8]	1	1	1	1	1	1	1	1	1	1
K01925	murD; UDP-N-acetylglucosamine-D-glutamate ligase [EC:6.3.2.9]	1	1	1	1	1	1	0	1	1	1
K01926	redX; redox-sensing transcriptional repressor	1	1	1	0	0	0	0	0	0	0
K01928	murE; UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase [EC:6.3.2.13]	1	1	1	1	1	1	1	1	1	1
K01929	murF; UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase [EC:6.3.2.10]	1	1	1	1	1	1	1	1	1	1
K01933	purM; phosphoribosylformylglycine amidinohydrolase [EC:6.3.3.1]	1	1	1	1	1	1	1	1	1	1
K01934	MTHFS; 5-formyltetrahydfolate cyclo-ligase [EC:6.3.3.2]	1	1	1	1	1	1	0	0	0	0
K01935	bioB; diethibiotin synthetase [EC:6.3.3.3]	0	0	0	0	1	0	0	0	0	0
K01937	pyrG; CTPS; CTP synthase [EC:6.3.4.2]	1	1	1	1	1	1	1	1	1	1
K01938	fhs; formate-tetrahydfolate ligase [EC:6.3.4.3]	1	1	1	2	1	1	0	1	1	1
K01939	purA; ADPS; adenylosuccinate synthase [EC:6.3.4.4]	1	1	2	1	1	1	1	1	1	1
K01940	argE; AS51; argininosuccinate synthase [EC:6.3.4.5]	1	1	1	1	1	1	1	1	1	1
K01945	purD; phosphoribosylamine—glutamine ligase [EC:6.3.4.13]	1	1	1	1	1	1	1	1	1	1
K01950	E6.3.5.1; NADSYN1; QNS1; nadE; NAD+ synthase (glutamine-hydrolysing) [EC:6.3.5.1]	1	1	0	1	1	1	2	1	1	1
K01951	guA; GMPs; GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]	2	2	2	2	1	1	0	1	1	1
K01952	PEAS; purU; phosphoribosylformylglycine synthase [EC:6.3.5.3]	1	1	1	1	1	1	0	1	1	1
K01953	aasB; ASN; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]	0	1	3	0	1	1	0	1	1	1
K01955	carB; CP42; carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]	3	0	4	1	1	3	0	1	2	2
K01956	carA; CPA1; carbamoyl-phosphate synthase small subunit [EC:6.3.5.5]	0	0	1	1	1	0	0	1	1	1
K01958	PC; pyc; pyruvate carboxylase [EC:6.4.1.1]	1	0	0	1	1	1	0	1	1	1
K01961	accC; accY; CoA-carboxylase; biotin carboxylase subunit [EC:6.4.1.2.6.3.4.14]	1	1	4	0	0	1	1	1	1	1
K01962	ACC_A; accY; CoA-carboxylase; carboxyl transferase subunit alpha [EC:6.4.1.2.2.1.3.15]	0	0	0	0	1	1	0	0	0	0
K01963	accD; accY; CoA-carboxylase; carboxyl transferase subunit beta [EC:6.4.1.2.2.1.3.15]	0	0	0	0	1	1	0	0	0	0
K01966	PCCB; pccB; propionyl-CoA carboxylase beta chain [EC:6.4.1.3.2.1.3.15]	1	1	4	0	0	1	1	1	1	1
K01971	ligD; bifunctional non-homologous end joining protein Ugo [EC:6.5.1.1]	1	2	1	0	0	0	0	0	1	1
K01972	E6.5.1.2; ligA; ligB; DNA ligase (NAD+) [EC:6.5.1.2]	1	1	1	1	1	1	1	1	1	1
K01975	thpR; RNA 2'-3'-cyclic 3'-phosphodiesterase [EC:3.1.4.58]	1	1	1	0	0	0	0	0	0	0
K01989	KO1989; putative tryptophan/tryptidine transport system substrate-binding protein	1	1	1	1	1	1	0	0	0	0
K01990	ABC-2.A; ABC-2 type transport system ATP-binding protein	9	3	22	2	12	3	3	6	5	5
K01992	ABC-2.P; ABC-2 type transport system permease protein	9	3	15	2	9	2	2	1	1	1
K01993	ABC-2.TK; HlyD family secretion protein	2	1	3	0	0	0	1	1	0	0
K01994	gevE; LuxR family transcriptional regulator; transcriptional regulator of spore coat protein	0	0	1	0	0	0	0	0	0	0
K01995	livG; branched-chain amino acid transport system ATP-binding protein	2	2	11	1	0	0	2	0	0	0
K01996	livF; branched-chain amino acid transport system ATP-binding protein	2	3	12	1	0	0	2	1	0	0
K01997	livH; branched-chain amino acid transport system permease protein	2	2	10	1	0	0	2	0	0	0
K01998	livM; branched-chain amino acid transport system substrate-binding protein	2	2	10	1	0	0	1	1	0	0
K01999	livK; branched-chain amino acid transport system substrate-binding protein	1	2	16	1	0	1	2	1	0	0
K02000	proV; glycine betaine/proline transport system ATP-binding protein [EC:7.6.2.9]	0	0	0	0	1	0	1	1	0	0
K02001	proW; glycine betaine/proline transport system permease protein	0	0	0	0	1	0	1	1	0	0
K02002	proX; glycine betaine/proline transport system substrate-binding protein	0	1	1	0	1	0	1	1	0	0
K02003	ABC.CD_A; putative ABC transport system ATP-binding protein	6	2	14	3	5	1	2	2	7	5
K02005	ABC.CD_TK; HlyD family secretion protein	6	2	15	3	5	1	2	2	7	5
K02006	cbiO; cobalt/nickel transport system ATP-binding protein	1	1	8	0	0	0	1	1	1	1
K02007	cbiM; cobalt/nickel transport system permease protein	2	1	4	2	2	0	1	0	1	1
K02008	cbiQ; cobalt/nickel transport system permease protein	2	1	4	2	2	0	2	0	1	1
K02009	cbiN; cobalt/nickel transport protein	1	1	1	1	0	1	0	1	0	0
K02010	afuC; fbpC; iron(III) transport system ATP-binding protein [EC:7.2.2.7]	0	0	1	0	0	0	0	0	0	0
K02013	ABC.FEV_A; iron complex transport system ATP-binding protein [EC:7.2.2.-]	4	2	1	1	1	1	3	0	0	0
K02015	ABC.FEV_P; iron complex transport system permease protein	4	2	1	1	1	1	0	0	0	0
K02016	ABC.FEV_S; iron complex transport system substrate-binding protein	3	2	1	1	1	1	3	0	0	0
K02017	modC; modylate transport system ATP-binding protein [EC:7.3.2.5]	1	1	0	0	0	2	1	1	2	2
K02018	modB; modylate transport system permease protein	1	1	0	0	0	2	1	1	1	1
K02019	modI; modylate transport system regulatory protein	2	1	1	0	0	0	1	0	2	2
K02020	modA; modylate transport system substrate-binding protein	1	1	0	0	0	2	2	2	2	2
K02022	ABC.MR_TK; HlyD family secretion protein	0	0	1	0	0	0	0	0	0	0
K02025	ABC.MS_P; multiple sugar transport system permease protein	0	0	1	0	0	0	1	0	0	0
K02027	ABC.MS_S; multiple sugar transport system substrate-binding protein	0	0	3	0	0	0	0	0	0	0
K02028	ABC.PA_A; polar amino acid transport system ATP-binding protein [EC:7.4.2.1]	2	2	7	4	2	1	0	2	1	1
K02029	ABC.PA_P; polar amino acid transport system permease protein	3	7	4	2	1	0	2	1	1	1
K02030	ABC.PA_S; polar amino acid transport system substrate-binding protein	3	2	5	3	2	1	0	2	2	2
K02031	ddEP; peptide/nickel transport system ATP-binding protein	0	2	13	3	1	0	0	0	0	0
K02032	ddEP; peptide/nickel transport system permease protein	0	1	7	3	1	0	0	0	0	0
K02033	ABC.PE_P; peptide/nickel transport system permease protein	0	3	16	3	1	0	0	0	0	0
K02034	ABC.PE_P1; peptide/nickel transport system permease protein	0	2	16	1	1	0	0	0	0	0
K02035	ABC.PE_S; peptide/nickel transport system substrate-binding protein	0	3	17	3	1	0	0	0	0	0
K02036	psb; phosphate transport system ATP-binding protein [EC:7.3.2.1]	1	0	2	0	1	1	0	1	1	1
K02037	pscC; phosphate transport system permease protein	1	0	2	0	1	1	1	1	1	1
K02038	pscA; phosphate transport system permease protein	1	0	1	0	1	1	1	1	1	1
K02039	psbU; phosphate transport system protein	1	0	1	0	1	1	1	1	1	1
K02040	pscT; phosphate transport system substrate-binding protein	1	1	0	2	0	1	1	1	1	1
K02041	phnC; phosphate transport system ATP-binding protein [EC:7.3.2.2]	0	0	1	0	0	0	0	0	0	0
K02042	phnE; phosphate transport system permease protein	0	0	2	0	0	0	0	0	0	0
K02044	phnD; phosphate transport system substrate-binding protein	0	0	1	0	0	0	0	0	0	0
K02049	ABC.SN_A; NifT/TauF family transport system ATP-binding protein	3	3	1	0	1	3	2	0	2	2
K02050	ABC.SN_P; NifT/TauF family transport system permeate protein	4	2	1	0	1	3	2	0	1	1
K02051	ABC.SN_S; NifT/TauF family transport system substrate-binding protein	3	2	1	0	1	3	2	0	1	1
K02052	ABC.SPA; putative spermidine/putrescine transport system ATP-binding protein	0	2	0	0	0	0	0	0	0	0
K02053	ABC.SPB; putative spermidine/putrescine transport system permease protein	0	0	3	0	0	0	0	0	0	0
K02054	ABC.SPB1; putative spermidine/putrescine transport system permease protein	0	0	3	0	0	0	0	0	0	0
K02055	ABC.SPS; putative spermidine/putrescine transport system substrate-binding protein	0	0	3	0	0	0	0	0	0	0
K02056	ABC.SSS_A; simple sugar transport system ATP-binding protein [EC:7.5.2.-]	1	1	4	0	0	0	2	1	0	0
K02057	ABC.SSS_P; simple sugar transport system ATP-binding protein	2	2	9	1	1	0	2	2	0	0
K02071	metN; D-methionine transport system permease protein	1	1	1	1	0	0	0	0	0	0

K02114	ATPF1_E, atpC; F-type H ⁺ -transporting ATPase subunit epsilon	1	1	1	1	1	1	1	1	1	1
K02115	ATPF1_G, atpG; F-type H ⁺ -transporting ATPase subunit gamma	1	1	1	1	1	1	1	1	1	1
K02117	ATPV_A, atpA; V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit A [EC:7.1.2.2.7.2.2.1]	0	0	0	0	0	1	0	0	0	0
K02118	ATPV_B, atpB; V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit B	0	0	0	0	0	1	0	0	0	0
K02119	ATPV_C, atpC; V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit C	0	0	0	0	0	1	0	0	0	0
K02120	ATPV_D, atpD; V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit D	0	0	0	0	0	1	0	0	0	0
K02121	ATPV_E, atpE; V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit E	0	0	0	0	0	1	0	0	0	0
K02122	ATPV_F, atpF; V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit F	0	0	0	0	0	1	0	0	0	0
K02123	ATPV_I, atpI; V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit I	0	0	0	0	0	1	0	0	0	0
K02124	ATPV_K, atpK; V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit K	0	0	0	0	0	1	0	0	0	0
K02160	acbB, bccP; acetyl-CoA carboxylase biotin carboxyl carrier protein	0	0	2	0	1	1	0	0	0	0
K02168	betT, betS; choline/glycine/proline betaine transport protein	1	1	1	1	3	0	0	0	0	0
K02171	blaI; blaI family transcriptional regulator, penicillinase repressor	2	0	2	0	1	0	1	0	0	0
K02172	blaR1; blaI regulatory protein blaR1	0	0	1	0	0	0	0	0	0	0
K02188	cblD; cobalt-precorrin-58 (C1)-methyltransferase [EC:2.1.1.195]	1	1	1	1	1	0	1	0	0	0
K02189	cblG; cobalt-precorrin 5A hydrolase [EC:3.7.1.12]	0	0	1	1	1	0	1	0	0	0
K02190	cblK; sirohydrochlorin cobaltochelatase [EC:4.99.1.3]	0	0	0	1	1	0	1	0	0	0
K02191	cblT; cobalt-precorrin-6B (C15)-methyltransferase [EC:2.1.1.196]	1	1	1	0	0	0	0	0	0	0
K02193	ccmH; heme exporter protein A [EC:7.6.2.5]	1	1	0	0	0	0	0	0	0	0
K02194	ccmB; heme exporter protein B	1	1	0	0	0	0	0	0	0	0
K02195	ccmC; heme exporter protein C	1	1	0	0	0	0	0	0	0	0
K02197	ccmE; cytochrome c-type biogenesis protein CcmE	1	1	0	0	0	0	0	0	0	0
K02198	ccmF; cytochrome c-type biogenesis protein CcmF	1	1	0	0	0	0	0	0	0	0
K02199	ccmG; cytochrome c biogenesis protein CcmG, thiol:disulfide interchange protein DsbE	0	0	0	1	0	0	0	0	0	0
K02204	thrB2; homoserine kinase type II [EC:2.7.1.2.39]	1	1	3	1	5	0	0	0	0	0
K02205	rocE, cbaC; arginine/ornithine permease	0	1	0	0	0	0	0	0	0	0
K02221	ygtT; YgtT family protein	1	1	1	1	1	0	1	1	0	0
K02224	cobB-cbaI; cobrynic acid a,c-diamide synthase [EC:6.3.5.9.6.3.5.11]	3	1	2	1	1	0	1	0	0	0
K02226	cobC, phbP; alpha-ribazole phosphatase [EC:3.1.3.73]	1	1	2	1	1	0	1	0	1	1
K02227	cobB, cobD; adenosylcobinamide-phosphate synthase [EC:6.3.3.10]	1	1	1	1	1	0	1	0	0	0
K02231	cobP, cobU; adenosylcobinamide kinase / adenosylcobinamide-phosphate guanyltransferase [EC:2.7.1.156.2.7.7.62]	1	1	1	1	1	0	1	0	0	0
K02232	cobQ, cobP; adenosylcobyrinic acid synthase [EC:3.6.3.5.10]	1	1	1	1	1	0	1	0	0	0
K02233	E2.7.8.26, cobS, cobV; adenosylcobinamide-GDP ribazoletransferase [EC:2.7.8.26]	2	1	1	1	1	0	1	1	0	0
K02234	cobW; cobalamin biosynthesis competitor CobW	0	0	2	0	0	0	0	0	0	0
K02237	comA; competence protein ComEA	1	1	1	0	0	1	1	0	1	1
K02338	comC; competence protein ComEC	2	1	1	1	1	1	1	1	1	1
K02421	comF; competence protein ComFB	0	1	1	0	0	0	0	0	1	1
K02424	comFC; competence protein ComFC	1	1	0	1	1	1	1	1	1	1
K02479	cpaA, tadv; prepilin peptidase CpaA [EC:3.4.23.43]	0	1	1	0	0	0	0	0	0	0
K0279	cpaB, rcpC; pilus assembly protein CpaB	3	1	1	0	1	0	0	1	1	1
K0282	cpaE, tadZ; pilus assembly protein CpaE	0	0	1	0	0	0	0	1	1	1
K0283	cpaF, tadA; pilus assembly protein CpaF [EC:7.4.2.8]	3	1	1	0	1	0	0	1	1	1
K0292	crtO; beta-carotene ketolase (CrtO type)	0	0	1	0	0	0	0	0	0	0
K0304	MET3; precorrin-2 dehydrogenase / sirohydrochlorin ferrochelatase [EC:1.3.1.76.499.1.4]	1	1	1	0	1	0	1	0	0	0
K0313	dnaA; chromosomal replication initiator protein	1	1	1	1	1	1	0	1	1	1
K0314	dnaB; replicative DNA helicase [EC:5.6.2.3]	1	1	1	1	1	1	1	1	1	1
K0315	dnaC; DNA replication protein DnaC	1	1	2	2	1	1	1	1	1	1
K0316	dnaG; DNA primase [EC:2.7.7.10]	0	0	0	0	0	0	0	0	0	1
K0334	dpo; DNA polymerase bacteriophage-type [EC:2.7.7.7]	0	0	0	0	0	0	0	0	0	1
K0335	polA; DNA polymerase [EC:2.7.7.7]	1	1	1	1	1	1	1	1	1	1
K0337	polB; DNA polymerase III subunit alpha [EC:2.7.7.7]	1	2	1	1	1	1	1	1	1	1
K0338	polB; DNA polymerase III subunit beta [EC:2.7.7.7]	1	1	1	1	1	1	1	1	1	1
K0340	holA; DNA polymerase III subunit delta [EC:2.7.7.7]	1	1	1	1	1	1	1	1	1	1
K0341	holB; DNA polymerase III subunit delta' [EC:2.7.7.7]	1	1	1	1	0	1	1	1	1	1
K0342	holD; DNA polymerase III subunit epsilon [EC:2.7.7.7]	0	0	1	0	0	0	0	0	0	0
K0343	dnaX; DNA polymerase III subunit gamma/tau [EC:2.7.7.7]	1	1	1	1	1	1	0	1	1	1
K0346	dinB; DNA polymerase IV [EC:2.7.7.7]	3	1	2	1	1	0	0	0	1	1
K0347	poxX; dpx; DNA polymerase (family X)	0	0	1	0	0	0	0	0	0	0
K0348	elaA; ElaA protein	1	0	2	2	2	2	1	1	1	2
K0355	fusA; GFM, EFG; elongation factor G	2	1	1	1	1	1	1	1	1	1
K0357	tst; TSFM; elongation factor Ts	1	0	1	1	1	1	1	1	1	1
K0358	tuf; TUFM; elongation factor Tu	2	1	2	0	0	0	1	1	1	1
K0363	entE, dhbE, vibE, mxeE, 2,3-dihydroxybenzoate--[aryl-carrier protein] ligase [EC:6.3.2.14.6.2.1.71]	0	0	1	0	0	0	0	0	0	0
K0371	fabK; enoyl-[acyl-carrier protein] reductase II [EC:1.3.1.9]	1	1	1	0	1	1	2	1	1	1
K0372	fabZ; 3-hydroxacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]	1	1	1	0	1	1	1	1	1	1
K0379	fdhB; FdhB protein	1	1	1	0	0	0	0	1	0	0
K0385	flbD; flagellar protein FlbD	0	1	1	0	0	0	0	1	1	1
K0387	flgB; flagellar basal-body rod protein FlgB	0	1	1	0	1	0	1	0	1	1
K0388	flgC; flagellar basal-body rod protein FlgC	0	1	1	0	1	0	1	0	1	1
K0389	flgD; flagellar basal-body rod modification protein FlgD	0	1	1	0	1	0	1	0	1	1
K0390	flgE; flagellar hook protein FlgE	0	1	1	0	1	0	1	0	2	1
K0392	flgF; flagellar basal-body rod protein FlgF	0	2	0	0	2	0	2	0	1	2
K0396	flgK; flagellar hook-associated protein 1	0	1	1	0	1	0	1	0	1	1
K0397	flgL; flagellar hook-associated protein 3 FlgL	0	1	0	0	1	0	0	0	0	0
K0398	flgM; negative regulator of flagellin synthesis FlgM	0	1	0	0	0	0	0	0	0	0
K0400	flhA; flagellar biosynthesis protein FlhA	0	1	1	0	1	0	1	0	1	1
K0401	flhB; flagellar biosynthesis protein FlhB	0	1	1	0	1	0	1	0	1	1
K0404	flfF; flagellar biosynthesis protein FlfF	0	1	1	0	0	0	0	0	0	0
K0405	fliA; whiG; RNA polymerase sigma factor FliA	0	1	1	0	1	0	1	0	1	1
K0406	fliC; hac; flagellin	0	0	1	0	1	0	0	0	1	1
K0407	fliD; flagellar hook-associated protein 2	0	0	0	0	0	0	0	0	1	1
K0408	fliE; flagellar hook-basal body complex protein Flie	0	1	1	0	1	0	1	0	1	1
K0409	fliF; Flagellar M-ring protein Flf	0	1	1	0	1	0	1	0	1	1
K0410	fliG; flagellar motor switch protein Flig	0	1	1	0	1	0	1	0	1	1
K0412	fliJ; flagellum-specific ATP synthase [EC:7.4.2.8]	0	1	0	0	1	0	1	0	1	1
K0413	fliL; flagellar protein Flil	0	1	1	0	0	0	0	0	0	0
K0415	fliM; flagellar motor switch protein Flim	0	1	1	0	0	0	0	0	0	0
K0416	fliN; flagellar motor switch protein Flin	0	1	2	0	1	0	1	0	1	1
K0417	fliO; fliZ; flagellar protein FlfO/FlfZ	0	1	0	0	0	0	0	0	0	0
K0419	fliP; flagellar biosynthesis protein Fip	0	1	1	0	1	0	1	0	1	1
K0420	fliQ; flagellar biosynthesis protein Flfq	0	1	1	0	1	0	1	0	1	1
K0421	fliR; flagellar biosynthesis protein Flir	0	1	1	0	1	0	1	0	1	1
K0422	fliS; flagellar secretion chaperone Flis	0	1	1	0	1	0	1	0	1	0
K0423	gatA; QSL1; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit A [EC:6.3.5.6.6.3.5.7]	2	2	1	1	1	2	2	1	1	1
K0424	gatB; PET112; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B [EC:6.3.5.6.6.3.5.7]	2	2	1	1	1	1	1	1	1	1
K0425	gatC; GATC; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit C [EC:6.3.5.6.6.3.5.7]	2	2	2	1	1	1	1	1	1	1
K0427	goV; GGS; glycine cleavage system H protein	2	1	3	2	0	0	0	0	1	1
K0440	GLPF; glycerol uptake facilitator protein	0	1	1	0	0	0	0	0	0	0
K0443	glyP; glycerol uptake operon antiterminator	0	0	1	0	0	0	0	0	0	0
K0446	glpX; fructose-1,6-bisphosphatase II [EC:3.1.3.11]	0	1	1	1	1	0	0	0	0	0
K0450	gspA; general secretion pathway protein A	0	0	1	0	0	0	0	0	0	0
K0456	gspG; general secretion pathway protein G	1	2	1	0	0	0	0	0	0	0
K0469	gyrA; DNA gyrase subunit A [EC:5.6.2.2]	1	1	1	1	1	1	1	1	1	1
K0470	gyrB; DNA gyrase subunit B [EC:5.6.2.2]	1	1	1	2	0	0	0	0	1	1
K0472	wecC; UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.336]	1	0	2	0	0	0	0	0	1	1
K0473	wbpP; UDP-N-acetylglucosamine/UDP-N-acetylgalactosamine 4-epimerase [EC:5.1.3.7.5.1.3.]	0	0	0	0	0	1	0	0	0	0
K0474	wbpO; UDP-N-acetyl-D-glucosamine/UDP-N-acetyl-D-galactosamine dehydrogenase [EC:1.1.1.136 1.1.1.1.]	0	0	0	0	0	1	0	0	0	0
K0477	K02477; two-component system, LytTR family, response regulator	2	0	1	0	0	0	0	0	0	0
K0478	K02478; two-component system, LytTR family, sensor kinase [EC:2.7.13.3]	0	0	1	0	0	0	0	0	0	0
K0479	K02479; two-component system, Narl family, response regulator	0	0	3	0	0	0	0	0	0	0
K0481	flgR; two-component system, NtrC family, response regulator	3	0	2	0	0	0	0	0	0	0
K0482	flgS; two-component system, NtrC family, sensor kinase [EC:2.7.13.3]	2	0	0	0	0	0	0	0	0	0
K0483	K02483; two-component system, OmpR family, response regulator	5	1								

K03117	tatB; sec-independent protein translocase protein TatB	0	0	0	0	1	0	0	0	0
K03118	tatC; sec-independent protein translocase protein TatC	1	1	1	1	1	0	0	0	0
K03147	thiC; phosphomethylpyrimidine synthase [EC:4.1.99.17]	2	0	0	0	1	0	0	1	0
K03148	thiF; sulfur carrier protein thiF adenylyltransferase [EC:2.7.7.73]	0	0	0	1	0	0	0	0	0
K03149	thiH; thiazole synthase [EC:3.8.1.10]	0	0	0	1	0	0	0	0	0
K03150	thiH; 2-aminooacetate synthase [EC:4.1.99.19]	0	0	1	2	1	0	0	1	1
K03151	thiI; RNA uracil 4-sulfurtransferase [EC:2.8.1.4]	1	1	1	1	1	0	1	1	1
K03152	thiJ; protein deglycase [EC:3.5.1.124]	0	0	1	1	1	0	0	2	0
K03153	thiS; sulfur carrier protein	0	1	1	1	1	1	1	1	1
K03168	topA; DNA topoisomerase I [EC:5.6.2.1]	0	1	1	1	1	0	0	1	0
K03169	topB; DNA topoisomerase III [EC:5.6.2.1]	1	1	1	1	1	1	1	1	1
K03177	truB; PUS4; TRU81; RNA pseudouridine55 synthase [EC:5.4.99.25]	4	0	2	1	2	0	0	1	2
K03179	ubqA; 4-hydroxybenzene polyynehydride synthase [EC:2.5.1.39]	1	1	1	1	0	1	1	1	0
K03182	ubqB; 4-hydroxy-3-polyperoxybenzoate decarboxylase [EC:4.1.1.98]	0	0	1	2	1	0	0	0	0
K03183	ubqE; demethylmenaquinone methyltransferase / 2-methoxy-4-polyperoxy-1,4-benzoquinol methylase [EC:2.1.1.163 2.1.1.201]	1	1	2	0	0	0	1	0	0
K03184	ubqX; bsdB; PADD1; flavin prenyltransferase [EC:2.5.1.129]	0	1	4	0	1	1	0	1	1
K03205	virD4; lvhd4; type IV secretion system protein VirD4 [EC:7.4.2.8]	5	0	0	0	1	0	0	0	0
K03210	yajC; preprotein translocase subunit YajC	1	0	1	1	1	1	1	1	1
K03215	rnm4; 23S rRNA [uracil39-C5]-methyltransferase [EC:2.1.1.190]	1	1	1	1	1	1	1	1	1
K03216	trml; cspR; tRNA (cytidine/uridine-2'-O)-methyltransferase [EC:2.1.1.207]	1	1	1	1	1	1	1	1	1
K03217	yidC; spoIIIE; OXA1; cfcA; YidC/Oxa1 family membrane protein insertase	2	0	2	1	0	0	1	0	0
K03218	rlnB; 23S rRNA [guanosine225-2'-O]-methyltransferase [EC:2.1.1.185]	1	1	1	1	1	1	1	1	1
K03224	yscN; sctN; hrcN; ssaT; ATP synthase in type III secretion protein N [EC:7.4.2.8]	0	0	1	0	0	0	0	0	0
K03276	waafA; waafB; rfaD; UDP-glucose:galactose:(glucosyl)LPs alpha-1,2-glucosyl/galactosyltransferase [EC:2.4.1.-]	1	0	0	0	0	0	0	0	0
K03281	Tc,CIC; chloride channel protein; CIC family	0	0	1	0	0	1	0	0	0
K03282	mscL; large conductance mechanosensitive channel	1	1	0	1	1	0	0	1	1
K03284	corA; magnesium transporter	2	0	3	0	0	1	1	2	2
K03293	TC.AAA1; amino acid transporter, AAT family	0	0	4	0	0	1	0	1	1
K03294	TC.APA1; basic amino acid/polypeptide antiporter, APA family	0	2	0	0	1	0	0	0	0
K03296	TC.HAE1; hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family	1	0	6	1	2	1	1	1	0
K03297	emfE; qac; mrr; smr; small multidrug resistance pump	1	0	0	0	0	0	0	0	0
K03298	TC.DME; drug/metabolite transporter, DME family	0	0	1	2	0	0	0	0	1
K03303	IctP; lactate permease	0	1	2	0	0	1	0	1	0
K03306	TC.PIT1; inorganic phosphate transporter, PIT family	1	1	1	0	1	1	1	2	2
K03307	TC.SSS1; solute:Na+ symporter, SSS family	0	1	6	2	1	0	1	2	1
K03308	TC.NSS1; neurotransmitter:Na+ symporter, NSS family	1	1	1	1	0	0	0	0	0
K03310	TC.AGCS1; alanine or glycine:cation symporter, AGCS family	0	0	1	1	1	0	1	1	1
K03312	gltS; glutamate:Na+ symporter, ESS family	0	0	1	0	0	1	0	0	0
K03313	nhaA; Na+H+ antiporter; NhaA family	0	0	0	0	1	0	0	0	0
K03315	nhaC; Na+H+ antiporter; NhaC family	0	1	2	0	0	0	2	0	0
K03319	TC.DASS1; divalent anion:Na+ symporter, DASS family	0	0	1	0	0	0	0	0	0
K03320	amrAMT; MEP; ammonium transporter, Amt family	0	0	3	2	3	0	0	2	1
K03322	mntrB; manganese transport protein	0	0	1	0	0	0	0	1	0
K03324	yibB; phosphate:Na+ symporter	1	1	2	0	1	0	0	0	0
K03325	ACR8; acrB; arsenite transporter	0	0	1	0	0	0	0	0	0
K03328	TC.PST1; polysaccharide transporter, PST family	1	0	0	0	0	0	0	0	0
K03378	morA; morphine-6-dehydrogenase [EC:1.1.1.218]	0	0	0	0	0	0	1	0	0
K03382	atbB; hydroxycleohoroatrazine ethylaminohydrolase [EC:3.5.4.43]	0	0	2	0	0	0	1	0	0
K03385	nrflX; nitrite reductase (cytochrome c-552) [EC:1.7.2.2]	1	1	0	0	0	0	0	0	0
K03386	PRDX2; ahpC; peroxiredoxin 04-Feb [EC:1.11.1.24]	1	0	0	0	2	0	0	1	0
K03388	hdrA2; heterodisulfide reductase subunit A2 [EC:1.8.7.3-1.8.98.4 1.8.98.5 1.8.98.6]	2	2	3	0	0	1	2	0	0
K03389	hdrB2; heterodisulfide reductase subunit B2 [EC:1.8.7.3-1.8.98.4 1.8.98.5 1.8.98.6]	1	1	1	0	1	1	0	0	0
K03390	hdrC2; heterodisulfide reductase subunit C2 [EC:1.8.7.3-1.8.98.4 1.8.98.5 1.8.98.6]	1	1	1	0	0	1	1	0	0
K03392	ACMSD1; aminocarboxymuconate-semialdehyde decarboxylase [EC:4.1.1.45]	0	0	0	0	0	0	1	0	0
K03394	cobI-cbtI; precorin-2/cobalt-factor-2 C20-methyltransferase [EC:2.1.1.130 2.1.1.151]	0	1	1	1	1	0	1	0	0
K03399	cbtE; cobalt-precorin-7 (CS)-methyltransferase [EC:2.1.1.289]	1	1	1	0	0	0	0	0	0
K04020	argH; CtrC; transcriptional regulator of arginine metabolism	1	1	1	1	1	1	1	1	1
K04046	mcpP; methyl-accepting chemotaxis protein	0	3	14	0	6	0	1	2	2
K04047	cheA; two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3]	0	2	3	0	1	0	0	1	1
K04048	cheW; purine-binding chemotaxis protein CheW	0	2	4	0	2	0	2	0	1
K04049	cheX; chemotaxis protein CheX	0	1	1	0	0	0	0	0	0
K04140	cheC; chemotaxis protein CheC	0	1	1	0	1	0	1	1	1
K04141	cheD; chemotaxis protein CheD [EC:3.5.1.44]	0	1	1	0	1	0	1	1	1
K04142	cheB; two-component system, chemotaxis family, protein-glutamate methyltransferase/glutaminase [EC:3.1.1.61 3.5.1.44]	0	1	2	0	1	0	1	1	1
K04143	cheY; two-component system, chemotaxis family, chemotaxis protein CheY	0	2	4	0	1	0	1	0	1
K04242	tatD; TatD DNase family protein [EC:3.1.21.-]	1	1	1	1	1	1	1	1	1
K04246	E3.6.1.22, NUOT12, nudC; NAD+ diphosphatase [EC:3.6.1.22]	1	1	1	0	1	0	0	0	1
K04247	hsdM; type I restriction enzyme M protein [EC:2.1.1.172]	1	0	0	0	3	0	0	1	0
K04249	ugtP; presumptive 1,2-diacylglycerol beta-glucosyltransferase [EC:2.4.1.315]	0	1	2	0	0	0	1	1	0
K04340	phnW; 2-aminoethylphosphonate-pyruvate transaminase [EC:2.6.1.37]	0	0	1	0	0	0	0	0	0
K04341	glmM; phosphoglucomamine mutase [EC:5.4.2.10]	1	1	1	1	1	1	1	1	1
K04346	fruR2; fruR; DeoR family transcriptional regulator, fructose operon transcriptional repressor	0	0	1	0	0	0	0	0	0
K04347	spoU; RNA methyltransferase TrmH family	1	1	1	1	1	0	1	1	1
K04348	rnrW; rsmH; 16S rRNA [cytosine1402-N4]-methyltransferase [EC:2.1.1.199]	1	1	1	1	1	0	1	1	1
K04349	trmB; METT11; TRM8; tRNA (guanine-N7)-methyltransferase [EC:2.1.1.133]	1	0	1	1	1	0	0	1	1
K04346	emmB; MFS transporter, CP family, multidrug resistance protein	0	0	3	0	0	0	0	1	0
K04449	TC.BCT1; betaine/carnitine transporter, BCCT family	2	0	5	3	2	0	0	0	0
K04533	TC.BASS1; bili acid:Na+ symporter, BASS family	0	0	0	0	0	0	1	0	0
K04545	TC.KEF1; monovalent cation:H+ antiporter-2, CPA2 family	0	0	1	1	1	0	0	1	1
K04547	TC.NCS1; nucleobase:cation symporter-1, NCS1 family	0	1	6	1	1	0	0	2	0
K04548	TC.NCS2; nucleobase:cation symporter-2, NCS2 family	0	0	2	0	0	0	0	2	0
K04546	thyX; thyZ; thymidylate synthase FAD) [EC:2.1.1.148]	1	1	0	0	0	1	0	1	1
K04546	FtsK; SpoIIIE; DNA segregation ATPase FtsK/SpoIIIE, S-DNA-T family	1	1	1	0	1	1	1	2	2
K04549	rnhA; RNASEH1; ribonuclease HI [EC:3.1.26.4]	1	1	1	1	1	1	1	1	1
K04549	gldA; mmrB; MT01; 16S rRNA 5'-carboxymethylaminomethyl modification enzyme	1	1	1	1	1	1	1	1	1
K04549	parA; soj; chromosome partitioning protein	5	1	1	1	3	1	2	1	1
K04549	parB; spoII; ParB family transcriptional regulator, chromosome partitioning protein	5	1	1	1	2	1	1	1	1
K04549	trkH; trkG; trkB; trkD; trk system potassium uptake protein	2	1	2	1	2	2	0	1	1
K04549	trkA; trkC; HtrC; trkA system potassium uptake protein	3	1	4	1	2	2	1	1	1
K05000	rsnB; sun; 16S rRNA [cytosine67-C5]-methyltransferase [EC:2.1.1.176]	1	1	1	1	1	1	1	1	1
K05011	gidB; rsmG; 16S rRNA [guanine527-N7]-methyltransferase [EC:2.1.1.170]	1	1	1	1	1	1	1	1	1
K05020	umuC; DNA polymerase V	0	0	0	1	0	0	1	0	0
K05117	adaQ; quinolinate synthase [EC:2.5.1.72]	0	0	1	0	1	2	1	1	2
K05118	coxS; ae obc carbon-monoxide dehydrogenase small subunit [EC:1.2.5.3]	4	5	21	0	0	2	1	6	3
K05119	coxM; cutM; aerobic carbon-monoxide dehydrogenase medium subunit [EC:1.2.5.3]	3	4	9	0	0	1	2	5	1
K05120	coxL; cutL; aerobic carbon-monoxide dehydrogenase large subunit [EC:1.2.5.3]	0	0	3	0	0	0	0	3	0
K05121	fixB; ethR; electron transfer flavoprotein beta subunit	3	1	4	0	0	0	0	4	1
K05122	fixB; ethR; electron transfer flavoprotein alpha subunit	3	1	4	0	0	0	2	4	1
K05123	bioY; biotin transport system substrate-specific component	1	1	1	0	2	1	1	1	1
K05124	birA; BirA family transcriptional regulator, biotin operon repressor / biotin--[acetyl-CoA-carboxylase] ligase [EC:6.3.4.15]	1	1	1	2	2	1	1	1	1
K05125	coxA; type III panthenote kinase [EC:2.7.1.33]	1	1	1	1	1	0	1	1	1
K05126	gopG; (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase [EC:1.17.7.1 1.17.7.3]	1	0	1	1	1	1	1	1	1
K05129	smc; chromosome segregation protein	1	1	1	1	1	0	1	1	1
K05303	hupB; HupB; binding protein HU-beta	1	1	1	1	1	1	0	0	0
K05311	ftsZ; cell division protein FtsZ	1	1	1	1	1	1	0	1	1
K05335	gudP; MFS transporter, ACS family, glucurate transporter	2	0	0	0	0	0	0	0	0
K05336	rnpA; ribonuclease P protein component [EC:3.1.26.5]	0	0	1	1	1	1	1	1	1
K05344	clpX; CLPX; ATP-dependent Clp protease ATP-binding subunit ClpX	1	0	1	1	1	1	1	1	1
K05345	tig; trigger factor	1	1	1	1	1	1	1	1	1
K05346	sbcC; rad50; DNA repair protein SbcC/Rad50	1	0	1	1	0	0	0	0	0
K05347	sbcD; mre11; DNA repair protein SbcD/Mre11	1	1	1	1	0	1	0	1	0
K05348	perM; putative permease	0	1	1	0	0	0	0	1	1
K05350	ruvA; holliday junction DNA helicase RuvA [EC:5.6.2.4]	1	1	1	1	1	1	1	1	1
K05511	ruvB; holliday junction DNA helicase RuvB [EC:5.6.2.4]	1	1	1	1	1	1	1	1	1
K05533	recA; recombination protein RecA	1	1	1	1	1	1	1	1	1
K05555	mutS; DNA mismatch repair protein MutS	0	1	2	1	1	1	1	1	1
K05566	matP; LuxR family transcriptional regulator, mato regulon positive regulatory protein	0								

K03572	mutL; DNA mismatch repair protein MutL	1	1	1	1	1	1	1	1	1	1
K03574	mutT; NIUT15, MTH2; 2'-deoxy-DGTP diphosphatase [EC:3.6.1.55]	1	0	2	0	0	0	0	0	1	0
K03575	mutV; A/G-specific adenine glycosylase [EC:3.2.2.21]	0	0	1	1	0	0	0	1	0	0
K03577	acrR; smtA; TetR/AcrR family transcriptional regulator, acrB operon repressor	0	0	1	0	0	0	0	0	0	0
K03581	recD; exodeoxyribonuclease V alpha subunit [EC:3.1.11.5]	1	1	1	0	0	0	0	0	0	0
K03584	recO; DNA repair protein RecO (recombination protein O)	1	1	1	1	1	1	1	1	1	1
K03585	acrA; mcaX; adeI; smdE; mtbC; cmeA; membrane fusion protein, multidrug efflux system	0	0	0	0	0	0	1	0	0	0
K03588	ftsW; spvE; cell division protein FtsW	2	2	2	1	1	1	1	1	1	1
K03589	ftsQ; cell division protein FtsQ	1	1	1	0	0	0	1	0	1	1
K03590	ftsA; cell division protein FtsA	1	1	1	1	1	1	0	0	0	0
K03592	pmbA; PmbA protein	1	1	2	1	1	1	0	0	2	2
K03593	mmpB; NupBL; ATP-binding protein involved in chromosome partitioning	1	1	2	2	1	1	1	0	0	0
K03594	bfr; bacterioferritin [EC:3.16.3.1]	1	1	1	1	1	1	0	0	1	1
K03595	era; ERA1; GTPase	1	1	1	1	1	1	0	1	1	1
K03596	lepA; GTP-binding protein LepA	1	0	1	1	1	1	0	1	1	1
K03601	xseA; exodeoxyribonuclease VII large subunit [EC:3.1.11.6]	1	1	1	1	1	1	0	1	1	1
K03602	xseB; exodeoxyribonuclease VII small subunit [EC:3.1.11.6]	0	1	1	1	1	0	0	0	0	0
K03605	hydA; hydD; hydrogenase maturation protease [EC:3.4.23.-]	1	0	1	0	0	0	1	0	1	1
K03606	wcaL; undecaprenyl-phosphate glucose phosphotransferase [EC:2.7.8.31]	0	1	1	0	0	0	0	0	0	0
K03608	minD; septum site-determining protein MinD	1	1	1	1	1	1	1	0	1	1
K03610	minC; septum site-determining protein MinC	2	2	2	1	1	1	2	0	2	2
K03612	rnfG; H+/Na+-translocating ferredoxin:NAD+ oxidoreductase subunit G	0	0	1	0	1	0	0	1	0	1
K03613	rnfE; H+/Na+-translocating ferredoxin:NAD+ oxidoreductase subunit E	0	0	1	0	1	0	0	1	0	0
K03614	rnfH; H+/Na+-translocating ferredoxin:NAD+ oxidoreductase subunit D [EC:7.1.1.11.7.2.1.2]	0	0	1	0	1	0	0	1	0	0
K03615	rnfC; H+/Na+-translocating ferredoxin:NAD+ oxidoreductase subunit C [EC:7.1.1.11.7.2.1.2]	0	0	1	0	1	0	0	1	0	0
K03616	rnfB; H+/Na+-translocating ferredoxin:NAD+ oxidoreductase subunit B [EC:7.1.1.11.7.2.1.2]	0	0	1	0	1	0	0	1	0	0
K03617	rnfA; H+/Na+-translocating ferredoxin:NAD+ oxidoreductase subunit A	0	0	1	0	1	0	0	1	0	0
K03620	hydA; Ni/Fe-hydrogenase 1 8-type cytochrome subunit	0	0	0	1	0	0	0	0	0	0
K03621	plxS; phosphate acyltransferase [EC:2.3.1.274]	1	1	1	1	1	1	1	1	1	1
K03624	greA; transcription elongation factor GreA	1	1	1	1	1	1	1	1	1	1
K03625	nusB; transcription antitermination protein NusB	1	1	1	1	1	1	1	1	1	1
K03628	rho; transcription termination factor Rho	1	1	0	0	0	0	0	0	0	0
K03629	recF; DNA replication and repair protein RecF	1	1	1	1	1	1	1	1	1	1
K03630	radC; DNA repair protein RadC	4	1	2	1	1	1	1	1	1	1
K03631	recN; DNA repair protein RecN (Recombination protein N)	1	1	1	1	1	1	1	1	1	1
K03633	MOC52B; moeA; molybdopterin synthase catalytic subunit [EC:2.8.1.12]	1	0	1	0	0	0	0	0	0	0
K03634	moeA; cytochrome sulfur-carrier protein	0	0	0	0	0	0	0	0	1	1
K03637	moeA; CNX3; cyclic pyranopterin monophosphate synthase [EC:4.6.1.17]	1	1	1	0	0	1	1	1	1	1
K03639	moeA; CNX2; GTP 3'-R-cyclase [EC:4.1.99.22]	1	1	2	0	0	1	1	1	1	1
K03641	tolB; TolB protein	0	0	1	0	0	0	0	0	0	0
K03644	lipA; LIA1; UPI1; UPI5; lipoyl synthase [EC:2.8.1.8]	0	0	1	0	0	0	0	0	0	0
K03648	UNG; UDG; uracil-DNA glycosylase [EC:3.2.2.27]	1	1	0	0	0	0	0	0	0	0
K03649	mug; double-stranded uracil-DNA glycosylase [EC:3.2.2.28]	0	0	0	1	1	0	1	1	1	1
K03650	mmmt; trmL; MSS1; RNA modification GTase [EC:3.6.-.-]	1	1	1	1	1	1	0	1	1	1
K03652	MPG; DNA-3-methyladenine glycosylase [EC:3.2.2.1]	1	1	0	0	0	1	0	0	0	0
K03654	recQ; ATP-dependent DNA helicase RecQ [EC:5.6.2.4]	2	0	0	1	1	0	0	0	0	0
K03655	recG; ATP-dependent DNA helicase RecG [EC:5.6.2.4]	0	0	1	1	1	0	1	1	1	1
K03657	uvrD; pcrA; ATP-dependent DNA helicase UvrD/PcrA [EC:5.6.2.4]	2	1	4	1	1	1	1	1	1	1
K03664	smpB; SmpB-binding protein	1	1	1	1	1	1	0	1	1	1
K03665	hfq; Hfq protein	1	1	0	0	0	1	1	1	1	1
K03666	hfq; host factor-I protein	1	1	1	1	1	1	0	1	1	1
K03667	hsuU; ATP-dependent HsUUV protease ATP-binding subunit HsuU	1	1	1	1	1	1	1	1	1	1
K03671	trxA; thioredoxin 1	4	3	6	1	2	2	1	3	3	3
K03676	grxC; GLRX; GLRX2; glutaredoxin 3	0	0	1	0	0	0	0	0	0	0
K03685	rnc; DRDASHA; RNT1; ribonuclease III [EC:3.1.26.3]	1	1	1	1	1	1	0	1	1	1
K03686	dnaJ; molecular chaperone DnaJ	2	2	2	2	2	2	1	2	1	1
K03687	GrpE; molecular chaperone GrpE	1	1	1	0	1	1	1	1	1	1
K03688	ubiB; aafF; ubiquinone biosynthesis protein	1	0	1	0	0	0	0	1	0	0
K03691	cipB; ATP-dependent Cip protease ATP-binding subunit CipB	1	1	1	1	1	1	1	1	1	1
K03694	cipC; ATP-dependent Cip protease ATP-binding subunit CipC	1	1	0	0	0	0	1	0	0	0
K03698	cifB; bifL; 3'-exoribonuclease [EC:3.1.-]	1	1	0	0	0	0	0	0	0	0
K03700	tlyC; magnesium and cobalt exporter, CNNM family	1	0	1	1	1	0	0	1	1	1
K03701	recU; recombination protein U	0	0	1	0	0	0	0	0	1	0
K03702	uvrA; excinuclease ABC subunit A	1	1	1	1	1	1	1	1	1	1
K03702	uvrB; excinuclease ABC subunit B	1	1	1	1	1	1	1	1	1	1
K03703	uvrC; excinuclease ABC subunit C	2	0	1	1	1	1	0	1	1	1
K03704	cspA; cold shock protein	2	2	3	0	1	2	1	2	2	2
K03705	hrmA; heat-inducible transcriptional repressor	0	1	1	1	1	1	1	1	1	1
K03706	cody; transcriptional pleiotropic repressor	1	1	0	0	0	0	1	1	1	1
K03707	tenA; thiaminase (transcriptional activator TenA) [EC:3.5.99.2]	1	0	0	0	0	0	2	0	0	0
K03708	ctsR; transcriptional regulator of stress and heat shock response	1	1	1	1	1	1	1	1	1	1
K03709	trR; DtxR family transcriptional regulator, Mn-dependent transcriptional regulator	1	1	2	0	2	2	1	2	1	1
K03710	DtxR; DtxR family transcriptional regulator	0	0	13	0	1	0	0	0	0	0
K03711	fur; zur; Fur family transcriptional regulator, ferric uptake regulator	1	1	1	1	1	1	0	1	3	2
K03716	spib; sporoprotidol lyase [EC:4.1.99.14]	0	1	1	0	0	0	0	0	1	1
K03718	asnC; Lrp; AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	1	1	1	1	1	1	0	0	0	0
K03721	tyrR; transcriptional regulator of arfO, aroG, tyrA and aromatic amino acid transport	6	6	18	6	5	0	0	0	0	0
K03722	dinG; ATP-dependent DNA helicase DinG [EC:5.6.2.3]	1	1	1	1	1	1	1	1	1	1
K03723	mfd; peptidyl-prolyl cis-trans-peptidyl-isomerase (superfamily II helicase) [EC:5.6.2.4]	1	1	1	1	1	1	1	1	1	1
K03733	xerC; integrase/recombinase XerC	1	1	1	1	1	1	1	1	1	1
K03734	apbE; APB-protein FMN transferase [EC:2.7.1.180]	1	1	2	2	2	0	0	0	0	0
K03735	eutB; ethanoline ammonia-lyase large subunit [EC:4.3.1.7]	1	2	2	2	2	0	0	0	0	0
K03737	por; nifI; pyruvate-ferredoxin/flavodoxin oxidoreductase [EC:1.2.7.1.1.2.7.-]	1	1	0	0	0	1	1	1	1	1
K03738	aoR; aldehyde-ferredoxin oxidoreductase [EC:1.2.7.5]	1	4	1	0	0	0	0	0	5	4
K03741	arsC; arsenate reductase (thioredoxin) [EC:3.10.4.4]	0	0	0	0	0	0	0	0	1	1
K03742	pncC; nicotinamide-nucleotide amidase [EC:3.5.1.42]	0	0	0	0	0	0	0	0	1	0
K03743	pncC; nicotinamide-nucleotide amidase [EC:3.5.1.42]	1	1	1	1	1	1	1	1	1	0
K03744	lemM; LemM protein	2	2	1	0	1	1	1	1	1	1
K03748	sanA; SanA protein	0	0	1	0	0	0	0	0	0	0
K03750	moeA; molybdopterin molybdenum cofactor guanylyltransferase [EC:2.10.1.1]	2	1	3	0	0	1	2	0	1	1
K03752	mobA; molybdenum cofactor guanine dinucleotide biosynthesis adapter protein	1	1	2	1	0	0	1	0	3	3
K03762	proP; MFS transporter, MHS family, proline/betaine transporter	0	0	2	0	0	0	0	0	0	0
K03763	polC; DNA polymerase III subunit alpha, Gram-positive type [EC:2.7.7.7]	1	1	1	0	0	0	0	0	0	0
K03767	PPHA; peptidyl-prolyl cis-trans-isomerase A (cyclophilin A) [EC:5.2.1.8]	0	0	1	0	0	0	0	0	0	0
K03768	PPIB; ppb; peptidyl-prolyl cis-trans-isomerase B (cyclophilin B) [EC:5.2.1.8]	1	0	2	2	1	0	1	1	1	1
K03769	ppC; peptidyl-prolyl cis-trans-isomerase C [EC:5.2.1.8]	1	1	1	1	1	0	1	0	0	0
K03781	katE; CAT; catB; srpA; catalase [EC:1.11.1.1]	2	2	1	1	0	2	0	2	2	2
K03782	katG; catalase-peroxidase [EC:3.1.1.21]	0	0	1	0	0	0	1	0	0	0
K03783	punA; PNP; purine-nucleoside phosphorylase [EC:2.4.2.1]	0	0	0	0	1	1	1	1	0	0
K03785	aroD; 3-dehydroquinate dehydratase I [EC:4.2.1.10]	0	0	1	0	0	0	0	0	0	0
K03786	aroQ; quE; 3-dehydroquinate dehydratase II [EC:4.2.1.10]	1	1	1	1	2	2	0	1	1	1
K03787	surE; 5'3'-nucleotidase [EC:3.1.3.5.3.1.3.6]	1	1	1	1	1	1	1	1	1	1
K03789	rimI; ribosomal protein S18-alanine N-acetyltransferase [EC:2.3.1.266]	1	1	2	0	0	1	1	1	1	1
K03790	rimI; ribosomal protein S18-alanine N-acetyltransferase [EC:2.3.1.267]	0	0	1	0	1	0	0	0	0	0
K03795	cbxII; silychrochlorin cobaltochelatase [EC:4.99.1.3]	1	1	1	0	0	0	1	0	0	0
K03797	E3.4.21.102; prc; ctpA; carboxy-terminal processing protease [EC:3.4.21.102]	2	2	2	1	1	2	0	2	2	2
K03798	ftsH; ftfB; cell division protease FtsH [EC:3.4.24.-]	2	1	1	2	1	1	1	1	1	1
K03800	lpxA; lpxB; lipote—protein ligase [EC:6.3.2.10]	2	1	2	1	0	0	1	1	1	2
K03801	lipB; lipoyl[octanoyl] transferase [EC:2.3.1.181]	1	1	2	0	0	0	0	0	0	0
K03802	cphA; cyanophycin synthetase [EC:6.3.2.29.6.3.2.30]	1	1	1	0	0	0	0	0	0	0
K03803	rseC; sigma-E factor negative regulatory protein RseC	0	0	1	0	1	0	0	0	1	0
K03813	modD; molybdenum transport protein [EC:2.4.2.-]	0	0	1	0	0	0	0			

K03852	xsc; sulfocetaldehyde acetyltransferase [EC:2.3.3.15]	1	0	0	0	0	0	0	0	0	0
K03855	fixX; ferredoxin like protein	3	1	2	0	0	0	2	1	0	0
K03856	ARO2, proA; 3-deoxy-7-phosphogluconate synthase [EC:2.5.1.54]	2	2	3	1	1	2	1	2	1	1
K03892	arsR; ArsR family transcriptional regulator, arsenate/arsenite/antimonite-responsive transcriptional repressor	1	1	3	1	2	2	2	1	2	3
K03924	moxR; MoxR-like ATPase [EC:3.6.3.-]	1	0	3	0	1	0	0	0	0	0
K03925	mrA2; transcriptional regulator MrA2	1	1	1	1	1	1	0	1	1	1
K03969	pspA; phage shock protein A	1	0	0	0	0	0	0	0	0	0
K03972	pspE; phage shock protein E	0	0	0	0	0	0	0	0	0	0
K03973	pspC; phage shock protein C	0	0	0	0	1	0	1	1	1	1
K03975	dedA; membrane-associated protein	1	1	0	0	1	0	1	0	0	0
K03976	ybaK, ebsC; Cys-tRNA(Pro)/tCys-tRNA(Cys) deacylase [EC:3.1.1.-]	1	1	2	1	1	1	1	0	0	0
K03977	engA, der; GTPase	1	1	1	1	1	1	1	1	1	1
K03978	engB; GTP-binding protein	1	1	1	1	1	1	1	1	1	1
K03979	obgE, cgtA, MTG2; GTPase [EC:3.6.5.-]	1	1	1	1	1	1	1	1	1	1
K03980	murI, mwN; putative peptidoglycan lipid II flippe	2	2	2	2	3	2	1	2	2	2
K04019	eutA; ethanolamine utilization protein EutA	1	1	1	1	1	0	0	0	0	0
K04023	eutH; ethanolamine transporter	0	1	2	3	4	0	0	0	0	0
K04024	eutU; ethanolamine utilization protein EutJ	1	2	2	1	1	0	0	0	0	0
K04026	eutU; ethanolamine utilization protein EutL	1	1	1	1	1	0	0	0	0	0
K04027	eutM; ethanolamine utilization protein EutM	4	3	4	1	1	0	0	0	0	0
K04028	eutN; ethanolamine utilization protein EutN	1	2	2	0	1	0	0	0	0	0
K04029	eutP; ethanolamine utilization protein EutP	1	2	2	1	1	0	0	0	0	0
K04030	eutQ; ethanolamine utilization protein EutQ	1	1	0	0	0	0	0	0	0	0
K04031	eutS; ethanolamine utilization protein EutS	1	2	2	1	1	0	0	0	0	0
K04032	eutT; ethanolamine utilization cobalamin adenosyltransferase [EC:2.5.1.154]	1	1	1	1	1	0	0	0	0	0
K04034	bchE; anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase [EC:1.21.98.3]	1	1	1	0	1	0	1	1	1	1
K04041	frbP3; fructose-1,6-bisphosphatase III [EC:3.1.3.11]	1	0	0	0	0	0	0	0	0	0
K04042	glmN; bifunctional UDP-N-acetylglucosamine pyrophosphorylase / glucosamine-1-phosphate N-acetyltransferase [EC:2.7.7.23 2.3.1.157]	1	1	1	1	1	1	1	1	1	1
K04043	dnaK, HSP49; molecular chaperone DnaK	3	1	2	1	1	1	1	1	1	1
K04061	flhB2; flagellar biosynthesis protein	0	1	1	0	1	0	1	0	0	0
K04066	priA; primosomal protein N' (replication factor Y) (superfamily II helicase) [EC:5.6.2.4]	1	1	1	1	1	1	1	1	1	1
K04068	ndrG; anaerobic ribonucleoside-triphosphate reductase activating protein [EC:1.97.1.4]	1	1	1	1	0	1	1	0	1	1
K04069	pflA, pflC, pflE; pyruvate formate lyase activating enzyme [EC:1.97.1.4]	6	3	5	1	2	1	2	1	1	1
K04070	pflX; putative pyruvate formate lyase activating enzyme [EC:1.97.1.4]	0	1	0	0	0	0	0	1	0	0
K04072	adhE; acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]	1	1	0	0	0	0	0	0	0	0
K04075	tis5, mes; tRNA([leu]-lysine synthase [EC:6.3.4.19]	0	1	1	1	1	1	1	1	1	1
K04076	lonB; ATP-dependent Lon protease [EC:3.4.21.53]	1	0	1	0	0	0	0	0	0	0
K04077	groEL, HSPD1; chaperonin GroEL [EC:5.6.1.7]	1	1	1	1	1	1	1	1	1	1
K04078	groES, HSPF1; chaperonin GroES	1	1	1	1	1	1	0	1	1	1
K04079	HSP90A, Hsp90; molecular chaperone HtpG	1	1	1	1	1	0	0	0	1	1
K04083	hsfQ; molecular chaperone Hsp33	1	1	0	0	0	1	1	1	0	0
K04085	tusA, sraA; tRNA 2-thiouridine synthesizing protein A [EC:2.8.1.-]	3	0	5	0	1	0	3	2	2	2
K04094	trmF0, gfd; methylenetetrahydrofolate-tRNA-(uracil-5)-methyltransferase [EC:2.1.1.74]	1	1	1	1	1	1	1	1	1	1
K04096	smf; DNA processing protein	1	1	1	1	1	1	1	1	1	1
K04102	phtS; 4,5-dihydroxyphthalate decarboxylase [EC:4.1.1.55]	0	0	1	0	0	0	0	0	0	0
K04108	hcrA, hbcA; 4-hydroxybenzyl-CoA reductase subunit alpha [EC:1.1.7.1]	0	0	0	0	0	0	0	0	1	0
K04114	bcrA, bafD; benzyl-CoA reductase subunit A [EC:1.3.7.8]	2	2	2	0	0	0	0	1	1	1
K04177	ycdX; putative hydrolase	1	1	2	0	0	0	0	0	0	0
K04180	mtaB; methanol—5-hydroxybenzimidazolylcobamide Co-methyltransferase [EC:2.1.1.90]	1	0	1	1	1	0	0	0	0	0
K04185	radA, smr; DNA repair protein RadA/Gms	1	1	1	1	1	1	1	1	1	1
K04186	E3.1.3.5B; histidine-phosphotransferase (HPH family) [EC:3.1.3.15]	2	2	4	1	1	1	1	2	2	2
K04187	tscS, NFS1; cysteine desulfurase [EC:2.8.1.7]	2	2	3	4	2	1	1	2	2	3
K04188	tscU, nifH; nitrogen fixation protein NifH and related proteins	2	2	2	1	1	0	1	2	2	3
K04196	aroA1, aroA; chorismate mutase [EC:5.4.99.5]	0	0	0	0	1	0	0	0	0	0
K04197	tyrA2; prephenate dehydrogenase [EC:1.3.1.12]	1	0	1	1	1	1	1	1	1	1
K04198	pheA2; prephenate dehydratase [EC:2.1.5.1]	1	1	1	0	0	0	0	0	0	0
K04199	flhG; fimbrial biosynthesis protein FlhG	0	0	1	0	0	0	0	0	0	0
K04204	SOD2; superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	0	0	0	1	0	1	0	1	1	1
K04205	SOD1; superoxide dismutase, Cu-Zn family [EC:1.15.1.1]	1	1	1	0	0	1	0	1	1	1
K04207	KARS, lysS; lysyl-tRNA synthetase, class II [EC:6.1.1.6]	1	1	1	1	1	1	1	1	1	1
K04651	hypA, hypB; hydrogenase nickel incorporation protein HypA/HybF	0	0	1	1	1	0	1	0	1	1
K04652	hypB; hydrogenase nickel incorporation protein HypB	0	0	1	1	1	0	1	1	1	1
K04653	hypC; hydrogenase expression/formation protein HypC	2	0	1	1	1	0	2	0	1	1
K04654	hypD; hydrogenase expression/formation protein HypD	1	0	1	1	1	0	1	0	1	1
K04655	hypE; hydrogenase expression/formation protein HypE	1	0	1	1	1	0	0	0	1	1
K04656	hypF; hydrogenase maturation protein HypF	1	0	1	1	1	0	1	0	1	1
K04719	blub; 5,6-dimethylbenzimidazole synthase [EC:1.13.11.79]	0	1	0	0	0	0	0	0	0	0
K04720	cobD; threonine-phosphate decarboxylase [EC:4.1.4.181]	1	1	1	1	1	0	1	0	0	0
K04749	rsvB; anti-sigma B factor antagonist	0	0	4	0	0	0	0	0	0	0
K04750	phnB; PhnB protein	1	0	3	0	0	0	0	0	0	0
K04751	glbN; nitrogen regulatory protein P-II 1	0	0	0	0	1	0	0	2	0	0
K04752	glkN; nitrogen regulatory protein P-II 2	0	0	1	0	0	0	0	0	0	0
K04757	rsvB; serine/threonine-protein kinase RsvBW [EC:2.7.11.1]	0	0	2	0	0	0	0	0	0	1
K04758	feoA; ferrous iron transport protein A	2	1	4	0	4	4	1	3	4	4
K04759	feoB; ferrous iron transport protein B	2	1	3	1	3	3	0	3	2	3
K04761	oxyR; LysR family transcriptional regulator, hydrogen peroxide-inducible genes activator	0	0	1	0	0	0	0	0	0	0
K04763	xerD; integrase/recombinase XerD	2	1	4	1	1	1	0	1	2	1
K04766	aouA; acetoacetate utilization protein AouA [EC:2.3.1.-]	1	0	0	0	0	0	0	0	0	0
K04767	aouB; aceto utilization protein AcuB	2	1	1	0	0	0	0	0	0	0
K04768	aouC; acetoacet utilization protein AcuC	1	0	0	0	0	0	0	1	0	0
K04769	spoVt; AbfB family transcriptional regulator, stage V sporulation protein T	1	1	1	1	1	1	1	1	1	1
K04771	degP; HtrA; serine protease D [EC:3.4.21.107]	2	3	3	2	2	1	1	1	1	2
K04773	sppA; protease IV [EC:3.4.21.1]	0	0	0	0	0	0	0	0	0	1
K04780	dhbF; glycine-[lycyl-carrier protein] ligase [EC:6.2.1.66]	0	0	0	1	0	0	0	0	0	0
K04833	mal; methylaspartate ammonia-lyase [EC:4.3.1.2]	0	0	1	0	0	0	0	0	0	0
K04940	odh; opine dehydrogenase [EC:1.5.1.28]	0	0	3	0	0	0	0	0	0	0
K05020	opuB, betP; glycine betaine transporter	2	0	8	2	4	0	0	0	0	0
K05245	catT; L-carnitine/gamma-butyrobetaine antipporter	1	0	1	1	0	0	0	0	0	0
K05297	rubB, alkR; rubredoxin—NAD+ reductase [EC:1.18.1.1]	0	0	0	0	0	0	0	1	0	0
K05299	fdhA; formate dehydrogenase (NADP+) alpha subunit [EC:1.17.1.10]	0	0	0	1	0	0	0	0	0	0
K05306	pnfx; phosphonocetaldehyde hydrolase [EC:3.11.1.1]	1	0	0	0	0	0	0	0	0	0
K05327	fer; ferredoxin	0	0	0	0	1	0	0	0	1	0
K05339	lrgB; holin-like protein LrgB	0	0	0	0	0	0	0	1	0	0
K05346	deoR; deoxyribonucleoside regulato	0	0	2	0	0	0	0	0	0	0
K05364	pbpA; penicillin-binding protein A	1	1	1	1	1	0	0	0	0	0
K05366	mrkC; penicillin-binding protein 1A [EC:2.4.1.129 3.4.16.4]	1	1	1	0	0	1	0	1	1	1
K05396	doyD; D-cysteine desulphydrase [EC:4.4.1.15]	0	0	1	0	0	0	0	0	1	0
K05515	mrkD; penicillin-binding protein 2 [EC:3.4.16.4]	2	2	2	2	2	2	1	2	2	2
K05516	cbpA; curved DNA-binding protein	1	0	1	0	0	0	0	0	1	0
K05521	draG; ADP-ribofyl-[dinitrogen reductase] hydrolase [EC:3.2.2.24]	0	0	1	0	0	0	0	0	0	0
K05540	tsdB; tRNA-dihydrouridine synthase B [EC:3.2.2.-]	1	1	1	1	1	1	1	1	1	1
K05548	benK; PTS transporter, AARS family, benzate transport protein	0	0	1	0	0	0	0	0	0	0
K05563	mnhA, mnP; multicomponent Na+-H+ antipporter subunit A	0	0	0	0	0	0	1	0	1	1
K05564	mnhB, mnP; multicomponent Na+-H+ antipporter subunit B	1	0	0	0	0	0	0	0	0	0
K05567	mnhC, mnP; multicomponent Na+-H+ antipporter subunit C	1	0	0	0	0	0	0	0	0	0
K05568	mnhD, mnP; multicomponent Na+-H+ antipporter subunit D	1	0	0	0	0	0	0	2	0	1
K05569	mnhE, mnP; multicomponent Na+-H+ antipporter subunit E	1	0	0	0	0	0	0	0	0	0
K05570	mnhF, mnP; multicomponent Na+-H+ antipporter F	1	0	0	0	0	0	0	0	0	0
K05571	mnhG, mnP; multicomponent Na+-H+ antipporter G	1	0	0	0	0	0	0	0	0	0
K05572	deaD, cshA; ATP-dependent RNA helicase DeaD [EC:3.6.4.13]	2	0	1	0	1	2	1	1	0	1
K05601	hcp; hydroxylamine reductase [EC:1.7.99.1]	2	1	1	2	0	1	1	1	1	1
K05606	MCEE, epi; methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1]	0	1	2	0	0	0	1	0	1	1
K05770	TSP0, B2ZP; translocator protein	0	0	0	1	0	1	1	0		

K05837	rodA, mrdB; rod shape determining protein RodA	2	1	1	1	1	0	1	1	1
K05844	rimK; ribosomal protein S6-L-glutamate ligase [EC:6.3.2.-]	0	0	1	0	0	0	0	0	0
K05845	opuC; omoprotectant transport system substrate-binding protein	0	2	2	0	0	0	0	0	0
K05846	opuD; omoprotectant transport system permease protein	0	3	4	0	1	0	0	0	0
K05847	opuA; omoprotectant transport system ATP-binding protein [EC:7.6.2.9]	0	2	2	0	1	0	0	0	0
K05882	E1.1.1.91; aryl-alcohol dehydrogenase (NADP+)[EC:1.1.1.91]	0	0	0	1	0	0	0	0	0
K05884	comC; L-2-hydroxyoxaloate dehydrogenase (NAD+)[EC:1.1.1.337]	1	1	1	1	1	0	1	0	0
K05895	cobK-cbiJ; precorrin-6A/cobalt-precorrin-6A reductase [EC:1.3.1.54 1.3.1.106]	1	0	1	1	1	1	1	1	1
K05896	scpA; segregation and condensation protein A	1	0	0	0	0	0	0	0	0
K05897	kstD; 3-oxosteroid 1-dehydrogenase [EC:1.3.99.4]	1	1	1	1	1	0	1	0	0
K05919	dfx; superoxide reductase [EC:1.15.1.2]	2	2	2	1	1	0	1	0	0
K05921	hpaG; 5-oxopent-3-ene-1,2,5-tricarboxylic decarboxylase / 2-hydroxyhepta-2,4-diene-1,7-diole isomerase [EC:4.1.1.68 5.3.3.-]	0	0	1	1	1	1	1	1	1
K05934	cobI; cobI; precorrin-3B C17-methyltransferase / cobalt-factor III methyltransferase [EC:2.1.1.131 2.1.1.272]	0	0	1	1	1	0	1	0	0
K05936	cobM; cbiF; precorrin-4/cobalt-precorrin-4 C11-methyltransferase [EC:2.1.1.137 2.1.1.271]	2	2	1	1	1	0	1	0	0
K05937	K05937; uncharacterized protein	2	2	0	0	0	0	0	0	0
K05940	tagA, tarA; N-acetylglucosaminylidiphosphudacaprol N-acetyl-beta-D-mannosaminyltransferase [EC:2.4.1.187]	2	2	0	1	1	1	1	1	1
K05964	citX; holo-ACP synthase [EC:2.7.7.61]	0	0	1	0	0	0	0	0	0
K05966	citG; triphosphoribosyl-dephospho-CoA synthase [EC:2.4.2.52]	0	0	2	0	0	0	0	0	0
K05967	K05967; uncharacterized protein	0	0	0	0	0	0	1	0	0
K05979	comb; 2-phosphosulfonate phosphatase [EC:3.1.3.71]	0	0	1	0	0	0	1	1	1
K06001	trpB; tryptophan synthase beta chain [EC:4.2.1.20]	1	1	1	0	1	1	2	1	1
K06012	gpr; spore protease [EC:3.4.24.78]	1	1	1	1	1	0	1	1	1
K06015	E3.5.1.81; N-Acyl-D-amino-acid deacylase [EC:3.5.1.81]	1	0	2	0	0	0	1	0	0
K06016	pycD; beta-ureidopropionate N-carbamoyl-L-amino-acid hydrolase [EC:3.5.1.6 3.5.1.87]	0	1	0	0	0	0	0	0	0
K06019	ppkA; pyrophosphatase PpkA [EC:3.6.1.1]	1	1	1	1	1	1	1	1	1
K06020	etta; energy-dependent translational throttle protein Etta	0	1	0	0	0	0	0	0	0
K06024	scpB; segregation and condensation protein B	1	1	1	1	1	1	1	1	1
K06027	NSF, SEC18; vesicle-fusing ATPase [EC:3.6.4.6]	1	1	1	0	0	0	0	0	0
K06034	comD; sulfopyruvate decarboxylase subunit alpha [EC:4.1.1.79]	0	0	1	0	0	0	0	0	0
K06042	cobH-cbcI; precorrin-8/cobalt-precorrin-8 methylmutase [EC:5.4.99.61 5.4.99.60]	1	1	1	1	1	0	0	0	0
K06075	slyA; MarR family transcriptional regulator, transcriptional regulator for hemolysin	0	0	1	0	0	0	0	0	0
K06121	dhcB; glycerol dehydratase medium subunit [EC:4.2.1.30]	0	1	0	0	0	0	0	0	0
K06131	cfaA; cardiolipin synthase A/B [EC:2.7.8.-]	2	1	2	1	1	0	1	1	1
K06133	LYS5, acpT; 4'-phosphopantetheinyl transferase [EC:2.7.8.-]	1	0	0	0	0	0	1	1	0
K06140	rnlE; regulator of nucleoside diphosphate kinase	1	1	0	0	0	0	0	0	0
K06147	ABC-B-ABC; ATP-binding cassette subfamily B, bacterial	8	1	6	4	4	2	0	2	2
K06148	ABC-C-ABC; ATP-binding cassette subfamily C, bacterial	0	1	5	0	0	0	0	0	0
K06149	uspA; universal stress protein A	5	0	1	0	0	0	0	2	1
K06153	baeA; undecaprenyl-diphosphatase [EC:3.6.1.27]	1	1	1	1	3	1	1	1	1
K06158	ABC/F3; ATP-binding cassette, subfamily F, member 3	2	1	3	1	1	0	2	1	1
K06162	phnM; alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase [EC:3.6.1.63]	0	0	1	0	0	0	0	0	0
K06163	phnI; alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase [EC:4.7.1.1]	0	0	1	0	0	0	0	0	0
K06164	phnI; alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnI [EC:2.7.8.37]	0	0	1	0	0	0	0	0	0
K06165	phnII; alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnII [EC:2.7.8.37]	0	0	1	0	0	0	0	0	0
K06166	phnIII; alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnIII [EC:2.7.8.37]	0	0	1	0	0	0	0	0	0
K06167	phnP; phosphoribosyl 1,2-cyclic phosphate phosphodiesterase [EC:3.1.4.55]	0	0	1	0	0	0	0	0	0
K06168	misA; tRNA-2-methylinosine synthase [EC:2.8.4.3]	1	1	1	0	1	1	1	1	1
K06173	trueA; tRNA pseudouridine38-40 synthase [EC:5.4.99.12]	1	1	1	1	1	1	1	1	1
K06178	rluB; 23S rRNA pseudouridine260S synthase [EC:5.4.99.22]	1	1	1	1	1	1	1	1	1
K06180	rluD; 23S rRNA pseudouridine1911/1917 synthase [EC:5.4.99.23]	2	1	2	2	2	1	1	2	2
K06187	recR; recombinase protein RecR	1	1	1	1	1	1	1	1	1
K06188	aqp2; aquaporin 2	0	0	1	0	0	0	0	0	0
K06191	nrdH; glutaredoxin-like protein NrdH	1	0	1	0	0	0	0	0	0
K06194	nlpD; lipoprotein NlpD	0	0	0	0	0	0	0	1	0
K06196	ccdB; cytochrome c-type biogenesis protein	1	1	1	1	0	1	1	1	1
K06199	crcB; FEX; fluoride exporter	1	0	1	0	0	0	1	0	2
K06200	cstA; carbon starvation protein	0	0	2	0	0	0	0	0	0
K06206	sfaA; sugar fermentation stimulation protein A	1	1	1	2	1	0	0	0	0
K06207	typA; bipA; GTP-binding protein	1	1	1	1	1	1	1	2	1
K06208	aroH; chorismate mutase [EC:5.4.99.5]	1	1	1	0	0	0	0	0	0
K06209	pheB; chorismate mutase [EC:5.4.99.5]	1	1	1	0	0	0	0	0	0
K06213	mgtE; magnesium transporter	1	0	0	1	1	0	0	0	0
K06215	pdkS; pdx1; pyridoxal 5'-phosphate synthase pdxS subunit [EC:4.3.3.6]	0	0	2	0	1	1	1	0	0
K06217	phoN; phoN; phosphate starvation-inducible protein PhoH and related proteins	1	1	1	1	1	1	1	1	1
K06218	relE; rRNA interference RelE/StBE	2	0	2	1	0	0	0	0	0
K06221	degA; 2,5-diketogluconate reductase A [EC:1.1.1.346]	1	0	1	3	0	0	0	0	0
K06223	dam; DNA adenine methylase [EC:2.1.1.72]	1	0	0	0	0	0	0	0	0
K06281	hydA, hydB; hydrogenase large subunit [EC:1.12.99.6]	2	0	2	0	0	0	0	0	1
K06282	hydA, hydB; hydrogenase small subunit [EC:1.12.99.6]	1	0	2	0	0	0	1	0	1
K06283	spollD; putative DeoR family transcriptional regulator, stage III sporulation protein D	1	1	1	1	1	0	1	1	1
K06284	abrB; AbrB family transcriptional regulator, transcriptional pleiotropic regulator of transition state genes	1	1	1	0	0	0	0	0	0
K06285	mttrB; transcription attenuation protein (tryptophan RNA-binding attenuator protein)	1	1	1	0	0	1	0	0	0
K06287	yhdE; nucleoside triphosphate pyrophosphatase [EC:3.6.1.-]	1	1	1	1	1	0	1	1	1
K06295	gerK8; spore germination protein KA	3	2	3	1	4	1	0	1	2
K06296	gerK8; spore germination protein KB	3	2	4	0	4	0	0	0	0
K06297	gerK8C; spore germination protein KC	4	2	3	0	3	0	0	0	1
K06298	gerM; germination protein M	1	1	1	0	0	1	1	1	1
K06306	yaah; spore germination protein	1	0	1	0	0	2	1	1	2
K06310	yndD; spore germination protein	0	0	1	0	0	0	0	0	0
K06311	yndE; spore germination protein	0	0	1	0	0	0	0	0	0
K06313	ypeB; spore germination protein	1	1	1	0	0	1	0	0	0
K06317	bofA; inhibitor of the pro-sigma K processing machinery	1	1	1	0	0	0	0	0	0
K06329	cotF; spore coat protein F	0	1	0	0	0	0	0	0	0
K06331	cotF; spore coat protein I	1	3	1	1	0	1	1	0	0
K06333	cotIB; spore coat protein IB	0	1	2	1	1	1	0	1	0
K06334	cotIC; spore coat protein IC	1	2	1	1	1	1	1	1	1
K06337	cotS; spore coat-associated protein S	2	0	1	0	0	0	0	0	0
K06346	jag; spollI-associated protein	1	1	1	1	1	1	1	1	1
K06373	spmA; spore maturation protein A	1	1	1	1	1	1	0	1	1
K06374	spmb; spore maturation protein B	1	1	1	1	1	1	1	1	1
K06378	spoliaA; stage II sporulation protein AA (anti-sigma F factor antagonist)	1	1	1	1	1	1	1	1	1
K06379	spoliaB; stage II sporulation protein AB (anti-sigma F factor) [EC:2.7.11.1]	3	3	3	1	2	2	2	1	1
K06381	spoliaD; stage II sporulation protein D	3	3	3	1	2	2	2	1	1
K06382	spoliaE; stage II sporulation protein E [EC:3.1.3.16]	1	1	0	1	1	1	1	1	1
K06383	spoliaGA; stage II sporulation protein GA (sporulation sigma-E factor processing peptidase) [EC:3.4.23.-]	1	1	1	1	1	1	1	1	1
K06384	spollM; stage II sporulation protein M	1	1	1	0	0	1	0	0	0
K06385	spollP; stage II sporulation protein P	2	2	2	0	0	0	1	0	0
K06386	spollQ; stage II sporulation protein Q	0	0	1	0	0	0	0	0	0
K06387	spollR; stage II sporulation protein R	1	1	1	0	1	1	1	2	1
K06390	spollIAA; stage III sporulation protein AA	1	1	1	1	1	1	1	1	1
K06391	spollIAB; stage III sporulation protein AB	1	1	1	1	0	1	1	1	1
K06392	spollIAC; stage III sporulation protein AC	1	0	1	1	1	0	1	1	1
K06393	spollIAD; stage III sporulation protein AD	1	1	1	1	1	1	1	1	1
K06394	spollIAE; stage III sporulation protein AE	1	1	1	1	1	1	1	1	1
K06395	spollIAF; stage III sporulation protein AF	0	1	1	0	0	0	1	0	0
K06396	spollIAG; stage III sporulation protein AG	1	1	1	0	1	0	1	1	1
K06397	spollIAH; stage III sporulation protein AH	0	0	1	0	0	0	0	0	0
K06398	spolvA; stage IV sporulation protein A	1	1	1	1	1	1	1	1	1
K06399	spolvB; stage IV sporulation protein B [EC:3.4.21.16]	1	1	1	1	1	1	1	1	1
K06400	spolvCA; site-specific DNA recombinase	3	0	0	1	0	0	1	0	2
K06402	spolvFB; stage IV sporulation protein FB [EC:3.4.24.-]	1	1	1	0	0	0	0	0	0
K06405	spolvAC; stage V sporulation protein AC	2	2	2	1	1	1	1	1	1
K06406	spolvAD; stage V sporulation protein AD	2	2	3	2	1	1	1	1	1
K06407	spolvAE; stage V sporulation protein AE	3	3	3	1	1	1	2	1	1
K06408	spolvAF; stage V sporulation protein AF	1	1	1	0	0	0	0	0	0
K06409	spolvB; stage V sporulation protein B	2	1	1	1	1	1	1	1	1
K06410	spolvFA; dipicolinate synthase subunit A	1	1	1	1	1	1	1	1	2
K06411	spolvFB; dipicolinate synthase subunit B	1	1	1	1	1	1	0	1	2
K06412	spolvG; stage V sporulation protein G	2	1	1	1	1	0	0	1	1
K06413	spolvK; stage V sporulation protein K	1	1	1	0	0	1	1	1	1
K06415	spolvR; stage V sporulation protein R	1	1	1	0	0	0	0	0	0

K06436	yabG; spore coat assembly protein	1	1	1	1	0	0	0	0	0	0
K06438	yqf0; similar to stage IV sporulation protein	1	1	1	0	1	1	1	1	1	1
K06442	tlyA; 23S rRNA (cytidine1920-2'-O)16S rRNA (cytidine1409-2'-O)-methyltransferase [EC:2.1.1.226 2.1.1.227]	1	1	1	1	1	1	1	1	1	1
K06446	DCAa; acyl-CoA dehydrogenase [EC:1.3.99.-]	1	0	0	0	0	0	0	0	0	0
K06518	cida; hly-like protein	0	0	0	0	0	0	1	0	0	0
K06580	SLC42A4, RHAG, RHBC, CD241; ammonium transporter Rh	0	0	0	0	0	0	0	0	0	0
K06599	chiP; ArcA family transcriptional regulator, chemosensory pilus system protein ChpD	1	0	0	0	0	0	0	0	0	0
K06714	rocR; arginyl utilization regulatory protein	7	3	23	5	16	0	0	0	0	0
K06857	tupC; vnuC; tungstate transport system ATP-binding protein [EC:7.3.2.6]	1	1	0	0	0	1	0	1	1	1
K06864	farE; pyridinium-3,5-biscarboxylic acid mononucleotide sulfurtransferase [EC:4.4.1.37]	1	1	1	1	2	0	1	0	1	1
K06871	K06871; uncharacterized protein	1	1	5	1	1	1	0	1	1	1
K06872	K06872; uncharacterized protein	0	1	1	0	0	0	0	1	0	0
K06881	nnmA; bifunctional oligonuclelease and PAP phosphatase NrnA [EC:3.1.3.7 3.1.13.3]	1	1	1	1	1	1	1	1	1	1
K06884	K06884; uncharacterized protein	1	1	4	1	1	1	0	0	1	1
K06889	K06889; uncharacterized protein	1	0	2	1	1	0	0	1	2	1
K06894	yfHM; alpha-2-macroglobulin	1	1	1	0	0	1	0	1	1	1
K06897	K06897; 7,8-dihydropteroate-5'-methyl-4-(beta-D-ribofuranosyl)aminobenzene 5'-phosphate synthase [EC:2.5.1.105]	1	0	1	0	0	1	0	1	1	1
K06898	larB; pyridinium-3,5-biscarboxylic acid mononucleotide synthase [EC:2.5.1.143]	1	1	1	1	2	0	0	0	1	1
K06900	capV; cGMP-activated phosphoplasma [EC:3.1.1.32 3.1.1.-]	0	0	0	0	0	0	1	0	0	0
K06902	UMF1; MFS transporter, UMF1 family	0	0	1	0	0	0	0	0	0	0
K06904	K06904; uncharacterized protein	1	0	0	0	0	0	0	0	1	1
K06905	xtnB; phage terminase large subunit	0	0	0	1	1	1	0	1	0	0
K06910	PEBP1; TFS1; phosphatidylethanolamine-binding protein	0	0	0	0	1	0	0	1	0	0
K06911	PIR; queretin 2,3-dioxogenase [EC:1.13.11.24]	1	0	0	0	0	0	0	0	0	0
K06914	mfnD; tyrosine--l-glutamate ligase [EC:6.3.4.24]	0	0	1	0	0	0	0	0	0	0
K06915	herA; DNA double-strand break repair helicase HerA and related ATPase	0	0	0	1	0	0	0	0	0	0
K06917	selU; mmh1; RNA 2-selenouridine synthase [EC:2.9.1.3]	0	1	1	0	0	1	1	1	0	0
K06919	K06919; putative DNA primase/helicase	1	0	0	0	0	0	0	0	0	0
K06920	queC; 7-cyano-7-deazaguanine synthase [EC:6.3.4.20]	1	1	1	0	0	0	0	0	0	0
K06923	K06923; uncharacterized protein	1	1	1	0	1	1	1	1	1	1
K06924	K06924; uncharacterized protein	0	1	1	0	0	0	0	0	0	0
K06925	tsAE; tRNA threonylcarambyladenine biosynthesis protein TsAE	1	1	1	1	1	1	1	1	1	1
K06926	K06926; uncharacterized protein	1	0	0	0	0	0	0	0	0	0
K06927	DPH6; diphthine-ammonia ligase [EC:6.3.1.14]	0	0	0	0	0	0	0	0	1	0
K06928	NTPCR; nucleoside-triphosphatase [EC:3.6.1.15]	0	0	0	0	0	1	1	0	1	1
K06929	K06929; uncharacterized protein	1	0	1	0	0	0	0	0	0	0
K06933	K06933; uncharacterized protein	2	1	1	0	1	0	0	1	0	0
K06934	K06934; glycerol dibiphytanyl glycerol tetraether/macrocycle archaeol synthase	1	1	1	1	0	0	0	0	0	0
K06937	K06937; glycerol dibiphytanyl glycerol tetraether/macrocycle archaeol synthase	0	1	1	0	0	0	0	0	1	1
K06941	rlnC; 23S rRNA (adenine2503-C2)-methyltransferase [EC:2.1.1.192]	1	0	1	1	1	1	1	1	0	0
K06942	ychF; ribosome-binding ATPase	1	1	1	1	1	1	1	1	1	1
K06945	rsgA; engC; ribosome biogenesis GTPase / thiamine phosphate phosphatase [EC:3.6.1.- 3.3.1.100]	1	1	1	1	2	1	1	1	1	1
K06950	K06950; uncharacterized protein	3	2	4	2	2	0	1	1	1	1
K06951	K06951; uncharacterized protein	0	1	0	0	0	0	0	0	0	0
K06952	yfdR; S'-nucleotidase [EC:3.1.3.89]	0	0	0	0	1	0	0	0	0	0
K06953	rapZ; RNA adapter protein RapZ	1	1	1	1	1	1	1	1	1	1
K06955	tex; protein Tex	1	0	1	0	0	0	1	0	0	0
K06960	K06960; uncharacterized protein	1	1	1	1	1	1	1	1	1	1
K06962	K06962; uncharacterized protein	1	1	1	0	0	0	0	0	0	0
K06967	trmK; rNA (adenine22-N1)-methyltransferase [EC:2.1.1.217]	1	1	1	1	1	1	1	1	1	1
K06971	K06971; uncharacterized protein	0	0	1	0	0	0	0	0	0	0
K06973	K06973; uncharacterized protein	1	1	1	1	1	1	1	1	1	1
K06975	K06975; uncharacterized protein	0	0	0	0	1	0	0	0	0	0
K06984	K06984; beta-ribofuranosylaminobenzene 5'-phosphate synthase [EC:2.4.2.54]	0	0	1	0	0	0	0	0	0	0
K06990	MEMO1; MEMO1; Merozoite surface protein	2	2	2	1	1	1	0	1	2	2
K06997	yggS; PROSC; PLP dependent protein	1	1	1	1	1	1	1	1	1	1
K06998	phzF; trans-2,3-dihydro-3-hydroxyanthranilate isomerase [EC:5.3.3.17]	0	0	1	0	0	0	0	0	0	0
K07001	K07001; NTE family protein	1	0	0	2	0	1	1	1	1	1
K07003	K07003; uncharacterized protein	0	0	0	0	0	1	0	0	0	0
K07005	K07005; uncharacterized protein	2	2	1	2	1	1	0	0	2	1
K07006	K07006; uncharacterized protein	3	0	2	1	1	0	0	0	0	0
K07007	balN; 3-dehydro- bile acid Delta4,6-reductase [EC:1.3.1.114]	2	2	2	1	2	1	1	1	1	1
K07010	K07010; putative glutamine amidotransferase	1	1	1	1	0	0	0	1	1	1
K07012	cas3; CRISPR-associated endonuclease/helicase Cas3 [EC:3.1.- 5.6.2.4]	2	1	1	0	0	0	1	0	0	0
K07013	K07013; uncharacterized protein	0	1	1	0	0	0	0	0	0	0
K07015	yogG; putative phosphatase [EC:3.1.3.-]	1	1	1	1	1	1	1	1	1	1
K07016	csm1, cas10; CRISPR-associated protein Csm1	0	1	0	0	0	0	0	0	0	0
K07017	K07017; uncharacterized protein	0	0	0	1	0	0	0	0	0	0
K07023	YGK1, HDCD2; 5'-deoxynucleotidase [EC:3.1.3.89]	0	0	2	0	0	0	0	0	0	0
K07024	SPP; sucrose-6-phosphatase [EC:3.1.3.24]	0	0	1	0	0	0	0	0	0	0
K07025	K07025; putative hydrolase of the HAD superfamily	1	1	4	0	0	1	1	1	0	0
K07027	K07027; glycosytransferase 2 family protein	0	0	2	0	0	0	0	0	0	0
K07029	dagK; diacylglycerol kinase [ATP] [EC:2.7.1.107]	0	0	2	2	1	0	1	1	1	1
K07030	fakA; fatty acid kinase [EC:2.7.2.18]	1	1	1	1	1	1	1	1	1	1
K07033	K07033; uncharacterized protein	1	1	1	1	1	1	0	1	0	0
K07034	K07034; uncharacterized protein	1	0	0	0	1	1	0	1	0	0
K07035	K07035; uncharacterized protein	0	0	1	1	1	0	0	0	0	0
K07037	pgpH; cyclic-di-AMP phosphodiesterase PgpH [EC:3.1.4.-]	1	1	1	1	1	1	1	1	1	1
K07040	yceD, yLN; DUF177 domain-containing protein	1	1	1	1	1	1	1	1	0	0
K07042	ybeV, ygfG; probable rRNA maturation factor	1	1	1	1	1	1	1	1	1	1
K07043	upp; UTP pyrophosphatase [EC:3.6.1.-]	1	1	1	0	1	0	0	1	0	0
K07045	K07045; uncharacterized protein	1	1	3	2	2	0	0	1	4	1
K07048	PTEB; ppp; phosphotriesterase-related protein	0	0	0	0	0	0	0	1	0	0
K07052	K07052; CAAx protease family protein	3	1	2	0	1	1	0	1	3	2
K07053	K07053; uncharacterized protein	2	3	4	1	1	1	1	1	1	1
K07057	rsmF; 16S rRNA (cytidine1402-2'-O)-methyltransferase [EC:2.1.1.198]	1	1	1	1	1	1	1	1	1	1
K07061	cmr1; CRISPR-associated protein Cmr1	1	0	0	0	0	0	0	0	0	0
K07067	disA; diadenylate cyclase [EC:2.7.7.85]	0	0	1	1	1	0	0	0	0	0
K07068	K07068; uncharacterized protein	0	0	1	0	0	0	0	0	0	0
K07069	K07069; uncharacterized protein	0	1	1	0	0	0	0	0	0	0
K07072	K07072; uncharacterized protein	0	0	1	0	0	0	0	0	0	0
K07074	K07074; uncharacterized protein	0	0	1	0	0	0	0	0	0	0
K07075	K07075; uncharacterized protein	2	2	0	0	0	0	0	0	1	1
K07076	K07076; uncharacterized protein	1	1	2	4	4	4	0	0	2	2
K07079	K07079; uncharacterized protein	1	1	1	2	4	4	0	0	0	0
K07080	K07080; uncharacterized protein	0	0	4	0	0	2	0	0	0	0
K07082	K07082; UP0755 protein	1	1	1	2	2	1	1	1	1	1
K07089	K07089; uncharacterized protein	1	1	1	3	0	1	0	0	0	1
K07094	pcrB; heptaprenylglyceryl phosphate synthase [EC:2.5.1.-]	1	1	3	3	1	2	0	1	0	0
K07095	K07095; uncharacterized protein	1	1	3	3	1	2	0	1	0	0
K07096	K07096; uncharacterized protein	0	0	1	0	0	0	0	0	0	0
K07098	K07098; uncharacterized protein	0	1	3	0	1	0	0	0	2	1
K07099	K07099; uncharacterized protein	1	1	1	1	1	1	1	1	1	1
K07100	K07100; putative phosphoribosyl transferase	0	0	0	0	0	0	0	0	0	1
K07105	K07105; uncharacterized protein	0	1	0	0	1	0	0	0	0	0
K07107	ybgC; acyl-CoA thiolester hydrolase [EC:3.1.2.-]	1	0	0	0	1	1	3	0	0	0
K07112	K07112; uncharacterized protein	3	3	0	0	0	1	1	3	0	0
K07113	fxsA; UP0716 protein FxsA	0	0	1	0	0	0	0	0	0	0
K07120	K07120; uncharacterized protein	0	0	7	0	0	0	0	0	0	0
K07124	K07124; uncharacterized protein	0	0	0	0	0	1	0	0	0	0
K07130	kynB; arylformamidase [EC:3.5.1.9]	0	0	1	0	0	0	0	0	1	0
K07133	K07133; uncharacterized protein	2	0	1	1	0	0	0	0	0	0
K07137	K07137; uncharacterized protein	2	2	2	2	0	0	0	2	1	1
K07138	K07138; uncharacterized protein	1	1	1	1	0	0	0	0	0	0
K07141	mocA; molybdenum cofactor cytidyltransferase [EC:2.7.7.76]	1	1	1	0	0	1	1	2	1	1
K07144	mifE; 5-(aminomethyl)-3-furamethanol phosphate kinase [EC:2.7.4.31]	0	0								

K07181	cdgI; c-di-GMP phosphodiesterase [EC:3.1.4.52]	0	0	2	0	0	0	0	0	0	0	0
K07182	K07182; CBS domain-containing protein	0	0	1	0	0	0	0	1	0	0	0
K07213	ATOX1, ATX1, copZ, golB; copper chaperone	2	1	2	0	0	1	0	0	0	0	0
K07216	hr; hemerythrin	0	2	1	0	0	0	0	0	0	0	0
K07217	K07217; Mn-containing catalase	0	1	1	1	0	0	0	1	1	1	1
K07219	K07219; putative molybdoprotein biosynthesis protein	0	0	1	0	0	0	0	1	0	0	1
K07220	K07220; uncharacterized protein	1	1	1	0	1	0	0	1	2	2	2
K07228	K07228; TrkA domain protein	0	0	1	0	0	0	0	0	0	0	0
K07230	p19, ftrA; periplasmic iron binding protein	0	0	1	0	0	0	0	0	0	0	0
K07238	TC.ZipP, upf1, ZRT3, ZIP2; zinc transporter, ZIP family	2	3	2	3	2	3	3	0	0	0	0
K07240	chrA; chromate transporter	2	2	2	2	2	2	2	2	2	2	2
K07243	FTR, FTH1, fefH; high-affinity iron transporter	0	0	1	0	0	0	0	0	0	0	0
K07250	gabI; 4-aminobutyrate aminotransferase / (S)-3-amino-2-methylpropionate transaminase / 5-aminovalerate transaminase [EC:2.6.1.19 2.6.1.22 2.6.1.48]	0	0	2	0	0	0	0	0	0	0	0
K07258	dacC, dacA, dacB; serine-type II-DnaA-DnaC carboxypeptidase (penicillin-binding protein 5/6) [EC:3.4.16.4]	4	3	6	2	2	2	2	3	3	3	3
K07263	pgql; zinc protease [EC:3.4.24.-]	0	0	0	0	0	1	0	0	0	0	0
K07282	capA, pgmA; gamma-polyglutamate biosynthesis protein CapA	1	1	1	0	1	1	1	1	1	1	1
K07284	srtA; sortase A [EC:3.4.2.7.0]	1	0	0	0	1	3	0	0	2	0	1
K07300	chaA, CAX; Ca2+H+ antipporter	0	0	0	0	0	1	0	0	0	0	0
K07301	yrbG; cation:H+ antipporter	0	1	0	1	1	0	0	1	0	0	0
K07306	dmsA5; anaerobic dimethyl sulfoxide reductase subunit A [EC:1.8.5.3]	0	0	1	0	0	1	0	0	0	0	0
K07307	dmsB5; anaerobic dimethyl sulfoxide reductase subunit B	1	0	1	1	0	1	0	0	0	0	0
K07310	ytfF; Tat-targeted selenate reductase subunit YtfF [EC:1.97.1.9]	0	0	0	1	0	0	0	0	0	0	0
K07313	pphA; serine/threonine protein phosphatase 1 [EC:3.1.3.16]	0	0	0	1	1	0	0	0	0	0	0
K07315	rsbU_P; phosphoserine phosphatase RsbU/P [EC:3.1.3.3]	0	0	2	0	0	0	0	0	0	0	0
K07316	mod; adenine-specific DNA-methyltransferase [EC:2.1.1.172]	3	0	0	0	0	0	1	0	0	0	0
K07317	K07317; adenine-specific DNA-methyltransferase [EC:2.1.1.72]	1	0	0	0	0	0	0	0	0	0	0
K07321	cocA; CO dehydrogenase maturation factor	3	2	2	3	3	0	0	0	0	0	0
K07322	ytfE, sdaA; regulator of cell morphogenesis and NO signaling	1	1	0	0	0	0	0	0	0	0	0
K07335	bmpA, bmpB, bmpC; basic membrane protein A and related proteins	1	1	5	1	1	0	0	1	0	0	0
K07343	tfoX; DNA transformation protein and related proteins	0	0	0	1	0	0	1	0	0	0	0
K07391	comM; magnesium chelatase family protein	1	1	1	1	1	1	1	1	1	1	1
K07397	yhfA; putative redox protein	1	0	0	0	0	0	0	0	1	1	1
K07399	resB, ccs1; cytochrome c biogenesis protein	0	0	1	0	0	0	0	0	0	0	0
K07402	xdhC; xanthine dehydrogenase accessory factor	0	0	1	0	0	3	3	3	2	2	2
K07403	nfbD; membrane-bound serine protease (ClpP class)	1	1	1	0	0	0	1	1	0	1	1
K07406	melA; alpha-galactosidase [EC:3.2.1.22]	0	0	0	0	0	0	1	0	0	0	0
K07443	ybaZ; methylated-DNA-protein-cysteine methyltransferase related protein	0	0	1	0	0	0	0	0	0	0	0
K07444	ypcI; putative N6-adenine-specific DNA methylase [EC:2.1.1.-]	1	0	1	0	0	0	1	1	1	1	1
K07447	ruxX; putative pre-tGS RNA nuclelease [EC:3.1.-.-]	1	1	1	1	1	1	1	1	1	1	1
K07451	mcrA; 5-methylcytosine-specific restriction enzyme A [EC:3.1.21.-]	0	0	0	0	0	0	0	0	0	0	1
K07452	mcrB; 5-methylcytosine-specific restriction enzyme B [EC:3.1.21.-]	1	0	0	0	0	0	0	0	0	0	0
K07454	mutS2; DNA mismatch repair protein MutS2	1	2	2	1	1	1	0	1	1	2	2
K07459	ybjD; putative ATP-dependent endonuclease of the OLD family	1	0	0	0	0	0	0	0	0	0	0
K07460	yraN; putative endonuclease	2	0	1	1	0	1	0	0	1	1	1
K07461	K07461; putative endonuclease	1	1	1	0	0	1	1	1	1	1	1
K07462	recJ; single-stranded-DNA-specific exonuclease [EC:3.1.-.-]	2	1	1	0	1	0	1	0	0	0	0
K07464	cas4; CRISPR-associated exonuclease Cas4 [EC:3.1.12.1]	0	1	6	0	0	0	1	0	2	2	2
K07469	mop; aldehyde oxidoreductase [EC:1.2.99.7]	0	1	6	0	0	0	0	1	0	0	0
K07473	dinJ; DNA-damage-inducible protein J	3	0	1	0	0	0	0	0	0	0	0
K07474	xtnM; phage terminase small subunit	1	0	0	0	0	1	0	0	0	0	0
K07475	cas3; CRISPR-associated endonuclease Cas3-HD [EC:3.1.-.-]	0	0	0	0	1	0	0	0	0	0	0
K07478	casI; putative ATPase	1	1	1	1	1	1	1	1	1	1	1
K07481	K07481; transposase, ISS family	0	0	1	0	0	0	0	0	0	0	0
K07482	K07482; transposase, IS10 family	0	1	1	0	0	0	0	0	0	0	0
K07483	K07483; transposase	6	0	8	0	1	0	0	2	0	0	0
K07484	K07484; transposase	14	0	3	0	0	0	0	0	0	0	0
K07486	K07486; transposase	1	0	2	0	0	0	0	0	0	0	0
K07487	K07487; transposase	1	1	0	0	0	0	0	0	0	0	0
K07491	rayT; REP-associated tyrosine transposase	0	0	3	0	0	0	0	0	0	0	0
K07493	K07493; putative transposase	4	0	7	0	0	0	0	0	0	0	0
K07494	K07494; putative transposase	1	0	0	0	0	0	0	0	0	0	0
K07495	K07495; putative transposase	0	1	0	0	0	0	0	0	0	0	0
K07497	K07497; putative transposase	7	0	10	0	4	0	0	2	0	0	0
K07504	K07504; predicted type IV restriction endonuclease	0	0	1	0	0	0	0	0	0	0	0
K07506	K07506; AraC family transcriptional regulator	0	1	0	0	0	0	0	0	0	0	0
K07507	mgtC; putative Mg2+ transporter-Mgt (Mgt) family protein	1	1	1	1	1	1	1	1	1	1	1
K07533	prsA; foldase protein PrsA [EC:5.2.1.8]	0	0	1	0	0	0	0	0	0	0	1
K07540	E4.1.99.11; benzylsuccinate synthase [EC:4.1.99.11]	0	0	1	0	0	0	0	0	0	0	0
K07550	bbIB; benzylsuccinyl-CoA thiolester Bb8 subunit [EC:2.3.1.310]	0	0	1	1	0	0	0	0	0	0	0
K07552	bcr; tcAB; MFS transporter, DH1 family, multidrug resistance protein	0	0	1	0	0	0	0	0	0	0	0
K07559	kptA; putative RNA 2'-phosphotransferase [EC:2.7.1.-]	0	0	1	0	0	0	0	0	0	0	0
K07560	ddt; DTD; D-aminoacyl-RNA deacylase [EC:3.1.1.96]	1	1	1	1	1	1	1	1	1	1	1
K07566	tsaC, rIM7, SUAS, YRDc; L-threonylcarbamoyladenylate synthase [EC:2.7.7.87]	1	1	1	1	1	1	1	1	1	1	1
K07568	queA; S-adenosylmethionine:RNA ribosyltransferase-isomerase [EC:2.4.99.17]	1	1	1	1	1	1	1	1	1	1	1
K07571	K07571; S11 RNA binding domain protein	1	0	1	0	0	1	0	1	1	1	1
K07574	yhbR; RNA-binding protein	1	1	1	1	1	1	1	1	0	0	0
K07576	K07576; metallo-beta-lactamase family protein	1	1	1	1	1	1	1	1	1	1	1
K07588	MMAA, argK; GTPase [EC:3.6.5.-]	0	1	2	0	0	0	0	0	1	1	1
K07590	RP-L7A, rplGB; large subunit ribosomal protein L7A	1	1	1	1	1	1	1	1	0	0	0
K07636	phoR; two-component system, OmpR family, phosphate regulon sensor histidine kinase PhoR [EC:2.7.13.3]	1	0	1	0	1	1	1	1	1	1	1
K07642	baeS, smrE; two-component system, OmpR family, sensor histidine kinase BaeS [EC:2.7.13.3]	0	0	1	0	0	0	0	0	0	0	0
K07644	cusS, copS, sllS; two-component system, OmpR family, heavy metal sensor histidine kinase CusS [EC:2.7.13.3]	0	0	0	0	1	0	0	0	0	0	0
K07646	kdpD; two-component system, OmpR family, sensor histidine kinase KdpD [EC:2.7.13.3]	2	0	1	0	0	0	1	0	0	0	0
K07651	resE; two-component system, OmpR family, sensor histidine kinase ResE [EC:2.7.13.3]	2	0	0	0	0	0	0	0	0	0	0
K07658	phoB1; phoP; two-component system, OmpR family, alkaline phosphatase synthesis response regulator PhoB	1	0	6	0	1	1	1	1	2	1	1
K07665	cusR, copR, sllR; two-component system, OmpR family, copper resistance phosphate regulon response regulator CusR	0	0	1	0	0	0	0	0	0	0	0
K07666	qseB; two-component system, OmpR family, response regulator QseB	0	0	1	0	0	0	0	0	0	0	0
K07667	kdpE; two-component system, OmpR family, KDP operon response regulator KdpE	2	0	1	2	1	0	0	0	0	0	0
K07668	vicR; two-component system, OmpR family, response regulator VicR	0	0	2	1	1	0	0	0	0	0	0
K07669	mprA; two-component system, OmpR family, response regulator MprA	0	0	0	0	1	0	0	0	0	0	0
K07692	degU; two-component system, NarL family, response regulator DegU	1	0	0	0	0	0	0	0	1	1	1
K07694	vraR; two-component system, NarL family, vancomycin resistance associated response regulator VraR	0	0	0	0	0	0	0	0	0	1	1
K07696	nreC; two-component system, NarL family, response regulator NreC	0	0	1	0	0	0	0	0	0	0	0
K07699	spoA; two-component system, response regulator, stage D sporulation protein A	1	1	1	1	1	1	2	1	1	1	1
K07705	lytT, lytR; two-component system, LytR family, response regulator LytT	0	0	2	0	0	0	0	0	0	1	0
K07707	agrA, bfpR, fsrA; two-component system, LytR family, response regulator AgrA	0	0	0	0	0	0	0	0	0	1	1
K07708	ginL, ntrB; two-component system, NtrC family, nitrogen regulation sensor histidine kinase GinL [EC:2.7.13.3]	0	0	1	0	0	0	0	0	0	0	0
K07710	atoS; two-component system, NtrC family, sensor histidine kinase AtoS [EC:2.7.13.3]	1	2	1	0	0	0	0	0	0	0	0
K07713	zraR, hydG; two-component system, NtrC family, response regulator HydG	1	0	0	0	0	0	0	0	0	0	0
K07717	glnK; two-component system, sensor histidine kinase GlnK [EC:2.7.13.3]	0	0	1	0	0	0	0	0	0	0	0
K07719	yesM; two-component system, sensor histidine kinase YesM [EC:2.7.13.3]	0	0	1	0	0	0	0	0	0	0	0
K07720	yesN; two-component system, response regulator YesN	4	2	10	2	2	0	0	0	0	0	0
K07723	ndoA; CopG gene transcriptional regulator / antitoxin EndoAI	1	1	1	0	0	0	0	0	0	0	0
K07727	K07727; putative transcriptional regulator	2	0	3	0	1	0	0	0	1	1	1
K07729	K07729; putative transcriptional regulator	0	0	3	2	4	0	0	3	4	2	2
K07736	carD; CarD family transcriptional regulator, regulator of rRNA transcription	1	1	2	1	1	1	1	1	1	2	2
K07738	ndrD; transcriptional repressor NrdR	1	1	1	0	0	1					

K08151	tetA; MFS transporter, DHA1 family, tetracycline resistance protein	0	0	1	0	0	0	0	0	0	0	0
K08161	mdtG; MFS transporter, DHA1 family, multidrug resistance protein	0	0	5	0	0	0	0	0	0	0	0
K08169	yebC; MFS transporter, DHA2 family, multidrug resistance protein	1	1	2	0	1	0	0	0	0	1	0
K08177	oxiT; MFS transporter, OFA family, oxalate/formate antiporter	1	0	0	0	0	1	0	0	0	0	0
K08191	exuT; MFS transporter, ACS family, hexuronate transporter	1	0	0	0	0	0	0	0	0	0	0
K08217	mef; MFS transporter, DHA2 family, macrolide efflux protein	1	1	2	0	1	0	1	0	0	0	0
K08223	fsr; MFS transporter, FSR family, fosfomycin resistance protein	1	1	2	1	0	0	0	1	0	0	0
K08255	cdt; CoA-disulfide reductase [EC:1.8.1.14]	0	0	0	0	0	0	0	1	0	0	0
K08260	cbzI; adenosylcobinamide hydrolase [EC:3.5.1.90]	0	0	0	2	0	0	0	0	0	0	0
K08264	hdhR; heterodisulfide reductase subunit D [EC:1.8.98.1]	0	0	0	2	1	0	0	0	0	0	0
K08279	caE; carnitine operon protein CaE	0	0	1	0	0	0	0	0	0	0	0
K08281	pncA; nicotiamidase/pyrazinamidase [EC:3.5.1.19 3.5.1.1]	0	0	1	0	1	1	0	0	0	0	0
K08282	E2.7.11.1; non-specific serine/threonine protein kinase [EC:2.7.11.1]	1	1	0	0	0	0	0	0	0	0	0
K08296	sixA; phosphoinositide phosphatase [EC:3.1.3.3]	1	0	0	0	0	0	0	0	0	0	0
K08297	caIA; crotonobutyryl-CoA dehydrogenase [EC:1.3.8.13]	1	0	0	0	0	0	0	0	0	0	0
K08301	rng; rnfA; ribonuclease G [EC:3.1.2.6...]	1	1	1	1	1	1	1	1	1	1	1
K08303	prtC, trhP; U32 family peptidase [EC:3.4.-.-]	2	2	2	2	3	3	1	2	1	1	1
K08309	slt; soluble lytic murein transglycosylase [EC:4.2.2.-]	1	1	1	0	0	1	1	1	0	0	0
K08315	hyd; hydronase 3 maturation protease [EC:3.4.23.51]	0	0	0	0	0	0	1	0	1	1	1
K08316	rsmD; 16S rRNA (guanine-966-N2)-methyltransferase [EC:2.1.1.171]	1	1	1	1	1	1	0	1	1	1	1
K08352	phsA, psrA; thiosulfate reductase / polysulfide reductase chain A [EC:1.8.5.5]	1	0	2	0	0	0	0	0	0	0	0
K08368	MFS transporter, putative metabolite transport protein	0	0	0	4	0	0	0	0	0	0	0
K08369	ydjE; MFS transporter, putative metabolite:H+ symporter	2	1	2	0	0	0	0	1	0	0	0
K08384	spoVD; stage V sporulation protein D (sporulation-specific penicillin-binding protein)	0	1	1	1	1	1	1	1	1	1	1
K08590	nit; 2-oxoglutarate amidase [EC:3.5.1.111]	0	0	0	1	0	0	0	0	0	0	0
K08591	plyA; acyl phosphate:glycerol 3-phosphate acyltransferase [EC:2.3.1.275]	2	1	1	1	1	2	1	1	1	1	1
K08600	srbT; sortase B [EC:3.4.22.71]	0	0	0	1	3	0	0	0	0	0	0
K08602	pepF; pepB; oligopeptidase F [EC:3.4.24.-]	1	1	2	1	1	1	1	1	1	1	1
K08641	vanX; zinc-D-Ala-D-Ala dipeptidase [EC:3.4.13.22]	0	0	1	2	0	1	0	0	0	1	1
K08659	pepPA, pepB; dipeptidase [EC:3.4.-.-]	1	0	0	0	0	0	0	0	0	0	0
K08678	UXS1, uxs; UDP-glucurone decarboxylase [EC:4.1.1.35]	0	1	0	0	0	0	0	0	0	0	0
K08679	GAE, cap1; UDP-glucuronate 4-epimerase [EC:5.1.3.6]	1	0	0	0	0	0	0	0	0	0	0
K08681	pdxT, pdx2; pyridoxal 5'-phosphate synthase pdxT subunit [EC:4.3.3.6]	1	1	2	0	1	1	1	1	0	0	0
K08687	E3.5.1.59; N-carbamoylsarcosine amidase [EC:3.5.1.59]	1	0	0	0	0	0	0	0	0	0	0
K08722	yfbR; 5'-deoxyribonucleotidase [EC:3.1.3.89]	1	1	1	1	1	1	1	1	1	1	1
K08764	SCP2, SCPX; sterol carrier protein 2 [EC:3.3.1.176]	0	0	1	0	0	0	0	0	0	0	0
K08963	mtmA; methylthioribose-1-phosphate isomerase [EC:5.3.1.23]	1	1	1	1	1	1	0	1	1	1	1
K08965	mtmN; 2,3-diketo-3-methylthiopentyl-1-phosphate enolase [EC:5.3.2.5]	1	0	1	0	0	0	0	0	0	0	0
K08966	mtmX; 2-hydroxy-3-keto-5-methylthiopentyl-1-phosphate phosphatase [EC:3.1.3.87]	0	0	1	0	0	0	0	0	0	0	0
K08968	msrC; L-methionine (R)-S-oxide reductase [EC:1.8.4.14]	0	0	0	1	0	0	0	0	0	0	0
K08972	K08972; putative membrane protein	2	2	3	0	0	1	0	0	0	0	0
K08974	K08974; putative membrane protein	0	0	0	0	0	0	1	0	0	0	0
K08978	TC_BAT1; bacterial/archaeal transporter family protein	0	0	0	2	0	0	0	0	0	0	0
K08984	yidF; putative membrane protein	0	0	1	0	0	0	0	0	0	0	0
K08986	ycgQ; putative membrane protein	0	0	2	0	0	0	0	0	0	0	0
K08997	SELENOO, selD; protein adenyltransferase [EC:2.7.7.108]	1	0	0	0	0	0	0	0	0	0	0
K08998	uncharacterized protein	0	0	0	1	1	0	1	1	0	1	1
K09000	cmr4; CRISPR-associated protein Cmr4	1	0	0	0	0	0	0	0	0	0	0
K09002	csm3; CRISPR-associated protein Csm3	0	1	0	0	0	0	0	0	0	0	0
K09005	K09005; uncharacterized protein	0	1	1	0	0	0	0	0	0	1	1
K09013	suFC; Fe-S cluster assembly ATP-binding protein	1	1	1	1	1	1	1	0	1	0	0
K09017	rutR; TefA/ActfA family transcriptional regulator	0	0	0	4	0	0	0	0	0	0	0
K09020	rubB; 1,6-dioleoyl-2-palmitoyl glycerol acyl transferase [EC:3.1.1.110]	0	0	1	0	0	0	0	0	0	0	0
K09022	ridA, tdcF, RIDA; 2-limonobutanate-2-limonopropanoate deaminase [EC:3.5.99.10]	0	1	3	0	1	1	1	3	0	0	0
K09065	argF; N-acetylornithine carbamoyltransferase [EC:2.1.3.9]	0	0	2	0	0	0	0	0	0	0	0
K09116	K09116; damage-control phosphatase, subfamily I [EC:3.1.3.-]	0	0	0	0	0	1	0	0	0	0	0
K09117	K09117; uncharacterized protein	1	0	1	1	1	0	0	0	0	0	1
K09118	K09118; uncharacterized protein	1	1	1	0	0	0	0	0	0	0	0
K09121	lacC; pyridine-3,3'-bisthiocarboxylic acid mononucleotide nickel chelatase [EC:4.99.1.12]	1	1	2	0	2	0	0	0	1	1	1
K09123	lhpI; cis-3-hydroxyproline dehydratase [EC:4.2.1.171]	0	0	2	4	0	0	1	0	0	0	0
K09124	uncharacterized protein	0	0	1	0	0	0	0	0	0	0	0
K09125	yhQ; queuosin precursor transporter	0	0	0	1	1	1	1	1	1	1	1
K09126	uncharacterized protein	1	1	1	0	1	0	0	0	0	0	0
K09128	acnX2; mevalonate 5-phosphate dehydratase small subunit [EC:4.2.1.-]	0	2	4	0	0	1	0	0	0	0	0
K09131	K09131; uncharacterized protein	1	1	1	0	0	0	0	0	0	0	0
K09133	K09133; uncharacterized protein	0	0	3	0	0	0	1	1	0	1	1
K09137	K09137; uncharacterized protein	0	0	1	0	0	0	0	0	0	0	0
K09138	K09138; uncharacterized protein	0	0	1	0	0	0	1	1	1	2	2
K09153	small membrane protein	0	1	1	1	0	1	1	1	1	1	1
K09154	K09154; small membrane protein	0	0	1	0	0	0	0	0	0	0	0
K09157	K09157; uncharacterized protein	1	0	1	1	1	1	1	1	0	0	0
K09165	dodein	1	0	1	0	0	0	0	0	0	0	0
K09251	pataA; putrescine aminotransferase [EC:2.6.1.82]	1	1	1	0	0	0	0	0	0	0	0
K09384	uncharacterized protein	0	0	1	0	0	0	0	0	0	0	0
K09457	queF; 7-cyano-7-deazaguanine reductase [EC:1.7.1.13]	1	0	0	0	0	0	1	0	0	0	0
K09458	fabF, OXMS, CEM1, 3-oxoacyl-acyl-carrier-protein) synthase II [EC:2.3.1.179]	2	1	1	0	2	1	1	1	1	1	1
K09493	CCT1, TCP1; T-complex protein 1 subunit epsilon	1	0	1	0	0	0	0	0	0	0	0
K09497	CTC5; T-complex protein 1 subunit epsilon	0	1	0	0	0	0	0	0	0	0	0
K09581	glnC; LysR family transcriptional regulator, transcription activator of glutamate synthase operon	1	0	1	2	0	0	0	0	0	0	0
K09583	hutP; hutP; operon positive regulatory protein	0	1	1	0	0	0	0	0	0	0	0
K09588	pucR; Puc family transcriptional regulator, purine catabolism regulatory protein	1	1	2	0	0	0	0	1	0	0	0
K09589	purR; purine operon repressor	1	1	1	0	0	0	0	0	0	0	0
K09590	wzm, rfbB; lipopolysaccharide transport system permease protein	0	0	1	0	0	0	0	0	1	0	0
K09591	nodI; lipopolysaccharide transport system ATP-binding protein	0	0	1	0	0	0	0	0	0	0	0
K09595	glkX; nondiscriminating glutamyl-tRNA synthetase [EC:6.1.1.24]	0	1	1	1	1	1	1	1	0	0	0
K09705	K09705; uncharacterized protein	0	0	0	1	1	0	0	0	0	0	0
K09707	K09707; uncharacterized protein	0	0	0	1	0	0	0	0	0	0	0
K09710	ybeB; ribosome-associated protein	1	1	1	1	0	0	1	1	1	1	1
K09711	lipS1; lipoI synthase	0	0	1	1	0	0	0	0	0	0	0
K09729	K09729; uncharacterized protein	1	1	1	0	0	0	0	0	0	0	0
K09733	mfnb; 5-formylfuran-3-yl)methyl phosphate synthase [EC:4.2.3.153]	0	0	1	0	0	0	0	0	0	0	0
K09740	K09740; uncharacterized protein	1	1	2	0	0	1	0	0	0	1	1
K09747	eBfC; nucleoid-associated protein EbfC	1	1	1	1	1	1	1	1	1	1	1
K09748	rimP; ribosome maturation factor RimP	1	1	1	1	0	1	1	1	1	1	1
K09749	K09749; uncharacterized protein	0	1	0	0	0	0	0	0	0	0	0
K09760	rnuC; DNA recombinase protein RnuC	1	0	1	1	1	1	0	0	1	1	1
K09761	rsmE; 16S rRNA (uracil-1498-N3)-methyltransferase [EC:2.1.1.193]	1	1	1	1	1	1	1	0	0	0	0
K09762	whiA; cell division protein WhiA	1	1	1	1	1	1	1	1	1	1	1
K09764	uncharacterized protein	1	1	1	1	0	0	0	0	1	0	0
K09765	queE; epoxyqueuosin reductase [EC:1.17.99.6]	1	1	1	1	1	1	1	1	1	1	1
K09767	yqQ; cyclic-di-GMP-binding protein	1	1	1	1	1	0	0	0	0	0	0
K09768	K09768; uncharacterized protein	1	1	1	1	0	0	0	1	1	1	1
K09769	yndB; 2',3'-cyclic-nucleotide 2'-phosphodiesterase [EC:3.1.4.16]	1	1	1	1	1	1	1	1	1	1	1
K09770	K09770; uncharacterized protein	0	1	0	0	0	0	0	0	0	0	0
K09771	TC_SMR3; small multidrug resistance family-3 protein	1	0	1	0	0	0	0	0	0	0	0
K09772	sepF; cell division inhibitor SepF	1	1	1	1	0	1	1	1	1	1	1
K09773	pprS; [pyruvate, water dikinase]-phosphate phosphotransferase / [pyruvate, water dikinase] kinase [EC:2.7.4.28.2.7.11.33]	1	0	1	1	1	0	0				

K98200	ABC.MNAs; manganese/iron transport system ATP-binding protein	0	0	0	0	0	1	0	0
K98201	perF; Fur family transcriptional regulator, peroxide stress response regulator	1	0	3	0	1	1	1	0
K98611	K9861; uncharacterized protein	0	0	0	1	0	0	0	0
K98888	zapA; cell division protein ZapA	1	0	1	0	0	1	0	1
K99093	pyrH; uridylyl kinase [EC:2.7.4.22]	1	1	1	1	1	0	1	1
K99113	ppnB; purine/pyrimidine-nucleoside phosphorylase [EC:2.4.2.1 2.4.2.2]	0	0	0	1	0	0	0	0
K99228	K992; uncharacterized protein	0	0	1	0	0	0	0	0
K99336	IC.BA12; bacterial/archaeal transporter family-2 protein	2	1	2	2	2	1	1	1
K99400	K9940; uncharacterized protein	1	1	1	0	0	0	0	0
K99492	K9942; uncharacterized protein	0	0	1	0	0	0	0	0
K99951	cas2; CRISPR-associated protein Cas2	3	2	1	1	1	0	0	0
K99952	csn1, Cas9; CRISPR-associated endonuclease Csn1 [EC:3.1.-.-]	1	0	0	1	0	0	0	0
K99974	K9974; uncharacterized protein	0	0	0	1	1	0	0	1
K10026	queE; 7-carboxy-7-deazaguanine synthase [EC:4.3.99.3]	1	1	1	0	0	0	0	0
K10112	msmX, msmK, mslK, sucG, ggtA, msK; multiple sugar transport system ATP-binding protein [EC:7.5.2.-.]	0	0	1	0	0	0	0	0
K10117	msmE; serine/stachyose/melibiose transport system substrate-binding protein	0	0	0	0	0	0	1	0
K10118	msmF; raffinose/stachyose/melibiose transport system permease protein	0	0	0	0	0	0	1	0
K10206	E2.6.1.83; LL-diaminopimelate aminotransferase [EC:2.6.1.83]	1	1	2	1	2	1	1	1
K10216	dmpD, xyfD; hydroxymuconate-semialdehyde hydrolase [EC:3.7.1.9]	0	0	0	1	0	0	0	0
K10218	lglK, galC; 4-hydroxy-4-methyl-2-oxoglutarate aldolase [EC:4.1.3.17]	0	0	1	0	0	0	0	0
K10439	rbsB; ribose transport system substrate-binding protein	0	0	1	0	0	0	0	0
K10440	rbsC; ribose transport system permease protein	0	1	1	0	0	0	1	0
K10441	rbsA; ribose transport system ATP-binding protein [EC:7.5.2.7]	0	0	1	0	0	0	0	0
K10549	albS; D-allose transport system substrate-binding protein	0	1	1	0	0	0	1	0
K10554	fruC; fructose transport system ATP-binding protein	0	1	1	0	0	0	0	0
K10563	mutM, fog; formamidopyrimidine-DNA glycosylase [EC:3.2.2.23 4.2.99.18]	1	1	2	1	1	1	1	1
K10670	grdB; glycine reductase complex component A [EC:1.21.4.2 1.21.4.3 1.21.4.4]	7	4	9	0	0	0	0	0
K10672	grdB; glycine reductase complex component B subunit gamma [EC:1.21.4.2]	6	4	4	0	0	0	0	0
K10679	fnfB; nitroreductase / dihydroopteridine reductase [EC:1.1.-.- 1.5.1.34]	1	0	0	0	0	0	0	0
K10680	nemA; N-ethylmaleimide reductase [EC:1.1.-.-]	1	0	0	0	0	0	0	0
K10681	saeS; two-component system, Ompf family, sensor histidine kinase SaeS [EC:2.7.13.3]	0	0	0	0	1	0	0	0
K10716	mttb; methane-tetrahydromethanopterin dehydrogenase [EC:1.5.1.-.]	0	0	1	0	0	0	0	0
K10733	NTH; endonuclease III [EC:4.2.9.18]	1	1	1	1	1	1	1	1
K10797	enz; 2-enolate reductase [EC:1.3.1.31]	0	0	4	0	0	0	0	0
K10819	E2.7.13.3; histidine kinase [EC:2.7.13.3]	1	0	2	0	0	0	0	0
K10823	oppP; oligopeptide transport system ATP-binding protein	1	0	6	0	0	0	0	0
K10907	K10907; aminotransferase [EC:2.6.1.-.]	1	1	2	1	1	1	2	2
K10913	lpxB, luxR, TetR/AcR family transcriptional regulator, hemagglutinin/protease regulatory protein	0	0	0	0	0	0	0	0
K10914	crp; CRP/FNR family transcriptional regulator, cyclic AMP receptor protein	4	1	2	0	0	0	0	0
K10941	fliR, fliQ, fliK; sigma-54 dependent transcriptional regulator, flagellar regulatory protein	0	1	0	1	0	0	0	0
K10943	fliC, fliM; two-component system, response regulator FliC	0	0	1	0	0	0	0	0
K10947	padR; PadR family transcriptional regulator, regulatory protein PadR	2	1	5	1	3	0	1	0
K10977	aksA; methanoglycolic acid synthase [EC:2.3.3.14 2.3.3.-.]	0	0	1	0	0	1	1	0
K10979	ku; DNA end-binding protein Ku	1	1	1	0	0	0	0	1
K11014	eta; exfoliative toxin A/B	1	0	0	1	0	0	0	0
K11050	cYhA; multidrug/hemolysin transport system ATP-binding protein	0	0	0	0	1	0	1	0
K11068	cYhB; multidrug/hemolysin transport system permease protein	0	0	0	0	1	0	1	0
K11069	hlyH; hemolysin III	0	0	1	1	2	0	1	0
K11070	potD; spermidine/putrescine transport system substrate-binding protein	0	0	1	1	0	0	0	0
K11070	potC; spermidine/putrescine transport system permease protein	0	1	1	0	0	0	0	0
K11071	potB; spermidine/putrescine transport system permease protein	0	1	1	0	0	0	0	0
K11072	potA; spermidine/putrescine transport system ATP-binding protein [EC:7.6.2.11]	0	1	1	0	0	0	0	0
K11105	cvaR; hmpB; potassium/hydrogen antiporter	0	0	0	0	0	0	1	0
K11145	mrnC; mini-1-bromoducte III [EC:3.1.26.-.]	1	1	1	1	1	1	1	1
K11175	purN; phosphoribosylglycaminide formyltransferase I [EC:2.1.2.2]	1	1	1	1	1	1	1	1
K11178	yagS; xanthine dehydrogenase YagS FAD-binding subunit [EC:1.17.7.14]	0	0	1	0	0	0	0	0
K11179	tusC; dTCA-tRNA (cytosine1407-C5)-methyltransferase [EC:2.1.1.178]	0	1	2	0	0	0	0	0
K11180	dsrA; dissimilatory sulfite reductase alpha subunit [EC:1.8.99.5]	1	1	1	0	0	0	0	0
K11181	dsrB; dissimilatory sulfite reductase beta subunit [EC:1.8.99.5]	1	1	1	0	0	0	0	0
K12161	fmdE; fmdE; formylmethanofuran dehydrogenase subunit E [EC:1.2.7.12]	1	1	3	0	2	0	1	0
K12158	ylhdB; aspartate aminotransferase [EC:2.6.1.1]	0	0	0	0	0	0	1	0
K13183	kinB; two-component system, NirC family, sensor histidine kinase KinB [EC:2.7.13.3]	0	0	1	0	0	0	0	0
K13192	rsfM; 16S rRNA (cytosine1407-C5)-methyltransferase [EC:2.1.1.178]	0	0	1	0	0	0	0	0
K14444	wspR; two-component system, chemotaxis family, response regulator WspR [EC:2.7.7.65]	0	0	1	0	0	0	0	0
K14743	glcF; glycolate dehydrogenase iron-sulfur subunit [EC:1.19.9.14]	1	0	7	0	0	0	0	0
K14745	vanR; GntR family transcriptional regulator, vanilate catabolism transcriptional regulator	0	0	4	0	0	0	1	1
K15127	K15127; two-component system, sensor histidine kinase and response regulator [EC:2.7.13.3]	0	1	0	0	0	0	0	0
K16161	maeN; malate:Na+ symporter	0	0	0	0	0	1	0	0
K16168	dctP; C4-dicarboxylate-binding protein DctP	1	0	0	0	0	0	0	0
K16169	dcm; C4-dicarboxylate transporter, DctM subunit	1	0	1	0	0	1	2	1
K16193	temP; peptidoglycan pentaglycine linkage peptidyl transferase (the first glycine) [EC:2.3.2.16]	1	1	1	0	0	1	1	1
K17177	sufS; cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]	2	2	1	1	1	1	2	2
K17177	lysP; lysine-specific permease	0	0	1	0	0	0	0	0
K17177	cyaD; Serine/D-alanine/glycine transporter	1	0	0	0	0	0	1	0
K17179	sugE; quaternary ammonium compound-resistance protein SugE	0	0	1	0	0	0	1	0
K17179	rsfE; regulator of sigma E protease [EC:3.4.24.-]	1	1	1	1	1	1	1	1
K17179	ribD; dihydroxydiphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosamino)uracil reductase [EC:3.5.4.26 1.1.1.193]	1	0	1	1	1	1	1	1
K17179	ribF; riboflavin kinase / FMN adenyltransferase [EC:2.7.1.26 2.7.7.2]	1	1	2	0	1	1	1	1
K17174	folD; dihydrofolate synthase / folylpolyglutamate synthase [EC:3.6.3.12 3.6.3.27]	1	1	1	1	1	0	1	1
K17175	hisF; phosphoribosyl carboxylic acid cyclohydrolase / phosphoribosyl ATP phosphohydrolase [EC:3.5.4.19 3.6.1.31]	0	0	0	1	0	0	1	1
K19211	cynR; cynS family transcriptional regulator, cyan operon transcriptional activator	0	0	0	1	0	0	0	0
K19212	mntrB; DtxR family transcriptional regulator, manganese transport regulator	0	0	0	1	1	0	0	1
K19217	rhdE; ATP-dependent RNA helicase RhdE [EC:3.6.4.13]	0	0	0	0	1	0	1	1
K1936	pgcA; poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:4.1.-]	0	0	1	0	0	0	0	0
K19566	natA; neutral amino acid transport system ATP-binding protein	0	0	1	0	0	0	1	0
K19911	adaC; RNA(dinucleotide) deaminase [EC:3.5.4.33]	1	1	1	1	1	1	1	1
K21232	prtc; stkP; eukaryotic-like serine/threonine-protein kinase [EC:2.7.11.11]	1	1	1	1	2	1	1	2
K21237	hybF; hydrogenase-4 component F [EC:1.1.-.-]	0	0	0	0	0	0	0	0
K21238	hybC; hydrogenase-4 component C [EC:1.1.-.-]	2	0	0	0	0	0	0	0
K21239	hybD; hydrogenase-4 component D [EC:1.1.-.-]	0	0	0	0	0	0	0	0
K21240	hybE; hydrogenase-4 component E [EC:1.1.-.-]	2	0	0	0	0	0	1	0
K21241	hybF; hydrogenase-4 component F [EC:1.1.-.-]	1	1	2	0	0	0	0	0
K22511	aguB; N-carbamoylputrescine amidase [EC:3.5.1.53]	1	0	1	0	0	0	0	0
K22526	spuC; putrescine--putravate transaminase [EC:2.6.1.113]	2	1	2	1	1	0	1	1
K22564	norV; anaerobic nitric oxide reductase flavurobedoxin	0	0	1	1	1	1	0	0
K22677	msrAB; peptide methionine sulfoxide reductase msrA/B [EC:1.8.4.11 1.8.4.12]	1	1	1	1	1	0	1	1
K23399	cysM; D-Sulfato-L-cysteine synthase (O-acetyl-L-serine-dependent) [EC:2.5.1.144]	1	0	0	0	0	0	0	0
K24240	nrdA; NAD-dependent decetylase [EC:2.3.1.26]	0	0	1	0	0	0	0	0
K25027	fadC; acyl-CoA synthetase [EC:6.6.2.1.-]	1	0	0	0	0	0	0	0
K25028	ftsC; feruloyl-CoA synthase [EC:6.6.2.1.34]	0	0	0	0	0	0	1	0
K25029	ftsB; tight adherence protein B	1	1	1	0	0	0	0	1
K25111	cadC; tight adherence protein C	1	1	1	0	0	0	1	1
K25277	vgfK; putative selenate reductase [EC:1.97.1.9]	0	0	1	0	0	0	0	0
K25278	xdhD; putative selenate reductase molybdopterin-binding subunit	1	0	0	0	0	0	0	0
K25273	rnr; vacB; ribonuclease J [EC:3.1.13.1]	1	1	1	1	1	0	0	1
K25274	rnr; ribonuclease I [EC:3.1.13.1]	1	1	1	1	1	1	1	1
K25274	phosphatidylinositol alpha 1,6-mannosyltransferase [EC:2.4.1.-]	0	0	1	0	0	0	0	0
K25275	pmnS; 2-phosphomimiclylate synthase [EC:2.3.3.18]	1	0	0	0	0	0	0	0
K25276	rhcC; manganese-transporting P-type ATPase C [EC:7.2.2.22]	1	1	5	1	2	1	1	1
K25276	mttB; O-antigen biosynthesis alpha-1,3-mannosyltransferase [EC:2.4.1.139]	2	2	4	2	2	2	0	0
K25277	wpbP; O-antigen biosynthesis protein WpbP	0	0	0	0	0	0	2	1
K25305	wpaP; UDP- α -acetamido-D-glucosamine dehydrogenase [EC:1.1.1.136]	0	2	2	0	0	0	0	0
K25307	wbgC; wbcB; UDP-2-acetamido-2-deoxy-D-glucuronate dehydrogenase [EC:1.2.6.1.98]	0	1	0	0	0	0	0	0
K25308	wbaL; wbaP; UDP-2-acetamido-2-deoxy-D-glucuronate dehydrogenase [EC:1.1.1.335]	0	1	0	0	0	0	0	0
K25309	coaBC; coaE; phosphatidophenylcysteine decarboxylase/phosphopantothenate--cysteine ligase [EC:4.1.16.6 3.2.5]	1	1	1	1	1	1	1	1
K25309	comC; comE; sulphydryl decarboxylase subunit beta [EC:4.1.1.79]	0	0	1	0	0	0	0	0

K31617	mttC; dimethylaminomorronidate protein	1	0	7	0	0	0	1	0	0
K31618	pylB; methionyl-tRNA synthase [EC:5.4.1.99.58]	1	1	4	1	1	0	0	0	0
K31618	pylC; 3-methylnorlathione-L-lysine ligase [EC:6.3.2.59]	1	1	2	1	1	0	0	0	0
K31618	pylD; 3-methylnorlathione-NL-lysine dehydrogenase [EC:1.4.1.-]	1	0	1	1	1	0	0	0	0
K31618	ypbB; tetraprenyl-beta-curcumene synthase [EC:4.2.3.130]	1	1	1	0	0	0	0	0	0
K31623	est; estP; ethanalamine permease	1	0	3	0	0	0	0	1	0
K31626	K1630G; farnesyl-bisphosphate adelalase 2'-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase [EC:4.1.2.13 2.2.1.10]	0	0	1	0	0	0	0	0	0
K31627	K16327; putative LysE/RhtB family amino acid efflux pump	0	0	1	0	0	0	0	0	0
K31641	mxaA; myxamalid-type nonribosomal peptide synthetase MxaA	0	0	0	0	0	0	0	0	1
K31673	biot; biotin transport system permease protein	0	0	0	0	0	0	0	0	0
K31674	bioM; biotin transport system ATP-binding protein [EC:7.6.2.-]	0	0	0	0	0	0	0	0	0
K31675	ecf1; energy-coupling factor transport system permease protein	3	4	6	1	4	1	2	3	5
K31676	ecf1A; energy-coupling factor transport system ATP-binding protein [EC:7.-.-.]	1	1	3	0	0	1	1	2	3
K31677	ecf2A; energy-coupling factor transport system ATP-binding protein [EC:7.-.-.]	1	1	3	0	0	1	0	1	2
K31678	naicN; naicin transporter	0	0	0	0	0	0	0	1	0
K31681	hpwA; allantoin racemase [EC:5.1.99.3]	0	1	3	0	0	0	0	0	0
K316845	suA; (2R)-sulfafolate sulfo-lyase subunit alpha [EC:4.4.1.24]	2	0	0	0	0	0	1	0	0
K316846	suB; (2R)-sulfafolate sulfo-lyase subunit beta [EC:4.4.1.24]	2	0	0	0	0	0	0	0	0
K316849	uxaA1; altronate dehydratase small subunit [EC:4.2.1.7]	0	0	2	0	0	0	0	0	0
K316850	uxaA2; altronate dehydratase large subunit [EC:4.2.1.7]	0	0	2	0	0	0	1	0	0
K316874	hmfF; 2,5-furandicarboxylate decarboxylase	1	0	3	0	1	1	0	0	0
K316881	lmann81; mannose-1-phosphate lyase/transferase / phosphomannomutase [EC:2.7.7.13 5.4.2.8]	1	1	1	0	0	0	0	0	0
K316888	addB; ATP-dependent helicase/nuclease subunit A [EC:5.6.2.4.3.1.-]	1	1	1	1	1	1	1	1	1
K316899	addB; ATP-dependent helicase/nuclease subunit B [EC:5.6.2.4.3.1.-]	1	1	1	0	0	1	0	1	1
K316904	DCTPP1; DCTP diphosphatase [EC:3.6.1.12]	0	0	1	1	0	0	0	0	0
K316905	I1690S; fluoroquinolone transport system permease protein	1	0	0	0	0	0	0	0	0
K316906	I1690S; fluoroquinolone transport system permease protein	1	0	0	0	0	0	0	0	0
K316907	I1690T; fluoroquinolone transport system ATP-binding protein [EC:7.6.2.-]	1	0	0	0	0	0	0	0	0
K316923	qrtT; energy-coupling factor transport system substrate-specific component	1	0	0	0	0	0	0	0	0
K316925	ykE; energy-coupling factor transport system permease protein	0	0	1	0	0	0	1	0	0
K316926	htsT; energy-coupling factor transport system substrate-specific component	0	0	2	0	0	0	0	2	3
K316927	cbfT; energy-coupling factor transport system substrate-specific component	1	2	1	0	0	0	0	1	0
K316937	doxD; thioflavin dehydrogenase (quinone) large subunit [EC:1.8.5.2]	0	0	2	0	0	0	0	0	0
K316950	arsA; arsenic sulfite reductase subunit B	1	1	2	0	0	1	1	0	0
K316951	arsB; arsenic sulfite reductase subunit B	1	0	2	0	0	1	1	0	0
K316957	tryC; L-cystine transport system substrate-binding protein	0	0	2	0	0	0	0	0	0
K316959	tryM; L-cystine transport system permease protein	0	0	2	0	0	0	0	0	0
K316960	tryN; L-cystine transport system ATP-binding protein [EC:7.4.2.1]	0	0	2	0	0	0	0	0	0
K317037	lyxX1; putative lysine transport system substrate-binding protein	0	0	0	0	1	2	0	0	0
K317074	lyxX2; putative lysine transport system permease protein	0	0	0	1	1	0	0	0	0
K317076	lyxY; putative lysine transport system ATP-binding protein	0	0	0	1	1	0	0	0	0
K317093	CHO1; CPSA; CDP-diacylglycerol—serine O-phosphatyltransferase [EC:2.7.8.8]	1	1	1	0	0	0	0	0	0
K317218	sqr; sulfate quinolone oxidoreductase [EC:1.8.5.4]	1	1	1	0	0	0	0	0	0
K317248	pgII; N-acetylglucosamine-N,N'-diacyltadecanoyl-diphospho-undecaprenol 4-alpha-N-acetylglactosaminyltransferase [EC:2.4.1.291]	0	0	0	1	0	0	0	0	0
K317472	cymR; Rf2 for Rf1; transcriptional regulator; cytochrome metabolism repressor	1	1	2	0	0	0	1	2	1
K317675	SUPV3L1; SUPV3; ATP-dependent RNA helicase SUPV3L1/SUPV3 [EC:3.6.4.13]	0	0	0	0	0	0	0	0	1
K317686	copa; CPA17; F-type Cu+ transporter [EC:7.2.2.8]	1	1	2	0	1	1	2	1	1
K317723	preA; dihydropyrimidine dehydrogenase (NAD+) subunit PreA [EC:1.3.1.1]	0	0	6	0	0	0	0	1	1
K317727	PMPBC; MAS1; mitochondrial-processing peptidase subunit beta [EC:3.4.24.64]	1	1	1	1	1	0	1	1	1
K317733	cmkI; peptidoglycan LD-endopeptidase Cmkl [EC:3.4.-.-.]	0	0	1	0	0	0	0	0	0
K317754	cpnA; peptidoglycan endopeptidase [EC:1.1.1.163]	0	0	1	0	0	0	0	0	0
K317828	pyrD1; dihydoroorotate dehydrogenase (NAD+) catalytic subunit [EC:1.3.1.14]	1	0	2	1	1	1	1	1	1
K317830	GGR; diguanidylglycerophospholipid reductase [EC:3.3.1.101 1.3.7.11]	0	0	2	1	0	0	0	0	0
K317865	croB; hydroxybutyryl-CoA dehydratase [EC:4.2.1.55]	0	0	1	0	0	0	0	0	0
K317929	hndB; NADP-reducing hydrogenase subunit HndB [EC:1.12.1.3]	1	1	2	0	0	0	0	0	0
K317995	hydG; sulphydrylogenase subunit gamma (sulfur reductase) [EC:1.12.98.4]	0	0	1	0	0	0	0	0	0
K318009	budC; meso-butenediol dehydrogenase (S,S)-butenediol dehydrogenase / diacetyl reductase	0	0	0	0	0	0	0	1	0
K318011	kanE; beta-5,6-aminomutase beta subunit [EC:5.4.3.3]	0	0	1	0	0	0	0	0	0
K318012	kkdI; L-erythrose-3,5-diaminohexanoate dehydrogenase [EC:1.4.1.11]	0	0	1	0	0	0	0	0	0
K318013	kceC; 3-ke-to 5-aminohexanoate cleavage enzyme [EC:3.2.1.247]	0	0	2	0	0	0	0	2	0
K318118	aarc1; cat1; succinyl-CoA:acetate CoA-transferase [EC:2.3.2.18]	0	0	1	1	1	1	0	0	1
K318122	cat2; abfF; 4-hydroxybutyrate CoA-transferase [EC2.8.3.-]	1	1	2	0	0	0	0	1	0
K318148	rcbC; release factor H-coupled RcbB family protein	0	0	1	0	0	0	0	0	0
K318164	NDUFK7; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex assembly factor 7	1	1	0	0	0	0	0	0	0
K318166	FOXRED1; FAD-dependent oxidoreductase domain-containing protein 1	0	0	1	0	0	0	0	0	0
K318189	TACO1; translational activator of cytochrome c oxidase 1	0	0	1	0	0	0	0	1	0
K318199	inhA; cyclohexyl-isocyanide hydrolase [EC:4.2.1.103]	0	0	2	0	0	0	0	1	1
K318209	ifrA; fumurate reductase [ComQ/Cob] subunit A [EC:1.3.4.1]	0	0	1	0	0	0	0	0	0
K318235	rsmV; rsmR; macrolide transport system ATP-binding/permease protein	1	0	0	0	0	0	0	0	0
K318234	vat; virginiamycin A acetyltransferase [EC:2.3.1.-]	0	0	0	0	0	0	0	0	1
K318290	ichY; itaconyl-CoA hydratase [EC:4.2.1.56]	0	0	2	0	0	0	0	0	0
K318302	mekI; membrane fusion protein, multidrug efflux system	0	0	1	0	0	0	0	0	0
K318303	mekII; multidrug efflux pump	0	0	1	0	0	0	0	0	0
K318303	mekIII; membrane fusion protein, multidrug efflux system	1	0	0	0	0	0	0	0	0
K318330	hndA; NADP-reducing hydrogenase subunit HndA [EC:1.12.1.3]	2	1	1	0	0	1	0	0	0
K318331	hndC; NADP-reducing hydrogenase subunit HndC [EC:1.12.1.3]	0	0	0	0	0	0	1	0	0
K318332	hndB; NADP-reducing hydrogenase subunit HndB [EC:1.12.1.3]	0	0	0	0	0	0	1	0	1
K318345	vanS8; vanS; vanSD; two-component system, OmpR family, sensor histidine kinase VanS [EC:2.7.13.3]	1	0	1	0	0	0	0	0	0
K318346	vanW; vanCm; vanR; vanNC; vanS; vanSD; two-component system, OmpR family, sensor histidine kinase VanR [EC:2.7.13.3]	1	0	2	0	1	0	0	0	1
K318347	vanD; D-specific alpha-keto acid dehydrogenase [EC:1.1.1.-]	0	0	1	0	0	0	0	0	0
K318349	vanR; vanNC; vanR; vanNC; two-component system, OmpR family, response regulator VanR	1	1	2	0	2	0	0	0	1
K318350	vanS; vanS; vanS; vanSD; two-component system, OmpR family, sensor histidine kinase VanS [EC:2.7.13.3]	0	0	1	0	0	1	0	0	0
K318359	padH; phenylglyoxalate dehydrogenase epsilon subunit [EC:1.2.1.58]	0	0	2	0	0	0	0	0	0
K318367	CoADr; CoA-dependent NAD(P)H sulfur oxidoreductase [EC:1.8.1.18]	1	1	1	0	0	0	0	0	0
K318369	adhZ; alcohol dehydrogenase [EC:1.1.1.-]	0	0	0	0	0	0	1	0	0
K318429	legG; neuf2; GDP-DPN-N,N-diacetylβ-D-glucosamine 2-epimerase (hydrolysing) [EC:3.2.1.184]	0	0	1	0	0	0	0	0	0
K318430	legI; neuf2; N,N-diacetylβ-D-glucosamine synthase [EC:2.5.1.101]	0	0	1	0	0	0	0	0	0
K318431	legJ; ptmb; CMP-N,N-diacetylβ-D-glucosamine acid synthase [EC:2.2.7.62]	0	0	1	0	0	0	0	0	0
K318445	ndx1; diadenosine triphosphate hydrolase (ATP-forming) [EC:3.6.1.61]	1	0	1	1	1	0	0	0	0
K318456	E3.5.4.32; 8-oxoguanine deaminase [EC:3.5.4.32]	0	0	1	0	0	0	0	0	0
K318471	ydgG; methylglyoxal reductase [EC:1.1.1.-]	0	0	1	0	0	0	0	0	0
K318501	hmeD; heterodisulfide reductase iron-sulfur subunit	1	1	0	0	0	0	0	0	0
K318563	thnl; methyltransferase [EC:2.1.1.-]	0	0	1	0	0	0	0	0	0
K318608	ptdA; pyridoxamine—pyruvate transaminase [EC:2.6.1.30]	0	0	0	0	0	0	0	0	2
K318672	daca; diadenylate cyclase [EC:2.7.7.85]	1	1	1	1	1	1	1	1	1
K318682	rny; ribonuclease Y [EC:3.1.-.-.]	1	1	1	0	0	0	1	1	1
K318700	fkf; fluorocetyl-CoA thioesterase [EC:3.3.1.229]	0	0	1	0	0	0	0	0	0
K318702	uctC; CoA:oxidase CoA-transferase [EC:2.8.3.19]	0	0	3	0	0	0	0	0	0
K318707	mtAB; threonylcaramylobinoside tRNA methylthiotransferase MtAb [EC:2.8.4.5]	1	1	1	1	1	1	1	1	1
K318785	mpz2; beta-1,4-mannoooligosaccharide-beta-1,4-mannoN-Acetylglucosamine phosphorylase [EC:2.4.1.319 2.4.1.320]	0	0	0	0	0	0	1	0	0
K318814	icbt; putative inorganic carbon (hco3-) transporter	0	0	0	0	1	1	0	0	0
K318899	mfdA; smda; ATP-binding cassette subfamily B, multidrug efflux pump	0	0	0	0	0	0	0	0	1
K318906	mfdB; smda; multiple small multidrug resistance pump	0	0	0	0	0	0	0	0	1
K318934	ycckC; paired small multidrug resistance pump	1	0	0	0	0	0	0	0	0
K318925	yckkD; paired small multidrug resistance pump	1	0	0	0	0	0	0	0	0
K318934	imr5; MFS transporter, DHA2 family, multidrug resistance protein	0	0	0	0	0	0	1	0	0
K318935	sdrM; MFS transporter, DHA2 family, multidrug resistance protein	1	0	1	0	0	0	0	0	0
K318940	arlS; two-component system, OmpR family, sensor histidine kinase ArlS [EC:2.7.13.3]	1	0	0	0	0	0	0	0	0
K318941	arlF; two-component system, OmpR family, response regulator ArlF	1	0	1	0	1	1	0	0	0
K318979	queG; epoxypeptidase reductase [EC:1.17.99.6]	1	0	2	0	0	0	0	0	0
K318997	cbpM; chaperone modulatory protein CbpM	1	0	0	0	0	0	0	0	0
K319005	tdkX; UDP-2-acetamido-2,6-beta-L-arabinohex-4-ose reductase [EC:2.4.1.337]	1	0	0	0	0	0	0	0	0
K319005	tdkX; UDP-2-acetamido-2,6-beta-L-arabinohex-4-ose reductase Cas6 [EC:3.1.1.367]	1	0	2	0	0	0	0	0	0
K319075	ct31; ct37; CRISPR-associated protein Ct32	0	0	1	0	0	0	0	1	0
K319081	bras; bcsL; two-component system, OmpR family, sensor histidine kinase Bras/Bcs5 [EC:2.7.13.3]	0	0	0	0	0	0	1	0	1
K319082	braR; bceC; two-component system, OmpR family, response regulator protein BraR/BceR	0	0	0	1	0	0	0	1	0
K319090	casSt; CRISPR-associated protein CasSt	0	0	1	0	0	0	0	0	0
K319091	casS; CRISPR-associated endoribonuclease Cas6 [EC:3.1.-.-.]	2	0	2	0	0	0	0	0	0
K319092	parE1_3_4; toxin ParE1/3/4	1	0	0	0	0	0	0	1	0
K319114	csh1; CRISPR-associated protein Csh1	1	0	0	0	0	0	0	0	0
K319115	csh2; CRISPR-associated protein Csh2	2	0	1	0	0	0	0	0	0
K319116	cas9; CRISPR-associated protein Cas9	2	0	1	0	0	0	0	0	0
K319117	cas1; cas8; CRISPR-associated protein Csd1	0	1	0	0	0	0	0	1	0

K19118	csd2, cas7; CRISPR-associated protein Csd2	0	1	0	0	1	0	0	2	0	0
K19119	cas5d; CRISPR-associated protein Cas5d	0	0	0	0	1	0	0	1	0	0
K19134	csx10; CRISPR-associated protein Csx10	1	0	0	0	0	0	0	0	0	0
K19137	cnn2; CRISPR-associated protein Cnn2	1	0	0	0	0	0	0	0	0	0
K19138	csm2; CRISPR-associated protein Csm2	0	1	0	0	0	0	0	0	0	0
K19139	csm4; CRISPR-associated protein Csm4	0	1	0	0	0	0	0	0	0	0
K19140	csm5; CRISPR-associated protein Csm5	0	1	0	0	0	0	0	0	0	0
K19141	csm5; CRISPR-associated protein Cmr5	1	0	0	0	0	0	0	0	0	0
K19147	mcrC; S-methylcytosine-specific restriction enzyme subunit McrC	1	0	0	0	0	0	0	1	0	1
K19157	yafQ; mRNA interferase YafQ [EC:3.1.-.-]	2	0	1	0	0	0	0	0	0	0
K19158	yoeB; toxin YoeB [EC:3.1.-.-]	1	0	1	0	0	0	0	0	0	0
K19159	yefM; antitoxin YefM	1	0	0	0	0	0	0	0	0	0
K19171	dndD; DNA sulfur modification protein DndD	0	0	1	0	0	0	0	0	0	0
K19200	IA1; saponin-N-acetyltransferase like protein	0	0	1	0	0	0	0	0	0	0
K19221	cobA, btuB; cob(I)alanyl adenyltransferase [EC:2.5.1.17]	1	0	4	1	1	1	1	1	1	1
K19222	menI, DHNAT; 1,4-dihydroxy-2-naphthoyl-CoA hydrolase [EC:3.1.2.28]	0	0	0	0	0	0	0	1	0	0
K19224	lytE, cwfL; peptidoglycan DL-endopeptidase LytE [EC:3.4.-.-]	1	1	1	0	0	0	0	0	0	0
K19239	sapZ; predicted membrane protein	1	1	1	0	0	0	0	0	0	0
K19244	alaD; alanine dehydrogenase [EC:1.4.1.1]	0	0	1	0	0	0	0	0	0	0
K19270	hpxA; mannosid-1-sugar-/sorbitol-6-phosphatase [EC:3.1.3.22 3.1.3.23 3.1.3.50]	1	0	0	0	0	0	0	1	0	0
K19294	algI; alginate O-acetyltransferase complex protein AlgI	1	0	1	0	1	0	0	1	1	1
K19302	bcrC; undecaprenyl-diphosphatase [EC:3.6.1.27]	2	1	3	1	1	1	0	1	1	1
K19333	kdgR; ICR family transcriptional regulator, Kdg regulon repressor	0	0	2	0	1	0	0	0	0	0
K19350	lsa; lincosamide and streptogramin A transport system ATP-binding/permease protein	0	0	1	0	1	0	0	0	0	1
K19405	mcsA; protein arginine kinase [EC:2.7.14.1]	1	1	1	1	1	1	1	1	0	0
K19411	mcsA; protein arginine kinase activator	1	1	1	1	1	1	0	1	0	0
K19421	epsC; polysaccharide biosynthesis protein EpsC	1	1	2	0	1	1	0	0	0	0
K19422	epsD; glycosyltransferase EpsD [EC:2.4.-.-]	1	0	0	1	0	1	0	0	0	0
K19423	epsE; glycosyltransferase EpsE [EC:2.4.-.-]	1	0	0	0	1	1	0	0	0	0
K19424	epsF; glycosyltransferase EpsF [EC:2.4.-.-]	0	0	0	0	0	1	0	0	0	0
K19425	epsH; glycosyltransferase EpsH [EC:2.4.-.-]	1	0	0	0	0	0	0	0	0	0
K19427	epsI; glycosyltransferase EpsI [EC:2.4.-.-]	1	0	0	0	1	0	0	0	0	0
K19428	epsL; sugar transferase EpsL [EC:2.4.-.-]	0	0	1	0	1	0	0	0	0	0
K19430	epsN; pyridoxal phosphate-dependent aminotransferase EpsN [EC:2.6.1.-.]	1	0	1	0	1	1	0	0	0	0
K19545	InuA_C_D_E; Inosamidase nucleotidytransferase A/C/D/E	0	0	0	0	1	0	0	0	0	0
K19689	ampS, pepS, ampT; aminopeptidase [EC:3.4.11.-.]	1	1	1	1	1	1	1	1	1	0
K19709	ydif; acetate CoA-transferase [EC:2.8.3.8]	0	0	1	0	0	0	0	0	0	0
K19736	aerF; TeiR/Acrf family transcriptional regulator, regulator of autoinduction and epiphytic fitness	0	0	0	0	0	0	0	1	0	0
K19784	chrN; NOR; chromate reductase, NAD(P)H dehydrogenase (quinone)	1	0	1	0	1	0	0	0	0	0
K19802	ycjG, ykfB; L-Ala-D-Lys epimerase [EC:5.1.1.20]	0	0	1	0	0	0	0	0	0	0
K19814	eam; glutamate 2,3-aminotransferase [EC:5.4.3.9]	2	1	0	0	0	0	0	0	0	0
K19955	adh2; alcohol dehydrogenase [EC:1.1.1.-.]	1	0	0	0	0	0	1	1	1	0
K19960	chnA; cyclohexanol dehydrogenase [EC:1.1.1.245]	1	0	0	0	0	0	0	0	0	0
K20036	cutC; choline trimethylamine-lyase [EC:4.3.99.4]	1	1	1	0	0	0	0	0	0	0
K20074	ppcP; ppM family protein phosphatase [EC:3.1.3.16]	1	1	1	2	1	1	1	1	1	1
K20156	sggG; 2-amino-4-deoxychorismate dehydrogenase [EC:3.1.3.8.16]	2	0	0	0	0	0	0	0	0	0
K20265	gadC; glutamate/GABA antiporter	0	0	0	2	2	0	0	0	0	0
K20249	vioA; dTDP-4-amino-4-deoxy-D-glucose transaminase [EC:2.6.1.33]	1	0	1	0	0	0	0	0	0	0
K20445	ndhF; nicotinate dehydrogenase FAD-subunit [EC:1.17.1.5]	0	1	4	0	0	1	0	0	0	0
K20446	ndhS; nicotinate dehydrogenase small FeS subunit [EC:1.17.1.5]	0	0	1	0	0	0	0	0	0	0
K20447	ndhL; nicotinate dehydrogenase large molybdopterin subunit [EC:1.17.1.5]	2	3	9	0	0	1	1	3	0	0
K20448	ndhM; nicotinate dehydrogenase medium molybdopterin subunit [EC:1.17.1.5]	0	0	1	0	0	0	0	1	0	0
K20449	hnr; 6-hydroxyacetone reductase [EC:1.3.7.1]	0	0	1	0	0	0	0	0	0	0
K20451	mlr; methylitaconate Delta-isomerase [EC:5.3.3.6]	0	0	4	0	0	0	0	0	0	0
K20454	dnl; 2,3-dimethylmalate lyase [EC:4.1.3.32]	0	0	0	0	0	0	0	1	0	0
K20459	nukF, mcdP, sbcD; lantibiotic transport system ATP-binding protein	0	0	0	0	0	0	0	0	1	0
K20460	nukE, mcdP, sbcD; lantibiotic transport system permease protein	0	0	0	0	0	0	0	0	1	0
K20487	nisK, spaR two-component system, OmpP family, lantibiotic biosynthesis sensor histidine kinase NisK/SpaK [EC:2.7.13.3]	1	0	0	0	0	0	0	0	1	1
K20488	nisR, spaR two-component system, OmpP family, lantibiotic biosynthesis response regulator NisR/SpaR	1	0	0	0	1	0	0	0	1	1
K20609	sgcP; putative aminopeptidase [EC:3.4.1.-.]	0	0	1	0	0	0	0	0	0	0
K20625	ahy; acetylene hydratase [EC:4.2.1.12]	0	0	3	0	0	0	0	0	0	0
K20680	fdtB; dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase [EC:2.6.1.90]	0	0	1	0	0	0	0	0	0	0
K20763	naaA; 5-nitroanthranilic acid aminohydrolase [EC:3.5.99.8]	0	0	1	0	0	0	0	0	0	0
K20859	phnPP; phosphoribosyl 1,2-cyclic phosphate 1,2-diphosphodiesterase [EC:3.1.4.57]	0	0	1	0	0	0	0	0	0	0
K20882	hadA; (R)-2-hydroxy-4-methylpentanolate CoA-transferase [EC:2.8.3.24]	1	0	0	0	0	0	0	0	0	0
K20922	vpsI; polysaccharide biosynthesis protein VpsI	1	0	0	0	0	0	0	0	0	0
K21020	siaD; diguanylate cyclase [EC:2.7.7.65]	0	0	1	0	0	0	0	0	0	0
K21022	roeA; diguanylate cyclase [EC:2.7.7.65]	0	0	0	0	0	0	0	1	0	0
K21028	ynjE; molybdopterin synthase sulfurtransferase [EC:2.8.1.11]	0	0	1	0	0	0	0	0	0	0
K21029	moeB; molybdopterin-synthase adenylyltransferase [EC:2.7.7.80]	0	0	1	1	0	0	0	0	1	2
K21030	tarI; D-ribitol-5-phosphate cytidylyltransferase [EC:2.7.7.40]	0	0	0	1	1	0	0	0	0	0

Table S5. Recipe for trace element solution A, 500 mL solution

Description	Volume (mg, unless stated)
HCl	10 mL
FeCl ₂ .4H ₂ O	750
CoCl ₂ .6H ₂ O	95
MnCl ₂ .4H ₂ O	50
ZnCl ₂	35
H ₃ BO ₃	3
Na ₂ MoO ₄ .H ₂ O	18
NiCl ₂ .6H ₂ O	12
CuCl ₂ .2H ₂ O	1
Water (MilliQ)	500 mL

Table S6. Recipe for trace element solution B, 500 mL solution

Description	Volume (mg, unless stated)
Na ₂ SeO ₃ .5H ₂ O	3
NaWO ₄ .2H ₂ O	4
NaOH	250
Water (MilliQ)	500 mL

Table S7. Recipe for 1000X vitamin, 1L solution. After dissolving all the reagents in the water, the solution water was filter-sterilized three times into serum bottles and capped with sterile septa. The solution was then purged with sterile N₂ for 30 minutes.

Description	Volume (mg, unless stated)
p-aminobenzoate	20
Biotin	5
Nicotinic acid	50
Pantothenic acid	25
Pyridoxine	75
Thiamine	50
Cyanocobalamin	50
Water (MilliQ)	1 L

FASP Protocol

All centrifugation steps were done at 14,000 rcf for 10 minutes unless indicated otherwise.

1. Each extract sample was diluted to a final concentration of 0.8 µg/µl using ammonium bicarbonate buffer (ABC, 0.05 M stock, pH 9.0). The proteins in the diluted sample were denatured by adding dithioreitol to a final concentration of 5 mM and incubating the mixture at 30° C for 30 minutes.
2. The samples were mixed with 200 µl of urea solution (UA, 8 M stock) and the filter units were centrifugated twice. The flow-through from each filter unit was discarded from the collection tube after each centrifugation step.
3. 100 µl of iodoacetamide solution (IAA, 0.05 M) was added to the filter units and was mixed using a thermomixer temperature at 600 rpm. The filter unites were incubated for 20 minutes in the dark before being centrifugated.
4. 100 µl of UA was added to the filter units which were then centrifugated twice.
5. 100 µl of ABC was added to the filter units which were then centrifugated twice.
6. 40 µl of ABC and 0.9 µl of trypsin stock solution (0.4 ng/µl) were added to the filter units and were mixed at 600 rpm in thermomixer for 1 minute. The flow-through from each filter unit was then discarded from the collection tube.
7. 500 µl of MilliQ H₂O was added to the filter units, which were incubated at 37° C in dark for 12 hours.
8. The filter component from each unit was relocated to a new container tube and was centrifugated.
9. 20 µl of ABC was added to the filter units, which were then centrifugated twice. The flow-through containing peptides were transferred to 1.5 mL tubes and were stored at -20° C until proteomics analysis.

Table S8. List of proteins identified in all three replicates of *D. formicoceticum* grown in DCM

The protein sequence coverage (95%) refers to the percentage of matching amino acids from the identified peptides having confidence greater than or equal to 95% divided by the total number of amino acids in the sequence

NCBI Protein ID	Protein Description	Protein Name	Pathway	Protein Scores			Number of peptides			Protein sequence coverage (95%)			
				Average	STDEV	% STDEV	Average	STDEV	% STDEV	Average	STDEV	% STDEV	
WP_089610968.1	(R)-phenylalanyl-CoA dehydratase beta subunit	MetH	Amino Acid fermentation - L-Phenyl-Lactate	31.1	2.8	0.1	19.3	3.3	0.2	49.4	5.6	0.1	
WP_089611000.1	Malate synthase		Amino acid synthesis	9.0	0.9	0.1	5.0	0.5	0.3	25.4	8.2	0.3	
WP_242965479.1	Branched-chain-amino-acid aminotransferase 2		Amino Acids	29.5	4.5	0.2	20.3	2.1	0.1	50.6	6.5	0.1	
WP_089612575.1	S-adenosylmethionine synthase	Xsc	Amino Acids - Enzyme cofactors	30.1	4.5	0.1	17.0	2.2	0.1	46.1	5.8	0.1	
WP_089610166.1	Sulfacetaldelyde acetyltransferase		Amino Acids	37.0	2.0	0.1	20.7	1.7	0.1	32.0	1.9	0.1	
WP_089611605.1	Hypotaurine/taurine-pryuvate aminotransferase		Amino Acids - Glutamate	31.9	4.7	0.1	22.7	2.5	0.1	46.0	4.7	0.1	
WP_089609398.1	NADP-specific glutamate dehydrogenase	DAP	Amino Acids - Glutamate	56.1	4.4	0.1	72.3	5.2	0.1	67.7	3.7	0.1	
WP_089609283.1	LL-diaminopimelate aminotransferase		Amino Acids - Lysole	33.1	2.9	0.1	22.7	2.1	0.1	55.8	8.5	0.2	
WP_089609252.1	Diaminopimelate decarboxylase		Amino Acids - Lysole	35.2	3.9	0.1	27.7	0.5	0.0	47.0	1.6	0.0	
WP_193064971.1	Maleate-semialdehyde dehydrogenase	IoA	Amino Acids - betaine, alanine, aspartate	38.7	4.5	0.1	24.0	3.6	0.1	44.5	3.4	0.1	
WP_089612390.1	Maleate-semialdehyde dehydrogenase	Meth	Amino Acids - Methionine	30.2	0.8	0.0	46.7	0.9	0.0	78.8	0.1	0.1	
WP_089611707.1	Methionine synthase	Meth	Amino Acids - Tryptophan	49.0	2.2	0.0	39.0	2.2	0.1	57.1	4.2	0.1	
WP_089612390.1	Methionine synthase		Amino Acids - Arginine and pyrimidine precursor	52.1	5.7	0.1	29.7	2.5	0.1	27.8	3.1	0.1	
WP_089612137.1	Tryptophan synthase beta chain		C1 pathway	2.3	0.1	0.0	1.0	0.0	0.0	4.6	0.0	0.0	
WP_242965392.1	Carbamoyl-phosphate synthase large chain	Mch	C1 pathway	49.7	1.7	0.0	49.3	3.1	0.1	61.4	4.1	0.1	
WP_089608723.1	Methenyl-coenzyme M methyltransferase	Mtb8	C1 pathway	52.1	2.5	0.0	65.0	1.6	0.0	73.0	2.7	0.0	
WP_157677303.1	Methylcrotonyl-tetrahydrolipofate methyltransferase	Mtrf1	C1 pathway	12.5	1.3	0.1	7.7	0.5	0.1	18.9	1.7	0.1	
WP_089608939.1	Glycine betaine methyltransferase	Mtb8	C1 pathway	1.9	0.2	0.1	1.0	0.0	0.0	1.9	0.0	0.0	
WP_089608646.1	Glycine betaine methyltransferase	Mtb8	C1 pathway	9.5	3.6	0.1	6.9	2.3	0.1	49.6	14.5	0.1	
WP_19306644.1	Glycine betaine methyltransferase	Mtb8	C1 pathway	13.5	1.4	0.1	7.7	0.5	0.1	33.5	2.8	0.1	
WP_089612392.1	Glycine betaine methyltransferase	Mtb8	C1 pathway	15.6	3.3	0.2	8.7	1.2	0.1	23.4	4.1	0.2	
WP_089608588.1	Chaperone protein DnaK		Chaperone	80.7	5.5	0.1	49.0	3.3	0.1	52.6	7.9	0.2	
WP_089608782.1	60 kDa chaperonin		Chaperone	70.9	4.1	0.1	77.0	7.3	0.1	65.0	4.7	0.1	
WP_089608882.1	Chaperone protein ClpB		Chaperone	48.6	1.9	0.0	30.0	1.4	0.0	36.0	0.9	0.0	
WP_089608885.1	Chaperone protein dnaK2		Chaperone	54.4	2.4	0.0	32.7	3.3	0.1	49.5	3.4	0.1	
WP_089609257.1	Chaperone protein HtpG		Chaperone	57.6	9.9	0.2	33.0	3.6	0.1	50.8	4.0	0.1	
WP_089612371.1	Nucleic acid ligase of genetic competence CipC/MedB	CysG	Cofactor biosynthesis	31.5	3.6	0.1	16.7	1.2	0.1	37.3	4.7	0.1	
WP_089611628.1	NADPH-quinone oxidoreductase subunit 1, chloroplastic		Complex I	70.0	7.4	0.1	59.1	5.5	0.1	47.1	4.3	0.1	
WP_089611627.1	NADH-quinone oxidoreductase subunit 4	NuoC	Complex I	4.3	2.4	0.6	2.7	0.9	0.4	31.1	12.3	0.4	
WP_089611863.1	NAD(+)-translocating NADH-quinone reductase subunit F	NuoD	Complex I	15.6	4.4	0.3	8.3	1.7	0.2	27.6	4.9	0.2	
WP_089611621.1	NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic	NuoF	Complex I	10.5	1.0	0.1	5.0	0.0	0.0	12.3	1.0	0.1	
WP_193067331.1	NADH-quinone oxidoreductase subunit K	NuoL	Complex I	5.7	0.2	0.0	3.0	0.0	0.0	30.0	0.6	0.0	
WP_089611617.1	NADH-quinone oxidoreductase subunit L	NuoK	Complex I	2.0	0.6	0.0	1.0	0.0	0.0	12.7	0.0	0.0	
WP_089611615.1	NAD(P)H-quinone oxidoreductase subunit L	NuoM	Complex I	4.2	1.4	0.3	3.3	0.5	0.1	5.8	0.7	0.1	
WP_089611614.1	NAD(P)H-quinone oxidoreductase subunit 2	NuoN	Complex I	4.7	0.7	0.1	3.0	0.8	0.3	6.1	0.8	0.1	
WP_089612430.1	Sulfite reductase, dissimilatory-type subunit alpha	DsrA	Dissimilatory sulfite reduction	3.2	0.3	0.1	2.3	0.5	0.2	6.9	0.8	0.1	
WP_089612473.1	Sulfite reductase, dissimilatory-type subunit beta	DsrB	Dissimilatory sulfite reduction	40.5	4.0	0.1	25.0	0.0	0.0	51.0	2.6	0.1	
WP_089612474.1	Sulfite reductase, dissimilatory-type subunit gamma	DsrC	Dissimilatory sulfite reduction	7.0	2.1	0.3	5.3	0.5	0.1	51.7	10.3	0.2	
WP_242965458.1	FAD-dependent oxidoreductase	GltB/StnC	Electron bifurcation	62.9	3.0	0.0	39.0	0.0	0.0	49.9	0.7	0.0	
WP_089609841.1	NADP-reducing hydrogenase subunit HndA	HndA	Electron bifurcation	9.3	3.2	0.3	7.3	1.2	0.2	37.3	3.0	0.1	
WP_089609810.1	NADP-reducing hydrogenase subunit HndA	HndB	Electron bifurcation	6.3	0.2	0.0	3.3	0.5	0.1	33.3	1.0	0.0	
WP_157677371.1	NADP-reducing hydrogenase subunit HndA	HndC	Electron bifurcation	7.6	3.1	0.4	7.0	1.4	0.2	44.9	7.0	0.2	
WP_242965457.1	FAD-dependent NADH oxidoreductase	HndD	Electron bifurcation	80.8	6.1	0.1	56.7	2.9	0.1	45.4	7.0	0.2	
WP_089609815.1	Ion-translocating oxidoreductase complex subunit C	HndE	Electron bifurcation	29.1	1.5	0.1	17.3	1.1	0.1	32.3	0.7	0.0	
WP_089609814.1	NAD(P)-reducing hydrogenase subunit HndD	HndF	Fermentation producing ethanol	61.8	10.6	0.2	46.0	6.5	0.1	56.1	4.7	0.1	
WP_089611701.1	Aldehyde-alcohol dehydrogenase		Fermentation producing ethanol	39.6	4.2	0.1	32.0	0.0	0.0	63.0	6.9	0.1	
WP_089612456.1	Valine-tRNA ligase		General cellular functions	30.3	2.1	0.1	18.0	2.2	0.1	24.6	1.4	0.1	
WP_089608704.1	Trigger factor		General cellular functions	35.5	0.9	0.0	19.0	0.8	0.0	45.1	0.6	0.0	
WP_089608919.1	Methionine-tRNA ligase		General cellular functions	29.5	3.5	0.1	14.7	1.2	0.1	28.1	2.6	0.1	
WP_089612510.1	Lysine-tRNA ligase		General cellular functions	34.7	2.1	0.1	18.7	1.2	0.1	47.1	2.8	0.1	
WP_089609461.1	DNA-directed RNA polymerase subunit beta		General cellular functions	53.6	6.1	0.1	27.0	3.6	0.1	29.2	4.3	0.1	
WP_193064941.1	DNA-directed RNA polymerase subunit beta'		General cellular functions	50.2	1.9	0.0	23.7	0.5	0.0	25.8	0.0	0.0	
WP_089609460.1	Elongation factor G		General cellular functions	39.0	1.3	0.0	25.1	1.4	0.1	39.1	2.5	0.1	
WP_089609453.1	Elongation factor G		General cellular functions	64.1	3.0	0.1	74.3	6.5	0.1	50.9	4.6	0.1	
WP_089609452.1	Elongation factor G		Glycine cleavage system	5.8	0.7	0.1	3.0	0.0	0.0	16.1	0.0	0.0	
WP_089609451.1	Glycine-tRNA ligase beta subunit	GcvH	Glycine cleavage system	6.4	0.6	0.1	6.0	1.6	0.3	24.9	1.9	0.1	
WP_089612299.1	Aminomethyltransferase	GcvT	Glycine cleavage system	36.3	1.8	0.1	24.3	1.7	0.1	52.5	3.7	0.1	
WP_089608877.1	Glyceraldehyde-3-phosphate dehydrogenase	GapA	Glycolysis	26.6	1.7	0.1	17.0	1.6	0.1	42.5	4.4	0.1	
WP_089609613.1	3-bisphosphoglycerate-independent phosphoglycerate mutase	GpmI	Glycolysis	24.8	6.0	0.2	12.7	1.9	0.1	42.5	10.6	0.2	
WP_089609361.1	Phosphohexitose isomerase	Pgi	Glycolysis	14.2	1.2	0.1	9.0	0.8	0.1	31.1	5.1	0.2	
WP_089608821.1	Pyruvate kinase	Pyk	Glycolysis	2.2	0.2	0.1	1.0	0.0	0.0	2.9	0.0	0.0	
WP_089609452.1	Enolase		Glycolysis/Gluconeogenesis	34.5	3.2	0.1	23.7	1.7	0.1	51.7	5.3	0.1	
WP_089609451.1	Fructose-bisphosphate aldolase	Fba	Glycolysis/Gluconeogenesis	36.9	2.1	0.1	21.3	0.9	0.0	46.6	3.7	0.1	
WP_089609450.1	Phosphoglucomutase	Pgm	Glycolysis/Gluconeogenesis	36.9	2.1	0.1	21.3	0.9	0.0	46.6	3.7	0.1	
WP_089609452.1	Pyruvate kinase	Pdk	Glycolysis/Gluconeogenesis	36.9	5.7	0.1	21.7	1.3	0.1	37.3	3.5	0.1	
WP_089609453.1	Putative phosphate kinase Ywf	GcvT	Glycine cleavage system	5.8	0.7	0.1	3.0	0.0	0.0	16.1	0.0	0.0	
WP_089609454.1	Transaldolase		Glycine cleavage system	6.4	0.6	0.1	6.0	1.6	0.3	24.9	1.9	0.1	
WP_089609453.1	Apulse-4-phosphate transketolase subunit A		HktA	heme biosynthesis	31.2	3.0	0.1	34.7	4.8	0.1	57.4	6.7	0.1
WP_089609338.1	Apulse-4-phosphate transketolase subunit B		HktB	heme biosynthesis	63.2	2.7	0.0	88.7	1.9	0.0	74.7	2.1	0.0
WP_089609339.1	Apulse-4-phosphate transketolase subunit B		Isoprenoid synthesis	34.0	4.0	0.1	21.7	2.1	0.1	30.4	2.6	0.1	
WP_089613021.1	Inosine-5'-monophosphate dehydrogenase	KtA	Isoprenoid synthesis	51.1	0.5	0.0	35.7	0.5	0.0	39.9	2.2	0.1	
WP_089609737.1	GMP synthase [glutamine-hydrolyzing]	guAA	Metabolism - interconversion NADH-NADPH	29.5	3.0	0.1	17.7	1.9	0.1	50.5	1.5	0.0	
WP_089612687.1	Putative sugar phosphate isomerase		Purine biosynthesis	36.9	1.8	0.0	22.7	1.7	0.1	49.7	3.0	0.1	
WP_089609454.1	Acetyl-CoA acetyltransferase		Purine biosynthesis	33.1	2.0	0.1	18.3	1.2	0.1	42.8	4.3	0.1	
WP_089609453.1	4Fe-4S cluster domain-containing protein	AckA	Purine biosynthesis	31.2	3.0	0.1	17.7	1.7	0.1	19.7	1.3	0.1	
WP_089609932.1	FAD/(NADP)-binding protein	PdtU	Purine biosynthesis	30.6	1.1	0.0	20.0	1.4	0.1	75.5	3.7	0.0	
WP_089609931.1	4Fe-4S binding protein	Pyr	Purine biosynthesis	11.9	8.7	0.1	94.7	7.0	0.1	51.7	2.0	0.0	
WP_089612053.1	Glycine reductase complex component B subunit gamma	GrdB	Purine biosynthesis	87.8	3.6	0.1	59.3	0.9	0.0	49.4	2.7	0.1	
WP_089609511.1	Glycine reductase complex component C subunit beta	GrdC	Purine biosynthesis	26.6	5.4	0.2	20.7	5.3	0.3	28.9	6.3	0.2	
WP_089608591.1	Glycine reductase complex component C subunit beta	GrdD	Purine biosynthesis	6.0	0.0	0.0	3.0	0.5	0.1	51.2	0.0	0.0	
WP_089609521.1	Glycine reductase complex component C subunit alpha	GrdB	Purine biosynthesis	49.8	3.4	0.1	48.0	3.6	0.1	75.6	3.3	0.0	
WP_089609541.1	Glycine reductase complex component B subunit alpha and beta	GrdE	Purine biosynthesis	6.7	1.2	0.2	3.3	0.5	0.1	68.3	0.8	0.0	
WP_089612054.1	Glycine reductase complex component B subunits alpha and beta	GrdF	Purine biosynthesis	33.8	2.4	0.1	21.7	1.2	0.1	69.4	1.0	0.0	
WP_089609511.1	Glycine reductase complex component C subunit beta	GrdG	Purine biosynthesis	48.6	6.3	0.1	33.7</td						

WP_089608521.1	secondary thiamine-phosphate synthase enzyme YjbQ							
WP_089608530.1	Ig-like domain-containing protein							
WP_089608538.1	Ethanalamine utilization protein EutL							
WP_198306554.1	aryl-sulfate sulfotransferase							
WP_089608533.1	Ferredoxin–NADP reductase							
WP_089608541.1	Thioredoxin 1							
WP_089608542.1	DUF169 domain-containing protein							
WP_198306679.1	flotillin-like protein Flot1							
WP_089608544.1	nodulation protein NefD							
WP_089608545.1	30S ribosomal protein S21							
WP_089612441.1	Purine nucleoside phosphorylase							
WP_089608561.1	Ribosomal RNA small subunit methyltransferase E							
WP_089612443.1	Ribosomal protein L11 methyltransferase							
WP_089608571.1	Chaperone protein DnaJ							
WP_089608581.1	Protein GrpE							
WP_089608582.1	60 kDa chaperonin							
WP_089612444.1	Elongation factor 4							
WP_089608578.1	30S ribosomal protein S20							
WP_089612456.1	Leucine–tRNA ligase							
WP_089610002.1	Leucine–tRNA ligase subunit alpha							
WP_089608583.1	hemolysin family protein							
WP_157677240.1	Sodium/pantothenate symporter							
WP_089608591.1	ATP-binding protein							
WP_089608594.1	hypothetical protein							
WP_089608595.1	Phage-shock protein A							
WP_089608599.1	cupin domain-containing protein							
WP_089608600.1	hypothetical protein							
WP_089608603.1	Release factor glutamine methyletransferase							
WP_089608619.1	Sensor protein KdpD							
WP_089608622.1	Potassium-transferring ATPase potassium-binding subunit							
WP_089608623.1	Potassium-transferring ATPase ATP-binding subunit							
WP_089608624.1	hypothetical protein							
WP_089608625.1	Potassium-transferring ATPase KdpC subunit							
WP_089608626.1	Regulatory Y							
WP_089608641.1	RNA-binding protein							
WP_089608643.1	50S ribosomal protein L27							
WP_089608645.1	50S ribosomal protein L21							
WP_089608686.1	Ribonuclease G							
WP_089608693.1	Septum-site-determining protein MinD							
WP_242965343.1	Peptidoglycan D,D-transpeptidase MrdA							
WP_089608697.1	Cell shape-determining protein MreB							
WP_089608698.1	Regulatory transcriptional repressor Rex							
WP_089608700.1	Poly(γ-glutamate) synthase							
WP_089612458.1	Lon protease 1							
WP_089608702.1	ATP-dependent Clp protease ATP-binding subunit ClpX							
WP_089608703.1	ATP-dependent Clp protease proteolytic subunit							
WP_089608707.1	2-methoxy-5-polypropenyl-1,4-benzonanol methylase, mitochondrial							
WP_089608711.1	Bifunctional uridylyltransferase/uridyl-removing enzyme							
WP_089608712.1	Phenylacetate coenzyme A ligase							
WP_089608716.1	Formate dehydrogenase, cytochrome b56G(d) subunit							
WP_089608719.1	Oligopeptide-binding protein OppA							
WP_089608721.1	Methionine synthase							
WP_089608724.1	Zinc-binding GTase YerR							
WP_089608726.1	Hypoxanthine-guanine phosphoribosyltransferase							
WP_089608729.1	10 kDa chaperonin							
WP_157677251.1	hypothetical protein							
WP_089608735.1	Imidazolidineopenopeptidase							
WP_198306737.1	Alanyl-tRNA synthetase							
WP_089608740.1	Bifunctional NADPH-hydride repair enzyme Nnr							
WP_089608742.1	Protoxanthophorein oxidase							
WP_089608748.1	Uroporphyrinogen decarboxylase							
WP_089608753.1	Pyruvate synthase subunit PorC							
WP_089608758.1	Pyruvate synthase subunit PorD							
WP_089608759.1	Pyruvate synthase subunit PorA							
WP_089608760.1	Oxalate oxidoreductase subunit beta							
WP_089608761.1	DUF86 domain-containing protein							
WP_089608762.1	Cytidine deaminase subunit Smc							
WP_089608769.1	TIGR02678 family protein							
WP_089608774.1	DUF360 domain-containing protein							
WP_089608791.1	Pyridinium-3,5-bis(hydroxyacetic acid) mononucleotide nickel insertion protein							
WP_089608800.1	Macrolide export ATP-binding/permease protein MacB							
WP_089608817.1	Ribonuclease							
WP_089608821.1	Putative K+-stimulated pyrophosphate-energized sodium pump							
WP_089608822.1	putative protein-export membrane protein SecG							
WP_242965438.1	2,3-bisphosphoglycerate-independent phosphoglycerate mutase							
WP_089608824.1	Transketolase							
WP_089608825.1	Phosphoglycerate kinase							
WP_089608830.1	RNA polymerase sigma-54 factor							
WP_089608836.1	Reverse rubrerythrin							
WP_089608852.1	Large-conductance mechanosensitive channel							
WP_089608854.1	Aspartate aminotransferase							
WP_089608855.1	Phosphoserine aminotransferase							
WP_089608858.1	2-hydroxyisocaproyl-CoA dehydratase activator							
WP_089608859.1	Cysteine desulfurase Subunit							
WP_089608860.1	Cytochrome c nitroreductase subunit NrfA							
WP_089608863.1	5-layer homology domain-containing protein							
WP_242965363.1	putative protein [GBAA_0001/BASCE63]							
WP_089608869.1	K+-stimulated pyrophosphate-energized proton pump							
WP_089608870.1	DUF169 domain-containing protein							
WP_089608873.1	Molybdate binding protein ModA							
WP_089608875.1	1-pyrroline-5-carboxylate dehydrogenase 1							
WP_089608877.1	Hydroxycycloglutathione hydrolase							
WP_089608879.1	Cysteine desulfurase							
WP_089608880.1	Hydroxymethyl/propanolylaine family protein							
WP_089608884.1	N-acetylglucosaminidase/phosphoheundecaprenol-N-acetyl-beta-D-mannosaminyltransferase							
WP_089608892.1	polysaccharide lyase							
WP_089611195.1	MULTISPECIES: DUF5320 domain-containing protein							
WP_089611882.1	MULTISPECIES: NifB/NifX family molybdenum-iron cluster-binding protein							
WP_089609235.1	Ribonuclease BN							
WP_089611870.1	Iron-sulfur cluster carrier protein							
WP_242965352.1	putative protein							
WP_242965353.1	DUF169 domain-containing protein							
WP_089609236.1	DUF169 domain-containing protein							
WP_089609241.1	stage 0 sporulation family protein							
WP_157677267.1	Sodium/pantothenate symporter							
WP_089609241.1	stage 0 sporulation family protein							
WP_089609241.1	Anaerobic nitric oxide reductase transcription regulator NorR							
WP_089609411.1	Putative Na(+)/nicotinamide transporter NaIP							
WP_198306631.1	putative xanthine dehydrogenase subunit D							
WP_089609461.1	Nucleoid-associated protein							
WP_157677268.1	DNA gyrase subunit gamma/tau							
WP_089609470.1	Random fork protein							
WP_157677269.1	ferritin family protein							
WP_089610940.1	Acid shock protein							
WP_089609892.1	TIR domain-containing protein							
WP_089609933.1	TIR domain-containing protein							
WP_089609981.1	site-specific DNA-methyltransferase							
WP_089609004.1	helix-turn-helix domain-containing protein							
WP_089609025.1	ATP-binding protein							
WP_089609041.1	pyrophosphate-5'-nucleotide oxidase family protein							
WP_089609045.1	DUF169 domain-containing protein							
WP_089609056.1	Na(+)/H(+)-K(+)-antporter GenR							
WP_089609057.1	Uroporphyrinogen decarboxylase							
WP_089609058.1	Na(+)-translocating NADH-quinone reductase subunit F							
WP_089609059.1	DUF1638 domain-containing protein							
WP_089609072.1	putative response regulatory protein							
WP_242965363.1	PoC1 ligand-binding domain-containing protein							
WP_157677269.1	IS661 family transposase ISSwo2							
WP_089609071.1	hypothetical protein							
WP_089609072.1	NdD domain							
WP_089609087.1	hypothetical protein							
WP_089609088.1	hypothetical protein							
WP_089609094.1	Serine–tRNA ligase							
WP_242965445.1	DNA gyrase subunit A							
WP_089609097.1	DNA gyrase subunit B							
WP_157677307.1	DUF370 domain-containing protein							
WP_089609100.1	Beta sliding clamp							
WP_089609101.1	Chromatin-remodeling initiator protein DnaA							
WP_242965362.1	Membrane protein inserase YhdC							
WP_089609104.1	Transcription termination/antitermination protein NusA							
WP_157677309.1	Stage 0 sporulation protein J							
WP_198306619.1	Lipoprotein LopJ							
WP_089609112.1	L-seryl-tRNA(Sec) selenium transferase							
WP_089609113.1	Selenocysteine-specific elongation factor							
WP_089609116.1	Lipopolysaccharide export system ATP-binding protein LptB							
2.0	0.0	0.0	1.0	0.0	0.0	8.5	0.0	0.0
25.4	2.8	0.1	11.7	2.1	0.2	10.4	1.5	0.1
1.8	0.2	0.1	1.0	0.0	0.0	7.3	0.0	0.0
3.0	1.2	0.4	2.0	0.8	0.4	5.5	2.2	0.4
11.2	3.1	0.3	7.3	1.7	0.2	23.2	7.3	0.3
6.8	0.0	0.0	5.0	0.0	0.0	46.3	0.0	0.0
9.3	1.5	0.1	5.7	0.9	0.2	19.5	4.1	0.1
27.0	2.0	0.1	16.3	0.9	0.1	53.8	3.0	0.1
6.9	1.1	0.2	3.7	0.5	0.1	10.0	1.4	0.1
5.5	1.2	0.2	3.7	1.2	0.3	44.3	6.5	0.1
7.7	1.6	0.2	4.3	0.9	0.2	39.5	0.0	0.0
4.4	1.4	0.3	2.7	0.5	0.2	18.4	4.3	0.2
9.0	1.6	0.2	6.0	0.0	0.0	18.5	3.3	0.2
25.4	1.3	0.1	14.7	1.2	0.1	44.4	5.0	0.1
15.0	2.5	0.2	10.0	1.6	0.2	48.7	2.2	0.0
6.0	1.7	0.1	3.7	0.5	0.1	10.4	3.4	0.1
9.3	3.8	0.4	5.0	1.4	0.3	13.6	5.1	0.4
2.6	1.2	0.5	1.7	0.5	0.3	25.7	0.5	0.0
8.1	2.1	0.3	4.0	0.8	0.2	15.7	2.3	0.1
15.2	3.1	0.2	9.3	2.5	0.3	21.6	6.5	0.3
4.8	2.2	0.5	3.0	0.8	0.3	7.8	4.4	0.6
2.6	1.2	0.5	1.3	0.5	0.4	3.6	1.6	0.5
7.9	2.7	0.3	4.7	1.2	0.3	26.0	2.6	0.3
7.7	1.7	0.2	4.0	0.8	0.2	15.6	4.3	0.3
29.5	2.1	0.1	28.7	0.9	0.1	73.1	4.5	0.1
3.2	0.3	0.1	2.3	0.5	0.2	27.1	4.4	0.2
7.5	0.3	0.0	4.3	0.5	0.1	50.0	0.0	0.0
15.3	1.2	0.1	9.0	0.8	0.1	53.4	0.0	0.0
4.1	0.2	0.0	2.0	0.0	0.0	6.2	0.3	0.0
3.1	1.3	0.4	2.3	0.9	0.4	3.5	1.7	0.5
5.6	2.1	0.4	3.0	0.8	0.3	5.1	1.6	0.3
19.3	0.7	0.0	10.3	0.9	0.1	21.7	1.7	0.1
4.1	0.1	0.0	2.0	0.0	0.0	17.2	0.0	0.0
4.6	1.1	0.2	2.7	0.9	0.4	23.5	3.8	0.2
2.0	0.0	0.0	1.0	0.0	0.0	7.5	0.0	0.0
3.2	0.3	0.1	2.3	0.5	0.2	10.1	1.2	0.1
3.2	0.3	0.1	2.3	0.5	0.2	32.4	0.0	0.0
2.0	0.0	0.0	1.0	0.0	0.0	19.7	0.0	0.0
2.0	0.0	0.0	1.0	0.0	0.0	16.1	0.0	0.0
4.1	0.2	0.0	2.0	0.0	0.0	6.2	0.3	0.0
3.1	1.3	0.4	2.3	0.9	0.4	3.5	1.7	0.5
5.6	2.1	0.4	3.0	0.8	0.3	36.4	1.6	0.0
19.3	0.7	0.0	10.3	0.9	0.1	21.7	1.7	0.1
4.1	0.1	0.0	2.0	0.0	0.0	17.2	0.0	0.0
6.0	2.5	0.4	3.3	1.2	0.2	45.6	4.8	0.2
5.5	1.1	0.2	3.3	0.5	0.1	10.1	1.2	0.1
3.2	0.3	0.1	2.3	0.5	0.2	11.0	3.2	0.1
2.0	0.0	0.0	1.0	0.0	0.0	11.7	0.0	0.0
4.1	2.0	0.5	2.3	1.2	0.5	11.4	7.3	0.6
5.5	1.5	0.3	3.0	0.8	0.3	16.7	4.6	0.3
14.0	0.9	0.1	10.7	0.5	0.0	76.6	3.9	0.1
2.9	0.9	0.3	1.7	0.5	0.3	39.3	12.3	0.3
8.1	2.0	0.3	4.7	0.9	0.2	15.7	3.3	0.2
10.6	3.2	0.3	6.3	1.2	0.2	23.7	5.1	0.0
23.5	1.8	0.1	13.3	0.9	0.1	32.0	2.4	0.1
10.4	1.1	0.1	7.3	0.5	0.1	22.8	1.4	0.1
5.9	0.5	0.1	3.7	0.5	0.1	18.0	5.1	0.3
8.8	2.3	0.3	6.0	1.6	0.3	40.1	12.5	0.3
22.1	1.7	0.1	13.7	1.2	0.1	28.9	2.5	0.1
29.2	2.3	0.1	27.3	5.0	0.2	49.0	0.0	0.0
2.1	0.1	0.0	1.3	0.5	0.4	5.4	1.6	0.3
7.5	2.3	0.3	4.3	0.9	0.2	11.0	3.2	0.1
2.0	0.0	0.0	1.0	0.0	0.0	11.7	0.0	0.0
4.1	2.0	0.5	2.3	1.2	0.5	11.4	7.3	0.6
5.5	1.5	0.3	3.0	0.8	0.3	16.7	4.6	0.3
13.5	2.5	0.2	8.3	1.2	0.2	15.2	3.4	0.2
7.8	1.2	0.1	6.3	1.2	0.2	21.8	2.2	0.1
17.9	3.0	0.2	14.7	2.4	0.2	76.6	4.4	0.1
6.1	0.9	0.1	4.3	0.5	0.1	17.4	1.0	0.1
24.4	1.3	0.1	12.7	1.2	0.1	20.1	2.7	0.1
21.0	0.9	0.0	12.3	1.2	0.1	16.1	1.0	0.1
2.0	0.0	0.0	1.7	0.5	0.3	24.0	0.0	0.0
8.2	1.6	0.2	5.0	0.8	0.2	15.7	2.3	0.1
7.8	1.2	0.2	4.7	0.5	0.2	21.8	2.2	0.1
24.9	2.5	0.1	17.0	0.8	0.0	17.6	1.7	0.1
7.8	0.5	0.1	4.7	0.5	0.1	28.3	2.4	0.1
20.8	1.2	0.1	17.7	0.9	0.1	50.9		

WP_089609118.1	hypothetical protein	25.2	2.6	0.1	16.7	2.5	0.1	40.7	3.3	0.1
WP_089609120.1	hypothetical protein	21.9	3.3	0.2	13.0	1.4	0.1	32.4	3.7	0.1
WP_089609123.1	GTP-binding protein TypA/BipA	7.3	1.8	0.2	4.7	1.7	0.4	8.8	2.3	0.3
WP_089609130.1	indolepyruvate oxidoreductase subunit beta	11.4	2.3	0.2	7.3	0.9	0.1	38.2	4.3	0.1
WP_089609132.1	Oligopeptidase F, plasmid	14.2	4.0	0.3	8.0	1.4	0.2	17.9	4.4	0.2
WP_089609133.1	Trx/DksA C4-type zinc finger protein	3.4	0.8	0.2	2.3	0.5	0.2	15.6	0.0	0.0
WP_089609134.1	hypothetical protein	3.1	1.1	0.2	2.7	0.2	0.2	5.1	0.8	0.1
WP_089609137.1	Acetylacetate synthase large subunit	20.8	5.4	0.3	11.7	3.3	0.3	25.6	5.6	0.2
WP_089609138.1	Acetylacetate synthase small subunit	9.0	1.6	0.2	5.7	0.5	0.1	27.6	3.1	0.1
WP_089609140.1	Aminopeptidase T	4.4	1.7	0.4	2.7	0.5	0.2	11.2	1.7	0.2
WP_089609142.1	Ornithine carbamoyltransferase	15.9	3.3	0.2	9.3	2.1	0.2	31.3	7.4	0.2
WP_089609144.1	Thiol-disulfide oxidoreductase ResA	5.0	1.6	0.3	3.3	0.9	0.3	22.3	3.7	0.2
WP_089609147.1	ABC transporter permease	3.6	0.5	0.1	2.0	0.0	0.0	8.0	0.0	0.0
WP_089609148.1	Ribose import ATP-binding protein RbsA	3.2	0.5	0.2	2.3	0.5	0.2	7.2	1.0	0.1
WP_089612490.1	Putative protein	26.0	3.3	0.1	15.7	2.1	0.1	51.3	10.3	0.2
WP_089612491.1	SAM-dependent methyltransferase	5.7	1.0	0.2	3.5	0.5	0.1	15.1	2.1	0.1
WP_19306622.1	peptidoglycan-binding protein	2.0	0.0	0.0	1.0	0.0	0.0	4.0	0.0	0.0
WP_089609153.1	Inosine-5'-monophosphate dehydrogenase	12.6	2.3	0.2	7.3	0.9	0.1	39.0	8.7	0.2
WP_089609154.1	lactate utilization protein	11.5	0.7	0.1	6.7	0.9	0.1	27.4	1.4	0.1
WP_19306623.1	Signal peptidase I P	6.9	1.1	0.2	5.3	0.9	0.2	41.2	9.9	0.2
WP_089609156.1	HTH-type transcriptional regulator CysL	4.8	2.8	0.6	2.7	0.9	0.4	9.3	2.1	0.2
WP_089609171.1	Ribosome-binding ATPase YchF	18.0	4.7	0.3	9.7	2.5	0.3	32.7	6.7	0.2
WP_089609181.1	Putative HMP/HMG-impinger ATP-binding protein YkoD	2.9	0.1	0.0	2.0	0.0	0.0	4.5	0.2	0.0
WP_089609184.1	5-hydroxy-beta-methylaspartate synthase BasA	18.3	2.6	0.1	13.3	1.2	0.1	28.6	3.8	0.1
WP_089609185.1	Anaerobic magnesium-corrugoporphyrin IX monomethyl ester cyclase	13.4	1.8	0.1	7.5	0.5	0.1	23.1	2.4	0.1
WP_157677319.1	Epoxyquinoxine reductase	7.7	1.4	0.2	4.3	0.5	0.1	12.1	1.1	0.1
WP_089609187.1	Selenide, water dikinase	2.7	1.2	0.4	1.3	0.5	0.4	8.4	2.7	0.3
WP_089609188.1	30S ribosomal protein S6	13.7	3.1	0.2	8.0	1.4	0.2	32.3	3.6	0.1
WP_089609189.1	Single-stranded DNA-binding protein A	9.6	1.4	0.1	7.0	0.8	0.1	54.4	6.0	0.1
WP_089609190.1	30S ribosomal protein S18	11.7	0.3	0.0	6.7	0.5	0.1	49.2	0.0	0.0
WP_089609191.1	50S ribosomal protein L9	7.2	1.4	0.2	4.7	0.5	0.1	40.9	0.0	0.0
WP_089609193.1	Alkylated acetyl ester cyclase DnrD	10.5	1.3	0.1	6.0	0.8	0.1	38.3	0.3	0.0
WP_089609194.1	hypothetical protein	4.0	0.0	0.0	2.0	0.0	0.0	13.4	0.0	0.0
WP_089609195.1	Ketol-acid reductoisomerase (NAD(+))	5.7	1.0	0.2	3.0	0.5	0.1	9.4	2.2	0.1
WP_089609196.1	2-hydroxymuconate tautomerase	23.6	0.3	0.0	21.3	0.5	0.0	47.0	2.3	0.0
WP_089609200.1	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase	6.4	1.2	0.2	7.0	0.0	0.0	59.6	10.8	0.2
WP_089609203.1	Putrescine aminotransferase	10.8	1.1	0.1	6.3	0.5	0.1	20.0	0.0	0.0
WP_089609205.1	Adenylosuccinate synthetase	10.8	1.4	0.1	6.0	0.8	0.1	18.7	2.9	0.2
WP_089609209.1	hypothetical protein	14.7	3.1	0.2	9.0	2.2	0.2	24.2	5.3	0.2
WP_157677327.1	copper amine oxidase N-terminal domain-containing protein	1.9	0.2	0.1	1.0	0.0	0.0	3.6	0.0	0.0
WP_193066244.1	Methylallyl-CoA mutase	3.5	0.5	0.1	1.7	0.5	0.3	7.3	2.0	0.3
WP_089609244.1	putative protein YctU	21.7	4.8	0.2	15.0	2.2	0.1	27.7	2.6	0.1
WP_089609245.1	Thioredoxin reductase	3.1	1.1	0.4	2.0	0.0	0.0	20.0	0.0	0.0
WP_089609246.1	Copper chaperone CopZ	17.4	4.3	0.2	11.3	2.5	0.2	35.4	5.2	0.1
WP_089609277.1	hypothetical protein	3.8	1.2	0.3	3.0	0.8	0.3	36.7	4.8	0.1
WP_089611957.1	Polyphosphate kinase	5.8	1.9	0.3	3.7	0.9	0.3	17.6	3.1	0.2
WP_193066311.1	Exopolyphosphatase	4.4	0.6	0.1	2.7	0.5	0.2	6.7	1.4	0.2
WP_193066321.1	CYTH and CHAD domain-containing protein	2.8	1.3	0.5	1.7	0.5	0.3	4.8	1.1	0.2
WP_089609244.1	Uridyl transferase 1-cis-2-vinyldihydropyran-1-oxyltransferase 1	10.1	3.8	0.4	5.7	1.7	0.3	19.6	5.8	0.3
WP_089609245.1	Serine protease-like Inra	3.5	1.9	0.5	2.7	1.7	0.7	6.6	3.1	0.4
WP_089609249.1	Hypoxanthine-guanine phosphoribosyltransferase	11.0	2.0	0.2	6.0	0.8	0.1	20.4	2.8	0.1
WP_089609250.1	putative protein YctU	4.4	1.8	0.4	3.3	0.5	0.1	19.7	2.9	0.1
WP_089609250.1	Thioredoxin	11.4	0.6	0.1	7.3	1.2	0.2	25.5	3.9	0.2
WP_089609251.1	General stress protein CTC	22.3	0.1	0.0	16.0	0.8	0.1	54.9	4.0	0.1
WP_089609254.1	Cold shock-like protein CspLA	2.0	0.0	0.0	2.0	0.0	0.0	38.5	0.0	0.0
WP_089609246.1	DEAD-box ATP-dependent RNA helicase CshA	9.7	4.5	0.5	5.3	1.9	0.4	14.9	5.8	0.4
WP_089609247.1	SPFH domain-containing protein	3.3	0.6	0.2	2.0	0.0	0.0	10.1	1.9	0.2
WP_089609250.1	Hydroxylamine reductase	37.7	8.2	0.2	24.3	4.2	0.2	47.1	5.6	0.1
WP_193066371.1	hypothetical protein	6.5	2.2	0.3	3.3	0.9	0.3	11.0	2.3	0.2
WP_089609251.1	Insulin-5'-monophosphate dehydrogenase	5.4	1.7	0.3	3.3	0.5	0.1	25.1	1.0	0.0
WP_089609252.1	UFO182 family protein	9.9	2.2	0.3	5.3	0.9	0.2	8.5	0.2	0.0
WP_089609253.1	hypothetical protein	7.9	1.2	0.2	4.3	0.5	0.1	30.6	2.4	0.1
WP_089609254.1	Uridyl phosphoryltransferase	21.5	2.8	0.1	11.3	1.2	0.1	51.9	6.2	0.1
WP_089609255.1	ATP synthase subunit c	23.7	1.1	0.0	16.0	3.3	0.2	35.6	6.4	0.2
WP_089609256.1	ATP synthase subunit delta	24.6	0.8	0.0	28.3	3.3	0.1	51.6	4.1	0.1
WP_089609257.1	ATP synthase subunit alpha	4.7	1.3	0.3	2.3	0.5	0.2	15.1	3.3	0.2
WP_089609258.1	ATP synthase epsilon chain	3.5	1.9	0.5	2.7	1.7	0.6	8.4	0.2	0.0
WP_089609259.1	ATP synthase epsilon chain	3.6	1.3	0.4	3.7	0.5	0.1	7.4	2.2	0.3
WP_089609260.1	CTP synthase	8.4	2.6	0.3	4.0	0.8	0.2	20.4	3.6	0.2
WP_089609261.1	Transcription termination factor rho	2.1	0.1	0.0	1.0	0.0	0.0	8.2	0.0	0.0
WP_089609273.1	SOS ribosomal protein S1	5.5	0.4	0.1	3.3	0.5	0.1	10.8	1.1	0.1
WP_089609278.1	Peptide chain release factor 1	5.8	0.9	0.2	4.3	0.5	0.1	59.2	7.7	0.1
WP_089609279.1	Uracil phosphoribosyltransferase	19.9	3.0	0.2	12.7	0.9	0.1	34.6	3.5	0.1
WP_089609281.1	ATP synthase subunit c	5.7	0.8	0.1	3.7	0.5	0.1	20.3	1.9	0.1
WP_089609281.1	ATP synthase subunit delta	1.9	0.1	0.1	1.0	0.0	0.0	12.0	0.0	0.0
WP_089609281.1	ATP synthase subunit alpha	4.7	1.3	0.3	2.3	0.5	0.2	15.1	3.3	0.2
WP_089609282.1	ATP synthase epsilon chain	3.5	0.7	0.2	2.0	0.0	0.0	8.4	0.2	0.0
WP_089609283.1	Swarming motility protein SwrC	29.5	0.5	0.0	19.7	2.4	0.2	46.6	1.9	0.0
WP_089609284.1	ToIC family protein	4.4	2.3	0.5	2.7	0.9	0.4	22.4	7.0	0.1
WP_089609285.1	Cell shape-determining protein Mbl	19.3	1.0	0.1	11.7	0.5	0.0	39.5	1.8	0.0
WP_089609287.1	copper amine oxidase N-terminal domain-containing protein	3.7	2.5	0.7	2.7	0.9	0.4	15.4	6.3	0.4
WP_089609288.1	Uracil phosphoribosyltransferase	8.4	2.2	0.3	7.3	0.9	0.1	22.4	4.4	0.2
WP_089609310.1	S-layer homology domain-containing protein	176.8	19.7	0.1	343.0	26.7	0.1	82.8	3.5	0.0
WP_089609311.1	Membrane bound tyrosine transglycosylase F	20.1	2.7	0.1	13.7	0.9	0.1	37.9	4.6	0.1
WP_089609311.1	Glycosidase translocating ATP-binding protein GlnQ	3.9	1.4	0.3	2.3	0.5	0.2	13.5	1.8	0.1
WP_089609312.1	Multidrug resistance protein MdtA	12.0	2.8	0.2	9.0	0.5	0.3	28.0	6.2	0.2
WP_089609313.1	S-layer homology domain-containing protein	39.4	3.0	0.1	33.0	1.4	0.1	22.3	1.6	0.1
WP_089609314.1	ToIC family protein	46.8	6.3	0.1	30.0	2.4	0.1	61.3	3.0	0.0
WP_089609315.1	UvrABC system protein A	34.8	1.0	0.2	22.3	1.2	0.1	47.2	2.0	0.0
WP_089609316.1	Ion-translocating oxidoreductase complex subunit B	33.7	2.5	0.1	32.3	3.1	0.1	39.2	1.4	0.0
WP_089609317.1	hypothetical protein	4.8	0.8	0.2	2.7	0.5	0.2	5.0	0.1	0.0
WP_089609318.1	Cell division coordinator CpsB	20.4	3.3	0.2	14.0	1.4	0.1	60.6	5.7	0.1
WP_089609319.1	Ribosome hibernation promotion factor	12.4	2.4	0.2	7.7	1.2	0.2	34.9	0.8	0.0
WP_089609320.1	High-affinity branched-chain amino acid transport ATP-binding protein LivF	1.9	0.2	0.1	1.0	0.0	0.0	2.4	0.0	0.0
WP_089609321.1	Ion-translocating oxidoreductase complex subunit B	10.5	2.1	0.2	5.7	0.9	0.2	19.8	3.1	0.2
WP_089609322.1	Diaminopimelate epimerase	4.2	1.3	0.3	2.3	0.5	0.2	8.1	1.5	0.2
WP_089609331.1	Glutamine synthetase	6.4	2.1	0.3	3.3	0.9	0.3	14.2	4.6	0.3
WP_089609341.1	Glycogen synthase	9.4	1.5	0.2	5.3	0.5	0.1	17.3	0.4	0.0
WP_089609343.1	Alpha-1-glucan maltoase-1-phosphate maltoysyltransferase	5.5	3.3	0.6	3.3	1.2	0.4	6.3	2.8	0.4
WP_089609345.1	Glutamine synthetase	16.9	3.8	0.2	9.3	1.2	0.1	29.1	4.8	0.2
WP_089609346.1	Diaminopimelate epimerase	5.7	0.5	0.1	3.3	0.5	0.1	16.2	0.0	0.0
WP_089609347.1	Put operon repressor RspR	8.2	0.8	0.1	4.0	0.0	0.0	20.		

WP_089609458.1	50S ribosomal protein L1							
WP_242965451.1	50S ribosomal protein L10							
WP_089609460.1	50S ribosomal protein L1/L12							
WP_089609463.1	Ribosome-associated protein L7Ae-like protein							
WP_089609464.1	30S ribosomal protein S12							
WP_089609465.1	30S ribosomal protein S7							
WP_089609466.1	30S ribosomal protein S10							
WP_089609468.1	50S ribosomal protein L3							
WP_089609469.1	50S ribosomal protein L4							
WP_089609470.1	50S ribosomal protein L23							
WP_089609471.1	50S ribosomal protein L2							
WP_089609472.1	30S ribosomal protein S19							
WP_089609473.1	50S ribosomal protein L22							
WP_089609474.1	30S ribosomal protein S3							
WP_089609475.1	50S ribosomal protein L16							
WP_089609476.1	50S ribosomal protein L29							
WP_242965452.1	30S ribosomal protein S17							
WP_089609478.1	50S ribosomal protein L14							
WP_089609479.1	50S ribosomal protein L24							
WP_089609480.1	50S ribosomal protein L5							
WP_089609482.1	30S ribosomal protein S8							
WP_089609483.1	50S ribosomal protein L6							
WP_089609484.1	50S ribosomal protein L18							
WP_089609485.1	30S ribosomal protein S5							
WP_089609486.1	50S ribosomal protein L30							
WP_089609487.1	50S ribosomal protein L15							
WP_089609488.1	Protein translocase subunit SecY							
WP_089609489.1	Adenylate kinase							
WP_089609490.1	Methionine aminopeptidase 1							
WP_089609492.1	Translation initiation factor IF-1							
WP_089609494.1	30S ribosomal protein S13							
WP_089609495.1	30S ribosomal protein S11							
WP_089609496.1	30S ribosomal protein S4							
WP_089609497.1	DNA-directed RNA-polymerase subunit alpha							
WP_089609498.1	50S ribosomal protein L17							
WP_242965453.1	50S ribosomal protein L13							
WP_089609504.1	30S ribosomal protein S9							
WP_089609507.1	2,3-dihydroxyphenylpropionate/2,3-dihydroxycinnamic acid 1,2-dioxygenase							
WP_193066411.1	YajQ family cyclic di-GMP-binding protein							
WP_089609510.1	N-acetyl-gamma-glutamyl-phosphate reductase							
WP_089611521.1	Arginine biosynthesis bifunctional protein ArgJ							
WP_089609511.1	Adenylyltransferase							
WP_089609512.1	Acetyltransferase amino transferase							
WP_089609512.1	Arginosuccinate synthase							
WP_089609513.1	S-inoxyethyl-homocysteine hydrolase							
WP_089609515.1	Lactate racemase							
WP_089609519.1	Na(+)-translocating NADH-quinone oxidoreductase subunit F							
WP_089609531.1	Glutamine-dependent NAD(+) synthetase							
WP_089609536.1	Argininosuccinate lyase							
WP_089609539.1	Iron-sulfur protein IroB							
WP_089609540.1	hypothetical protein							
WP_193066421.1	Cytidine deaminase							
WP_089609541.1	GTPase Era							
WP_089609553.1	ABC transporter substrate-binding protein							
WP_089609557.1	Coenzyme A disulfide reductase							
WP_089609559.1	Glycine-tRNA ligase alpha subunit							
WP_089609563.1	type II toxin-antitoxin system RelB/DinI family antitoxin							
WP_089609566.1	hypothetical protein							
WP_157677330.1	Arginyl transferase							
WP_089609570.1	HTH-type transcriptional repressor RspR							
WP_089609578.1	Thioredoxin reductase							
WP_089609579.1	Thioredoxin							
WP_089609581.1	GrdX family protein							
WP_089609586.1	hypothetical protein							
WP_242965381.1	Vitamin B12-binding protein							
WP_089609590.1	CoO family nickel-binding protein							
WP_089609593.1	High-molarity zinc uptake system binding-protein ZnuA							
WP_089609596.1	Zinc-import ATP-binding protein ZnuC							
WP_089609598.1	Fattylinosopyrimidine-binding protein							
WP_089609601.1	DNA primase							
WP_089609602.1	RNA polymerase sigma factor SigA							
WP_089609604.1	GTP cyclohydrolase 1 type 2							
WP_157677332.1	Histidinol-phosphate aminotransferase							
WP_193067011.1	Glutamine transport ATP-binding protein GlnQ							
WP_089609618.1	Phosphate-binding protein PstS 1							
WP_089609622.1	Phosphate-specific transport system accessory protein PhoU							
WP_089609623.1	Iron-sulfur protein IroD							
WP_089609625.1	PDZ domain-containing protein							
WP_157677355.1	hypothetical protein							
WP_089609636.1	Bif/Mec/Cop1 family transcriptional regulator							
WP_157677356.1	copper amine oxidase N-terminal domain-containing protein							
WP_089609645.1	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase							
WP_089609647.1	Glutamate 2,3-ammonotransferase							
WP_089609650.1	Phospho-N-phosphoryltransferase pncB2							
WP_089609656.1	Phosphate ester phosphotriphosphopyrophosphate							
WP_089609661.1	3-azoxymethyl carrier protein synthase 3 protein 1							
WP_089609662.1	NADH quinone reductase							
WP_089609681.1	Malonyl-CoA carrier protein transacylase							
WP_089609690.1	3-oxoacyl-[acyl-carrier-protein] reductase FabG							
WP_089609691.1	Acyl carrier protein							
WP_089609692.1	Inosine-5'-monophosphate dehydrogenase							
WP_193066541.1	3-oxoacyl-[acyl-carrier-protein] synthase 2							
WP_242965394.1	Ribonuclease 3							
WP_089609696.1	UvrA445 domain-containing protein							
WP_089609697.1	MVII domain-containing protein							
WP_242965395.1	Signal recognition particle receptor FtsY							
WP_089609701.1	S-methyl-5'-thiouridine phosphorylase							
WP_089609702.1	Methylthioribose-1-phosphate isomerase							
WP_242965396.1	5-deoxy-D-ribulose-1-phosphate aldolase							
WP_089609703.1	5-methylthioadenosine/S-adenosylhomocysteine deaminase							
WP_089609706.1	hypothetical protein							
WP_089609709.1	Cobalt-dependent inorganic pyrophosphatase							
WP_089609710.1	Sugar nucleic acid nucleotide							
WP_089609711.1	30S ribosomal protein S10							
WP_089609712.1	KH domain-containing protein							
WP_193067051.1	Calcium-transporting ATPase							
WP_089609719.1	type II toxin-antitoxin system HicB family antitoxin							
WP_089609725.1	Protein GrpF							
WP_089609726.1	Chaperone protein DnaK							
WP_089612539.1	4-hydroxy-tetrahydronicotinic acid synthase							
WP_089609755.1	Endonuclease MspI							
WP_089609757.1	ATP-dependent metalloprotease							
WP_089609760.1	2-hydroxyacid hydrolase							
WP_089609761.1	ATP-dependent zinc metalloprotease FtsH 4							
WP_089609763.1	General stress protein A							
WP_089609765.1	Septum site-determining protein MinD							
WP_157677365.1	hypothetical protein							
WP_193066571.1	Protein LemA							
WP_089609791.1	Phosphorylated carbohydrates phosphatase							
WP_089609802.1	Arylsulfate sulfotransferase AssT							
WP_089609813.1	hypothetical protein							
WP_089609814.1	Ribonucleic acid subunit methyltransferase K/L							
WP_089609817.1	Threonine synthase							
WP_089609818.1	Hydrogenase maturation factor HypA							
WP_089609819.1	Cold-shock protein CspB							
WP_089609836.1	putative protein							
WP_089609838.1	Cobalt-precorrin-4 (C11)-methyltransferase							
WP_089609841.1	nucleotidyltransferase substrate binding protein							
WP_089609842.1	Thiamine thiazole synthase							
WP_089609844.1	Dihydroxy-acid dehydratase							
WP_089609845.1	Adenosine triphosphate S-ribosyltransferase							
WP_089609847.1	2-isopropylmalate synthase							
WP_089609848.1	2,3-dimethylmalate hydratase small subunit							
WP_089609850.1	3-isopropylmalate dehydrogenase							
WP_089609851.1	(R)-citramalate synthase							
WP_089609858.1	DUF881 domain-containing protein							
WP_089609864.1	Phosphoglucomamine mutase							
WP_089609868.1	putative glucosidase-6-phosphate deaminase 2							
WP_089609870.1	Adenosine triphosphate S-ribosyltransferase							
WP_089609874.1	Putative NAD(P)H nitroreductase							
WP_089609876.1	Bifunctional protein Paaz2							
WP_089609878.1	Iron-sulfur protein							
WP_257912016.1	NADPH-reducing hydrogenase subunit HindC							
WP_242965461.1	Carbon monoxide dehydrogenase 2							
WP_089609887.1	GTP 3'-cyclase							
WP_242965411.1	peroxiredoxin							
20.5	1.3	0.1	11.3	0.5	0.0	42.2	4.1	0.1
14.2	3.5	0.2	8.3	2.1	0.2	37.9	13.4	0.4
19.3	2.4	0.1	19.7	2.1	0.1	77.0	7.1	0.1
2.6	1.0	0.4	1.3	0.5	0.4	27.2	9.7	0.4
5.0	0.8	0.2	3.7	0.5	0.1	22.9	2.9	0.1
18.5	1.8	0.1	16.7	2.4	0.1	59.0	3.9	0.1
11.7	1.3	0.1	7.3	0.2	0.2	50.7	6.7	0.1
18.0	1.4	0.1	11.7	0.5	0.0	49.3	2.1	0.0
9.2	1.3	0.1	10.3	1.7	0.2	26.4	1.4	0.1
10.1	1.4	0.1	5.7	0.5	0.1	62.1	0.0	0.0
18.7	2.5	0.1	14.3	1.7	0.1	41.4	4.2	0.1
14.5	0.9	0.1	11.0	0.8	0.1	72.3	0.0	0.0
8.4	2.2	0.3	5.3	2.1	0.4	41.0	2.9	0.1
20.4	1.3	0.1	11.7	0.5	0.0	49.0	1.5	0.0
8.0	2.0	0.2	4.0	0.8	0.2	41.7	9.3	0.2
11.3	0.7	0.1	6.7	0.2	0.1	56.1	0.0	0.0
4.7	1.4	0.1	14.7	0.5	0.0	51.0	6.0	0.1
5.7	0.4	0.1	4.3	1.2	0.3	40.7	8.8	0.2
9.3	0.7	0.1	9.7	0.9	0.1	54.1	3.9	0.1
20.8	1.7	0.1	14.0	1.4	0.1	58.3	5.1	0.1
9.1	1.8	0.2	7.0	1.4	0.2	45.0	9.3	0.2
17.1	2.4	0.1	10.7	1.9	0.2	48.5	12.4	0.3
11.4	0.9	0.1	6.7	0.9	0.1	51.4	5.5	0.1
15.8	0.3	0.0	11.3	0.5	0.0	46.4	0.0	0.0
4.7	0.6	0.1	3.5	0.4	0.1	39.1	9.1	0.1
6.5	1.9	0.3	4.7	0.5	0.1	33.9	4.8	0.1
8.1	1.1	0.1	6.7	0.5	0.1	46.1	4.4	0.1
8.4	0.5	0.1	6.0	0.8	0.1	40.5	2.9	0.1
10.5	2.2	0.2	6.0	0.8	0.1	19.1	1.6	0.1
8.9	2.6	0.3	7.7	0.5	0.1	35.2	6.5	0.2
17.7	1.8	0.1	9.3	1.2	0.1	40.7	4.9	0.1
14.8	3.3	0.2	9.2	1.3	0.1	29.3	1.9	0.1
6.0	0.0	0.0	3.0	0.0	0.0	16.0	0.0	0.0
24.6	2.3	0.1	13.0	0.9	0.1	45.1	4.5	0.1
15.0	4.2	0.3	8.0	1.6	0.2	23.6	4.6	0.2
8.1	1.1	0.1	6.7	0.5	0.1	46.1	4.4	0.1
5.4	0.2	0.0	3.0	0.0	0.0	15.0	0.0	0.0
9.9	0.8	0.1	5.7	0.5	0.1	17.7	1.0	0.1
33.0	2.5	0.1	25.3	1.7	0.1	36.7	2.0	0.1
3.7	1.4	0.4	2.0	0.8	0.4	3.9	1.4	0.4
12.9	3.6	0.3	7.3	0.9	0.1	20.7	3.2	0.2
6.9	1.9	0.3	3.7	0.9	0.3	22.7	5.6	0.2
9.6	1.8	0.2	5.0	0.5	0.2	27.1	4.4	0.2
6.0	3.3	0.6	3.0	1.4	0.5	30.1	12.2	0.1
4.8	2.5	0.5	2.7	0.9	0.4	10.2	3.8	0.4
27.7	2.0	0.1	21.7	0.9	0.0	39.3	2.7	0.1
3.2	0.9	0.3	2.7	1.7	0.6	5.2	4.1	0.8
18.5	3.6	0.2	10.0	0.8	0.1	36.3	2.4	0.1
8.8	1.9	0.2	5.7	0.9	0.2	43.6	8.4	0.2
2.0	0.0	0.0	1.0	0.0	0.0	14.8	0.0	0.0
10.6	2.0	0.1	14.7	0.5	0.0	38.9	2.0	0.1
10.7	1.8	0.2	8.0	0.8	0.1	51.0	6.8	0.1
2.7	1.2	0.4	1.3	0.5	0.4	15.3	4.2	0.3
7.2	2.0	0.3	5.7	1.7	0.3	25.3	7.4	0.3
10.4	1.5	0.1	6.3	0.5	0.1	22.6	4.4	0.2
5.4	2.4	0.4	3.0	0.8	0.3	15.3	4.9	0.3
8.7	1.5	0.2	5.3	0.5	0.1	31.2	3.9	0.1
5.3	1.2	0.3	3.7	0.5	0.1	18.0	2.5	0.1
11.3	1.1	0.1	7.7	0.5	0.1	31.3	3.1	0.1
3.2	1.2	0.4	1.7	0.5	0.3	34.2	13.3	0.4
5.5	2.2	0.4	3.6	0.8	0.3	13.0	4.5	0.4
22.9	3.5	0.2	34.0	5.4	0.2	41.3	3.4	0.1
5.6	1.9	0.3	3.7	1.2	0.3	9.6	2.4	0.2
18.1	3.7	0.2	9.3	1.7	0.2	20.9	3.6	0.2
10.2	1.8	0.2	6.0	0.0	0.0	23.7	4.0	0.2
13.0	2.7	0.3	8.0	0.2	0.2	35.4	5.4	0.2
12.5	1.0	0.1	6.7	0.9	0.1	21.1	4.9	0.2
5.6	1.0	0.1	2.3	0.9	0.4	8.5	3.2	0.4
6.7	1.7	0.3	5.3	0.9	0.2	24.8	4.8	0.2
2.7	1.2	0.4	1.3	0.5	0.4	5.1	1.8	0.4
2.0	0.0	0.0	1.0	0.0	0.0	6.4	0.0	0.0
12.5	2.4	0.2	8.0	1.4	0.2	21.3	4.9	0.2
13.8	3.5	0.3	10.0	2.2	0.2	27.1	9.0	0.3
6.4	4.3	0.7	4.0	1.6	0.4	10.2	3.6	0.4
19.1	1.7	0.1	12.0	0.8	0.1	29.0	2.7	0.1
8.0	0.0	0.0	6.7	0.0				

WP_242965411.1	Selenocysteine-containing peroxiredoxin PrxU	8.1	0.1	0.0	5.0	0.8	0.2	60.2	6.4	0.1
WP_089609897.1	hypothetical protein	6.4	3.0	0.5	3.3	0.9	0.3	34.4	9.4	0.3
WP_089609911.1	Phospho-2-dehydro-3-deoxyheptonate aldolase	9.1	1.9	0.2	4.3	0.5	0.1	16.7	2.1	0.1
WP_089609914.1	Potassium transporter KmA	2.5	0.8	0.3	1.3	0.5	0.4	2.4	0.9	0.4
WP_089609918.1	Chromosomal replication initiator protein DnaA	4.8	1.2	0.3	2.7	0.9	0.4	6.9	2.0	0.3
WP_089609920.1	2-amino-4-deoxychorismate dehydrogenase	10.3	1.7	0.2	5.3	1.2	0.2	29.7	5.8	0.2
WP_089609941.1	33-kDa heat shock protein	10.1	2.9	0.5	5.3	1.2	0.2	33.1	6.7	0.1
WP_089609943.1	hypothetical protein	6.3	1.4	0.2	5.0	0.8	0.2	44.7	6.9	0.2
WP_242965417.1	Peroxide-responsive repressor PerR	4.5	0.7	0.2	2.7	0.5	0.2	24.1	4.0	0.2
WP_089609937.1	Holliday junction ATP-dependent DNA helicase RuvB	20.4	1.1	0.1	14.3	0.5	0.0	37.2	1.6	0.0
WP_089609939.1	Hydrogenase maturation factor HypA	2.0	0.0	0.0	1.0	0.0	0.0	26.9	0.0	0.0
WP_089609940.1	Photosystem I assembly protein Ycf3	20.2	1.0	0.0	11.0	1.4	0.1	33.9	3.9	0.1
WP_242965419.1	Stage V sporulation protein D	5.7	2.9	0.5	4.0	1.4	0.4	11.3	4.1	0.4
WP_089609945.1	UDP-N-acetylumuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase	14.3	4.1	0.3	8.0	1.4	0.2	19.1	4.1	0.2
WP_089609947.1	UDP-N-acetylumuramoyl-L-alanine ligase	6.8	1.1	0.2	3.7	0.9	0.3	12.0	2.1	0.2
WP_089609948.1	UDP-N-acetylumuramoyl-L-alanine ligase	15.5	2.1	0.1	8.5	0.5	0.1	25.1	2.4	0.1
WP_157677382.1	Cell division protein FtsA	5.5	1.8	0.3	3.0	0.8	0.3	11.1	3.6	0.3
WP_089609952.1	Cell division protein FtsZ	25.9	0.7	0.0	15.3	0.5	0.0	40.5	1.7	0.0
WP_089609957.1	2-oxoadid-ferredoxin oxidoreductase subunit beta	8.3	3.4	0.4	4.3	1.2	0.3	23.8	5.7	0.2
WP_089609971.1	Anaerobic ribonucleoside-triphosphatase	6.0	0.7	0.1	3.3	0.5	0.1	6.3	2.0	0.3
WP_089609994.1	Polyphenol oxidase	5.8	1.6	0.3	3.0	0.8	0.3	15.6	2.1	0.1
WP_242965424.1	Pyridoxal phosphate homeostasis protein	5.0	1.6	0.3	2.7	0.9	0.4	16.7	3.9	0.2
WP_089609998.1	Pyridoxal-5-carboxylate reductase	8.1	3.4	0.4	4.0	1.6	0.4	20.4	7.3	0.4
WP_089610001.1	Ideonine kinase	22.2	7.2	0.3	12.3	2.6	0.2	18.0	5.0	0.3
WP_089610003.1	PFL family protein	8.3	4.9	0.5	4.7	1.1	0.4	13.1	6.5	0.1
WP_089610005.1	sulfite reductase subunit beta (hemoprotein)	26.4	0.6	0.0	20.0	0.0	0.0	59.5	2.4	0.0
WP_089610008.1	Molybdenum cofactor cyclohydrolase	2.9	1.0	0.4	1.7	0.5	0.3	10.9	3.1	0.3
WP_089610009.1	EF2563 family selenium-dependent molybdenum hydroxylase system protein	25.1	1.2	0.0	16.3	0.5	0.0	30.6	1.0	0.0
WP_089610011.1	Putative competence-damage inducible protein	17.8	4.1	0.2	9.7	1.2	0.1	39.0	3.4	0.1
WP_089610783.1	Monomethylammonium methyltransferase MtmB	3.3	1.3	0.4	2.3	0.9	0.4	12.9	4.9	0.4
WP_089610051.1	HTH-type transcriptional repressor GlnR	2.3	0.4	0.2	1.3	0.5	0.4	7.7	2.1	0.3
WP_089610033.1	hypothetical protein	9.6	2.1	0.2	6.3	0.9	0.1	16.5	3.2	0.2
WP_089610041.1	beta-propionate:beta-hydroxybutyrate transporter	9.6	1.0	0.1	4.7	0.5	0.1	12.2	1.5	0.1
WP_089610044.1	Dihydroxyacetone phosphate (NAD(+)) electron transfer subunit	8.3	1.0	0.2	3.0	0.8	0.2	22.1	2.5	0.1
WP_089610083.1	Orotidine 5'-phosphate decarboxylase	12.1	1.3	0.1	6.7	0.9	0.1	35.4	3.0	0.1
WP_089610090.1	Orotate phosphoribosyltransferase	10.7	1.5	0.1	6.3	0.9	0.1	35.1	0.2	0.0
WP_089610051.1	Na/Pi cotransporter family protein	5.2	1.4	0.3	3.0	0.8	0.3	7.3	1.7	0.2
WP_089610052.1	Carbon sulfoxide hydrolase	2.9	1.5	0.5	1.7	0.9	0.6	9.7	5.1	0.5
WP_089610053.1	RqC2 RqD	5.4	4.3	0.8	3.3	1.9	0.6	8.5	4.7	0.6
WP_089610057.1	YicC family protein	2.0	0.0	0.0	1.3	0.5	0.4	5.1	0.0	0.0
WP_089610059.1	Extracellular matrix-regulating protein A	12.3	6.6	0.1	7.7	0.5	0.1	50.5	9.5	0.2
WP_089610055.1	alpha, ribbon-domain-containing protein	2.7	1.3	0.4	3.3	0.5	0.4	6.5	0.5	0.1
WP_089610056.1	TIGR03265 family protein	1.3	0.2	0.1	5.7	0.5	0.1	12.1	1.4	0.1
WP_19306677.1	Chromosome partition protein Smc	9.5	2.4	0.3	5.3	0.5	0.1	31.8	3.1	0.1
WP_089610071.1	hypothetical protein	3.2	1.2	0.4	2.0	0.0	0.0	9.0	0.6	0.1
WP_089610104.1	Uroporphyrinogen decarboxylase	13.0	0.6	0.0	9.0	0.0	0.0	19.3	0.8	0.0
WP_089610106.1	Uroporphyrinogen decarboxylase	16.5	1.3	0.1	9.7	1.2	0.1	32.4	1.7	0.1
WP_089610120.1	Trans-4-hydroxy-L-proline dehydratase	6.2	0.3	0.1	3.3	0.5	0.1	4.6	0.6	0.1
WP_089610130.1	Peptide deformylase 1	4.0	0.0	0.0	2.0	0.0	0.0	27.8	0.0	0.0
WP_089610131.1	alpha, beta-dihydronicotinamide nucleotide oxidoreductase	3.0	1.0	0.3	2.0	0.0	0.0	11.4	2.3	0.2
WP_089610132.1	Serine/threonine phosphatase zfp	5.7	0.3	0.1	3.3	0.5	0.1	18.1	3.7	0.2
WP_089610141.1	Serine/threonine-protein kinase PtkC	9.3	2.3	0.2	5.7	0.5	0.1	12.1	1.4	0.1
WP_089610149.1	Riboflavin biosynthesis protein RibBA	18.7	3.1	0.2	9.0	1.4	0.2	28.2	5.3	0.2
WP_089610151.1	6,7-dimethyl-8-ribityllumazine synthase	7.5	2.2	0.3	4.3	0.5	0.1	39.7	8.9	0.2
WP_242965082.1	NAD-dependent protein deacetylase Siruin-5, mitochondrial	2.0	0.4	0.2	2.0	0.0	0.0	3.4	0.0	0.0
WP_157677401.1	Putative ABC transporter periplasmic binding protein	26.5	2.7	0.1	17.0	1.6	0.1	47.1	3.4	0.1
WP_089610171.1	sodium/proton antiporter	7.3	0.4	0.1	6.7	0.9	0.1	8.2	0.0	0.0
WP_089610181.1	C-GCAxx-C-C family protein	7.3	1.8	0.2	3.7	0.9	0.3	24.4	3.3	0.1
WP_089610184.1	hypothetical protein	4.5	1.2	0.3	2.3	0.5	0.2	38.2	8.3	0.2
WP_089610186.1	hypothetical protein	5.1	1.9	0.4	4.0	0.5	0.2	30.0	6.6	0.2
WP_089610193.1	putative zinc-binding protein	6.3	0.3	0.0	3.3	0.5	0.1	34.6	0.0	0.0
WP_089610195.1	putative zinc-binding protein	4.8	1.1	0.2	2.7	0.5	0.2	27.3	8.1	0.3
WP_089610201.1	D-alanine-D-alanine ligase A	24.7	3.8	0.2	14.3	2.9	0.2	42.5	3.5	0.1
WP_089610216.1	DNA topoisomerase I	4.5	1.9	0.4	3.0	1.4	0.5	4.9	2.1	0.4
WP_089610218.1	Methylenetetrahydrofolate-triRNA-(uracil-5')-methyltransferase TrmFO	1.8	0.3	0.1	1.0	0.0	0.0	2.2	0.0	0.0
WP_089610219.1	ATP-dependent protease subunit Hsv	2.0	0.0	0.0	1.0	0.0	0.0	6.3	0.0	0.0
WP_089610221.1	ATP-dependent protease ATPase subunit ClpY	21.8	0.5	0.0	12.0	0.0	0.0	22.5	0.4	0.0
WP_089610224.1	Elongation factor Ts	28.2	1.1	0.2	21.3	1.2	0.1	58.1	2.7	0.0
WP_089610231.1	Unidomain kinase	5.8	1.3	0.2	3.0	0.8	0.3	13.0	4.1	0.3
WP_089610233.1	Ribosome-recycling factor	16.4	1.0	0.0	15.0	1.6	0.1	59.3	7.0	0.1
WP_089610237.1	Ferrredoxin	2.0	0.0	0.0	1.7	0.5	0.3	38.9	0.0	0.0
WP_089610248.1	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin)	3.7	0.7	0.2	2.3	0.5	0.2	8.1	2.4	0.3
WP_089610250.1	Proline-RNA ligase	21.2	1.2	0.1	10.3	0.5	0.0	24.6	2.6	0.1
WP_089610258.1	(R)-phenylalanyl-CoA dehydratase beta subunit	11.3	0.8	0.1	6.7	0.9	0.1	20.8	0.4	0.0
WP_089610273.1	suRf reduction protein Dsf	7.0	0.2	0.0	12.7	1.2	0.1	62.7	9.7	0.2
WP_19306719.1	(R)-phenylalanyl-CoA dehydratase beta subunit	23.6	3.0	0.1	14.3	0.5	0.0	41.7	3.2	0.1
WP_089610284.1	Alkyltransferase-like protein	16.6	4.3	0.3	10.3	1.2	0.1	27.6	6.9	0.3
WP_089610286.1	(R)-2-hydroxyglutamate-CoA dehydratase activating ATPase	4.8	1.1	0.2	2.7	0.5	0.2	27.3	8.1	0.3
WP_089610293.1	S-adenosylmethionine decarboxylase proenzyme	2.7	1.2	0.4	1.3	0.5	0.4	12.8	1.1	0.1
WP_089610338.1	Uroporphyrinogen decarboxylase	24.6	2.4	0.1	26.7	1.2	0.0	30.9	3.3	0.1
WP_089610351.1	Pantothenate synthase	2.1	1.0	0.5	1.3	0.5	0.4	5.1	2.3	0.5
WP_089610353.1	Aspartate 1-decarboxylase	3.2	0.4	0.1	2.0	0.0	0.0	8.7	0.0	0.0
WP_089610355.1	hypothetical protein	3.2	0.8	0.3	2.0	0.0	0.0	4.0	0.4	0.1
WP_089610381.1	Uroporphyrinogen decarboxylase	7.3	4.1	0.6	3.7	1.7	0.5	12.9	4.4	0.3
WP_089610385.1	hypothetical protein	2.5	0.4	0.1	2.0	0.0	0.0	11.0	0.0	0.0
WP_089610393.1	Akkoniac acid methyl ester cyclase DnrD	5.0	2.3	0.3	3.7	1.3	0.3	17.9	3.1	0.2
WP_089610403.1	hypothetical protein	7.7	0.8	0.1	5.0	0.0	0.0	15.6	1.8	0.1
WP_089610410.1	Elongation factor Ts, mitochondrial	2.0	0.0	0.0	1.0	0.0	0.0	2.1	0.0	0.0
WP_089610411.1	DUF1659 domain-containing protein	10.6	2.0	0.2	18.0	2.8	0.2	41.7	4.8	0.1
WP_089610414.1	DUF2922 domain-containing protein	6.7	0.7	0.1	3.3	0.5	0.1	39.1	6.3	0.2
WP_089610414.1	DUF3343 domain-containing protein	6.6	1.4	0.2	3.7	0.5	0.1	59.2	0.0	0.0
WP_089610507.1	ATP-dependent protease subunit dehydratase	5.7	2.1	0.4	3.7	1.7	0.5	15.4	4.4	0.3
WP_089610608.1	Uridyl transferase	1.9	0.5	0.1	8.0	1.9	0.2	34.0	1.6	0.0
WP_089610630.1	Uridyl transferase 1-phosphate uridylyltransferase	9.8	1.3	0.2	4.5	0.5	0.1	22.1	2.4	0.1
WP_089610635.1	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	18.5	2.0	0.1	10.7	0.9	0.1	28.7	1.6	0.1
WP_089610645.1	flavodoxin	4.0	1.4	0.4	2.3	0.5	0.2	20.5	3.4	0.2
WP_089610647.1	putative oxido-reductase/MsmeI_2347	6.8	2.5	0.4	3.7	1.2	0.3	19.1	5.2	0.3
WP_089610663.1	copper amine oxidase N-terminal domain-containing protein	7.7	0.8	0.1	6.7	0.5	0.1	51.1	2.1	0.0
WP_089610666.1	hypothetical protein	12.1	1.4	0.1	7.3	0.9	0.1	21.6	1.9	0.1
WP_089610783.1	Intracellular iron chaperone frataxin	2.0	0.0	0.0	1.0	0.0	0.0	10.0	0.0	0.0
WP_089610740.1	Transmembrane dipteridate	11.1	0.7	0.1	6.0	0.8				

WP_089608798.1	Uroporphyrinogen decarboxylase
WP_157674474.1	hypothetical protein
WP_19306530.1	DUF3050 domain-containing protein
WP_242965474.1	VOC family protein
WP_089610998.1	Tryptophan synthase alpha chain
WP_089611070.1	Tryptophan synthase beta chain
WP_089610992.1	ABC transporter substrate-binding protein
WP_089611004.1	Zinc-binding GTPase YerR
WP_089611006.1	Phospho-2-dehydro-3-deoxyheptone aldolase, Tyr-sensitive
WP_089611081.1	Glucose 1-dehydrogenase
WP_089611031.1	hypothetical protein
WP_089611044.1	D-3-phosphoglycerate dehydrogenase
WP_089611048.1	phosphodiester glycosidase family protein
WP_089611052.1	sulfatase-like self-cleaving metalloprotein YedF
WP_089611057.1	Duf3243 domain-containing protein
WP_089611057.1	DNA mismatch repair protein MutS
WP_089611059.1	Exodeoxyribonuclease T small subunit
WP_089611064.1	1-deoxy-D-xylulose-5-phosphate synthase
WP_089611083.1	NAD kinase
WP_089611073.1	DNA repair protein RecN
WP_089612621.1	Methanol dehydrogenase activator
WP_089611093.1	Putative universal stress protein
WP_089611096.1	Phosphotransferase
WP_089611099.1	Pyrimidine-nucleoside phosphorylase
WP_089611109.1	hypothetical protein
WP_089611131.1	A-adding tRNA nucleotidyltransferase
WP_089611136.1	Tryptophanyl-tRNA ligase
WP_089611147.1	D-alanyl-D-alanine carboxypeptidase DacF
WP_089611156.1	Corrinoid adenosyltransferase
WP_089611158.1	putative protein YstY
WP_089611166.1	Chorismate mutase AroH
WP_089611169.1	N-(S-phosphoglycan)-aminoalanilate isomerase
WP_089611173.1	Phospho-2-dehydro-3-deoxyheptone aldolase
WP_089611173.1	3-sulfotetrahydroaldehyde reductase
WP_089611175.1	3-phosphohikimiate 1-carboxyvinyltransferase 1
WP_089611207.1	GTPase Der
WP_089611211.1	Glycerol-3-phosphate dehydrogenase [NAD(P)+]
WP_242965182.1	Homoserine dehydrogenase
WP_089611224.1	Aspartokinase
WP_089611228.1	Transcription-termination/antitermination protein NusA
WP_089611236.1	Ribosomal-binding factor A
WP_157674474.1	30S ribosomal protein S15
WP_089611255.1	4-hydroxy-tetrahydronicolinate reductase
WP_089611262.1	Ribonuclease J1
WP_19306540.1	Protein RecA
WP_089611304.1	GTP-sensing transcriptional teichoic repressor CcdY
WP_089611306.1	Polyisoprenyl-teichoic acid-peptidoglycan teichoic acid transferase TagU
WP_089611308.1	Diadenosine hexaphosphate hydrolase
WP_089611311.1	YidB membrane protein
WP_089611315.1	Lysopolyphosphate assembly protein B
WP_089611347.1	Alkaline shock protein 23
WP_089611365.1	hypothetical protein
WP_089611367.1	Elongation factor P
WP_089611370.1	Metalloprotease PmbA
WP_089612639.1	Metalloprotease TldD
WP_089611372.1	3-dehydroquinate synthase
WP_089611376.1	Chorismate synthase
WP_19306541.1	TytR IseR regulatory system protein G
WP_089611404.1	Carboxygeranylgeranyl synthase
WP_089611406.1	Polymyxin aminopeptidyl transferase
WP_242965202.1	Arginine decarboxylase
WP_089611434.1	DUF1292 domain-containing protein
WP_19306560.1	Putative pre-16S rRNA nuclease
WP_089612644.1	Ireb family regulatory phosphoprotein
WP_089611525.1	Alanine-tRNA ligase
WP_089611876.1	Alanine-tRNA ligase
WP_089611877.1	Alanine-tRNA ligase
WP_089611447.1	tRNA-specific 2'-thiouridylase MnmA
WP_089611449.1	Thioredoxin
WP_089611459.1	Aspartate-tRNA ligase
WP_089611461.1	Histidine-tRNA ligase
WP_089611470.1	lipopolysaccharide assembly protein A
WP_242965207.1	Sec translocon accessory complex subunit YajC
WP_089611472.1	Queuine tRNA-ribosyltransferase
WP_089611479.1	anti-Sigma factor domain-containing protein
WP_089611500.1	Putative environmental regulatory protein
WP_089611502.1	Biosynthetic polyphosphate triacylglycerol
WP_089611503.1	NGG10 interacting factor NifE
WP_089611514.1	Phenylalanine-tRNA ligase alpha subunit
WP_089611518.1	23S RNA (guanosine-2'-O)-methyltransferase RlmB
WP_089611523.1	Translation initiation factor IF-3
WP_089611534.1	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase
WP_089611536.1	NAD(P)H-dependent FMM reductase
WP_089611540.1	Putative heat-shock stress protein
WP_089611542.1	Putative universal stress protein
WP_089611548.1	N-substituted formamide deformylase
WP_089612649.1	Ferrodoxin-NADP reductase
WP_089611555.1	UDP-2-acetamido-2,6-beta-L-arabinofuranosyl-4-ose reductase
WP_089611560.1	hypothetical protein
WP_089611562.1	GatB/YqeY domain-containing protein
WP_089611573.1	Tyrosine-protein kinase YwqD
WP_089611575.1	putative membrane polysaccharide biosynthesis protein YwqC
WP_089611582.1	Ribonuclease BN
WP_089611582.1	NADPH-dependent 7-cyano-7-deazaguanine reductase
WP_089611585.1	MRI fold metallo-hydrolase
WP_089611594.1	Lactate utilization protein A
WP_089611596.1	putative FAD-linked oxidoreductase
WP_089611600.1	Fructose-1,6-bisphosphatase class 3
WP_19306569.1	Peptidyl methionine sulfoxide reductase Msra/MsrB
WP_089611683.1	Long-chain-fatty-acid-CoA ligase FadD13
WP_089611700.1	Guanine-nucleotide pyrophosphorylase reductase
WP_089611703.1	Glutamine synthase
WP_089611703.1	Immunoglobulin (Ig) domain-containing protein
WP_089611709.1	Ion-translocating oxidoreductase complex subunit B
WP_089611726.1	D-inositol-3-phosphate glycosyltransferase
WP_089611728.1	N-acetyl-alpha-D-glucosaminyl-L-malate deacetylase
WP_089611754.1	DNA polymerase I
WP_089611763.1	DUF177 domain-containing protein
WP_089611769.1	hypothetical protein
WP_089611770.1	putative protein
WP_089611821.1	Elongation factor G
WP_089611836.1	5'-nucleotidase Surf
WP_089611881.1	YpmA family protein
WP_089611820.1	GTP cyclohydrolase 1
WP_089611822.1	7-carboxy-7-deazaguanine synthase
WP_089611830.1	Phosphatidylserine decarboxylase proenzyme
WP_089611833.1	2-oxoglutarate carboxylase large subunit
WP_089611837.1	Putative 2-oxo-FAA carboxylase beta chain
WP_089611838.1	Adenylylthiophosphate
WP_157674466.1	Ribonuclease
WP_242965235.1	DNA-binding transcriptional activator DecR
WP_089611857.1	5-methyltetrahydrofolate/corrinoid/iron-sulfur protein co-methyltransferase
WP_089611859.1	Corrinoid/iron-sulfur protein small subunit
WP_089611872.1	hypothetical protein
WP_089611874.1	hypothetical protein
WP_089611876.1	hypothetical cluster repair protein ScdA
WP_089611877.1	hypothetical protein
WP_089611879.1	Protein-L-isospartape O-methyltransferase
WP_089611880.1	Tyrosine-tRNA ligase
WP_089611882.1	NifB/NifX family molybdenum-iron cluster-binding protein
WP_089611883.1	Copper chaperone CopZ
WP_242965240.1	Tol-Pal system protein TolB
WP_089611892.1	Glyceraldehyde-3-phosphate dehydrogenase
WP_089611893.1	Putative mscS/nicotinamide transporter NalP
WP_242965244.1	Indole-3-glycerol phosphate synthase
WP_089611897.1	Anthranilate phosphoribosyltransferase
WP_089611898.1	Anthranilate synthase component 2
WP_089612664.1	Anthranilate synthase component 1
WP_157674740.1	primosomal protein N'
WP_089611904.1	Hydroxylamine reductase

WP_089611908.1	AbrB/MazE/SpoVt family DNA-binding domain-containing protein	1.7	0.3	0.2	1.0	0.0	0.0	15.4	0.0	0.0
WP_242965256.1	virulence RhMu family protein	8.6	1.7	0.2	4.3	0.5	0.1	18.4	1.7	0.1
WP_089611953.1	DUF1232 domain-containing protein	3.0	1.5	0.5	2.3	0.5	0.2	15.8	1.7	0.1
WP_089611954.1	UDP-N-acetylglucosamine 4-epimerase	13.4	0.7	0.1	6.7	0.5	0.1	23.6	1.5	0.1
WP_089611955.1	UDP-glucose 6-dehydrogenase YwqF	6.9	2.8	0.4	4.0	1.4	0.4	14.8	7.7	0.5
WP_089611956.1	DNA replicative and repair protein RecF	4.1	2.5	0.6	3.0	1.6	0.5	5.1	2.5	0.5
WP_089611966.1	3'-oxoacyl-(acyl-carrier-protein) synthase 3	3.4	1.4	0.4	2.7	0.4	0.4	8.3	3.5	0.4
WP_089611968.1	Putative pyridoxal phosphate-dependent aminotransferase EpiN	6.5	0.8	0.1	4.0	0.0	0.0	17.0	0.6	0.0
WP_089611971.1	HTH-type transcriptional repressor RspR	15.3	0.4	0.0	8.0	0.8	0.1	24.8	2.2	0.1
WP_089611973.1	Glutamate 1-semialdehyde 2,1-aminomutase	7.0	1.2	0.2	3.7	0.5	0.1	21.3	2.7	0.1
WP_089611975.1	Delta-aminoeuvicinic acid dehydratase	26.0	9.1	0.4	19.3	6.0	0.3	41.9	13.5	0.3
WP_089611976.1	Porphobilinogen deaminase	13.1	6.3	0.5	7.3	2.6	0.4	27.4	11.5	0.4
WP_089611978.1	dTDP-4-dehydrodhamnose 3,5-epimerase family protein	9.2	1.0	0.1	4.7	0.5	0.1	19.8	2.3	0.1
WP_089611980.1	UDP-glucose 4-epimerase	2.8	1.0	0.4	1.7	0.5	0.3	12.8	2.4	0.2
WP_089611981.1	UDP-glucuronic acid 4-epimerase	5.2	2.7	0.5	2.7	1.2	0.5	12.6	5.0	0.4
WP_089611982.1	vinyl-CoA reductase/reductase synthase	20.5	1.1	0.1	10.7	0.0	0.0	42.0	2.2	0.0
WP_089611984.1	GerN domain-containing protein	10.6	1.2	0.1	5.3	0.5	0.1	23.5	3.3	0.1
WP_089611985.1	N-acetylmuramoyl-alanine amidase	15.2	1.9	0.1	7.7	0.5	0.1	19.5	1.8	0.1
WP_242965258.1	Aspartate-semialdehyde dehydrogenase 2	14.0	4.4	0.3	10.3	2.5	0.2	32.5	7.8	0.2
WP_089611988.1	Nigentriose	16.2	1.6	0.1	9.3	0.9	0.1	51.2	0.0	0.0
WP_089612052.1	transposase	1.9	0.1	0.1	1.0	0.0	0.0	5.9	0.6	0.1
WP_089612055.1	GrdX family protein	4.8	1.3	0.3	3.0	0.0	0.0	32.0	4.4	0.1
WP_089612059.1	Transcriptional regulatory protein SrrA	3.5	2.9	0.8	2.7	0.9	0.4	8.8	4.6	0.5
WP_089612061.1	transient transoxamate transporter substrate binding protein	2.0	0.0	0.0	1.0	0.0	0.0	3.3	0.0	0.0
WP_089612070.1	hypothetical protein	3.5	1.4	0.3	1.5	0.8	0.4	13.3	4.4	0.0
WP_089612071.1	Bifunctional protein FofD protein	22.2	0.9	0.0	15.7	0.9	0.1	42.7	0.0	0.0
WP_198306571.1	hypothetical protein DCMF_0180S	2.8	0.7	0.2	1.7	0.5	0.3	4.0	1.0	0.3
WP_242965274.1	Oxaloacetate decarboxylase alpha chain	14.1	1.7	0.1	8.3	1.7	0.2	19.3	4.5	0.2
WP_089612078.1	pirin family protein	10.6	1.9	0.2	7.0	0.8	0.1	25.9	3.6	0.1
WP_089612092.1	sporulation protein	14.3	2.7	0.2	10.3	0.9	0.1	57.1	3.2	0.1
WP_089612100.1	dTDP-4-dehydrodhamnose 3,5-epimerase family protein	1.8	0.3	0.2	1.0	0.0	0.0	2.8	0.0	0.0
WP_089612101.1	Putative NAD(P)H nitroreductase YKO	8.3	1.8	0.2	4.7	0.9	0.2	22.5	5.1	0.2
WP_089612103.1	2,3-diketo-5-hydroxy-6-heptenoate epolase	11.4	3.1	0.3	6.0	1.6	0.3	21.8	5.7	0.3
WP_089612107.1	Uridylate-dependent prochlorophyllide reductase subunit B	8.7	1.4	0.1	4.5	0.9	0.2	35.4	3.8	0.0
WP_089612108.1	Nitrogenase Iron protein	14.2	3.1	0.2	6.7	1.2	0.2	14.2	3.4	0.2
WP_089612109.1	hypothetical protein	7.4	2.3	0.3	4.0	0.8	0.2	13.1	3.0	0.2
WP_198306574.1	Copper-exporting P-type ATPase B	3.6	2.0	0.6	3.3	1.2	0.4	6.3	2.1	0.3
WP_089612130.1	Flavodoxin	5.6	0.6	0.1	3.3	0.5	0.1	23.3	0.0	0.0
WP_089612134.1	Uroporphyrinogen decarboxylase	23.8	1.2	0.0	15.3	1.2	0.1	46.6	0.0	0.0
WP_089612136.1	Choline trimethylamine-lyase	7.1	4.8	0.7	3.7	2.4	0.6	7.5	4.7	0.6
WP_089612141.1	Uridylate kinase	5.0	2.5	0.5	3.7	2.1	0.6	10.6	5.3	0.5
WP_089612145.1	Ribonuclease	3.6	0.2	0.1	2.0	0.0	0.0	22.5	0.0	0.0
WP_089612147.1	Lactoylglutathione lyase	4.3	0.3	0.1	2.7	0.5	0.2	22.1	6.2	0.0
WP_089612148.1	Putative universal stress protein	11.0	1.3	0.1	6.0	0.0	0.0	49.2	0.6	0.0
WP_089612151.1	Bifunctional F420 biosynthesis protein FbiB	4.7	1.2	0.2	3.7	0.5	0.1	19.0	2.7	0.1
WP_198306577.1	Lipoate-protein ligase A	6.5	1.2	0.2	4.0	0.8	0.2	34.2	7.3	0.2
WP_089612161.1	Long-chain-alcohol dehydrogenase 2	16.4	2.5	0.2	9.0	1.6	0.2	27.3	5.9	0.2
WP_089612164.1	CGGC domain-containing protein	2.0	0.0	0.0	1.3	0.5	0.4	13.6	0.0	0.0
WP_089612165.1	putative protein	2.6	1.0	0.4	1.3	0.5	0.4	7.4	2.3	0.3
WP_242965251.1	Ribonuclease	3.0	1.2	0.4	1.7	0.5	0.3	13.4	3.9	0.3
WP_089612170.1	Flavodoxin	6.6	2.4	0.3	3.0	0.5	0.3	24.7	5.5	0.2
WP_089612174.1	Site-specific DNA-methyltransferase	10.4	3.6	0.3	6.3	1.2	0.2	10.9	3.2	0.1
WP_089609716.1	(S)-2-haloacid dehalogenase	17.0	1.1	0.1	12.7	2.4	0.2	41.6	4.3	0.1
WP_242965203.1	2,3-dihydro-2H-chromene-2-carboxylate isomerase	6.8	2.5	0.4	5.3	1.2	0.2	20.3	5.9	0.3
WP_089611960.1	MULTISPECIEC pyridoxamine 5'-phosphate oxidase family protein	14.5	2.2	0.2	13.3	0.9	0.1	73.4	14.0	0.2
WP_089610571.1	hypothetical protein C1063_0543	3.8	0.3	0.1	2.0	0.0	0.0	15.3	0.0	0.0
WP_089608534.1	MULTISPECIES: metal-binding protein	3.6	0.4	0.1	2.0	0.0	0.0	31.9	0.0	0.0
WP_089612244.1	hypothetical protein	3.4	0.7	0.2	2.7	0.5	0.2	11.7	2.7	0.2
WP_089612246.1	hypothetical transcriptional regulator	2.2	0.3	0.2	1.3	0.5	0.4	23.0	5.7	0.2
WP_089612247.1	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	25.1	2.8	0.3	11.3	0.1	0.1	30.1	3.0	0.1
WP_089612238.1	Glutamyl-tRNA(Gln) amidotransferase subunit A	26.9	2.8	0.0	14.3	0.9	0.1	39.5	2.6	0.1
WP_089612239.1	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	2.0	0.0	0.0	1.3	0.5	0.4	22.7	6.5	0.3
WP_089612240.1	D-gamma-glutamyl-meso-diaminopimelic acid endopeptidase Cwls	24.7	0.9	0.0	19.3	0.5	0.0	53.2	2.4	0.0
WP_089612242.1	3'-exoribonuclease YhM	2.0	0.0	0.0	1.0	0.0	0.0	3.7	0.0	0.0
WP_089612248.1	universal stress protein	4.0	0.0	0.0	2.3	0.5	0.2	24.3	0.0	0.0
WP_089612249.1	DNAbis	10.2	2.8	0.3	5.0	1.4	0.3	11.7	2.7	0.2
WP_089612251.1	hypothetical protein	6.0	0.0	0.0	3.0	0.0	0.0	30.9	0.0	0.0
WP_089612252.1	Aspartyl-glutamyl-tRNA(Gln) amidotransferase	20.7	1.1	0.1	10.7	0.9	0.1	71.2	1.0	0.0
WP_089612254.1	Methylbacteriofuran dinucleotide biosynthesis adapter protein	4.9	1.4	0.3	3.0	0.5	0.3	22.6	4.6	0.1
WP_089612255.1	GTP 3'-cyclase	3.7	0.8	0.1	1.7	0.5	0.3	6.5	1.3	0.2
WP_089612256.1	Molybdoenzyme molybdenumtransferase	25.7	0.9	0.0	14.3	1.2	0.1	41.9	2.4	0.1
WP_089612257.1	hypothetical protein	3.7	1.3	0.4	2.0	0.8	0.4	36.8	14.1	0.4
WP_089612261.1	hypothetical protein	11.7	0.4	0.0	10.0	1.4	0.1	49.3	8.1	0.2
WP_089612262.1	CGGC domain-containing protein	22.6	4.1	0.2	12.3	1.7	0.1	40.8	2.0	0.0
WP_089612263.1	imidazole-glycerol phosphate synthase subunit HisF	14.7	3.4	0.2	8.3	0.9	0.1	45.1	8.4	0.2
WP_089612264.1	imidazole-glycerol phosphate synthase subunit HisG	2.0	0.0	0.0	1.0	0.0	0.0	6.6	0.0	0.0
WP_089612265.1	HisF	10.2	1.8	0.2	5.3	0.5	0.1	19.3	4.0	0.1
WP_089612266.1	ATP phosphoribosyl transferase	17.5	2.8	0.1	11.7	1.2	0.1	33.1	3.2	0.1
WP_089612267.1	ATP phosphoribosyl transferase regulatory subunit	17.5	2.8	0.1	11.7	1.2	0.1	33.1	3.2	0.1
WP_089608934.1	IS21 family transposase	2.6	1.1	0.4	1.3	0.5	0.4	3.9	1.7	0.4
WP_089608935.1	IS21 family transposase IShahy12	9.6	1.9	0.2	5.0	0.8	0.2	27.3	4.8	0.2
WP_089612280.1	type I CRISPR-associated protein Cas7	3.1	1.8	0.6	1.7	0.9	0.6	7.0	3.4	0.5
WP_089612281.1	hypothetical protein	5.1	1.1	0.2	4.0	0.8	0.2	48.7	6.8	0.1
WP_089612691.1	TrpR-like protein YecF/YecD	2.5	1.3	0.5	1.3	0.5	0.4	14.4	5.1	0.4
WP_089612291.1	Uridylate kinase	20.4	2.2	0.1	11.7	1.2	0.1	32.0	4.2	0.1
WP_089612292.1	Dihydroxyacetone phosphate lyase	7.5	3.1	0.3	4.0	1.4	0.3	16.1	6.9	0.4
WP_089612293.1	Phosphoribosylglycine ligase	16.3	4.1	0.3	8.3	1.7	0.1	32.2	5.4	0.2
WP_089612301.1	Bifunctional purine biosynthesis protein PurH	6.8	1.9	0.3	3.3	0.9	0.3	16.0	4.0	0.3
WP_089612303.1	Amidophosphoributrate transferase	12.1	2.4	0.2	6.3	1.2	0.2	18.2	3.5	0.2
WP_089612304.1	Adenylosuccinate lyase	12.0	1.4	0.1	7.0	0.8	0.1	17.8	2.4	0.1
WP_089612305.1	NS-carboxyaminomimidazole ribonucleotide mutase	4.8	1.9	0.4	4.3	1.2	0.3	21.0	7.2	0.3
WP_089612311.1	hemerythrin domain-containing protein	7.1	2.3	0.3	4.0	0.8	0.2	28.5	9.7	0.3
WP_089612314.1	Uridylate kinase/phosphoribulamin biosynthesis protein CobU	4.2	1.3	0.3	2.7	0.9	0.4	10.1	3.9	0.4
WP_089612316.1	Desulfurylase	4.6	0.3	0.1	2.3	0.5	0.2	20.4	1.8	0.1
WP_089612316.1	Desulfurylase desuccinylase	3.3	2.2	0.1	2.7	0.5	0.2	8.1	2.0	0.1
WP_089612318.1	Methionine synthase	3.0	0.2	0.1	36.0	3.6	0.1	68.8	4.8	0.1
WP_089612353.1	Glutamyl-tRNA reductase	1.7	0.2	0.1	1.3	0.5	0.4	2.9	1.0	0.4
WP_089612360.1	Sirohydrochlorin cobalochlorolase	5.0	1.7	0.3	4.0	1.4	0.4	39.7	7.0	0.2
WP_089612361.1	Phosphoribosylinosimidazole-succinocarboxamide synthase	24.2	2.8	0.1	17.3	0.9	0.1	61.4	3.9	0.1
WP_089612364.1	Hydrogenase-4 component B	2.0	0.1	0.0	1.0	0.0	0.0	2.1	0.0	0.0
WP_089612370.1	pyridoxamine 5'-phosphate oxidase family									

WP_089612429.1 hypothetical protein
WP_089612433.1 Protein LemA

3.9 7.0	1.2 1.4	0.3 0.2	3.3 5.0	0.9 0.8	0.3 0.2	27.2 26.0	7.3 7.6	0.3 0.3
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Table S9. Protein assignments to 22 KEGG categories using BlastKOALA

KEGG Functional Category	Category Code	Raw number	% out of total annotated (702)	% out of proteins in proteome (1,012)
Genetic information processing	9120	115	16.4	11.4
Amino acid metabolism	9105	97	13.8	9.6
Energy metabolism	9102	90	12.8	8.9
Metabolism of cofactors and vitamins	9108	84	12.0	8.3
Carbohydrate metabolism	9101	80	11.4	7.9
Protein families: genetic information processing	9182	58	8.3	5.7
Environmental information processing	9130	49	7.0	4.8
Unclassified: metabolism	9191	38	5.4	3.8
Nucleotide metabolism	9104	36	5.1	3.6
Human diseases	9160	34	4.8	3.4
Protein families: signalling and cellular processing	9183	33	4.7	3.3
Cellular processes	9140	33	4.7	3.3
Metabolism of other amino acids	9106	23	3.3	2.3
Glycan biosynthesis and metabolism	9107	22	3.1	2.2
Xenobiotics degradation and metabolism	9111	22	3.1	2.2
Organismal systems	9150	20	2.8	2.0
Unclassified		19	2.7	1.9
Protein families: metabolism	9181	18	2.6	1.8
Unclassified: genetic information processing	9192	12	1.7	1.2
Unclassified: signalling and cellular processing	9193	11	1.6	1.1
Lipid metabolism	9103	10	1.4	1.0
Metabolism of terpenoids and polyketides	9109	4	0.6	0.4

Table S10. List of proteins identified from *D. formicacecum* proteome assigned to 22 KEGG functional categories using BlastKOALA

Query_GTDB	Query_Prokka	Best Hit	KEGG Functional Category	Category Code	Hit Description	Score
NZ_CPO22121_1_2554	JBMCGNCK_02618	K00003	Amino acid metabolism	9105	hom; homoserine dehydrogenase [EC:1.1.1.3]	231
NZ_CPO22121_1_3424	JBMCGNCK_03511	K00013	Amino acid metabolism	9105	hisD; histidin dehydrogenase [EC:1.1.1.23]	306
NZ_CPO22121_1_3067	JBMCGNCK_03149	K00133	Amino acid metabolism	9105	asd; aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	243
NZ_CPO22121_1_1158	JBMCGNCK_01199	K00145	Amino acid metabolism	9105	argC; N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]	201
NZ_CPO22121_1_2826	JBMCGNCK_02898	K00147	Amino acid metabolism	9105	proA; glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41]	255
NZ_CPO22121_1_2572	JBMCGNCK_02637	K00215	Amino acid metabolism	9105	dapB; 4-hydroxy-tetrahydropicolinate reductase [EC:1.17.1.8]	152
NZ_CPO22121_1_1730	JBMCGNCK_01783	K00286	Amino acid metabolism	9105	LYS1; saccharopine dehydrogenase (NAD+, L-lysine forming) [EC:1.5.1.7]	343
NZ_CPO22121_1_2663	JBMCGNCK_02728	K00290	Amino acid metabolism	9105	E1.2.1.88; L-pyrroline-5-carboxylate dehydrogenase [EC:1.2.1.88]	346
NZ_CPO22121_1_415	JBMCGNCK_00425	K00294	Amino acid metabolism	9105	OTC, argF, argI; ornithine carbamoyltransferase [EC2.3.1.3]	252
NZ_CPO22121_1_736	JBMCGNCK_00758	K00611	Amino acid metabolism	9105	glu; glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC2.3.1.35 5.2.3.1]	251
NZ_CPO22121_1_1160	JBMCGNCK_01200	K00620	Amino acid metabolism	9105	hisG; ATP phosphoribosyltransferase [EC2.4.2.17]	136
NZ_CPO22121_1_3425	JBMCGNCK_03512	K00765	Amino acid metabolism	9105	trpD; anthranilate phosphoribosyltransferase [EC:2.4.2.18]	230
NZ_CPO22121_1_2963	JBMCGNCK_03043	K00766	Amino acid metabolism	9105	mtaP, MTP; 5'-methylthioadenosine phosphorylase [EC:2.4.2.28]	218
NZ_CPO22121_1_1374	JBMCGNCK_01425	K00772	Amino acid metabolism	9105	metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]	302
NZ_CPO22121_1_1802	JBMCGNCK_01856	K00789	Amino acid metabolism	9105	araO; 3-phosphoshikimate 1-carboxyvinyltransferase [EC:2.5.1.19]	330
NZ_CPO22121_1_2531	JBMCGNCK_02595	K00800	Amino acid metabolism	9105	hisC; histidinol-phosphate aminotransferase [EC:2.6.1.9]	177
NZ_CPO22121_1_1268	JBMCGNCK_01311	K00817	Amino acid metabolism	9105	gD; acetylornithine/N-succinylalanopimelate aminotransferase [EC:2.6.1.11 2.6.1.1]	255
NZ_CPO22121_1_1162	JBMCGNCK_01202	K00821	Amino acid metabolism	9105	tyrB; aromatic-amino-acid transaminase [EC:2.6.1.57]	149
NZ_CPO22121_1_390	JBMCGNCK_00400	K00832	Amino acid metabolism	9105	lysC; aspartate kinase [EC:2.7.2.4]	244
NZ_CPO22121_1_2556	JBMCGNCK_02620	K00928	Amino acid metabolism	9105	argB; acetylglutamate kinase [EC:2.7.2.8]	228
NZ_CPO22121_1_1161	JBMCGNCK_01201	K00930	Amino acid metabolism	9105	prob; glutamate-5-kinase [EC:2.7.2.11]	274
NZ_CPO22121_1_2827	JBMCGNCK_02899	K00931	Amino acid metabolism	9105	E3.3.1.1, ahcY; adenosylhomocysteine [EC:3.3.1.1]	296
NZ_CPO22121_1_2907	JBMCGNCK_02983	K01251	Amino acid metabolism	9105	speA; arginine decarboxylase [EC:4.1.1.19]	352
NZ_CPO22121_1_2666	JBMCGNCK_02731	K01585	Amino acid metabolism	9105	trpC; indole-3-glycerol phosphate synthase [EC:4.1.1.48]	124
NZ_CPO22121_1_2962	JBMCGNCK_03042	K01609	Amino acid metabolism	9105	speD, AMD1; S-adenosylmethionine decarboxylase [EC:4.1.1.50]	122
NZ_CPO22121_1_2001	JBMCGNCK_02059	K01611	Amino acid metabolism	9105	trpA; tryptophan synthase alpha chain [EC:4.2.1.20]	159
NZ_CPO22121_1_2420	JBMCGNCK_02483	K01695	Amino acid metabolism	9105	trpB; tryptophan synthase beta chain [EC:4.2.1.20]	158
NZ_CPO22121_1_2422	JBMCGNCK_02485	K01696	Amino acid metabolism	9105	trpB; tryptophan synthase beta chain [EC:4.2.1.20]	67
NZ_CPO22121_1_2421	JBMCGNCK_02484	K01696	Amino acid metabolism	9105	dapA; 4-hydroxy-tetrahydronicotinate synthase [EC:4.3.3.7]	169
NZ_CPO22121_1_1414	JBMCGNCK_01468	K01714	Amino acid metabolism	9105	aroB; 3-dehydroquinate synthase [EC:4.2.3.5]	319
NZ_CPO22121_1_2640	JBMCGNCK_02705	K01735	Amino acid metabolism	9105	metV; O-acetylserine (thiol)-lyase [EC:4.2.5.1.49]	340
NZ_CPO22121_1_2642	JBMCGNCK_02707	K01736	Amino acid metabolism	9105	parE; diaminopimelate epimerase [EC:5.1.1.7]	160
NZ_CPO22121_1_3563	JBMCGNCK_03651	K01740	Amino acid metabolism	9105	hisF; imidazole-glycerol-phosphate synthase subunit HisF [EC:4.3.2.10]	84
NZ_CPO22121_1_1189	JBMCGNCK_01229	K01755	Amino acid metabolism	9105	hisH; imidazole-glycerol-phosphate synthase subunit HisH [EC:4.3.2.10]	108
NZ_CPO22121_1_995	JBMCGNCK_01023	K01778	Amino acid metabolism	9105	hisZ; ATP phosphoribosyltransferase regulatory subunit	120
NZ_CPO22121_1_3421	JBMCGNCK_03508	K01814	Amino acid metabolism	9105	AROA, aroA; 3-deoxy-7-phosphohexulonate synthase [EC:2.5.1.54]	222
NZ_CPO22121_1_2528	JBMCGNCK_02592	K01817	Amino acid metabolism	9105	AROA2, aroA2; 3-deoxy-7-phosphohexulonate synthase [EC:2.5.1.54]	156
NZ_CPO22121_1_227	JBMCGNCK_00236	K01912	Amino acid metabolism	9105	tyrA2; prephenate dehydrogenase [EC:1.3.1.12]	146
NZ_CPO22121_1_3599	JBMCGNCK_03687	K01912	Amino acid metabolism	9105	trpB2; tryptophan synthase beta chain [EC:4.2.1.20]	343
NZ_CPO22121_1_3420	JBMCGNCK_03507	K02500	Amino acid metabolism	9105	aroH; chorismate mutase [EC:5.4.99.5]	64
NZ_CPO22121_1_3422	JBMCGNCK_03509	K02501	Amino acid metabolism	9105	mtnA; methylthioribose-1-phosphate isomerase [EC:5.3.1.23]	191
NZ_CPO22121_1_3426	JBMCGNCK_03513	K02502	Amino acid metabolism	9105	patA; putrescine aminotransferase [EC:2.6.1.82]	301
NZ_CPO22121_1_1621	JBMCGNCK_01674	K02856	Amino acid metabolism	9105	E2.6.1.83; LL-diaminopimelate aminotransferase [EC:2.6.1.83]	452
NZ_CPO22121_1_2529	JBMCGNCK_02593	K02856	Amino acid metabolism	9105	hisorbyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphorylase [EC:3.5.4.18]	18
NZ_CPO22121_1_2530	JBMCGNCK_02594	K04517	Amino acid metabolism	9105	cysM; 5-Sulfo-L-cysteine synthase (O-acetyl-L-serine-dependent) [EC:2.5.1.144]	268
NZ_CPO22121_1_2830	JBMCGNCK_02903	K06001	Amino acid metabolism	9105	itdA; 5-methylthioadenosine/S-adenosylhomocysteine deaminase [EC:3.5.4.31 3.5.4.25]	250
NZ_CPO22121_1_2527	JBMCGNCK_02591	K06208	Amino acid metabolism	9105	pydJ; 3-methylthiorynamoyl-N6-L-lysine dehydrogenase [EC:1.4.1.-1]	66
NZ_CPO22121_1_1375	JBMCGNCK_01426	K08963	Amino acid metabolism	9105	pflD; trans-4-hydroxy-L-proline dehydratase [EC:4.2.1.172]	538
NZ_CPO22121_1_808	JBMCGNCK_00829	K09251	Amino acid metabolism	9105	E2.5.1.54, aroF, aroG, aroH; 3-deoxy-7-phosphohexulonate synthase [EC:2.5.1.54]	208
NZ_CPO22121_1_2787	JBMCGNCK_02856	K0926	Amino acid metabolism	9105	trpE; anthranilate synthase component I [EC:4.1.3.27]	309
NZ_CPO22121_1_3409	JBMCGNCK_03496	K11755	Amino acid metabolism	9105	trpG; anthranilate synthase component II [EC:4.1.3.27]	132
NZ_CPO22121_1_2955	JBMCGNCK_03035	K12339	Amino acid metabolism	9105	GDH; D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase [EC:1.1.1.95 1.3.1.5]	315
NZ_CPO22121_1_1377	JBMCGNCK_01428	K12960	Amino acid metabolism	9105	E1.4.1.4, gdhA; glutamate dehydrogenase (NAD+) [EC:1.4.1.4]	299
NZ_CPO22121_1_1165	JBMCGNCK_01205	K16182	Amino acid metabolism	9105	metaD; homoserine O-acetyltransferase/O-acetyltransferase [EC:2.3.1.46 2.3.1.31]	202
NZ_CPO22121_1_2363	JBMCGNCK_02432	K23121	Amino acid metabolism	9105	cysK; cysteine synthase [EC:2.5.1.47]	236
NZ_CPO22121_1_2429	JBMCGNCK_02492	K01626	Amino acid metabolism, Cellular processes	9105	E; UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase [EC:6.3.2.23]	233
NZ_CPO22121_1_2964	JBMCGNCK_03045	K01657	Amino acid metabolism, Cellular processes	9105	argA, SS51; argininosuccinate synthase [EC:6.3.4.5]	426
NZ_CPO22121_1_2452	JBMCGNCK_03216	K01658	Amino acid metabolism, Cellular processes	9105	ilvC, ilvD; branched-chain amino acid aminotransferase [EC:2.6.1.42]	355
NZ_CPO22121_1_1028	JBMCGNCK_01056	K02062	Amino acid metabolism, Energy metabolism	9105	serC, PSAT1; phosphoserine aminotransferase [EC:2.6.1.52]	249
NZ_CPO22121_1_3566	JBMCGNCK_03654	K00651	Amino acid metabolism, Energy metabolism	9105	methY; MTR; 5-methyltetrahydrofolate--homocysteine methyltransferase [EC:2.1.1.13]	51
NZ_CPO22121_1_1665	JBMCGNCK_03650	K01738	Amino acid metabolism, Energy metabolism	9105	trpE, SRM, SP3; spermidine synthase [EC:2.5.1.16]	218
NZ_CPO22121_1_1071	JBMCGNCK_01103	K00764	Amino acid metabolism, Nucleotide metabolism	9105	lysA; diaminopimelate decarboxylase [EC:4.1.1.20]	313
NZ_CPO22121_1_3469	JBMCGNCK_03555	K01756	Amino acid metabolism, Nucleotide metabolism	9105	trpF, PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]	298
NZ_CPO22121_1_810	JBMCGNCK_00831	K01939	Amino acid metabolism, Nucleotide metabolism	9105	purF, PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]	222
NZ_CPO22121_1_3237	JBMCGNCK_03318	K01955	Amino acid metabolism, Nucleotide metabolism	9105	purB, ADSL; adenylosuccinate lyase [EC:4.3.2.2]	312
NZ_CPO22121_1_1726	JBMCGNCK_01779	K05810	Amino acid metabolism, Nucleotide metabolism	9105	carB, CPA2; carbamoyl-phosphate synthase large subunit [EC:6.3.3.5]	807
NZ_CPO22121_1_1540	JBMCGNCK_01593	K01667	Amino acid metabolism, Metabolism of cofactors and vitamins	9105	-nucleoside/S-methyl-5-thiouridine phosphorylase / adenosine deaminase [EC:2.4.:-]	167
NZ_CPO22121_1_1560	JBMCGNCK_01562	K01733	Amino acid metabolism, Metabolism of cofactors and vitamins	9105	ilvD; dihydroxy-acid dehydratase [EC:2.1.2.19]	395
NZ_CPO22121_1_3282	JBMCGNCK_02851	K00104	Carbohydrate metabolism	9101	trhC, threonine synthase [EC:2.3.1.1]	292
NZ_CPO22121_1_3460	JBMCGNCK_03546	K02083	Carbohydrate metabolism	9101	glcD, glcE; glyceraldehyde oxidase [EC:1.1.1.19]	301
NZ_CPO22121_1_891	JBMCGNCK_00918	K00616	Carbohydrate metabolism	9101	govPB; glycine dehydrogenase subunit Z [EC:1.4.4.2]	333
NZ_CPO22121_1_988	JBMCGNCK_01016	K00700	Carbohydrate metabolism	9101	E2.2.1.2, taI, taII; transaldolase [EC:2.2.1.2]	179
NZ_CPO22121_1_3170	JBMCGNCK_03250	K01571	Carbohydrate metabolism	9101	GBE1, glgE; 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	346
NZ_CPO22121_1_1376	JBMCGNCK_01427	K01628	Carbohydrate metabolism	9101	oادا; oxaloacetate decarboxylase [Na+ extruding] subunit alpha [EC:7.2.4.2]	164
NZ_CPO22121_1_3248	JBMCGNCK_03329	K01759	Carbohydrate metabolism	9101	fucA; L-fucose-phosphate aldolase [EC:4.1.2.17]	122
NZ_CPO22121_1_3575	JBMCGNCK_03663	K01759	Carbohydrate metabolism	9101	GLO1, gloA; lactoylglutathione lyase [EC:4.4.1.5]	87
NZ_CPO22121_1_1564	JBMCGNCK_01617	K02564	Carbohydrate metabolism	9101	GLO1, gloA; lactoylglutathione lyase [EC:4.4.1.5]	74
NZ_CPO22121_1_1560	JBMCGNCK_01613	K03431	Carbohydrate metabolism	9101	nagB, GNPDAs; glucosamine-6-phosphate deaminase [EC:3.5.9.9.6]	152
NZ_CPO22121_1_3051	JBMCGNCK_03132	K05942	Carbohydrate metabolism	9101	glmB, PGPAs; glucosaminoglycan mutase [EC:5.4.2.10]	273
NZ_CPO22121_1_2781	JBMCGNCK_02850	K11473	Carbohydrate metabolism	9101	E2.3.3.3; citrate (Re)-synthase [EC:2.3.3.3]	430
NZ_CPO22121_1_987	JBMCGNCK_01015	K15916	Carbohydrate metabolism	9101	glcF; glycolate oxidase iron-sulfur subunit	134
NZ_CPO22121_1_1166	JBMCGNCK_01206	K22373	Carbohydrate metabolism	9101	pgl-pmu; glucose/mannose-6-phosphate isomerase [EC:5.3.1.9.5.1.8]	180
NZ_CPO22121_1_1546	JBMCGNCK_01599	K00052	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	larA; lactate racemase [EC:5.1.2.1]	202
NZ_CPO22121_1_3461	JBMCGNCK_03547	K00282	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	leuB, IMDH; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]	247
NZ_CPO22121_1_2259	JBMCGNCK_03248	K00382	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	gcpPA; glycine dehydrogenase subunit 1 [EC:1.4.4.2]	284
NZ_CPO22121_1_1547	JBMCGNCK_01600	K01649	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]	261
NZ_CPO22121_1_1543	JBMCGNCK_01596	K01649	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]	222
NZ_CPO22121_1_1544	JBMCGNCK_01597	K01703	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	leaU, IMS; 2-isopropylmalate synthase [EC:2.3.3.13]	383
NZ_CPO22121_1_1545	JBMCGNCK_01598	K01704	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	leaU, IMS; 2-isopropylmalate synthase [EC:2.3.3.13]	348
NZ_CPO22121_1_1921	JBMCGNCK_01978	K02437	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	M1-I; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33.4]	327
NZ_CPO22121_1_3462	JBMCGNCK_03548	K02437	Carbohydrate metabolism, Amino acid metabolism	9101, 9105	gcvH, GCH3; glycine cleavage system H protein	124
NZ_CPO22121_1_357	JBMCGNCK_03065	K15633	Carbohydrate metabolism, Amino acid metabolism, Energy metabolism	9101, 9105, 9102	gcvH, GCH3; glycine cleavage system H protein	67
NZ_CPO22121_1_1279	JBMCGNCK_01324	K15635	Carbohydrate metabolism, Amino acid metabolism, Energy metabolism	9101, 9105, 9102	gpmI; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]	320
NZ_CPO22121_1_993	JBMCGNCK_01021	K01915	Carbohydrate metabolism, Amino acid metabolism, Energy metabolism	9101, 9105, 9102, 9140, 9	apgM; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]	235
NZ_CPO22121_1_1069	JBMCGNCK_01099	K01915	Carbohydrate metabolism, Amino acid metabolism, Energy metabolism	9101, 9105, 9102, 9140, 9	glnA, GLU; glutamine synthetase [EC:6.3.1.2]	352
NZ_CPO22121_1_1068	JBMCGNCK_01098	K00820	Carbohydrate metabolism, Amino acid metabolism, Energy metabolism	9101, 9105, 9102, 9140, 9	glnA, GLU; glutamine synthetase [EC:6.3.1.2]	240
NZ_CPO22121_1_3463	JBMCGNCK_03549	K00605	Carbohydrate metabolism, Amino acid metabolism, Metabolism of cofactors and vitamins	9101, 9105, 9108	gcvT, AMT; aminomethyltransferase [EC:2.1.2.10]	268
NZ_CPO22121_1_731	JBMCGNCK_00753	K01652	Carbohydrate metabolism, Amino acid metabolism, Metabolism of cofactors and vitamins	9101, 9105, 9108	E2.2.1.6L, ilvB, ilvI, ilvJ; acetoacetate synthase [V/L/large subunit] [EC:2.2.1.6]	341
NZ_CPO22121_1_1542	JBMCGNCK_01595	K01652	Carbohydrate metabolism, Amino acid metabolism, Metabolism of cofactors and vitamins	9101, 9105, 9108	E2.2.1.6L, ilvB, ilvI, ilvJ; acetoacetate synthase [V/L/large subunit] [EC:2.2.1.6]	316
NZ_CPO22121_1_732	JBMCGNCK_00754	K01653	Carbohydrate metabolism, Amino acid metabolism, Metabolism of cofactors and vitamins	9101, 9105, 9		

NZ_CP022121_1_2780	JBMCGNCK_02849	K01624	Carbohydrate metabolism, Energy metabolism	9101, 9102	FBA,fbkA:fructose-bisphosphate aldolase, class I [EC:4.1.2.13]
NZ_CP022121_1_1588	JBMCGNCK_01641	K01678	Carbohydrate metabolism, Energy metabolism	9101, 9102	E4.1.2.1AB: fumC, fumarate hydratase subunit beta [EC:4.1.2.1]
NZ_CP022121_1_2741	JBMCGNCK_02808	K01681	Carbohydrate metabolism, Energy metabolism	9101, 9102	ACO, acnA, acnB: citrate hydratase [EC:2.4.1.3]
NZ_CP022121_1_358	JBMCGNCK_03066	K01803	Carbohydrate metabolism, Energy metabolism	9101, 9102	TPI, tpkA: triosephosphate isomerase (TPI) [EC:5.3.1.1]
NZ_CP022121_1_904	JBMCGNCK_00931	K01808	Carbohydrate metabolism, Energy metabolism	9101, 9102	rpiB: ribose-5-phosphate isomerase B [EC:5.3.1.6]
NZ_CP022121_1_360	JBMCGNCK_03688	K01958	Carbohydrate metabolism, Energy metabolism	9101, 9102	PC, pyc: pyruvate carboxylase [EC:6.4.1.1]
NZ_CP022121_1_495	JBMCGNCK_00507	K03737	Carbohydrate metabolism, Energy metabolism	9101, 9102	por, nifU: pyruvate-formate lyase/fluorodioxane oxidoreductase [EC:1.2.7.1.2.7.-]
NZ_CP022121_1_2786	JBMCGNCK_02855	K04041	Carbohydrate metabolism, Energy metabolism	9101, 9102	fbp3: fructose-1,6-diphosphatase III [EC:3.3.1.3]
NZ_CP022121_1_2738	JBMCGNCK_02805	K21071	Carbohydrate metabolism, Energy metabolism	9101, 9102	epend phosphofructokinase / diphosphate-dependent phosphofructokinase [EC:2.7.2.19]
NZ_CP022121_1_206	JBMCGNCK_00827	K21071	Carbohydrate metabolism, Energy metabolism	9101, 9102	epend phosphofructokinase / diphosphate-dependent phosphofructokinase [EC:2.7.2.19]
NZ_CP022121_1_1636	JBMCGNCK_01689	K00031	Carbohydrate metabolism, Energy metabolism	9101, 9102	IDH1, IDH2, lldC: isocitrate dehydrogenase [EC:2.1.1.42]
NZ_CP022121_1_359	JBMCGNCK_03067	K00097	Carbohydrate metabolism, Energy metabolism, Environmental information processing	9101, 9102	PGK, pgk: phosphoglycerate kinase [EC:2.7.2.3]
NZ_CP022121_1_360	JBMCGNCK_03658	K00134	Carbohydrate metabolism, Energy metabolism	9101, 9102	ackA: acetate kinase [EC:2.7.2.1]
NZ_CP022121_1_2861	JBMCGNCK_02935	K00925	Carbohydrate metabolism, Energy metabolism	9101, 9102	M2E, sfcA, maeA: malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
NZ_CP022121_1_275	JBMCGNCK_02823	K15024	Carbohydrate metabolism, Energy metabolism, Metabolism of other amino acids	9101, 9102, 9130	KAT, cat, catB, catP, catalase [EC:1.11.1.6]
NZ_CP022121_1_285	JBMCGNCK_00293	K00169	Carbohydrate metabolism, Energy metabolism, Metabolism of other amino acids	9101, 9102, 9130	ENO, eno, enolase [EC:4.2.1.11]
NZ_CP022121_1_286	JBMCGNCK_02924	K00170	Carbohydrate metabolism, Energy metabolism, Xenobiotics biodegradation and metabolism	9101, 9102, 9111	UGDH, ugd; UDP-glucose 6-dehydrogenase [EC:1.1.1.22]
NZ_CP022121_1_284	JBMCGNCK_02929	K00171	Carbohydrate metabolism, Energy metabolism, Xenobiotics biodegradation and metabolism	9101, 9102, 9111	murB; UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.3.1.9]
NZ_CP022121_1_283	JBMCGNCK_02921	K00172	Carbohydrate metabolism, Energy metabolism, Xenobiotics biodegradation and metabolism	9101, 9102, 9111	murA; UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.3.1.7]
NZ_CP022121_1_1589	JBMCGNCK_01642	K00027	Carbohydrate metabolism, Energy metabolism, Xenobiotics biodegradation and metabolism	9101, 9102, 9111	porD; pyruvate ferredoxin oxidoreductase delta subunit [EC:2.1.2.1]
NZ_CP022121_1_1379	JBMCGNCK_01430	K03781	Carbohydrate metabolism, Environmental information processing	9101, 9130	porC, porG; pyruvate ferredoxin oxidoreductase gamma subunit [EC:1.2.7.1]
NZ_CP022121_1_356	JBMCGNCK_03064	K01689	Carbohydrate metabolism, Environmental information processing	9101, 9130	ME2, sfcA, maeA: malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
NZ_CP022121_1_3034	JBMCGNCK_03115	K00012	Carbohydrate metabolism, Environmental information processing, Organismal systems	9101, 9130, 9160	K15024; putative phosphotransacetylase [EC:2.3.1.8]
NZ_CP022121_1_3482	JBMCGNCK_03568	K00075	Carbohydrate metabolism, Glycan biosynthesis and metabolism	9101, 9102, 9111	porA; pyruvate ferredoxin oxidoreductase alpha subunit [EC:1.2.7.1]
NZ_CP022121_1_923	JBMCGNCK_00500	K00790	Carbohydrate metabolism, Glycan biosynthesis and metabolism	9101, 9102, 9111	porB; pyruvate ferredoxin oxidoreductase beta subunit [EC:1.2.7.1]
NZ_CP022121_1_843	JBMCGNCK_00869	K00790	Carbohydrate metabolism, Glycan biosynthesis and metabolism	9101, 9102, 9111	porD; pyruvate ferredoxin oxidoreductase delta subunit [EC:2.1.2.1]
NZ_CP022121_1_2057	JBMCGNCK_02120	K00963	Carbohydrate metabolism, Glycan biosynthesis and metabolism	9101, 9102, 9111	porC, porG; pyruvate ferredoxin oxidoreductase gamma subunit [EC:1.2.7.1]
NZ_CP022121_1_3062	JBMCGNCK_03143	K01784	Carbohydrate metabolism, Glycan biosynthesis and metabolism	9101, 9102, 9111	ME2, sfcA, maeA: malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
NZ_CP022121_1_1001	JBMCGNCK_01029	K04042	Carbohydrate metabolism, Glycan biosynthesis and metabolism	9101, 9102, 9111	KAT, cat, catB, catP, catalase [EC:1.11.1.6]
NZ_CP022121_1_3033	JBMCGNCK_03114	K08679	Carbohydrate metabolism, Glycan biosynthesis and metabolism	9101, 9102, 9111	ENO, eno, enolase [EC:4.2.1.11]
NZ_CP022121_1_3059	JBMCGNCK_03140	K01790	Carbohydrate metabolism, Glycan biosynthesis and metabolism, Metabolism of terpenoids and polyphenols	9101, 9102, 9111	UDGDH, ugd; UDP-glucose 6-dehydrogenase [EC:1.1.1.22]
NZ_CP022121_1_960	JBMCGNCK_00987	K00615	Carbohydrate metabolism, Metabolism of terpenoids and polyketides	9101, 9102, 9111	murB; UDP-N-acetylglucosamine dehydrogenase [EC:3.1.3.98]
NZ_CP022121_1_1002	JBMCGNCK_01030	K00948	Carbohydrate metabolism, Nucleotide metabolism	9101, 9102, 9111	murA; UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.3.1.7]
NZ_CP022121_1_2484	JBMCGNCK_02548	K01839	Carbohydrate metabolism, Nucleotide metabolism	9101, 9102, 9111	murA; UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.3.1.7]
NZ_CP022121_1_3171	JBMCGNCK_03251	K00873	Carbohydrate metabolism, Organismal system, Human diseases	9101, 9150, 9160	UGP2, galU; galP; UDP-glucose 4-epimerase [EC:5.1.3.2]
NZ_CP022121_1_2904	JBMCGNCK_02980	K23351	Carbohydrate metabolism, Xenobiotics biodegradation and metabolism	9101, 9111	gale, GALE; UDP glucose 4-epimerase [EC:5.1.3.2]
NZ_CP022121_1_1674	JBMCGNCK_01727	K03531	Cellular processes	9140	i-acetylglucosaminyltransferase [EC:2.4.1.16]
NZ_CP022121_1_1673	JBMCGNCK_02019	K03544	Cellular processes	9140	GAP, capU; UDP-glucuronate 4-epimerase [EC:5.1.3.6]
NZ_CP022121_1_1002	JBMCGNCK_02020	K01358	Carbohydrate metabolism, Metabolism of nucleotides	9101, 9102, 9111	rbcM, rbcN; dTDP-4-dehydroaromatic 3-epimerase [EC:5.1.3.13]
NZ_CP022121_1_214	JBMCGNCK_02021	K01371	Carbohydrate metabolism, Nucleotide metabolism	9101, 9102, 9111	E2.2.1.1, IKA, tkB; transketolase [EC:2.2.1.1]
NZ_CP022121_1_1727	JBMCGNCK_02022	K01377	Carbohydrate metabolism, Organismal system, Human diseases	9101, 9150, 9160	PRPS, prsA; ribose-5-phosphate pyrophosphokinase [EC:2.7.6.1]
NZ_CP022121_1_1673	JBMCGNCK_01726	K03590	Carbohydrate metabolism, Xenobiotics biodegradation and metabolism	9101, 9111	deoK; phosphopentomutase [EC:5.4.2.7]
NZ_CP022121_1_1644	JBMCGNCK_02022	K01358	Cellular processes, Glycan biosynthesis and metabolism	9140	PK, pk; pyruvate kinase [EC:2.7.1.40]
NZ_CP022121_1_2820	JBMCGNCK_02023	K01358	Cellular processes, Organismal systems	9140	gdcD, mmDC; glutamoyl-CoA: methyImidolyl-CoA decarboxylase subunit gamma [EC:3.5.1.3]
NZ_CP022121_1_1504	JBMCGNCK_01558	K00335	Energy metabolism	9101, 9102, 9111	ion; ATP-dependent Lon protease [EC:3.24.21.53]
NZ_CP022121_1_1583	JBMCGNCK_01636	K00335	Energy metabolism	9101, 9102, 9111	rpoD; RNA polymerase primary sigma factor [EC:3.21.53]
NZ_CP022121_1_1496	JBMCGNCK_01550	K00335	Energy metabolism	9101, 9102, 9111	ftsZ; cell division protein FtsZ
NZ_CP022121_1_2798	JBMCGNCK_02870	K03338	Energy metabolism	9101, 9102, 9111	cpxA, CLPX; ATP-dependent Cpx protease AtpB-binding subunit CpxA [EC:3.21.53]
NZ_CP022121_1_2795	JBMCGNCK_02867	K03341	Energy metabolism	9101, 9102, 9111	cpxB; cpxA; cell division protein FtsA [EC:3.21.53]
NZ_CP022121_1_2794	JBMCGNCK_02866	K03342	Energy metabolism	9101, 9102, 9111	cpxC, CLPX; ATP-dependent Cpx protease, protease subunit [EC:3.24.21.53]
NZ_CP022121_1_2793	JBMCGNCK_02865	K03343	Energy metabolism	9101, 9102, 9111	icetylglucosaminidylphosphodiacylglycerol N-Acetyl-beta-D-mannosaminyltransferase [EC:2.3.1.20]
NZ_CP022121_1_1364	JBMCGNCK_01044	K04049	Energy metabolism	9101, 9102, 9111	clpP, CLPP; ATP-dependent Cpx protease, protease subunit [EC:3.24.21.53]
NZ_CP022121_1_218	JBMCGNCK_02020	K01358	Energy metabolism	9101, 9102, 9111	fdhB; formate dehydrogenase (cytochrome f420) beta subunit [EC:1.17.9.83.1.98.6]
NZ_CP022121_1_1646	JBMCGNCK_01699	K00125	Energy metabolism	9101, 9102, 9111	acsD; acetyl-CoA dehydrogenase/lyase, CDDH; ACS complex subunit delta [EC:2.1.1.26]
NZ_CP022121_1_2920	JBMCGNCK_02997	K00194	Energy metabolism	9101, 9102, 9111	icsC; acetyl-CoA decarbonylase/synthase, CODH/ACS complex subunit gamma [EC:2.1.2.28]
NZ_CP022121_1_2923	JBMCGNCK_03300	K00197	Energy metabolism	9101, 9102, 9111	nuoC; NADH-quinone oxidoreductase subunit C [EC:1.7.1.2]
NZ_CP022121_1_2801	JBMCGNCK_02873	K00332	Energy metabolism	9101, 9102, 9111	nuoD; NADH-quinone oxidoreductase subunit D [EC:1.7.1.2]
NZ_CP022121_1_2800	JBMCGNCK_02872	K00333	Energy metabolism	9101, 9102, 9111	nuoE; NADH-quinone oxidoreductase subunit E [EC:1.7.1.2]
NZ_CP022121_1_1504	JBMCGNCK_01558	K00335	Energy metabolism	9101, 9102, 9111	nuoF; NADH-quinone oxidoreductase subunit F [EC:1.7.1.2]
NZ_CP022121_1_1583	JBMCGNCK_01636	K00335	Energy metabolism	9101, 9102, 9111	nuoG; NADH-quinone oxidoreductase subunit G [EC:1.7.1.2]
NZ_CP022121_1_1793	JBMCGNCK_01847	K01673	Energy metabolism	9101, 9102, 9111	nuoH; NADH-quinone oxidoreductase subunit H [EC:1.7.1.2]
NZ_CP022121_1_1913	JBMCGNCK_00940	K02110	Energy metabolism	9101, 9102, 9111	nuoI; NADH-quinone oxidoreductase subunit I [EC:1.7.1.2]
NZ_CP022121_1_1916	JBMCGNCK_00943	K02111	Energy metabolism	9101, 9102, 9111	nuoJ; NADH-quinone oxidoreductase subunit J [EC:1.7.1.2]
NZ_CP022121_1_1919	JBMCGNCK_00946	K02112	Energy metabolism	9101, 9102, 9111	nuoM; NADH-quinone oxidoreductase subunit M [EC:1.7.1.2]
NZ_CP022121_1_1915	JBMCGNCK_00942	K02113	Energy metabolism	9101, 9102, 9111	nuoN; NADH-quinone oxidoreductase subunit N [EC:1.7.1.2]
NZ_CP022121_1_1920	JBMCGNCK_00947	K02114	Energy metabolism	9101, 9102, 9111	nuoP; nitrite reductase [cytochrome c552] [EC:1.7.1.2]
NZ_CP022121_1_1364	JBMCGNCK_00406	K03345	Energy metabolism	9101, 9102, 9111	nuoQ; nitrite reductase [cytochrome c] [EC:1.7.1.2]
NZ_CP022121_1_1313	JBMCGNCK_00655	K00584	Energy metabolism	9101, 9102, 9111	nuoR; nitrite reductase [cytochrome b] [EC:1.7.1.2]
NZ_CP022121_1_1643	JBMCGNCK_01697	K01677	Energy metabolism	9101, 9102, 9111	nuoT; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_1642	JBMCGNCK_01696	K03348	Energy metabolism	9101, 9102, 9111	nuoU; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_1641	JBMCGNCK_01694	K03349	Energy metabolism	9101, 9102, 9111	nuoV; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_241	JBMCGNCK_00249	K04480	Energy metabolism	9101, 9102, 9111	tabB; methanol--5-hydroxybenzimidazolylcamobide Co-methyltransferase [EC:2.1.1.391]
NZ_CP022121_1_2796	JBMCGNCK_02868	K05576	Energy metabolism	9101, 9102, 9111	ndHE; NAD(P)H-quinone oxidoreductase subunit 4L [EC:7.1.1.2]
NZ_CP022121_1_1863	JBMCGNCK_00889	K05601	Energy metabolism	9101, 9102, 9111	fhdE, fmfdE; formylmethanofuran dehydrogenase subunit E [EC:2.7.12]
NZ_CP022121_1_2975	JBMCGNCK_03056	K05601	Energy metabolism	9101, 9102, 9111	mttB; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_726	JBMCGNCK_00748	K12161	Energy metabolism	9101, 9102, 9111	mttD; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_3527	JBMCGNCK_03613	K14083	Energy metabolism	9101, 9102, 9111	mttE; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_3572	JBMCGNCK_03660	K14083	Energy metabolism	9101, 9102, 9111	mttF; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_1690	JBMCGNCK_01743	K14083	Energy metabolism	9101, 9102, 9111	mttG; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_491	JBMCGNCK_00503	K14083	Energy metabolism	9101, 9102, 9111	tabD; methanol--5-hydroxybenzimidazolylcamobide Co-methyltransferase [EC:2.1.1.391]
NZ_CP022121_1_3526	JBMCGNCK_03612	K14083	Energy metabolism	9101, 9102, 9111	ndHE; NAD(P)H-quinone oxidoreductase subunit 4L [EC:7.1.1.2]
NZ_CP022121_1_1645	JBMCGNCK_01698	K14127	Energy metabolism	9101, 9102, 9111	mttB; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_2924	JBMCGNCK_03001	K14138	Energy metabolism	9101, 9102, 9111	mttD; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_2919	JBMCGNCK_02996	K15023	Energy metabolism	9101, 9102, 9111	mttE; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_3571	JBMCGNCK_03659	K15023	Energy metabolism	9101, 9102, 9111	mttF; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_1382	JBMCGNCK_01433	K15986	Energy metabolism	9101, 9102, 9111	mttG; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_1746	JBMCGNCK_01799	K16176	Energy metabolism	9101, 9102, 9111	mttH; trimethylamine--corrinoid protein Co-methyltransferase [EC:2.1.1.250]
NZ_CP022121_1_2405	JBMCGNCK_02468	K16179	Energy metabolism	9101, 9102, 9111	mttI; dimethylaminoleucine corrinoid protein
NZ_CP022121_1_1580	JBMCGNCK_01633	K00196	Energy metabolism, Xenobiotics biodegradation and metabolism	9102, 9111	cooF; anaerobic carbon-monoxide dehydrogenase iron-sulfur subunit [EC:1.2.1.47]
NZ_CP022121_1_1585	JBMCGNCK_01638	K00198	Energy metabolism, Xenobiotics biodegradation and metabolism	9102, 9111	cooS, acsA; anaerobic carbon-monoxide dehydrogenase catalytic subunit [EC:1.2.1.47]
NZ_CP022121_1_2925	JBMCGNCK_03002	K00198	Energy metabolism, Xenobiotics biodegradation and metabolism	9102, 9111	cooS, acsA; anaerobic carbon-monoxide dehydrogenase catalytic subunit [EC:1.2.1.47]
NZ_CP022121_1_3205	JBMCGNCK_03285	K02558	Energy metabolism, Xenobiotics biodegradation and metabolism	9102, 9111	nifD; nitrogenase iron protein NifH
NZ_CP022121_1_2097	JBMCGNCK_02161	K02558	Energy metabolism, Xenobiotics biodegradation and metabolism	9102, 9111	nifE; nitrogenase iron protein NifH
NZ_CP022121_1_3616	JBMCGNCK_03704	K11180	Energy metabolism, Xenobiotics biodegradation and metabolism	9102, 9111	dsrA; dissimilatory sulfite reductase alpha subunit [EC:1.8.99.5]
NZ_CP022121_1_2405	JBMCGNCK_02472	K02703	Environmental information processing	9130, 9140	dsrB; dissimilatory sulfite reductase beta subunit [EC:1.8.99.5]
NZ_CP022121_1_121	JBMCGNCK_00112	K07646	Environmental information processing	9130, 9140	nupA; general nucleoside transport system ATP-binding protein
NZ_CP022121_1_122	JBMCGNCK_00123	K07720	Environmental information processing	9130, 9140	nupB; general nucleoside transport system ATP-binding protein
NZ_CP022121_1_3155	JBMCGNCK_03236	K07795	Environmental information processing	9130, 9140	kdpD; potassium-transporting ATPase KdpD subunit [EC:7.2.2.6]
NZ_CP022121_1_1253	JBMCGNCK_01294	K09815	Environmental information processing	9130, 9140	kdpC; potassium-transporting ATPase KdpC subunit [EC:7.2.2.6]
NZ_CP022121_1_1254	JBMCGNCK_01295	K09817	Environmental information processing	9130, 9140	ctbD; cobalt/nickel transport system ATP-binding protein
NZ_CP022121_1_1260	JBMCGNCK_01301	K15598	Environmental information processing	9130, 9140	ctbM; cobalt/nickel transport system permease protein
NZ_CP022121_1_2049	JBMCGNCK_02472	K02703	Environmental information processing	9130, 9140	modA; molybdate transport system substrate-binding protein
NZ_CP022121_1_1932	JBMCGNCK_02111	K18940	Environmental information processing	9130, 9140	bmpA, bmpB, bmpC; basic membrane protein A and related proteins
NZ_CP022121_1_1742	JBMCGNCK_00764	K23535	Environmental information processing	9130, 9140	ddPd; two-component system, OmpF family, sensor histidine kinase NifD subunit [EC:7.13.3]
NZ_CP022121_1_706	JBMCGNCK_00727	K02313	Environmental information processing	9130, 9140	yesN; two-component system, response regulator YesN
NZ_CP022121_1_967	JBMCGNCK_00994	K01996	Environmental information processing, Cellular processes	9130, 9140	tctC; putative tricarboxylic transport membrane protein
NZ_CP022121_1_703	JBMCGNCK_00724	K01999	Environmental information processing, Cellular processes	9130, 9140	znuA; zinc transport system substrate-binding protein
NZ_CP022121_1_962	JBMCGNCK_00899	K01999	Environmental information processing, Cellular processes	9130, 9140	znuC; zinc transport system ATP-binding protein [EC:7.2.2.20]
NZ_CP022121_1_2409	JBMCGNCK_02111	K18940	Environmental information processing	9130, 9140	thiI; putative hydroxymethylpyrimidine transport system substrate-binding protein
NZ_CP022121_1_932	JBMCGNCK_00961	K23060	Environmental information processing	9130, 9140	arsI; arsT; arsC; arginine/lysine/histidine transporter system substrate-binding protein [EC:7.13.3]
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NZ_C022121_1_2567	JBMCGNCK_02632	K00562	Genetic information processing	9120	mmma, tRNA; uridine-2'-sulfurtransferase [EC.2.8.1.13]
NZ_C022121_1_2936	JBMCGNCK_03016	K01866	Genetic information processing	9120	pnpNPT1; polyribonucleotide nucleotidyltransferase [EC.2.7.7.8]
NZ_C022121_1_2509	JBMCGNCK_02573	K01867	Genetic information processing	9120	TARS, tyrosyl-tRNA synthetase [EC.6.1.1.1]
NZ_C022121_1_2733	JBMCGNCK_02800	K01868	Genetic information processing	9120	WARS, trpS; tryptophanyl-tRNA synthetase [EC.6.1.1.2]
NZ_C022121_1_76	JBMCGNCK_00077	K01869	Genetic information processing	9120	TARS, thrs; threonyl-tRNA synthetase [EC.6.1.1.3]
NZ_C022121_1_76	JBMCGNCK_00076	K01869	Genetic information processing	9120	LARS, leucyl-tRNA synthetase [EC.6.1.1.4]
NZ_C022121_1_1785	JBMCGNCK_01789	K01870	Genetic information processing	9120	LARS, leucyl-tRNA synthetase [EC.6.1.1.4]
NZ_C022121_1_2682	JBMCGNCK_02747	K01872	Genetic information processing	9120	IARS, lysyl-tRNA synthetase [EC.6.1.1.5]
NZ_C022121_1_2683	JBMCGNCK_02748	K01872	Genetic information processing	9120	AARS, alaS; alanyl-tRNA synthetase [EC.6.1.1.7]
NZ_C022121_1_213	JBMCGNCK_00215	K01873	Genetic information processing	9120	AARS, alaS; alanyl-tRNA synthetase [EC.6.1.1.7]
NZ_C022121_1_680	JBMCGNCK_00701	K01875	Genetic information processing	9120	SARS, serS; seryl-tRNA synthetase [EC.6.1.1.11]
NZ_C022121_1_2694	JBMCGNCK_02760	K01876	Genetic information processing	9120	DARS2, aspS; aspartyl-tRNA synthetase [EC.6.1.1.12]
NZ_C022121_1_1213	JBMCGNCK_01253	K01878	Genetic information processing	9120	glnQ; glycyl-tRNA synthetase alpha chain [EC.6.1.1.13]
NZ_C022121_1_1214	JBMCGNCK_01254	K01879	Genetic information processing	9120	glyS; glycyl-tRNA synthetase beta chain [EC.6.1.1.14]
NZ_C022121_1_1953	JBMCGNCK_02010	K01881	Genetic information processing	9120	PARS, proS; prolyl-tRNA synthetase [EC.6.1.1.15]
NZ_C022121_1_1091	JBMCGNCK_01127	K01883	Genetic information processing	9120	CARS, hisS; histidyl-tRNA synthetase [EC.6.1.1.16]
NZ_C022121_1_1096	JBMCGNCK_01132	K01886	Genetic information processing	9120	QARS, glnS; glutamyl-tRNA synthetase [EC.6.1.1.18]
NZ_C022121_1_888	JBMCGNCK_00900	K01887	Genetic information processing	9120	RARS, argS; arginyl-tRNA synthetase [EC.6.1.1.19]
NZ_C022121_1_2728	JBMCGNCK_02795	K01889	Genetic information processing	9120	FARSA, phes; phenylalanyl-tRNA synthetase alpha chain [EC.6.1.1.20]
NZ_C022121_1_2727	JBMCGNCK_02794	K01890	Genetic information processing	9120	FABPS, phent; phenylalanyl-tRNA synthetase beta chain [EC.6.1.1.20]
NZ_C022121_1_2695	JBMCGNCK_02761	K01892	Genetic information processing	9120	HARS, hisS; histidyl-tRNA synthetase [EC.6.1.1.21]
NZ_C022121_1_3407	JBMCGNCK_03494	K01972	Genetic information processing	9120	E6.5.1.2, liga, liga; DNA ligase (NAD+) [EC.6.5.1.2]
NZ_C022121_1_1263	JBMCGNCK_01304	K02316	Genetic information processing	9120	dnaG; DNA primase I [EC.2.7.7.101]
NZ_C022121_1_2856	JBMCGNCK_02930	K02335	Genetic information processing	9120	dnanA; DNA polymerase III subunit gamma/beta [EC.2.7.7.7]
NZ_C022121_1_680	JBMCGNCK_00707	K02338	Genetic information processing	9120	dnanA; DNA polymerase I subunit gamma [EC.2.7.7.7]
NZ_C022121_1_500	JBMCGNCK_00512	K02343	Genetic information processing	9120	RSL1; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit A [EC.6.3.5.6]
NZ_C022121_1_2392	JBMCGNCK_02455	K02433	Genetic information processing	9120	RSL1; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B [EC.6.3.5.6]
NZ_C022121_1_3389	JBMCGNCK_03476	K02433	Genetic information processing	9120	T112; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B [EC.6.3.5.6]
NZ_C022121_1_3388	JBMCGNCK_03475	K02434	Genetic information processing	9120	T112; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B [EC.6.3.5.6]
NZ_C022121_1_2393	JBMCGNCK_02456	K02434	Genetic information processing	9120	iATC; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit C [EC.6.3.5.6]
NZ_C022121_1_3390	JBMCGNCK_03477	K02435	Genetic information processing	9120	RP-L1, MPRL1, rplB; large subunit ribosomal protein L1
NZ_C022121_1_1102	JBMCGNCK_01143	K02863	Genetic information processing	9120	RP-L10, MPRL10, rplB; large subunit ribosomal protein L10
NZ_C022121_1_1103	JBMCGNCK_01144	K02864	Genetic information processing	9120	RP-L11, MPRL11, rplB; large subunit ribosomal protein L11
NZ_C022121_1_1101	JBMCGNCK_01142	K02867	Genetic information processing	9120	RP-L13, MPRL13, rplB; large subunit ribosomal protein L13
NZ_C022121_1_1148	JBMCGNCK_01180	K02871	Genetic information processing	9120	RP-L14, MPRL14, rplB; large subunit ribosomal protein L14
NZ_C022121_1_1223	JBMCGNCK_01164	K02874	Genetic information processing	9120	RP-L15, MPRL15, rplB; large subunit ribosomal protein L15
NZ_C022121_1_1132	JBMCGNCK_01173	K02876	Genetic information processing	9120	RP-L16, MPRL16, rplB; large subunit ribosomal protein L16
NZ_C022121_1_1220	JBMCGNCK_01161	K02878	Genetic information processing	9120	RP-L17, MPRL17, rplB; large subunit ribosomal protein L17
NZ_C022121_1_1143	JBMCGNCK_01184	K02879	Genetic information processing	9120	RP-L18, MPRL18, rplB; large subunit ribosomal protein L18
NZ_C022121_1_1229	JBMCGNCK_01170	K02881	Genetic information processing	9120	RP-L2, MPRL2, rplB; large subunit ribosomal protein L2
NZ_C022121_1_1116	JBMCGNCK_01157	K02886	Genetic information processing	9120	RP-L21, MPRL21, rplB; large subunit ribosomal protein L21
NZ_C022121_1_198	JBMCGNCK_00199	K02888	Genetic information processing	9120	RP-L22, MPRL22, rplB; large subunit ribosomal protein L22
NZ_C022121_1_1118	JBMCGNCK_01159	K02890	Genetic information processing	9120	RP-L23, MPRL23, rplB; large subunit ribosomal protein L23
NZ_C022121_1_1115	JBMCGNCK_01156	K02892	Genetic information processing	9120	RP-L24, MPRL24, rplB; large subunit ribosomal protein L24
NZ_C022121_1_1124	JBMCGNCK_01165	K02895	Genetic information processing	9120	RP-L25, rplB; large subunit ribosomal protein L25
NZ_C022121_1_852	JBMCGNCK_00878	K02897	Genetic information processing	9120	RP-L27, MPRL27, rplB; large subunit ribosomal protein L27
NZ_C022121_1_199	JBMCGNCK_00197	K02899	Genetic information processing	9120	RP-L29, rpmD; large subunit ribosomal protein L29
NZ_C022121_1_1221	JBMCGNCK_01162	K02904	Genetic information processing	9120	RP-L3, MPRL3, rplC; large subunit ribosomal protein L3
NZ_C022121_1_1113	JBMCGNCK_01154	K02906	Genetic information processing	9120	RP-L30, MPRL30, rpmD; large subunit ribosomal protein L30
NZ_C022121_1_1331	JBMCGNCK_01172	K02907	Genetic information processing	9120	RP-L31, rpmL; large subunit ribosomal protein L31
NZ_C022121_1_895	JBMCGNCK_00922	K02909	Genetic information processing	9120	RP-L4, MPRL4, rplD; large subunit ribosomal protein L4
NZ_C022121_1_1114	JBMCGNCK_01155	K02936	Genetic information processing	9120	RP-L5, MPRL5, rplE; large subunit ribosomal protein L5
NZ_C022121_1_1125	JBMCGNCK_01166	K02936	Genetic information processing	9120	RP-L6, MPRL6, rplF; large subunit ribosomal protein L6
NZ_C022121_1_1128	JBMCGNCK_01169	K02933	Genetic information processing	9120	RP-L7, MPRL7, rplH; large subunit ribosomal protein L7/L12
NZ_C022121_1_1104	JBMCGNCK_01145	K02935	Genetic information processing	9120	RP-L9, MPRL9, rplJ; large subunit ribosomal protein L9
NZ_C022121_1_781	JBMCGNCK_00809	K02939	Genetic information processing	9120	RP-S10, MPRL10, rpsJ; small subunit ribosomal protein S10
NZ_C022121_1_1112	JBMCGNCK_01153	K02946	Genetic information processing	9120	RP-S11, MPRL11, rpsK; small subunit ribosomal protein S11
NZ_C022121_1_1140	JBMCGNCK_01181	K02948	Genetic information processing	9120	RP-S12, MPRL12, rpsL; small subunit ribosomal protein S12
NZ_C022121_1_1108	JBMCGNCK_01149	K02950	Genetic information processing	9120	RP-S13, MPRL13, rpsM; small subunit ribosomal protein S13
NZ_C022121_1_1139	JBMCGNCK_01180	K02952	Genetic information processing	9120	RP-S15, MPRL15, rpsO; small subunit ribosomal protein S15
NZ_C022121_1_2566	JBMCGNCK_02631	K02956	Genetic information processing	9120	RP-S16, MPRL16, rpsP; small subunit ribosomal protein S16
NZ_C022121_1_1385	JBMCGNCK_01436	K02959	Genetic information processing	9120	RP-S17, MPRL17, rpsQ; small subunit ribosomal protein S17
NZ_C022121_1_1122	JBMCGNCK_01163	K02961	Genetic information processing	9120	RP-S19, rpmS; small subunit ribosomal protein S19
NZ_C022121_1_785	JBMCGNCK_00806	K02963	Genetic information processing	9120	RP-S2, MPRL2, rpsR; small subunit ribosomal protein S2
NZ_C022121_1_1117	JBMCGNCK_01158	K02965	Genetic information processing	9120	RP-S20, rpmT; small subunit ribosomal protein S20
NZ_C022121_1_1941	JBMCGNCK_01994	K02967	Genetic information processing	9120	RP-S21, MPRL21, rpsU; small subunit ribosomal protein S21
NZ_C022121_1_76	JBMCGNCK_00072	K02968	Genetic information processing	9120	RP-S3, rpsC; small subunit ribosomal protein S3
NZ_C022121_1_1141	JBMCGNCK_01182	K02986	Genetic information processing	9120	RP-S4, rpsD; small subunit ribosomal protein S4
NZ_C022121_1_1330	JBMCGNCK_01171	K02988	Genetic information processing	9120	RP-S5, MPRL5; small subunit ribosomal protein S5
NZ_C022121_1_781	JBMCGNCK_00804	K02990	Genetic information processing	9120	RP-S6, MPRL6; rpsF; small subunit ribosomal protein S6
NZ_C022121_1_2587	JBMCGNCK_02652	K02992	Genetic information processing	9120	RP-S7, MPRL7; rpsG; small subunit ribosomal protein S7
NZ_C022121_1_2461	JBMCGNCK_02525	K02962	Genetic information processing	9120	RP-S8, rpsH; small subunit ribosomal protein S8
NZ_C022121_1_892	JBMCGNCK_00919	K02968	Genetic information processing	9120	RP-S9, MPRL9; rpsI; small subunit ribosomal protein S9
NZ_C022121_1_2106	JBMCGNCK_00102	K02970	Genetic information processing	9120	rpoA; DNA-directed RNA polymerase subunit alpha [EC.2.7.7.6]
NZ_C022121_1_2106	JBMCGNCK_01046	K02976	Genetic information processing	9120	rpoB; DNA-directed RNA polymerase subunit beta [EC.2.7.7.6]
NZ_C022121_1_751	JBMCGNCK_00773	K03100	Genetic information processing	9120	lepB; signal peptide I [EC.3.4.21.89]
NZ_C022121_1_781	JBMCGNCK_00805	K03111	Genetic information processing	9120	ssb; single-strand DNA-binding protein
NZ_C022121_1_2587	JBMCGNCK_02653	K03153	Genetic information processing	9120	recA; recombination protein RecA
NZ_C022121_1_2461	JBMCGNCK_02525	K03162	Genetic information processing	9120	xseB; exodeoxyribonuclease VI small subunit [EC.3.1.1.16]
NZ_C022121_1_892	JBMCGNCK_00102	K03170	Genetic information processing	9120	rho; transcription termination factor Rho
NZ_C022121_1_2106	JBMCGNCK_02760	K03210	Genetic information processing	9120	uvrA; excinuclease ABC subunit A
NZ_C022121_1_1106	JBMCGNCK_01147	K03046	Genetic information processing	9120	tusA, sirA; RNA 2'-riboflavine synthetizing protein A [EC.2.8.1.-]
NZ_C022121_1_1106	JBMCGNCK_00773	K03100	Genetic information processing	9120	KARS, lysS; lysyl-tRNA synthetase, class II [EC.6.1.1.6]
NZ_C022121_1_1106	JBMCGNCK_03675	K03676	Genetic information processing	9120	deadA; chtD; ATP-dependent RNA helicase DeadA [EC.3.6.4.13]
NZ_C022121_1_3588	JBMCGNCK_02674	K03074	Genetic information processing	9120	RP-L7A, rpGL8; large subunit ribosomal protein L7A
NZ_C022121_1_1107	JBMCGNCK_01148	K03750	Genetic information processing	9120	rnr; rnc; ribonuclease I [EC.3.1..-1]
NZ_C022121_1_350	JBMCGNCK_00358	K12573	Genetic information processing	9120	HPG; molecular chaperone HPG
NZ_C022121_1_2577	JBMCGNCK_02642	K12574	Genetic information processing	9120	EARS, rRNA; ribonuclease III EC.3.26.3]
NZ_C022121_1_1149	JBMCGNCK_01424	K03110	Genetic information processing	9120	mrNA, CNTR; GTP 3'-cyclic [EC.4.19.99.22]
NZ_C022121_1_1373	JBMCGNCK_00447	K03110	Genetic information processing	9120	iscS, NFS1; cysteine desulfurase [EC.2.8.1.7]
NZ_C022121_1_3565	JBMCGNCK_03653	K04487	Genetic information processing	9120	selA; t-Ser-Lys(Amide) Ser leucinimuramoyltransferase [EC.2.9.1.1]
NZ_C022121_1_703	JBMCGNCK_00722	K01042	Genetic information processing	9120	MARS, metG; methionyl-tRNA synthetase [EC.6.1.1.10]
NZ_C022121_1_467	JBMCGNCK_00478	K01874	Genetic information processing	9120	groEL, HSPD1; chaperonin GroEL
NZ_C022121_1_871	JBMCGNCK_00899	K04043	Genetic information processing	9120	groES, HSPD2; HSP20; molecular chaperone GroES
NZ_C022121_1_1366	JBMCGNCK_00601	K04043	Genetic information processing	9120	groEL; molecular chaperone DnaK
NZ_C022121_1_1312	JBMCGNCK_01363	K01885	Genetic information processing	9120	groES; HSP20; molecular chaperone DnaK
NZ_C022121_1_3413	JBMCGNCK_03500	K03639	Genetic information processing	9120	groEL, HSPD1; molecular chaperone DnaK
NZ_C022121_1_3565	JBMCGNCK_03653	K04487	Genetic information processing	9120	groES; HSP20; molecular chaperone DnaK
NZ_C022121_1_703	JBMCGNCK_00722	K01042	Genetic information processing	9120	groEL; molecular chaperone DnaK
NZ_C022121_1_467	JBMCGNCK_00478	K01874	Genetic information processing	9120	igT_U_V; polyisoprenyl-teichoic acid-peptidoglycan teichoic acid transferase [EC.2.7.8]
NZ_C022121_1_871	JBMCGNCK_00899	K04043	Genetic information processing	9120	igT_U_V; polyisoprenyl-teichoic acid-peptidoglycan teichoic acid transferase [EC.2.7.8]
NZ_C022121_1_1366	JBMCGNCK_00601	K04043	Genetic information processing	9120	murC; UDP-N-acetyl muramoyl-alanine ligase [EC.6.3.2.8]
NZ_C022121_1_1312	JBMCGNCK_01363	K01885	Genetic information processing	9120	A, ddc; serine-type D-Ala-D-Ala carboxypeptidase [penicillin-binding protein 5] [EC.2.1.1.36.7]
NZ_C022121_1_3413	JBMCGNCK_03500	K03639	Genetic information processing	9120	spvD; stage V sporulation protein D (sporulation-specific penicillin-binding protein)
NZ_C022121_1_3565	JBMCGNCK_03653	K04487	Genetic information processing	9120	fmhB; peptidoglycan pentaglycine teichoic acid transferase [the first glycine] [EC.2.3.2.1.3]
NZ_C022121_1_703	JBMCGNCK_00722	K01042	Genetic information processing	9120	wbjC; UDP-2-acetamido-2,6-beta-D-alabio-hex-4-ose reductase [EC.1.1.1.36.7]
NZ_C022121_1_2515	JBMCGNCK_02579	K07258	Glycan biosynthesis and metabolism, Human diseases	9107	mrca; penicillin-binding protein 1A [EC.2.4.1.29.3.14.6.14]
NZ_C022121_1_1664	JBMCGNCK_01717	K03884	Glycan biosynthesis and metabolism	9107	mrdA; penicillin-binding protein 2 [EC.2.4.16.4]
NZ_C022121_1_1144	JBMCGNCK_00911	K11693	Glycan biosynthesis and metabolism	9107	amICB, N-acetylumuramoyl-L-alanine amidase [EC.3.5.1.28]
NZ_C022121_1_2757	JBMCGNCK_02825	K19068	Glycan biosynthesis and metabolism	9107	amICB, N-acetylumuramoyl-L-alanine amidase [EC.3.5.1.28]
NZ_C022121_1_2721	JBMCGNCK_02788	K05366	Glycan biosynthesis and metabolism	9107	amICB, N-acetylumuramoyl-L-alanine amidase [EC.3.5.1.28]
NZ_C022121_1_204	JBMCGNCK_02020	K05515	Glycan biosynthesis and metabolism, Human diseases	9107	amICB, N-acetylumuramoyl-L-alanine amidase [EC.3.5.1.28]
NZ_C022121_1_204	JBMCGNCK_01148	K01448	Human diseases	9107	blai; Blai family transcriptional regulator, penicilline repressor
NZ_C022121_1_204	JBMCGNCK_01148	K01448	Human diseases	9107	Human diseases
NZ_C022121_1_204	JBMCGNCK_01347	K02171	Human diseases	9107	Human diseases

NZ_CP022121_1_66	JBMCGNCK_00067	K03596	Human diseases	9160	lepA; GTP-binding protein LepA	463
NZ_CP022121_1_1233	JBMCGNCK_01264	K07755	Human diseases	9160	AS3MT; arsenite methyltransferase [EC.2.1.1.137]	107
NZ_CP022121_1_1775	JBMCGNCK_01829	K14475	Human diseases	9160	ICP; inhibitor of cysteine peptidase	57
NZ_CP022121_1_2548	JBMCGNCK_02612	K00057	Lipid metabolism	9103	gpsA; glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC.1.1.1.94]	189
NZ_CP022121_1_1361	JBMCGNCK_01412	K00645	Lipid metabolism	9103	fabD; MCAT; MCT1; [acyl-carrier-protein] 5-monoyltransferase [EC.2.3.1.139]	183
NZ_CP022121_1_1359	JBMCGNCK_01408	K00648	Lipid metabolism	9103	fabH; 3-oxacyl-[acyl-carrier-protein] synthase III [EC.2.3.1.180]	212
NZ_CP022121_1_3047	JBMCGNCK_03128	K00648	Lipid metabolism	9103	fabH; 3-oxacyl-[acyl-carrier-protein] synthase III [EC.2.3.1.180]	174
NZ_CP022121_1_3046	JBMCGNCK_03127	K00648	Lipid metabolism	9103	fabH; 3-oxacyl-[acyl-carrier-protein] synthase III [EC.2.3.1.180]	133
NZ_CP022121_1_2902	JBMCGNCK_02978	K01613	Lipid metabolism	9103	psd; PISD; phosphatidylserine decarboxylase [EC.4.1.1.65]	137
NZ_CP022121_1_1363	JBMCGNCK_01414	K02078	Lipid metabolism	9103	acPp; acyl carrier protein	45
NZ_CP022121_1_1360	JBMCGNCK_01411	K02371	Lipid metabolism	9103	fabK; enoyl-[acyl-carrier protein] reductase II [EC.1.3.1.9]	194
NZ_CP022121_1_1358	JBMCGNCK_01409	K03621	Lipid metabolism	9103	pIsk; phosphate acyltransferase [EC.2.3.1.274]	173
NZ_CP022121_1_270	JBMCGNCK_00278	K02331	Metabolism of cofactors and vitamins	9108	PPOX; hemY; protoporphyrinogen/coprotoporphyrin III oxidase [EC.1.3.3.4.13.3.15]	184
NZ_CP022121_1_1901	JBMCGNCK_01958	K03233	Metabolism of cofactors and vitamins	9108	NNT; H+-translocating NAD(P) transhydrogenase [EC.1.6.1.2.7.1.1]	82
NZ_CP022121_1_1899	JBMCGNCK_01956	K03234	Metabolism of cofactors and vitamins	9108	pntA; H+-translocating (NAD(P) transhydrogenase subunit alpha [EC.1.6.1.2.7.1.1]	259
NZ_CP022121_1_1318	JBMCGNCK_01369	K07633	Metabolism of cofactors and vitamins	9108	pncB; NAPRT1; nicotinate phosphoribosyltransferase [EC.6.3.4.21]	320
NZ_CP022121_1_1311	JBMCGNCK_01362	K00768	Metabolism of cofactors and vitamins	9108	obuB; cobT; nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase [232
NZ_CP022121_1_1893	JBMCGNCK_01950	K00794	Metabolism of cofactors and vitamins	9108	ribB; RIBB; 6,7-dimethyl-8-ribityllumazine synthase [EC.2.5.1.78]	157
NZ_CP022121_1_1048	JBMCGNCK_01078	K00796	Metabolism of cofactors and vitamins	9108	fopA; dihydropyroate synthase [EC.2.5.1.15]	214
NZ_CP022121_1_2466	JBMCGNCK_02530	K00858	Metabolism of cofactors and vitamins	9108	ppNk; NADK; NAD+ kinase [EC.2.7.1.23]	138
NZ_CP022121_1_286	JBMCGNCK_02355	K00868	Metabolism of cofactors and vitamins	9108	pdpx; pdxV; pyridoxine kinase [EC.2.7.1.35]	141
NZ_CP022121_1_1050	JBMCGNCK_01080	K00950	Metabolism of cofactors and vitamins	9108	oik; 2-amino-4-hydroxy-6-hydroxymethylhydriodopteridine diphosphokinase [EC.2.7.6.7]	102
NZ_CP022121_1_2897	JBMCGNCK_02973	K01495	Metabolism of cofactors and vitamins	9108	GCH1; folt; GTP cyclohydrolase IA [EC.3.5.4.16]	178
NZ_CP022121_1_272	JBMCGNCK_00280	K01599	Metabolism of cofactors and vitamins	9108	hemE; UROD; uroporphyrinogen decarboxylase [EC.4.1.1.37]	291
NZ_CP022121_1_1863	JBMCGNCK_01920	K01599	Metabolism of cofactors and vitamins	9108	hemE; UROD; uroporphyrinogen decarboxylase [EC.4.1.1.37]	207
NZ_CP022121_1_2404	JBMCGNCK_02467	K01599	Metabolism of cofactors and vitamins	9108	hemE; UROD; uroporphyrinogen decarboxylase [EC.4.1.1.37]	105
NZ_CP022121_1_3232	JBMCGNCK_03313	K01599	Metabolism of cofactors and vitamins	9108	hemE; UROD; uroporphyrinogen decarboxylase [EC.4.1.1.37]	68
NZ_CP022121_1_641	JBMCGNCK_00656	K01599	Metabolism of cofactors and vitamins	9108	hemE; UROD; uroporphyrinogen decarboxylase [EC.4.1.1.37]	25
NZ_CP022121_1_1865	JBMCGNCK_01922	K01599	Metabolism of cofactors and vitamins	9108	hemE; UROD; uroporphyrinogen decarboxylase [EC.4.1.1.37]	24
NZ_CP022121_1_2016	JBMCGNCK_02075	K01599	Metabolism of cofactors and vitamins	9108	hemE; UROD; uroporphyrinogen decarboxylase [EC.4.1.1.37]	18
NZ_CP022121_1_643	JBMCGNCK_00658	K01599	Metabolism of cofactors and vitamins	9108	B; 7,8-dihydroxyopterin aldolase/epimerase/oxygenase [EC.4.1.2.25.5.1.99.8.1.13.11]	55
NZ_CP022121_1_1049	JBMCGNCK_01079	K01633	Metabolism of cofactors and vitamins	9108	hemB; ALAD; porphobilinogen synthase [EC.2.5.1.61]	319
NZ_CP022121_1_3056	JBMCGNCK_03137	K01698	Metabolism of cofactors and vitamins	9108	hemC; HMBS; hydroxymethylbilane synthase [EC.2.5.1.61]	240
NZ_CP022121_1_3057	JBMCGNCK_03138	K01749	Metabolism of cofactors and vitamins	9108	hemL; glutamate-1-semialdehyde 2,1-aminomutase [EC.S.3.4.8]	297
NZ_CP022121_1_3054	JBMCGNCK_03135	K01845	Metabolism of cofactors and vitamins	9108	E6.3.5.1, NADSYN1, QNS1; NAD; synthase [glutamine-hydrolysing] [EC.6.3.5.1]	363
NZ_CP022121_1_1188	JBMCGNCK_01228	K01950	Metabolism of cofactors and vitamins	9108	cblD; cobalt-precorrin-58 (C1)-methyltransferase [EC.2.1.1.195]	225
NZ_CP022121_1_3509	JBMCGNCK_03595	K02188	Metabolism of cofactors and vitamins	9108	cblI; cobalt-precorrin-68 (C1)-methyltransferase [EC.2.7.1.12]	39
NZ_CP022121_1_3502	JBMCGNCK_03588	K02189	Metabolism of cofactors and vitamins	9108	cblT; cobalt-precorrin-68 (C1)-methyltransferase [EC.2.1.1.196]	71
NZ_CP022121_1_3507	JBMCGNCK_03593	K02191	Metabolism of cofactors and vitamins	9108	cobB; cbiA; cytochrome c aa 3-clamide synthase [EC.6.3.5.6.9.35.11]	206
NZ_CP022121_1_3511	JBMCGNCK_03597	K02224	Metabolism of cofactors and vitamins	9108	cobC; phbB; alpha-ribosyl phosphatase [EC.3.1.3.73]	76
NZ_CP022121_1_3515	JBMCGNCK_03601	K02226	Metabolism of cofactors and vitamins	9108	cobB; cobD; adenosylcobamide-phosphate synthase [EC.6.3.1.10]	172
NZ_CP022121_1_3513	JBMCGNCK_03599	K02227	Metabolism of cofactors and vitamins	9108	cobS; adenosylcobamide acyl transferase [EC.6.3.5.10]	280
NZ_CP022121_1_3516	JBMCGNCK_03602	K02231	Metabolism of cofactors and vitamins	9108	hemA; glutamyl-tRNA reductase [EC.1.2.1.70]	151
NZ_CP022121_1_3514	JBMCGNCK_03600	K02232	Metabolism of cofactors and vitamins	9108	cobI; cobB; cobalt-factor-2 C20-methyltransferase [EC.2.1.1.130 2.1.1.151]	69
NZ_CP022121_1_3515	JBMCGNCK_03622	K02492	Metabolism of cofactors and vitamins	9108	cblE; cobal-precorrin-7 (C5)-methyltransferase [EC.2.1.1.289]	109
NZ_CP022121_1_3501	JBMCGNCK_03587	K02394	Metabolism of cofactors and vitamins	9108	coxB; type III pantethenate kinase [EC.2.7.1.33]	238
NZ_CP022121_1_3508	JBMCGNCK_03590	K02399	Metabolism of cofactors and vitamins	9108	moeA; molybdoferredoxin molybdate transferase [EC.2.10.1.1]	183
NZ_CP022121_1_1060	JBMCGNCK_01090	K03525	Metabolism of cofactors and vitamins	9108	siR; siroheme chlorin ferrocetolate [EC.4.99.1.4]	14
NZ_CP022121_1_3414	JBMCGNCK_03501	K03750	Metabolism of cofactors and vitamins	9108	lipA; pli; lipL; lipote—protein ligase [EC.6.3.1.20]	169
NZ_CP022121_1_2536	JBMCGNCK_03623	K03794	Metabolism of cofactors and vitamins	9108	cobD; threonine-phosphate decarboxylase [EC.4.1.1.81]	118
NZ_CP022121_1_2522	JBMCGNCK_02586	K03900	Metabolism of cofactors and vitamins	9108	cobK; cbpB; precorrin-4-C6-ubiquinone reductase [EC.1.3.1.54]	83
NZ_CP022121_1_2512	JBMCGNCK_01741	K07141	Metabolism of cofactors and vitamins	9108	coxB; cobal-precorrin-4-C6-ubiquinone reductase [EC.2.1.1.130 2.1.1.151]	163
NZ_CP022121_1_3600	JBMCGNCK_03586	K08260	Metabolism of cofactors and vitamins	9108	bM; cbfB; precorrin-4/C6-ubiquinone-4-C11-methyltransferase [EC.2.1.1.133 2.1.1.2]	160
NZ_CP022121_1_3501	JBMCGNCK_03587	K08269	Metabolism of cofactors and vitamins	9108	bM; cbfB; precorrin-4/C6-ubiquinone-4-C11-methyltransferase [EC.2.1.1.133 2.1.1.2]	82
NZ_CP022121_1_3504	JBMCGNCK_03590	K08276	Metabolism of cofactors and vitamins	9108	cobB; cbpB; precorrin-4/C6-ubiquinone-4-C11-methyltransferase [EC.2.1.1.133 2.1.1.2]	82
NZ_CP022121_1_1353	JBMCGNCK_01588	K08536	Metabolism of cofactors and vitamins	9108	cobD; cbpD; 2-hydroxybenzimidazole methyltransferase [EC.5.4.9.9.15.4.9.60]	124
NZ_CP022121_1_3510	JBMCGNCK_03596	K08602	Metabolism of cofactors and vitamins	9108	hydoperpterin 6-yl-methyl-4-(beta-D-ribofuranosyl)aminoenzene 5'-phosphate synthetase [EC.2.7.7.7.6]	175
NZ_CP022121_1_461	JBMCGNCK_00472	K06897	Metabolism of cofactors and vitamins	9108	mcA; molybdenum cofactor cyclodydrolease [EC.3.5.1.90]	36
NZ_CP022121_1_1741	JBMCGNCK_01974	K07141	Metabolism of cofactors and vitamins	9108	cobZ; 2-carboxy-7-deazaguanine reductase [EC.1.7.1.13]	103
NZ_CP022121_1_3594	JBMCGNCK_03682	K08260	Metabolism of cofactors and vitamins	9108	queF; 7-carboxy-7-deazaguanine synthase [EC.4.3.99.3]	103
NZ_CP022121_1_2771	JBMCGNCK_02839	K09457	Metabolism of cofactors and vitamins	9108	folC; dihydروfolic synthase / folylpolyglutamate synthase [EC.6.3.2.12 6.3.2.17]	214
NZ_CP022121_1_2889	JBMCGNCK_02974	K10026	Metabolism of cofactors and vitamins	9108	cobA-hemD; uroporphyrin III methyltransferase / synthase [EC.2.1.1.107 4.2.1.7.5]	272
NZ_CP022121_1_212	JBMCGNCK_00214	K10174	Metabolism of cofactors and vitamins	9108	,4-dihydroxy-2-butanoate 4-phosphate synthase / GTP cyclohydrolase II [EC.4.1.99.12]	354
NZ_CP022121_1_3533	JBMCGNCK_03620	K10352	Metabolism of cofactors and vitamins	9108	cobA; btuB; cobT(l)alanin adenyltransferase [EC.2.5.1.17]	85
NZ_CP022121_1_1891	JBMCGNCK_01948	K10452	Metabolism of cofactors and vitamins	9108	bzaA; B; 5-hydroxybenzimidazole synthase [EC.4.1.99.23]	403
NZ_CP022121_1_2522	JBMCGNCK_02586	K10921	Metabolism of cofactors and vitamins	9108	bzaA; B; 5-hydroxybenzimidazole synthase [EC.4.1.99.23]	313
NZ_CP022121_1_1902	JBMCGNCK_00782	K10926	Metabolism of cofactors and vitamins	9108	btuB; 5-methoxybenzimidazole methyltransferase	262
NZ_CP022121_1_759	JBMCGNCK_00781	K2465	Metabolism of cofactors and vitamins	9108	metF, MTHFR; methylenetetrahydrofolate reductase (NAFH) [EC.1.5.1.54]	353
NZ_CP022121_1_2918	JBMCGNCK_02995	K02079	Metabolism of cofactors and vitamins	9108	trxB, TRR; thioiredoxin reductase (NADPH) [EC.1.8.1.9]	209
NZ_CP022121_1_3166	JBMCGNCK_03246	K01491	Metabolism of cofactors and vitamins	9108	trxB, TRR; thioiredoxin reductase (NADPH) [EC.1.8.1.9]	204
NZ_CP022121_1_3167	JBMCGNCK_03247	K01500	Metabolism of cofactors and vitamins	9108	trxB, TRR; thioiredoxin reductase (NADPH) [EC.1.8.1.9]	166
NZ_CP022121_1_2364	JBMCGNCK_02433	K02087	Metabolism of cofactors and vitamins	9108	selD; SEPHS; selenide water dikinase [EC.2.7.9.3]	119
NZ_CP022121_1_2478	JBMCGNCK_02542	K01515	Metabolism of cofactors and vitamins	9108	tpa; taurine-pyruvate aminotransferase [EC.2.6.1.77]	268
NZ_CP022121_1_2894	JBMCGNCK_02970	K03787	Metabolism of cofactors and vitamins	9108	tsuE; erotate phosphoribosyltransferase [EC.2.4.2.10]	148
NZ_CP022121_1_3465	JBMCGNCK_03551	K06002	Metabolism of cofactors and vitamins	9108	polyphosphatase / gamma-5'-phosphate nucleotidyl transferase [EC.3.6.3.195]	195
NZ_CP022121_1_1236	JBMCGNCK_01277	K03844	Metabolism of other amino acids	9108	purE; 5'-carboxyaminolinabutide ribonucleotide mutase [EC.5.4.99.18]	105
NZ_CP022121_1_424	JBMCGNCK_02684	K01591	Metabolism of other amino acids	9108	pyrF; orotidine 5'-phosphate decarboxylase [EC.4.1.1.23]	171
NZ_CP022121_1_1790	JBMCGNCK_02600	K09903	Metabolism of other amino acids	9108	purC; phosphoribosylaminodiazole-succinocarboxamide synthase [EC.6.3.2.6]	229
NZ_CP022121_1_1943	JBMCGNCK_01748	K21636	Metabolism of other amino acids	9108	purC; phosphoribosylaminodiazole-succinocarboxamide synthase [EC.6.3.2.6]	132
NZ_CP022121_1_1695	JBMCGNCK_00985	K01748	Metabolism of other amino acids	9108	purM; phosphoribosylformylglycaminidine cyclo-ligase [EC.6.3.3.1]	208
NZ_CP022121_1_1693	JBMCGNCK_01068	K01912	Metabolism of other amino acids	9108	pyrG; CTPS; CTP synthase [EC.6.3.4.2]	404
NZ_CP022121_1_1038	JBMCGNCK_01464	K01951	Metabolism of other amino acids	9108	PFAS; phosphoribosylamine—glycine ligase [EC.6.3.5.3]	852
NZ_CP022121_1_1411	JBMCGNCK_01152	K02358	Metabolism of other amino acids	9108	pyrD; dihydroorotate dehydrogenase electron transfer subunit	113
NZ_CP022121_1_2598	JBMCGNCK_02663	K00088	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	turP; triphosphate reductase (formate) [EC.1.1.98.6]	527
NZ_CP022121_1_2485	JBMCGNCK_02549	K00756	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	ndk, NME; nucleoside-diphosphate kinase [EC.2.7.4.6]	132
NZ_CP022121_1_848	JBMCGNCK_00874	K00760	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	guaA, GMPS, GMP synthase (glutamine-hydrolysing) [EC.6.3.5.2]	344
NZ_CP022121_1_848	JBMCGNCK_01097	K01923	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	IMPDH, guAB; IMP dehydrogenase [EC.1.1.20.5]	369
NZ_CP022121_1_1067	JBMCGNCK_03553	K01933	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	hprT, hpt, HPRT1; hypoxanthine phosphoribosyltransferase [EC.2.4.2.8]	130
NZ_CP022121_1_3467	JBMCGNCK_02531	K01945	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	ukd, UCK; uridine kinase [EC.2.7.1.48]	265
NZ_CP022121_1_882	JBMCGNCK_00909	K01937	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	cdd, CDA; cytidine deaminase [EC.3.5.4.5]	43
NZ_CP022121_1_3464	JBMCGNCK_03550	K01945	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	guaA, GMPS, GMP synthase (glutamine-hydrolysing) [EC.6.3.5.2]	295
NZ_CP022121_1_3396	JBMCGNCK_03483	K01952	Nucleotide metabolism	9104	ide metabolism, Environmental information processing, Xenobiotics biodegradation and metabolism	1
NZ_CP022121_1_1788	JBMCGNCK_01842	K02823	Nucleotide metabolism	9104	ide metabolism, Protein families; metabolism, Xenobiotics biodegradation and metabolism	1
NZ_CP022121_1_1943	JBMCGNCK_02000	K09903	Nucleotide metabolism	9104	ide metabolism, Xenobiotics biodegradation and metabolism	1
NZ_CP022121_1_1695	JBMCGNCK_01748	K21636	Nucleotide metabolism	9104	ide metabolism, Xenobiotics biodegradation and metabolism	1
NZ_CP022121_1_1038	JBMCGNCK_01068	K00940	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	Organismal systems, Human diseases	1
NZ_CP022121_1_1411	JBMCGNCK_01152	K01951	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	Organismal systems	1
NZ_CP022121_1_2598	JBMCGNCK_02663	K00088	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	Organismal systems	1
NZ_CP022121_1_2485	JBMCGNCK_02549	K00756	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	Organismal systems	1
NZ_CP022121_1_848	JBMCGNCK_00874	K00760	Nucleotide metabolism, Xenobiotics biodegradation and metabolism	9104	Organismal systems	1
NZ_CP022121_1_848	JBMCGNCK_03021	K02713	Nucle			

NZ_CP022121_1_211	JBMCGNCK_00213	K01926	Protein families: genetic information and processing	9182	rex; redox-sensing transcriptional repressor	138
NZ_CP022121_1_110	JBMCGNCK_01151	K02355	Protein families: genetic information and processing	9182	fusA, GFM; EFG: elongation factor G	558
NZ_CP022121_1_2892	JBMCGNCK_02968	K02355	Protein families: genetic information and processing	9182	fusA, GFM; EFG: elongation factor G	426
NZ_CP022121_1_2636	JBMCGNCK_02701	K02356	Protein families: genetic information and processing	9182	efp: elongation factor P	138
NZ_CP022121_1_1942	JBMCGNCK_01999	K02357	Protein families: genetic information and processing	9182	tsf, TSM; elongation factor Ts	200
NZ_CPO22121_1_682	JBMCGNCK_00207	K02369	Protein families: genetic information and processing	9182	gyrA; DNA gyrase subunit A [EC:5.6.2.2]	561
NZ_CPO22121_1_683	JBMCGNCK_00704	K02470	Protein families: genetic information and processing	9182	gyrB; DNA gyrase subunit B [EC:5.6.2.2]	465
NZ_CPO22121_1_1008	JBMCGNCK_01036	K02499	Protein families: genetic information and processing	9182	yabN; tetrapyrrole methylase family protein / MaxG family protein	89
NZ_CPO22121_1_1137	JBMCGNCK_01178	K02518	Protein families: genetic information and processing	9182	infA; translation initiation factor IF-1	66
NZ_CPO22121_1_2561	JBMCGNCK_02626	K02519	Protein families: genetic information and processing	9182	infB, MTF2; translation initiation factor IF-2	384
NZ_CPO22121_1_2732	JBMCGNCK_02799	K02520	Protein families: genetic information and processing	9182	infC, MTF3; translation initiation factor IF-3	101
NZ_CPO22121_1_2558	JBMCGNCK_02632	K02600	Protein families: genetic information and processing	9182	nusA; transcription termination antitermination protein NusA	238
NZ_CPO22121_1_200	JBMCGNCK_01441	K02601	Protein families: genetic information and processing	9182	nusG; transcription termination/antitermination protein NusG	156
NZ_CPO22121_1_58	JBMCGNCK_00059	K02687	Protein families: genetic information and processing	9182	prmA; ribosomal protein L11 methyletransferase [EC:2.1.1.-]	144
NZ_CPO22121_1_2562	JBMCGNCK_02627	K02834	Protein families: genetic information and processing	9182	rfaB; ribosome-binding factor A	57
NZ_CPO22121_1_896	JBMCGNCK_00923	K02835	Protein families: genetic information and processing	9182	prfA, MTRF1, MRF1; peptide chain release factor 1	261
NZ_CPO22121_1_1944	JBMCGNCK_02001	K02838	Protein families: genetic information and processing	9182	fr, MRFF, RRF; ribosome recycling factor	132
NZ_CPO22121_1_1933	JBMCGNCK_01990	K03168	Protein families: genetic information and processing	9182	topA; DNA topoisomerase I [EC:5.6.2.1]	424
NZ_CPO22121_1_1094	JBMCGNCK_01130	K03218	Protein families: genetic information and processing	9182	rlmB; 23S rRNA (guanosine2512'-O)-methyltransferase [EC:2.1.1.185]	94
NZ_CPO22121_1_2729	JBMCGNCK_02796	K03437	Protein families: genetic information and processing	9182	spoU; RNA methyltransferase, TrmT family	124
NZ_CPO22121_1_695	JBMCGNCK_00716	K03497	Protein families: genetic information and processing	9182	parB, spoU; ParB family transcriptional regulator, chromosome partitioning protein	123
NZ_CPO22121_1_1009	JBMCGNCK_01037	K03530	Protein families: genetic information and processing	9182	hubP; DNA-binding protein HU-beta	64
NZ_CPO22121_1_209	JBMCGNCK_00211	K03569	Protein families: genetic information and processing	9182	mreB; rod shape-determining protein MreB and related proteins	256
NZ_CPO22121_1_927	JBMCGNCK_00954	K03569	Protein families: genetic information and processing	9182	mreB; rod shape-determining protein MreB and related proteins	253
NZ_CPO22121_1_1203	JBMCGNCK_01243	K03595	Protein families: genetic information and processing	9182	era, ERA1; GTase	176
NZ_CPO22121_1_204	JBMCGNCK_00206	K03609	Protein families: genetic information and processing	9182	minD; septum site-determining protein MinD	202
NZ_CPO22121_1_1065	JBMCGNCK_01095	K03624	Protein families: genetic information and processing	9182	greA; transcription elongation factor GreA	106
NZ_CPO22121_1_2469	JBMCGNCK_02533	K03631	Protein families: genetic information and processing	9182	recN; DNA repair protein RecN (Recombination protein N)	144
NZ_CPO22121_1_1937	JBMCGNCK_01994	K03667	Protein families: genetic information and processing	9182	hsu1; ATP-dependent HisU protease ATP-binding subunit Hsu1	303
NZ_CPO22121_1_59	JBMCGNCK_00060	K03686	Protein families: genetic information and processing	9182	dnaJ; molecular chaperone DnaJ	216
NZ_CPO22121_1_61	JBMCGNCK_00062	K03687	Protein families: genetic information and processing	9182	GRPE; molecular chaperone GrpE	62
NZ_CPO22121_1_1081	JBMCGNCK_01117	K03696	Protein families: genetic information and processing	9182	clpC; ATP-dependent Clp protease ATP-binding subunit ClpC	539
NZ_CPO22121_1_3393	JBMCGNCK_03480	K03698	Protein families: genetic information and processing	9182	cbf1, cbf1'; 3'-exoribonuclease [EC:3.1.-.]	166
NZ_CPO22121_1_2599	JBMCGNCK_02664	K03706	Protein families: genetic information and processing	9182	codY; transcriptional pleiotropic repressor	164
NZ_CPO22121_1_1024	JBMCGNCK_01052	K03768	Protein families: genetic information and processing	9182	PPIB, ppIB; peptidyl-prolyl cis-isomerase B (cyclophilin B) [EC:5.2.1.8]	151
NZ_CPO22121_1_702	JBMCGNCK_00723	K03833	Protein families: genetic information and processing	9182	selB, EFSE; selenocysteine-specific elongation factor	321
NZ_CPO22121_1_2546	JBMCGNCK_02610	K03977	Protein families: genetic information and processing	9182	engA; der; GTase	301
NZ_CPO22121_1_246	JBMCGNCK_00254	K04078	Protein families: genetic information and processing	9182	groES, HSEPE1; chaperonin GroES	68
NZ_CPO22121_1_1632	JBMCGNCK_01685	K04083	Protein families: genetic information and processing	9182	hsIC; molecular chaperone Hsp33	208
NZ_CPO22121_1_1934	JBMCGNCK_01991	K04094	Protein families: genetic information and processing	9182	mFO, gID; methylenetetrahydrofolate--lRNA-(uracil-5-)methyltransferase [EC:2.1.1.7]	248
NZ_CPO22121_1_424	JBMCGNCK_00434	K05516	Protein families: genetic information and processing	9182	cbpA; curved DNA-binding protein	145
NZ_CPO22121_1_954	JBMCGNCK_00981	K05808	Protein families: genetic information and processing	9182	ybbI; putative sigma-54 modulation protein	112
NZ_CPO22121_1_468	JBMCGNCK_00479	K06284	Protein families: genetic information and processing	9182	rB family transcriptional regulator, transcriptional pleiotropic regulator of transition st:	64
NZ_CPO22121_1_755	JBMCGNCK_00777	K06942	Protein families: genetic information and processing	9182	ycf1; ribosome-binding ATPase	230
NZ_CPO22121_1_2860	JBMCGNCK_02934	K07040	Protein families: genetic information and processing	9182	ycf0, ybfN; DUF177 domain-containing protein	66
NZ_CPO22121_1_2678	JBMCGNCK_02743	K07447	Protein families: genetic information and processing	9182	ruvK; putative pre-16S rRNA nuclelease [EC:3.1.-.]	45
NZ_CPO22121_1_1006	JBMCGNCK_01034	K07533	Protein families: genetic information and processing	9182	prsA; foldase protein PrsA [EC:5.2.1.8]	24
NZ_CPO22121_1_192	JBMCGNCK_00194	K07574	Protein families: genetic information and processing	9182	ybfB; RNA-binding protein	70
NZ_CPO22121_1_1084	JBMCGNCK_01120	K07736	Protein families: genetic information and processing	9182	carD; CarD family transcriptional regulator	140
NZ_CPO22121_1_197	JBMCGNCK_00199	K08301	Protein families: genetic information and processing	9182	rgcA; ribonuclease G [EC:3.1.26.-]	329
NZ_CPO22121_1_999	JBMCGNCK_01027	K09685	Protein families: genetic information and processing	9182	purR; purine operon repressor	140
NZ_CPO22121_1_57	JBMCGNCK_00058	K09761	Protein families: genetic information and processing	9182	rsmE; 16S rRNA (uracil1498-N3)-methyltransferase [EC:2.1.1.193]	115
NZ_CPO22121_1_1653	JBMCGNCK_01706	K09825	Protein families: genetic information and processing	9182	perR; Fur family transcriptional regulator, peroxide stress response regulator	65
NZ_CPO22121_1_2395	JBMCGNCK_02458	K13628	Protein families: genetic information and processing	9182	queG; epoxypequinoic oxidoreductase [EC:1.17.99.6]	82
NZ_CPO22121_1_775	JBMCGNCK_00797	K13897	Protein families: genetic information and processing	9182	cct, ths; archaeal chaperone	392
NZ_CPO22121_1_62	JBMCGNCK_00063	K22447	Protein families: genetic information and processing	9182	K00666; fatty-acyl-CoA synthase [EC:6.2.1.-]	617
NZ_CPO22121_1_1316	JBMCGNCK_01367	K02066	Protein families: metabolism	9181	epsB, capB; protein-tyrosine kinase [EC:2.7.10.3]	87
NZ_CPO22121_1_2766	JBMCGNCK_02834	K02093	Protein families: metabolism	9181	map; methionyl aminopeptidase [EC:3.4.11.9]	158
NZ_CPO22121_1_1567	JBMCGNCK_01620	K02162	Protein families: metabolism	9181	pepF, pepB; oligopeptidopeptidase F [EC:3.4.24.-]	216
NZ_CPO22121_1_1135	JBMCGNCK_01176	K02165	Protein families: metabolism	9181	hsIV, clpQ; ATP-dependent HisU protease, peptidase subunit HisV [EC:3.4.25.]	132
NZ_CPO22121_1_1936	JBMCGNCK_01993	K02149	Protein families: metabolism	9181	tldD; TldD protein	287
NZ_CPO22121_1_2639	JBMCGNCK_02704	K02358	Protein families: metabolism	9181	pmbA; PmbA protein	239
NZ_CPO22121_1_971	JBMCGNCK_00998	K02359	Protein families: metabolism	9181	E3.4.21.102, prc; ctpA; carboxyl-terminal processing protease [EC:3.4.21.102]	161
NZ_CPO22121_1_1298	JBMCGNCK_01343	K02379	Protein families: metabolism	9181	E3.4.21.102, prc, ctpA; carboxyl-terminal processing protease [EC:3.4.21.102]	90
NZ_CPO22121_1_1438	JBMCGNCK_01492	K02378	Protein families: metabolism	9181	ftsH, hflB; HflB; division protease FtsH [EC:3.4.24.-]	413
NZ_CPO22121_1_1037	JBMCGNCK_01067	K02378	Protein families: metabolism	9181	ftsH, hflB; HflB; division protease FtsH [EC:3.4.24.-]	399
NZ_CPO22121_1_13	JBMCGNCK_00014	K06894	Protein families: metabolism	9181	yfhM; alpha-2-macroglobulin	475
NZ_CPO22121_1_725	JBMCGNCK_00747	K08602	Protein families: metabolism	9181	pepF, pepB; oligopeptidopeptidase F [EC:3.4.24.-]	376
NZ_CPO22121_1_1886	JBMCGNCK_01943	K12123	Protein families: metabolism	9181	prkC, stk2; eukaryotic-like serine/threonine-protein kinase [EC:2.7.11.1]	245
NZ_CPO22121_1_3391	JBMCGNCK_03478	K19224	Protein families: metabolism	9181	lytE, cwf1; peptidoglycan DL-endopeptidase LytE [EC:3.4.1.-.]	19
NZ_CPO22121_1_734	JBMCGNCK_00756	K19689	Protein families: metabolism	9181	amps, ampS, ampT; aminopeptidase [EC:3.4.11.-]	294
NZ_CPO22121_1_1885	JBMCGNCK_01942	K20074	Protein families: metabolism	9181	ppcP, pppC; PPV family protein phosphatase [EC:3.1.3.16]	91
NZ_CPO22121_1_3579	JBMCGNCK_03667	K20152	Protein families: signal and cellular processes	9183	ecfA; energy-coupling factor transport system ATP-binding protein [ATP:EC:7.-.-.]	301
NZ_CPO22121_1_756	JBMCGNCK_00778	K20152	Protein families: signal and cellular processes	9183	ecfA; energy-coupling factor transport system ATP-binding protein [ATP:EC:7.-.-.]	168
NZ_CPO22121_1_2900	JBMCGNCK_02982	K20164	Protein families: signal and cellular processes	9183	mmMDA; methylmalonyl-CoA decarboxylase subunit alpha [EC:7.2.4.3]	501
NZ_CPO22121_1_2423	JBMCGNCK_02486	K20189	Protein families: signal and cellular processes	9183	K01989; putative tryptophan/tyrosine transport system substrate-binding protein	173
NZ_CPO22121_1_334	JBMCGNCK_00342	K20203	Protein families: signal and cellular processes	9183	ABC.CDA; putative ABC transport system ATP-binding protein	104
NZ_CPO22121_1_2100	JBMCGNCK_02164	K20216	Protein families: signal and cellular processes	9183	ABC.FEVN; Irc complex transport system substrate-binding protein	124
NZ_CPO22121_1_1532	JBMCGNCK_01585	K20216	Protein families: signal and cellular processes	9183	ABC.FEVN; Irc complex transport system substrate-binding protein	74
NZ_CPO22121_1_1273	JBMCGNCK_01316	K20228	Protein families: signal and cellular processes	9183	ABC.PAA; polar amino acid transport system ATP-binding protein [EC:7.4.2.1]	131
NZ_CPO22121_1_1209	JBMCGNCK_01249	K20251	Protein families: signal and cellular processes	9183	ABC.SNS; NitT/TauT family transport system substrate-binding protein	141
NZ_CPO22121_1_2770	JBMCGNCK_02838	K20228	Protein families: signal and cellular processes	9183	comEC; competence protein ComEC	78
NZ_CPO22121_1_55	JBMCGNCK_00056	K20253	Protein families: signal and cellular processes	9183	HINT1, Hint1; histidine triad (HIT) family protein	61
NZ_CPO22121_1_388	JBMCGNCK_00398	K20328	Protein families: signal and cellular processes	9183	mscl; large conductance mechanosensitive channel	91
NZ_CPO22121_1_1792	JBMCGNCK_01846	K20334	Protein families: signal and cellular processes	9183	ybbB; phosphateNa ⁺ symporter	225
NZ_CPO22121_1_102	JBMCGNCK_00103	K20347	Protein families: signal and cellular processes	9183	hsdM; type I restriction enzyme M protein [EC:2.1.1.72]	408
NZ_CPO22121_1_2357	JBMCGNCK_02426	K20352	Protein families: signal and cellular processes	9183	fixB; fixF; electron transfer flavoprotein alpha subunit	207
NZ_CPO22121_1_77	JBMCGNCK_00078	K20369	Protein families: signal and cellular processes	9183	tlyC; magnesium and cobalt exporter, CNM family	225
NZ_CPO22121_1_1154	JBMCGNCK_01195	K20690	Protein families: signal and cellular processes	9183	MEMO1; MEMO1 family protein	224
NZ_CPO22121_1_1562	JBMCGNCK_00576	K20716	Protein families: signal and cellular processes	9183	mod; adenine-specific DNA-methyltransferase [EC:2.1.1.72]	211
NZ_CPO22121_1_3348	JBMCGNCK_02421	K20716	Protein families: signal and cellular processes	9183	mod; adenine-specific DNA-methyltransferase [EC:2.1.1.72]	208
NZ_CPO22121_1_1218	JBMCGNCK_02437	K20901	Protein families: signal and cellular processes	9183	dinD; DNA-damage-inducible protein J	42
NZ_CPO22121_1_2960	JBMCGNCK_03040	K20839	Protein families: signal and cellular processes	9183	ydjE; MFS transporter, putative metaboliteH ⁺ symporter	269
NZ_CPO22121_1_493	JBMCGNCK_00505	K20839	Protein families: signal and cellular processes	9183	ydjE; MFS transporter, putative metaboliteH ⁺ symporter	178
NZ_CPO22121_1_870	JBMCGNCK_00897	K20913	Protein families: signal and cellular processes	9183	sufC; Fe-S cluster assembly ATP-binding protein	163
NZ_CPO22121_1_80	JBMCGNCK_00081	K21392	Protein families: signal and cellular processes	9183	panF; sodium/potassium transporter	101
NZ_CPO22121_1_406	JBMCGNCK_00416	K21587	Protein families: signal and cellular processes	9183	hpaA; K(+)-stimulated pyrophosphate-energized sodium pump [EC:7.1.3.2]	792
NZ_CPO22121_1_354	JBMCGNCK_00362	K21587	Protein families: signal and cellular processes	9183	hpaA; K(+)-stimulated pyrophosphate-energized sodium pump [EC:7.1.3.2]	418
NZ_CPO22121_1_2368	JBMCGNCK_02437	K21591	Protein families: signal and cellular processes	9183	cas6; CRISPR-associated endoribonuclease Cas6 [EC:3.1.-.]	29
NZ_CPO22121_1_3443	JBMCGNCK_03529	K21915	Protein families: signal and cellular processes	9183	csh2; CRISPR-associated protein Csh2	237
NZ_CPO22121_1_2983	JBMCGNCK_03064	K21915	Protein families: signal and cellular processes	9183	prfF; sohA; antitoxin PrfF	12
NZ_CPO22121_1_2767	JBMCGNCK_02835	K21942	Protein families: signal and cellular processes	9183	epsA, capA; protein tyrosine kinase modulator	48
NZ_CPO22121_1_1247	JBMCGNCK_01288	K21954	Protein families: signal and cellular processes	9183	btuB; cobalamin transport system substrate-binding protein	114
NZ_CPO22121_1_721	JBMCGNCK_00743	K20179	Protein families: signal and cellular processes	9183	iorA; indolepyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.8]	409
NZ_CPO22121_1_722	JBMCGNCK_00744	K0180	Protein families: signal and cellular processes	9183	iorB; indolepyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.8]	119
NZ_CPO22121_1_2358	JBMCGNCK_02427	K00313	Protein families: signal and cellular processes	9183	fixC; electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]	248
NZ_CPO22121_1_2935	JBMCGNCK_03015	K00573	Unclassified	9183	E2.1.1.77, pcm; protein-Lissoapartate(D-aspartate)-O-methyltransferase [EC:2.1.1.77]	81
NZ_CPO22121_1_1486	JBMCGNCK_01540	K01023	Unclassified	9183	assT; arylsulfate sulfotransferase [EC:2.8.2.22]	287
NZ_CPO22121_1_1879	JBMCGNCK_01936	K01462	Unclassified	9183	PDF, def; peptide deformylase [EC:3.5.1.88]	46
NZ_CPO22121_1_2842	JBMCGNCK_02915	K01463	Unclassified	9183	bshB; N-acetylglucosamine malate deacetylase 1 [EC:3.5.1.-.]	28
NZ_CPO22121_1_3213	JBMCGNCK_03					

NZ_CPO22121_1_1882	JBMCGNCK_01939	K06973	Unclassified	K06973; uncharacterized protein	125
NZ_CPO22121_1_3271	JBMCGNCK_03354	K07006	Unclassified	K07006; uncharacterized protein	34
NZ_CPO22121_1_3546	JBMCGNCK_03634	K07006	Unclassified	K07006; uncharacterized protein	33
NZ_CPO22121_1_634	JBMCGNCK_00648	K07006	Unclassified	K07006; uncharacterized protein	14
NZ_CPO22121_1_2105	JBMCGNCK_02169	K07112	Unclassified	K07112; uncharacterized protein	244
NZ_CPO22121_1_973	JBMCGNCK_01000	K07138	Unclassified	K07138; uncharacterized protein	154
NZ_CPO22121_1_2701	JBMCGNCK_02767	K08992	Unclassified	lapA; lipopolysaccharide assembly protein A	13
NZ_CPO22121_1_2760	JBMCGNCK_02828	K09117	Unclassified	K09117; uncharacterized protein	33
NZ_CPO22121_1_868	JBMCGNCK_00895	K09118	Unclassified	K09118; uncharacterized protein	455
NZ_CPO22121_1_1193	JBMCGNCK_01233	K09126	Unclassified	K09126; uncharacterized protein	145
NZ_CPO22121_1_1727	JBMCGNCK_01790	K09157	Unclassified	K09157; uncharacterized protein	447
NZ_CPO22121_1_219	JBMCGNCK_00221	K03545	Unclassified: genetic information processing	fif; trigger factor	215
NZ_CPO22121_1_1510	JBMCGNCK_01564	K03704	Unclassified: genetic information processing	cspC; cold shock protein	71
NZ_CPO22121_1_858	JBMCGNCK_00884	K03704	Unclassified: genetic information processing	cspA; cold shock protein	67
NZ_CPO22121_1_1742	JBMCGNCK_01795	K07402	Unclassified: genetic information processing	xdhC; xanthine dehydrogenase accessory factor	36
NZ_CPO22121_1_53	JBMCGNCK_00054	K07403	Unclassified: genetic information processing	nfdD; membrane-bound serine protease (ClpP class)	184
NZ_CPO22121_1_647	JBMCGNCK_00662	K07484	Unclassified: genetic information processing	K07484; transposase	208
NZ_CPO22121_1_3144	JBMCGNCK_03226	K07491	Unclassified: genetic information processing	rayT; REP-associated tyrosine transposase	130
NZ_CPO22121_1_2915	JBMCGNCK_02992	K07576	Unclassified: genetic information processing	K07576; metallo-beta-lactamase family protein	238
NZ_CPO22121_1_499	JBMCGNCK_00511	K09747	Unclassified: genetic information processing	eblC; nucleoid-associated protein EblC	72
NZ_CPO22121_1_798	JBMCGNCK_01852	K09777	Unclassified: genetic information processing	remA; extracellular matrix regulatory protein A	91
NZ_CPO22121_1_1079	JBMCGNCK_01115	K19411	Unclassified: genetic information processing	mcsA; protein arginine kinase activator	81
NZ_CPO22121_1_684	JBMCGNCK_00705	K24648	Unclassified: genetic information processing	remB; extracellular matrix regulatory protein B	27
NZ_CPO22121_1_466	JBMCGNCK_00477	K30424	Unclassified: metabolism	tadT; TatB DNAse family protein [EC:3.1.21.-]	144
NZ_CPO22121_1_2356	JBMCGNCK_02425	K03521	Unclassified: metabolism	fixA, erfB; electron transfer flavoprotein beta subunit	147
NZ_CPO22121_1_25	JBMCGNCK_00026	K04026	Unclassified: metabolism	erfU; ethanamine utilization protein EufU	195
NZ_CPO22121_1_2362	JBMCGNCK_02431	K04069	Unclassified: metabolism	pflA, pflC, pflE; pyruvate formate lyase activating enzyme [EC:1.2.17.1.4]	154
NZ_CPO22121_1_3564	JBMCGNCK_03652	K04488	Unclassified: metabolism	iscU, nifU; nitrogen fixation protein NifU and related proteins	87
NZ_CPO22121_1_749	JBMCGNCK_00771	K04767	Unclassified: metabolism	acuB; acetoin utilization protein AcuB	110
NZ_CPO22121_1_3497	JBMCGNCK_03583	K05919	Unclassified: metabolism	dfc; superoxide reductase [EC:1.15.1.2]	68
NZ_CPO22121_1_2192	JBMCGNCK_02259	K06221	Unclassified: metabolism	dkgB; 2,5-diketo-D-gluconate reductase A [EC:1.1.1.346]	244
NZ_CPO22121_1_3184	JBMCGNCK_03264	K06911	Unclassified: metabolism	PIR; quercent 2,3-dioxogenase [EC:1.13.11.24]	179
NZ_CPO22121_1_1728	JBMCGNCK_01781	K06997	Unclassified: metabolism	yggS; PROSC; PLP dependent protein	119
NZ_CPO22121_1_2874	JBMCGNCK_02949	K07030	Unclassified: metabolism	fakA; fatty acid kinase [EC:2.7.2.18]	295
NZ_CPO22121_1_1506	JBMCGNCK_01560	K07444	Unclassified: metabolism	ypcS; putative N6-adenine-specific DNA methylase [EC:2.1.1.-]	250
NZ_CPO22121_1_323	JBMCGNCK_00331	K09121	Unclassified: metabolism	rC; pyridinum-3,5-bis(hydroxymethyl) acridine mononucleotide nickel chelatase [EC:4.99.1.1]	132
NZ_CPO22121_1_1238	JBMCGNCK_01279	K10670	Unclassified: metabolism	: glycine/sarcosine/betaine reductase complex component A [EC:1.21.4.2.1.21.3.12.-]	21
NZ_CPO22121_1_3147	JBMCGNCK_03229	K10671	Unclassified: metabolism	grdE; glycine reductase complex component B subunit alpha and beta [EC:1.21.4.2.]	355
NZ_CPO22121_1_1243	JBMCGNCK_01284	K10671	Unclassified: metabolism	grdE; glycine reductase complex component B subunit alpha and beta [EC:1.21.4.2.]	348
NZ_CPO22121_1_1244	JBMCGNCK_01285	K10672	Unclassified: metabolism	grdB; glycine reductase complex component B subunit gamma [EC:1.21.4.2.]	271
NZ_CPO22121_1_3146	JBMCGNCK_03228	K10672	Unclassified: metabolism	grdB; glycine reductase complex component B subunit gamma [EC:1.21.4.2.]	213
NZ_CPO22121_1_1245	JBMCGNCK_01286	K10672	Unclassified: metabolism	grdB; glycine reductase complex component B subunit gamma [EC:1.21.4.2.]	30
NZ_CPO22121_1_3145	JBMCGNCK_03227	K10672	Unclassified: metabolism	grdB; glycine reductase complex component B subunit gamma [EC:1.21.4.2.]	22
NZ_CPO22121_1_3540	JBMCGNCK_03628	K21237	Unclassified: metabolism	hydF; hydrogenase-4 component B [EC:3.-.-.-]	257
NZ_CPO22121_1_2330	JBMCGNCK_02399	K12264	Unclassified: metabolism	norV; anaerobic nitric oxide reductase flavourredoxin	288
NZ_CPO22121_1_2809	JBMCGNCK_02880	K12267	Unclassified: metabolism	msrAB; peptide methionine sulfoxide reductase msrA/msrB [EC:1.8.4.11.1.8.4.12.]	170
NZ_CPO22121_1_1503	JBMCGNCK_01557	K17992	Unclassified: metabolism	hndB; NAD(P)-reducing hydrogenase subunit HndB [EC:1.12.1.3]	39
NZ_CPO22121_1_1505	JBMCGNCK_01559	K18332	Unclassified: metabolism	hndD; NAD(P)-reducing hydrogenase subunit HndD [EC:1.12.1.3]	353
NZ_CPO22121_1_839	JBMCGNCK_00865	K38446	Unclassified: metabolism	ygfF; triphosphatase [EC:3.6.1.25]	67
NZ_CPO22121_1_2740	JBMCGNCK_02807	K39784	Unclassified: metabolism	chrR; NQR; chromate reductase, NAD(P)H dehydrogenase (quinone)	119
NZ_CPO22121_1_3135	JBMCGNCK_01366	K39814	Unclassified: metabolism	eam; glutamate 2,3-aminomutase [EC:5.4.3.9]	265
NZ_CPO22121_1_3235	JBMCGNCK_03316	K20038	Unclassified: metabolism	eutC; choline trimethylamine-lyase [EC:4.3.99.4]	402
NZ_CPO22121_1_1341	JBMCGNCK_01382	K21576	Unclassified: metabolism	a/sarcosine/betaine reductase complex component C subunit alpha [EC:1.21.4.2.1.21.1.-]	239
NZ_CPO22121_1_1240	JBMCGNCK_01281	K21577	Unclassified: metabolism	a/sarcosine/betaine reductase complex component C subunit beta [EC:1.21.4.2.1.21.4]	261
NZ_CPO22121_1_86	JBMCGNCK_00087	K21577	Unclassified: metabolism	a/sarcosine/betaine reductase complex component C subunit beta [EC:1.21.4.2.1.21.4]	182
NZ_CPO22121_1_1498	JBMCGNCK_01552	K22341	Unclassified: metabolism	fhdF2; formaldehyde dehydrogenase (formaldehyde dehydrogenase)	177
NZ_CPO22121_1_3613	JBMCGNCK_03701	K23077	Unclassified: metabolism	dsrC; dissimilatory sulfite reductase related protein	75
NZ_CPO22121_1_394	JBMCGNCK_00404	K23876	Unclassified: metabolism	tpdC; tpdD; tpdE; tpdF; tpdG; ferredoxin	182
NZ_CPO22121_1_1976	JBMCGNCK_02033	K23876	Unclassified: metabolism	tpdC; tpdD; tpdE; tpdF; tpdG; ferredoxin	182
NZ_CPO22121_1_259	JBMCGNCK_00267	K23997	Unclassified: metabolism	tpdC; tpdD; tpdE; tpdF; tpdG; ferredoxin	182
NZ_CPO22121_1_2108	JBMCGNCK_02172	K23997	Unclassified: metabolism	dependent NAD(P)H-hydrate dehydratase / NAD(P)H-hydrate epimerase [EC:4.2.1.136]	238
NZ_CPO22121_1_3558	JBMCGNCK_03646	K20205	Unclassified: signaling and cellular processes	ABC.CDTX; HydD family secretion protein	108
NZ_CPO22121_1_1289	JBMCGNCK_01334	K20239	Unclassified: signaling and cellular processes	phoU; phosphate transport system protein	126
NZ_CPO22121_1_937	JBMCGNCK_00564	K03296	Unclassified: signaling and cellular processes	TC.HAE1; hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family	207
NZ_CPO22121_1_489	JBMCGNCK_00501	K03307	Unclassified: signaling and cellular processes	TC.SS5; solute:N+ symporter, SSS family	62
NZ_CPO22121_1_700	JBMCGNCK_00721	K06298	Unclassified: signaling and cellular processes	gerM; germination protein M	52
NZ_CPO22121_1_3065	JBMCGNCK_03147	K06298	Unclassified: signaling and cellular processes	gerM; germination protein M	20
NZ_CPO22121_1_708	JBMCGNCK_00729	K06306	Unclassified: signaling and cellular processes	yaah; spore germination protein	128
NZ_CPO22121_1_690	JBMCGNCK_00711	K06346	Unclassified: signaling and cellular processes	jag; spoll1-associated protein	85
NZ_CPO22121_1_1000	JBMCGNCK_01028	K06412	Unclassified: signaling and cellular processes	spoVG; stage V sporulation protein G	85
NZ_CPO22121_1_1443	JBMCGNCK_01497	K07321	Unclassified: signaling and cellular processes	cooC; CO dehydrogenase maturation factor	108
NZ_CPO22121_1_1156	JBMCGNCK_01197	K09767	Unclassified: signaling and cellular processes	yajQ; cyclid-di-GMP-binding protein	110
NZ_CPO22121_1_3358	JBMCGNCK_03441	K01560	Xenobiotics biodegradation and metabolism	E3.8.1.2; 2-haloacid dehalogenase [EC:3.8.1.2]	110
NZ_CPO22121_1_805	JBMCGNCK_00826	K01821	Xenobiotics biodegradation and metabolism	prac, yhfH; 4-oxalocrotonate tautomerase [EC:5.3.2.6]	40
NZ_CPO22121_1_1539	JBMCGNCK_01592	K05898	Xenobiotics biodegradation and metabolism	kstD; 3-oxosteroid 1-dehydrogenase [EC:1.3.99.4]	199

Table S11. Similarity of electron bifurcation proteins identified from *D. formicoaceticum* proteome against proteins described in previous studies

	Query Prokka ID	Query NCBI ID	Query Description	Subject	Subject Description	Coverage	Identity	E-value	Score
StrA	JBMCGNCK_01549	WP_089609810.1	NADH-quinone oxidoreductase subunit E	WP_021167189.1	StrA (<i>S. ovata</i>)	84.0%	41.3%	3.00E-39	119
StrB	JBMCGNCK_01550	WP_242965405.1	NAD(P)H-quinone oxidoreductase subunit E	WP_021167190.1	StrB (<i>S. ovata</i>)	94.0%	57.3%	0	583
StrC	JBMCGNCK_01551	WP_089609812.1	FAD-dependent oxidoreductase	WP_021167191.1	StrC (<i>S. ovata</i>)	88.0%	40.7%	0	833
HndA	JBMCGNCK_01556	WP_089609814.1	NuoE-like protein	EF152768.1	NADH dehydrogenase (ubiquinone) 24 dKa subunit (<i>S. fructosivorans</i> JJ)	93%	40.4%	1.00E-45	134
HndB	JBMCGNCK_01557	WP_157677371.1	(2Fe-2S) ferredoxin domain-containing protein	EF152769.1	Putative NAD-reducing hydrogenase subunit (<i>S. fructosivorans</i> JJ)	90.0%	36.1%	4.00E-23	73.9
HndC	JBMCGNCK_01558	WP_242965405.1	NADH-quinone oxidoreductase subunit NuoF	EF152770.1	NADH dehydrogenase (quinone) (<i>S. fructosivorans</i> JJ)	75.0%	62.0%	0	567
HndD	JBMCGNCK_01559	WP_089609815.1	[FeFe] hydrogenase, group A	EF152771.1	Hydrogenase, Fe-only (<i>S. fructosivorans</i> JJ)	100.0%	54.3%	0	610
FloxA	JBMCGNCK_01698	WP_157677380.1	Hydrogenase iron-sulfur subunit	ABB38011.2	methyl-viologen-reducing hydrogenase delta subunit (<i>O. olaskensis</i> G20)	100.0%	52.2%	1.00E-26	85.5
FloxB	JBMCGNCK_01699	WP_089609931.1	4Fe-4S binding protein	ABB38012.1	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein (<i>O. olaskensis</i> G20)	91%	32.67%	1.00E-55	172
FloxC	JBMCGNCK_01700	WP_198306669.1	4Fe-4S dicluster domain-containing protein	ABB38013.1	Putative hydrogenase (<i>O. olaskensis</i> G20)	96%	33.73%	1.00E-65	201
FloxD	JBMCGNCK_01701	WP_089609932.1	FAD/NAD(P)-binding protein	ABB38014.1	Dihydroorotate dehydrogenase, electron transfer subunit (<i>O. olaskensis</i> G20)	97%	47.5	1.00E-99	283
HdrA	JBMCGNCK_01696	WP_089609930.1	Cob-CoM heterodisulfide reductase iron-sulfur subunit A family protein	ABB38010.1	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein (<i>O. olaskensis</i> G20)	99%	53.80%	2.00E-176	499
HdrA	JBMCGNCK_01697	WP_089609930.1	Cob-CoM heterodisulfide reductase iron-sulfur subunit A family protein	ABB38010.1	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein (<i>O. olaskensis</i> G20)	98%	60.20%	7.00E-80	240
HdrB	JBMCGNCK_01695	WP_089609929.1	Cob-CoM heterodisulfide reductase iron-sulfur subunit B family protein	ABB38009.1	Cob-CoM heterodisulfide reductase subunit B (<i>O. olaskensis</i> G20)	92%	42.91%	1.00E-86	251
HdrC	JBMCGNCK_01694	WP_198306668.1	4Fe-4S dicluster domain-containing protein	ABB38018.1	Heterodisulfide reductase C subunit (<i>O. olaskensis</i> G20)	91%	37.90%	2.00E-49	149

Figure S1. Distribution of genes encoding TCA cycle in the *Dehalobacteriia*

