Table S1. Samples used in this study

Sample	Site	Date	pH	Temperature (°C)	Reference
GS1					
Sample 4	C drift + 8-10 m	Nov-06	1.01	39.5	(1)
Sample 11	AB Muck +20 m	Jun-06	0.72	36.0	(1)
Sample 14	AB Muck +20 m	Jun-06	0.72	36.0	(1)
Sample 17	AB Muck	Jun-06	0.72	36.0	(1)
Sample 28	C drift + 8-10 m	Nov-05	0.5	40.0	(1)
Sample 29	C drift + 30 m	Nov-04	ND	41.0	(1)
Sample 30	C drift +20 m	Nov-04	ND	41.0	(1)
Sample 31	C drift	Nov-04	ND	41.0	(1)
Sample 39	B drif + 1-5m	May-07	0.99	46.0	(1)
Sample 41	AB Muck	Aug-07	0.83	37.1	(1)
GS2					
Sample 7	AB Muck	Nov-06	1.01	39.5	(1)
Sample 8	AB Muck	Nov-06	1.18	42.7	(1)
Sample 9	C drift +8-10 m	Nov-06	1	43.0	(1)
Sample 10	C drift + 75 m	Nov-06	0.7	43.0	(1)
Sample 20	C drift + 75 m	Aug-06	0.72	36.0	(1)
Sample 25	C drift + 75 m	Jun-06	0.92	39.3	(1)
Sample 33	AB Muck	Jun-06	0.93	42.0	(1)
Sample 40	C drift +8-10 m	Aug-06	1	41.0	(1)
Sample 49	B drift	Mar-05	1.12	40.2	(1)
5way Floating GS2	5way	Feb-08	0.98	38.0	*this study*
Submerged					
5way-Sunken1	5way	Feb-08	0.98	38.0	*this study*
5way-Sunken2	5way	Feb-08	0.98	38.0	*this study*
5way-Sunken3	5way	Feb-08	0.98	38.0	*this study*
UBA-Sunken1	UBA	Jun-09	1.1	38.0	*this study*
UBA-Sunken2	UBA	Jun-09	1.1	38.0	*this study*
UBA-Sunken3	UBA	Jun-09	1.1	38.0	*this study*

(1)**Mueller, R. S., V. J. Denef, L. H. Kalnejais, B. K. Suttle, B. C. Thomas, P. Wilmes, R. L. Smith, D. K. Nordstrom, R. B. McCleskey, M. Shah, N. VerBerkmoes, R. L. Hettich, and J. Banfield.** 2010. Ecological distribution and population physiology defined by proteomics in a natural microbial community. Molecular Systems Biology **6**.

Table S2: FISH analysis results for the sunken biofilm samples.

	5way-Sunken1	5way-Sunken2	UBA-Sunken1	UBA-Sunken2	UBA-Sunken3
EubMix	28.1 (8.9)	17.0 (8.75)	24.2 (8.5)	21.8 (10.3)	23.2 (9.9)
ARC915	50.1 (11.9)	65.4 (10.1)	73.1 (5.4)	78.2 (4.7)	76.9 (7.1)
LF655	10.8 (6.8)	<5	20.6 (7.9)	13.9 (10.1)	23.2 (5.9)
SUL230	15.6 (10.0)	13.1 (11.9)	<5	<5	<5
ARMAN 4/5	23.1 (7.4)	16.7 (6.5)	<1	<1	<1

*<1 and <5 indicates qualitative assessment only

Table S3: All archaeal proteins detected across samples

Protein	Annotation
IPL_15911_0581	hypothetical protein
IPL_15911_0573	oligopeptide ABC transporter Opp1, ATP binding protein; K02031 peptide/nickel transport system ATP-binding protein; K02032 peptide/nickel transport system ATP-binding protein
IPL_15911_0569	putative glycogen debranching enzyme
IPL_15911_0566	transcription regulator
IPL_15911_0558	icd; isocitrate dehydrogenase, nADP-dependent; K00031 isocitrate dehydrogenase [EC:1.1.1.42]
IPL_15911_0557	transcription factor; K03120 transcription initiation factor TFIID TATA-box-binding protein
IPL_15911_0498	rps28e; 30S ribosomal protein S28e; K02979 small subunit ribosomal protein S28e
IPL_15911_0419	thermosome
IPL_15911_0383	cobQ; cobyric acid synthase (EC:6.3.5.10); K02232 adenosylcobyric acid synthase [EC:6.3.5.10]
IPL_15911_0328	rps19p; 30S ribosomal protein S19P; K02965 small subunit ribosomal protein S19
IPL_15911_0321	rpl14p; 50S ribosomal protein L14P; K02874 large subunit ribosomal protein L14
IPL_15911_0268	2-oxoacid ferredoxin oxidoreductase subunit alpha; K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
IPL_15911_0264	seryl-tRNA synthetase (EC:6.1.1.11); K01875 seryl-tRNA synthetase [EC:6.1.1.11]
IPL_15911_0262	aspartyl-tRNA(Asn) amidotransferase, B subunit; K03330 glutamyl-tRNA(Gln) amidotransferase subunit E [EC:6.3.5.7]
IPL_15911_0253	putative deoxyhypusine synthase (EC:2.5.1.46); K00809 deoxyhypusine synthase [EC:2.5.1.46]

IPL_15911_0239	DNA-directed RNA polymerase subunit B; K13798 DNA-directed RNA polymerase subunit B [EC:2.7.7.6]
IPL_15911_0234	hypothetical protein
IPL_15911_0222	peptidase S16, Lon-like protease; K04076 Lon-like ATP-dependent protease [EC:3.4.21.-]
IPL_15911_0218	purE; phosphoribosylaminoimidazole carboxylase catalytic subunit; K01588 5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]
IPL_15911_0216	dnaG; DNA primase
IPL_15911_0207	small GTP-binding protein
IPL_15911_0147	hypothetical protein; K07029
IPL_15911_0127	chromosome hypothetical proteinregation protein SMC; K03529 chromosome hypothetical proteinregation protein
IPL_15911_0124	methionine adenosyltransferase (EC:2.5.1.6); K00789 S-adenosylmethionine synthetase [EC:2.5.1.6]
IPL_15911_0123	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (EC:3.5.4.10); K00602 phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]
IPL_15911_0107	AAA family ATPase, CDC48 subfamily (EC:3.6.1.3); K13525 transitional endoplasmic reticulum ATPase
IPL_15911_0090	serine/threonine protein kinase (EC:2.7.11.1); K00870 protein kinase [EC:2.7.1.37]
IPL_15911_0089	serine/threonine protein kinase (EC:2.7.11.1); K00870 protein kinase [EC:2.7.1.37]
IPL_15911_0083	transcription factor TFIIB cyclin-related protein; K03124 transcription initiation factor TFIIB
IPL_15911_0066	urocanate hydratase (EC:4.2.1.49); K01712 urocanate hydratase [EC:4.2.1.49]
IPL_15911_0014	hypothetical protein
IPL_13624_0384	arylsulfatase regulatory protein, putative; K06871
IPL_13624_0383	MFS general substrate transporter
IPL_13624_0382	Fe-S oxidoreductase
IPL_13624_0381	hypothetical protein
IPL_13624_0350	ef1a, tuf; elongation factor 1-alpha (EC:3.6.5.3); K03231 elongation factor EF-1 alpha subunit [EC:3.6.5.3]
IPL_13624_0347	ribosomal protein S7; K02992 small subunit ribosomal protein S7
IPL_13624_0326	superoxide dismutase (EC:1.15.1.1); K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
IPL_13624_0273	4-aminobutyrate aminotransferase (EC:2.6.1.19); K00823 4-aminobutyrate aminotransferase [EC:2.6.1.19]
IPL_13624_0267	aldehyde dehydrogenase; K07248 lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase [EC:1.2.1.22 1.2.1.21]
IPL_13624_0250	threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
IPL_13624_0240	thiamine pyrophosphate enzyme; K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
IPL_13624_0224	4-hydroxyphenylpyruvate dioxygenase (EC:1.13.11.27); K00457 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]
IPL_13624_0194	ABC transporter related; K02006 cobalt/nickel transport system ATP-binding protein

IPL_13624_0137	NAD-dependent aldehyde dehydrogenase; K00294 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]
IPL_13624_0135	carB; carbamoyl-phosphate synthase, large subunit (EC:6.3.5.5); K01955 carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]
IPL_13624_0071	valyl-tRNA synthetase; K01873 valyl-tRNA synthetase [EC:6.1.1.9]
IPL_13624_0064	proteasome endopeptidase complex, alpha subunit (EC:3.4.25.1); K03432 proteasome alpha subunit [EC:3.4.25.1]
IPL_13624_0044	membrane metalloprotease
IPL_13624_0040	translation initiation factor eIF-5A; K03263 translation initiation factor eIF-5A
IPL_13624_0007	DNA integration/recombination/invertion protein
IPL_13624_0004	molybdenum cofactor biosynthesis protein A; K06937
IPL_13624_0001	integrase/recombinase
IPL_13613_0001	integrase/recombinase
IPL_13606_0513	aldehyde:ferredoxin oxidoreductase; K03738 aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]
IPL_13606_0459	2,4-dienoyl-CoA reductase (NADPH) precursor related protein
IPL_13606_0441	pyruvate, phosphate dikinase (EC:2.7.9.1); K01006 pyruvate,orthophosphate dikinase [EC:2.7.9.1]
IPL_13606_0433	hypothetical protein
IPL_13606_0387	hypothetical protein
IPL_13606_0363	aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]
IPL_13606_0265	pyruvate flavodoxin/ferredoxin oxidoreductase domain-containing protein; K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
IPL_13606_0257	nucleoside-diphosphate-sugar epimerase; K01795 [EC:5.1.3.-]
IPL_13606_0201	V-type ATP synthase subunit A (EC:3.6.3.14); K02117 V-type H+-transporting ATPase subunit A [EC:3.6.3.14]
IPL_13606_0200	V-type ATP synthase subunit B (EC:3.6.3.14); K02118 V-type H+-transporting ATPase subunit B [EC:3.6.3.14]
IPL_13606_0192	protein of unknown function DUF255; K06888
IPL_13606_0135	katG; catalase (peroxidase I); K03782 catalase/peroxidase [EC:1.11.1.6 1.11.1.7]
IPL_13606_0121	dnaK; molecular chaperone DnaK; K04043 molecular chaperone DnaK
IPL_13606_0110	sdhA; succinate dehydrogenase flavoprotein subunit (EC:1.3.5.1); K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
IPL_13606_0079	ABC-type multidrug transport system, ATPase component; K01990 ABC-2 type transport system ATP-binding protein
IPL_13606_0059	oligopeptide/dipeptide ABC transporter, ATPase subunit
IPL_13606_0037	chaperonin GroEL
IPL_13606_0011	hypothetical protein
IPL_13448_0025	hypothetical protein

IPL_13448_0021	hypothetical protein
IPL_13448_0018	type III restriction enzyme, res subunit family
IPL_13448_0017	modification methylase
IPL_13249_0160	3-hydroxybutyryl-CoA dehydrogenase (EC:1.1.1.157); K00074 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
IPL_13249_0156	hypothetical protein
IPL_13249_0145	small nuclear ribonucleoprotein (snRNP)-like protein
IPL_13249_0140	glutamate dehydrogenase; K00261 glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]
IPL_13249_0100	inosine-5'-monophosphate dehydrogenase (EC:1.1.1.205); K00088 IMP dehydrogenase [EC:1.1.1.205]
IPL_13249_0090	methionyl-tRNA synthetase; K01874 methionyl-tRNA synthetase [EC:6.1.1.10]
IPL_13249_0061	tetrahydrofolylpolyglutamate synthase related protein; K11754 dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12 6.3.2.17]
GPL_13477_0077	aldo/keto reductase
GPL_13477_0075	formyltetrahydrofolate synthetase; K01938 formate--tetrahydrofolate ligase [EC:6.3.4.3]
GPL_13477_0072	hypothetical protein
GPL_13477_0068	multi drug ABC transporter ATP binding protein; K01990 ABC-2 type transport system ATP-binding protein
GPL_13477_0066	coenzyme A transferase
GPL_13477_0061	prefoldin subunit beta; K04798 prefoldin beta subunit
GPL_13477_0059	6,7-dimethyl-8-ribityllumazine synthase (EC:2.5.1.9); K00794 riboflavin synthase beta chain [EC:2.5.1.-]
GPL_13477_0057	glycerol-3-phosphate cytidylyltransferase (EC:2.7.7.39); K00980 glycerol-3-phosphate cytidylyltransferase [EC:2.7.7.39]
GPL_13477_0053	hypothetical protein; K00768 nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase [EC:2.4.2.21]
GPL_13477_0040	hypothetical protein
GPL_13477_0039	3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC:1.1.1.34); K00021 3-hydroxy-3-methylglutaryl-CoA reductase [EC:1.1.1.34]
GPL_13477_0037	hypothetical protein
GPL_13477_0036	long-chain-fatty-acid-CoA ligase ; K01897 long-chain acyl-CoA synthetase [EC:6.2.1.3]
GPL_13477_0032	hypothetical protein
GPL_13477_0028	aspartate carbamoyltransferase regulatory subunit (EC:2.1.3.2); K00610 aspartate carbamoyltransferase regulatory subunit
GPL_13477_0027	pyrB; aspartate carbamoyltransferase catalytic subunit (EC:2.1.3.2); K00609 aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]

GPL_13477_0026	hypothetical protein; K07442 tRNA (adenine-N1-)-methyltransferase [EC:2.1.1.36]
GPL_13477_0024	ATP-dependent RNA helicase; K03724 ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.1.-]
GPL_13477_0019	oxidoreductase
GPL_13475_0044	3-deoxy-7-phosphoheptulonate synthase; K03856 3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]
GPL_13475_0034	ilvE1; branched-chain amino acid aminotransferase (EC:2.6.1.42); K00826 branched-chain amino acid aminotransferase [EC:2.6.1.42]
GPL_13475_0029	putative cyclase; K07130
GPL_13475_0025	biphenyl dioxygenase, Rieske iron-sulfur component related protein
GPL_13475_0012	methionine aminopeptidase (EC:3.4.11.18); K01265 methionyl aminopeptidase [EC:3.4.11.18]
GPL_13459_0370	type III restriction-modification enzyme, helicase subunit
GPL_13459_0332	pyruvate ferredoxin/flavodoxin oxidoreductase; K00180 indolepyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.8]
GPL_13459_0331	indolepyruvate ferredoxin oxidoreductase, alpha subunit; K00179 indolepyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.8]
GPL_13459_0328	long-chain-fatty-acid--CoA ligase (EC:2.3.1.86); K00666 fatty-acyl-CoA synthase [EC:6.2.1.-]
GPL_13459_0324	hypothetical protein
GPL_13459_0323	proline dipeptidase related protein; K01271 X-Pro dipeptidase [EC:3.4.13.9]
GPL_13459_0321	gluconolactonase
GPL_13459_0310	neprilysin (EC:3.4.24.11); K07386 putative endopeptidase [EC:3.4.24.-]
GPL_13459_0309	N-acetylglucosamine kinase (EC:2.7.1.59); K00884 N-acetylglucosamine kinase [EC:2.7.1.59]
GPL_13459_0305	hypothetical protein
GPL_13459_0287	hypothetical protein
GPL_13459_0282	hypothetical protein
GPL_13459_0281	hypothetical protein
GPL_13459_0276	L-asparaginase related protein; K01424 L-asparaginase [EC:3.5.1.1]
GPL_13459_0274	hypothetical protein; K09730 hypothetical protein
GPL_13459_0273	ychF; translation-associated GTPase; K06942
GPL_13459_0269	electron transfer flavoprotein alpha and beta-subunit
GPL_13459_0268	biphenyl dioxygenase, Rieske iron-sulfur component related protein
GPL_13459_0265	methionine aminopeptidase (EC:3.4.11.18); K01265 methionyl aminopeptidase [EC:3.4.11.18]
GPL_13459_0263	cystathionine gamma-lyase (EC:4.4.1.1); K01739 cystathionine gamma-synthase [EC:2.5.1.48]
GPL_13459_0260	ABC-type multidrug transport system, ATPase component

GPL_13459_0259	L-3-hydroxyacyl-CoA dehydrogenase precursor related protein
GPL_13459_0258	sterol-binding domain-containing protein
GPL_13459_0255	2-methylcitrate synthase/citrate synthase II (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]
GPL_13459_0254	isochorismatase hydrolase
GPL_13459_0249	orotate phosphoribosyltransferase-like protein; K00762 orotate phosphoribosyltransferase [EC:2.4.2.10]
GPL_13459_0248	lysK; lysyl-tRNA synthetase (EC:6.1.1.6); K04566 lysyl-tRNA synthetase, class I [EC:6.1.1.6]
GPL_13459_0247	methionyl-tRNA synthetase (EC:6.1.1.10); K01874 methionyl-tRNA synthetase [EC:6.1.1.10]
GPL_13459_0246	rpoK; DNA-directed RNA polymerase subunit K (EC:2.7.7.6); K03055 DNA-directed RNA polymerase subunit K [EC:2.7.7.6]
GPL_13459_0242	nusG; transcription antitermination protein NusG; K02601 transcriptional antiterminator NusG
GPL_13459_0241	hypothetical protein
GPL_13459_0240	putative RNA-binding protein
GPL_13459_0239	thiol-specific antioxidant related protein; K03564 peroxiredoxin Q/BCP [EC:1.11.1.15]
GPL_13459_0238	nucleic-acid-binding protein; K07068
GPL_13459_0237	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
GPL_13459_0236	hypothetical protein
GPL_13459_0235	transcription regulator (HTH)
GPL_13459_0231	rpl11p; 50S ribosomal protein L11P; K02867 large subunit ribosomal protein L11
GPL_13459_0230	rpl1P; 50S ribosomal protein L1P; K02863 large subunit ribosomal protein L1
GPL_13459_0229	rplP0; acidic ribosomal protein P0; K02864 large subunit ribosomal protein L10
GPL_13459_0228	rpl12p; 50S ribosomal protein L12P; K02869 large subunit ribosomal protein L12
GPL_13459_0225	glutamate formiminotransferase; K01746 formiminotetrahydrofolate cyclodeaminase [EC:4.3.1.4]
GPL_13459_0224	formiminotransferase cyclodeaminase related protein
GPL_13459_0222	GTP-binding protein; K06944
GPL_13459_0221	purA; adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]
GPL_13459_0219	isocitrate dehydrogenase; K00031 isocitrate dehydrogenase [EC:1.1.1.42]
GPL_13459_0218	hypothetical protein
GPL_13459_0217	hypothetical protein
GPL_13459_0214	dihydrolipoamide dehydrogenase (EC:1.8.1.4); K00382 dihydrolipoamide dehydrogenase [EC:1.8.1.4]
GPL_13459_0213	branched-chain alpha-keto acid dehydrogenase subunit E2; K00627 pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
GPL_13459_0212	thiamine pyrophosphate-dependent dehydrogenase, E1 component beta subunit; K00162 pyruvate

	dehydrogenase E1 component subunit beta [EC:1.2.4.1]
GPL_13459_0211	3-methyl-2-oxobutanoate dehydrogenase alpha chain precursor; K00161 pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
GPL_13459_0208	CoA-binding domain-containing protein
GPL_13459_0206	prolyl endopeptidase; K01322 prolyl oligopeptidase [EC:3.4.21.26]
GPL_13459_0204	hypothetical protein
GPL_13459_0196	hypothetical protein
GPL_13459_0195	ABC transporter related protein
GPL_13459_0193	glycosyltransferase (EC:2.4.1.-)
GPL_13459_0191	hypothetical protein; K09723 hypothetical protein
GPL_13459_0188	proteasome subunit alpha (EC:3.4.25.1); K03432 proteasome alpha subunit [EC:3.4.25.1]
GPL_13459_0183	pyruvate ferredoxin oxidoreductase, alpha chain (EC:1.2.7.1); K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
GPL_13459_0182	2-oxoacid ferredoxin oxidoreductase subunit beta (EC:1.2.7.1); K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
GPL_13459_0179	rps12P; 30S ribosomal protein S12P; K02950 small subunit ribosomal protein S12
GPL_13459_0178	30S ribosomal protein S7P; K02992 small subunit ribosomal protein S7
GPL_13459_0173	gliding motility protein related
GPL_13459_0171	putative deoxyhypusine synthase (EC:2.5.1.46); K00809 deoxyhypusine synthase [EC:2.5.1.46]
GPL_13459_0167	tRNA CCA-pyrophosphorylase (EC:2.7.7.25 2.7.7.21); K07558 tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.25 2.7.7.21]
GPL_13459_0166	ferredoxin
GPL_13459_0165	phosphoribosylaminoimidazole synthetase (EC:6.3.3.1); K01933 phosphoribosylformylglycinamidine cyclo-ligase [EC:6.3.3.1]
GPL_13459_0163	hypothetical protein
GPL_13459_0162	aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]
GPL_13459_0161	tricorn protease; K08676 tricorn protease [EC:3.4.21.-]
GPL_13459_0159	hypothetical protein
GPL_13459_0158	geranylgeranyl pyrophosphate synthase (EC:2.5.1.1); K13787 geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10 2.5.1.29]
GPL_13459_0156	TPR repeat-containing protein
GPL_13459_0154	Zn-dependent hydrolase
GPL_13459_0152	sugar phosphate nucleotydyl transferase; K00992 [EC:2.7.7.-]

GPL_13459_0151	2-amino-3-ketobutyrate coenzyme A ligase (EC:2.3.1.29); K00639 glycine C-acetyltransferase [EC:2.3.1.29]
GPL_13459_0150	metal-dependent hydrolase related to alanyl-tRNA synthetase; K07050
GPL_13459_0142	geranylgeranyl reductase
GPL_13459_0140	CBS domain-containing protein
GPL_13459_0139	glycyl-tRNA synthetase (EC:6.1.1.14); K01880 glycyl-tRNA synthetase [EC:6.1.1.14]
GPL_13459_0137	hypothetical protein; K06869
GPL_13459_0136	glyceraldehyde-3-phosphate dehydrogenase (EC:1.2.1.59); K00150 glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]
GPL_13459_0135	radA; DNA repair and recombination protein RadA; K04483 DNA repair protein RadA
GPL_13459_0134	hypothetical protein; K07103
GPL_13459_0133	hypothetical protein
GPL_13459_0131	oligopeptide ABC transporter Opp1, extracellular binding protein
GPL_13459_0129	oligopeptide ABC transporter Opp1, permease protein; K02034 peptide/nickel transport system permease protein
GPL_13459_0128	oligopeptide ABC transporter Opp1, ATP binding protein; K02031 peptide/nickel transport system ATP-binding protein; K02032 peptide/nickel transport system ATP-binding protein
GPL_13459_0126	penicillin amidase (EC:3.5.1.11); K07116
GPL_13459_0122	aromatic acid decarboxylase; K03186 3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiX [EC:4.1.1.-]
GPL_13459_0120	cell division protein pelota related protein; K06965
GPL_13459_0117	Metallo-hydrolase/oxidoreductase
GPL_13459_0115	fabG; 3-ketoacyl-(acyl-carrier-protein) reductase (EC:1.1.1.100); K00059 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]
GPL_13459_0114	nth; endonuclease III; K10773 endonuclease III [EC:4.2.99.18]
GPL_13459_0112	signal recognition particle protein SRP54; K03106 signal recognition particle subunit SRP54
GPL_13459_0110	putative RNA-associated protein; K07582 hypothetical protein
GPL_13459_0109	exosome complex RNA-binding protein Rrp4; K03679 exosome complex component RRP4
GPL_13459_0108	exosome complex exonuclease Rrp41; K11600 exosome complex component RRP41
GPL_13459_0107	exosome complex RNA-binding protein Rrp42; K12589 exosome complex component RRP42
GPL_13459_0106	rpl37ae; 50S ribosomal protein L37Ae; K02921 large subunit ribosomal protein L37Ae
GPL_13459_0104	50S ribosomal protein L21e; K02889 large subunit ribosomal protein L21e
GPL_13459_0103	DNA-directed RNA-polymerase subunit F (EC:2.7.7.6); K03051 DNA-directed RNA polymerase subunit F [EC:2.7.7.6]
GPL_13459_0102	hypothetical protein; K07572 putative nucleotide binding protein
GPL_13459_0100	band 7 integral membrane protein-like protein

GPL_13459_0096	NAD-dependent aldehyde dehydrogenase; K00155 [EC:1.2.1.-]
GPL_13459_0095	acetolactate synthase (EC:2.2.1.6); K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
GPL_13459_0089	putative oxidoreductase; K00266 glutamate synthase (NADPH/NADH) small chain [EC:1.4.1.13 1.4.1.14]
GPL_13459_0087	seryl-tRNA synthetase (EC:6.1.1.11); K01875 seryl-tRNA synthetase [EC:6.1.1.11]
GPL_13459_0086	hypothetical protein; K07145
GPL_13459_0085	hypothetical protein
GPL_13459_0080	hypothetical protein; K00806 undecaprenyl diphosphate synthase [EC:2.5.1.31]
GPL_13459_0075	2,5-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine 1-reductase (EC:1.1.1.193); K00082 5-amino-6-(5-phosphoribosylamino)uracil reductase [EC:1.1.1.193]
GPL_13459_0074	S-adenosyl-L-homocysteine hydrolase (EC:3.3.1.1); K01251 adenosylhomocysteinase [EC:3.3.1.1]
GPL_13459_0073	cofactor-independent phosphoglycerate mutase (EC:5.4.2.1); K01834 phosphoglycerate mutase [EC:5.4.2.1]
GPL_13459_0072	phosphoglucomutase/phosphomannomutase (EC:5.4.2.8 5.4.2.2); K01835 phosphoglucomutase [EC:5.4.2.2]; K01840 phosphomannomutase [EC:5.4.2.8]
GPL_13459_0070	ef1B; elongation factor 1-beta; K03232 elongation factor EF-1 beta subunit
GPL_13459_0069	hypothetical protein
GPL_13459_0067	alaS; alanyl-tRNA synthetase (EC:6.1.1.7); K01872 alanyl-tRNA synthetase [EC:6.1.1.7]
GPL_13459_0065	hypothetical protein
GPL_13459_0063	chorismate synthase (EC:4.2.3.5); K01736 chorismate synthase [EC:4.2.3.5]
GPL_13459_0058	hypothetical protein
GPL_13459_0056	dTDP-glucose pyrophosphorylase; K00973 glucose-1-phosphate thymidylyltransferase [EC:2.7.7.24]
GPL_13459_0055	dTDP-4-dehydrorhamnose reductase; K00067 dTDP-4-dehydrorhamnose reductase [EC:1.1.1.133]
GPL_13459_0048	hypothetical protein
GPL_13459_0047	gcvH; glycine cleavage system protein H; K02437 glycine cleavage system H protein
GPL_13459_0043	hypothetical protein
GPL_13459_0042	hemB; delta-aminolevulinic acid dehydratase (EC:4.2.1.24); K01698 porphobilinogen synthase [EC:4.2.1.24]
GPL_13459_0041	ATPase
GPL_13459_0040	malate dehydrogenase (EC:1.1.1.37); K00024 malate dehydrogenase [EC:1.1.1.37]
GPL_13459_0037	short-chain dehydrogenase/reductase SDR (EC:1.3.1.34)
GPL_13459_0036	DNA polymerase sliding clamp; K04802 proliferating cell nuclear antigen
GPL_13459_0035	hypothetical protein
GPL_13459_0034	glycine dehydrogenase subunit 1 (EC:1.4.4.2); K00282 glycine dehydrogenase subunit 1 [EC:1.4.4.2]
GPL_13459_0033	glycine dehydrogenase subunit 2 (EC:1.4.4.2); K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2]

GPL_13459_0032	hypothetical protein; K09746 hypothetical protein
GPL_13459_0031	replication factor A; K07466 replication factor A1
GPL_13459_0030	5'-methylthioadenosine phosphorylase II (EC:2.4.2.28); K00772 5'-methylthioadenosine phosphorylase [EC:2.4.2.28]
GPL_13459_0029	hypothetical protein; K07577 putative mRNA 3-end processing factor
GPL_13459_0027	sulfolipid biosynthesis protein
GPL_13459_0026	peptidase S8/S53 subtilisin kexin sedolisin
GPL_13459_0014	pgk; phosphoglycerate kinase (EC:2.7.2.3); K00927 phosphoglycerate kinase [EC:2.7.2.3]
GPL_13459_0013	NUDIX hydrolase
GPL_13459_0010	50S ribosomal protein L15e; K02877 large subunit ribosomal protein L15e
GPL_13459_0009	replication factor C large subunit; K04800 replication factor C large subunit
GPL_13459_0008	kinase related to galactokinase and mevalonate kinase; K07031
GPL_13459_0006	chaperonin GroEL
GPL_13459_0004	acyl-CoA dehydrogenase; K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
GPL_13459_0002	inorganic pyrophosphatase; K01507 inorganic pyrophosphatase [EC:3.6.1.1]
GPL_13455_0104	hypothetical protein
GPL_13455_0103	CRISPR-associated protein
GPL_13455_0102	hypothetical protein
GPL_13455_0101	CRISPR-associated helicase Cas3; K07012
GPL_13455_0100	hypothetical protein
GPL_13455_0097	trehalose/maltose transport ATP-hydrolyzing subunit MalK; K02023 multiple sugar transport system ATP-binding protein
GPL_13455_0094	trehalose/maltose binding protein (MalE) related protein; K02027 multiple sugar transport system substrate-binding protein
GPL_13455_0089	GntR family transcriptional regulator
GPL_13455_0088	electron transfer flavoprotein subunit alpha; K03522 electron transfer flavoprotein alpha subunit
GPL_13455_0087	electron transfer flavoprotein subunit beta; K03521 electron transfer flavoprotein beta subunit
GPL_13455_0085	FixC protein related; K00313 electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]
GPL_13455_0081	spermidine synthase (EC:2.5.1.16); K00797 spermidine synthase [EC:2.5.1.16]
GPL_13455_0076	pirin-related protein; K06911
GPL_13455_0073	3-isopropylmalate dehydratase, small subunit; K01705 homoaconitate hydratase [EC:4.2.1.36]
GPL_13455_0069	30S ribosomal protein S6e; K02991 small subunit ribosomal protein S6e

GPL_13455_0068	translation initiation factor IF-2 subunit gamma; K03242 translation initiation factor eIF-2 gamma subunit
GPL_13455_0066	DNA-binding protein
GPL_13455_0065	hypothetical protein
GPL_13455_0064	hypothetical protein; K01151 deoxyribonuclease IV [EC:3.1.21.2]
GPL_13455_0063	DNA primase
GPL_13455_0062	hypothetical protein; K01338 ATP-dependent Lon protease [EC:3.4.21.53]
GPL_13455_0061	putative peroxiredoxin (EC:1.11.1.15); K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
GPL_13455_0058	hypothetical protein
GPL_13455_0057	sec-independent protein secretion pathway component; K03116 sec-independent protein translocase protein TatA
GPL_13455_0054	hypothetical protein
GPL_13455_0053	hypothetical protein
GPL_13455_0044	NADH dehydrogenase subunit I (EC:1.6.5.3); K00338 NADH dehydrogenase I subunit I [EC:1.6.5.3]
GPL_13455_0042	NADH dehydrogenase subunit D (EC:1.6.5.3); K00333 NADH dehydrogenase I subunit D [EC:1.6.5.3]
GPL_13455_0041	NADH dehydrogenase subunit C (EC:1.6.5.3); K00332 NADH dehydrogenase I subunit C [EC:1.6.5.3]
GPL_13455_0038	glutamyl-tRNA(Gln) amidotransferase subunit E; K03330 glutamyl-tRNA(Gln) amidotransferase subunit E [EC:6.3.5.7]
GPL_13455_0037	L-asparaginase, type I; K09482 glutamyl-tRNA(Gln) amidotransferase subunit D [EC:6.3.5.7]
GPL_13455_0035	acyl-CoA dehydrogenase; K00257 [EC:1.3.99.-]
GPL_13455_0034	purine phosphoribosyltransferase related protein; K07101
GPL_13455_0032	hypothetical protein
GPL_13455_0031	hypothetical protein
GPL_13455_0023	Fe-S oxidoreductase
GPL_13455_0021	DNA polymerase I (EC:2.7.7.7); K02319 DNA polymerase I [EC:2.7.7.7]
GPL_13455_0014	argS; arginyl-tRNA synthetase (EC:6.1.1.19); K01887 arginyl-tRNA synthetase [EC:6.1.1.19]
GPL_13455_0013	hypothetical protein
GPL_13455_0009	hypothetical protein
GPL_13455_0005	rfc; replication factor C small subunit; K04801 replication factor C small subunit
GPL_13455_0003	hypothetical protein
GPL_13447_0034	argC; N-acetyl-gamma-glutamyl-phosphate reductase (EC:1.2.1.38); K00145 N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]; K05829 N-acetyl-gamma-aminoadipyl-phosphate reductase [EC:1.2.1.-]
GPL_13447_0033	acetylglutamate kinase; K00930 acetylglutamate kinase [EC:2.7.2.8]; K05828 acetylaminoadipate kinase [EC:2.7.2.-]

GPL_13447_0032	acetylornithine aminotransferase (EC:2.6.1.11); K05830 acetylornithine/acetyl-lysine aminotransferase [EC:2.6.1.11 2.6.1.-]
GPL_13447_0031	RimK-like protein; K05827 lysine biosynthesis protein LysX
GPL_13447_0029	3-isopropylmalate dehydratase large subunit (EC:4.2.1.33); K01703 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
GPL_13447_0010	subtilase family protein
GPL_13374_0232	hypothetical protein
GPL_13374_0206	hypothetical protein
GPL_13374_0202	DNA-directed RNA polymerase subunit E'; K03049 DNA-directed RNA polymerase subunit E' [EC:2.7.7.6]
GPL_13374_0200	hypothetical protein; K09735 hypothetical protein
GPL_13374_0199	rps24e; 30S ribosomal protein S24e; K02974 small subunit ribosomal protein S24e
GPL_13374_0198	hypothetical protein
GPL_13374_0194	hypothetical protein; K03724 ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.1.-]
GPL_13374_0187	hypothetical protein
GPL_13374_0186	ATPase; K03924 MoxR-like ATPase [EC:3.6.3.-]
GPL_13374_0183	hypothetical protein
GPL_13374_0182	ATP-dependent protease Lon; K04076 Lon-like ATP-dependent protease [EC:3.4.21.-]
GPL_13374_0180	ribokinase related protein; K00852 ribokinase [EC:2.7.1.15]
GPL_13374_0179	acetyltransferase
GPL_13374_0178	eno; phosphopyruvate hydratase (EC:4.2.1.11); K01689 enolase [EC:4.2.1.11]
GPL_13374_0176	putative phosphatidylethanolamine-binding protein; K06910
GPL_13374_0175	GTP:adenosylcobinamide-phosphate guanylyltransferase
GPL_13374_0167	malA; alpha-glucosidase (EC:3.2.1.20); K01187 alpha-glucosidase [EC:3.2.1.20]
GPL_13374_0164	succinate-semialdehyde dehydrogenase [NADP+] (EC:1.2.1.16); K00135 succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]
GPL_13374_0162	hypothetical protein
GPL_13374_0156	ctaD; cytochrome c oxidase subunit I; K02274 cytochrome c oxidase subunit I [EC:1.9.3.1]
GPL_13374_0153	transcription factor; K03627 putative transcription factor
GPL_13374_0151	TPR repeat-containing protein
GPL_13374_0148	rps15p; 30S ribosomal protein S15P; K02956 small subunit ribosomal protein S15
GPL_13374_0141	hypothetical protein; K07151 dolichyl-diphosphooligosaccharide--protein glycosyltransferase [EC:2.4.1.119]
GPL_13374_0140	pheT; phenylalanyl-tRNA synthetase subunit beta (EC:6.1.1.20); K01890 phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]

GPL_13374_0139	hypothetical protein; K07722 CopG family transcriptional regulator, nickel-responsive regulator
GPL_13374_0138	hypothetical protein; K06937
GPL_13374_0136	pyruvoyl-dependent arginine decarboxylase (EC:4.1.1.19); K02626 arginine decarboxylase [EC:4.1.1.19]
GPL_13374_0134	short chain dehydrogenase
GPL_13374_0131	short chain dehydrogenase
GPL_13374_0128	aldehyde dehydrogenase related protein; K00294 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]
GPL_13374_0126	phosphoenolpyruvate carboxykinase (EC:4.1.1.32); K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
GPL_13374_0122	translation initiation factor IF-2; K03243 translation initiation factor IF-2 unclassified subunit
GPL_13374_0121	ndk; nucleoside diphosphate kinase; K00940 nucleoside-diphosphate kinase [EC:2.7.4.6]
GPL_13374_0119	rps28e; 30S ribosomal protein S28e; K02979 small subunit ribosomal protein S28e
GPL_13374_0118	rpl7ae; 50S ribosomal protein L7Ae; K02936 large subunit ribosomal protein L7Ae
GPL_13374_0117	dihydrodipicolinate synthetase; K01714 dihydrodipicolinate synthase [EC:4.2.1.52]
GPL_13374_0114	exosome complex RNA-binding protein Csl4; K07573 exosome complex component CSL4
GPL_13374_0112	small nuclear ribonucleoprotein (snRNP)-like protein
GPL_13374_0108	carboxymethylenebutenolidase (EC:3.1.1.45); K01061 carboxymethylenebutenolidase [EC:3.1.1.45]
GPL_13374_0107	ornithine carbamoyltransferase (EC:2.1.3.3); K00611 ornithine carbamoyltransferase [EC:2.1.3.3]
GPL_13374_0106	succinyl-CoA synthetase subunit alpha (EC:6.2.1.5); K01902 succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
GPL_13374_0105	sucC; succinyl-CoA synthetase subunit beta (EC:6.2.1.5); K01903 succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
GPL_13374_0104	thermosome, alpha chain
GPL_13374_0103	alternative thymidylate synthase
GPL_13374_0102	hypothetical protein; K07068
GPL_13374_0101	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
GPL_13374_0100	sugar ABC transporter extracellular solute binding protein
GPL_13374_0098	sugar ABC transporter ATP binding protein
GPL_13374_0097	HAD superfamily hydrolase
GPL_13374_0096	thioesterase; K07107
GPL_13374_0094	hypothetical protein
GPL_13374_0093	hypothetical protein
GPL_13374_0091	VAT ATPase (VCP-like ATPase); K13525 transitional endoplasmic reticulum ATPase
GPL_13374_0090	hypothetical protein

GPL_13374_0089	peptide chain release factor 1; K03265 peptide chain release factor eRF subunit 1
GPL_13374_0088	pyrH; uridylate kinase; K09903 uridylate kinase [EC:2.7.4.22]
GPL_13374_0087	2-oxoglutarate ferredoxin oxidoreductase subunit beta (EC:1.2.7.3); K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
GPL_13374_0086	2-oxoacid ferredoxin oxidoreductase subunit alpha; K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
GPL_13374_0085	hypothetical protein
GPL_13374_0084	phosphoribosylformylglycinamidine synthase I (EC:6.3.5.3); K01952 phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]
GPL_13374_0081	hypothetical protein
GPL_13374_0078	heat shock protein
GPL_13374_0075	DNA-directed RNA polymerase subunit L (EC:2.7.7.6); K03056 DNA-directed RNA polymerase subunit L [EC:2.7.7.6]
GPL_13374_0072	NAD(FAD)-dependent dehydrogenase
GPL_13374_0071	hypothetical protein
GPL_13374_0069	threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
GPL_13374_0068	fusA; elongation factor EF-2; K03234 elongation factor EF-2 [EC:3.6.5.3]
GPL_13374_0067	rps10p; 30S ribosomal protein S10P; K02946 small subunit ribosomal protein S10
GPL_13374_0066	ef1a, tuf; elongation factor 1-alpha (EC:3.6.5.3); K03231 elongation factor EF-1 alpha subunit [EC:3.6.5.3]
GPL_13374_0065	30S ribosomal protein S3Ae; K02984 small subunit ribosomal protein S3Ae
GPL_13374_0062	transcription regulator
GPL_13374_0061	asparagine synthetase A (EC:6.1.1.22); K01893 asparaginyl-tRNA synthetase [EC:6.1.1.22]
GPL_13374_0060	ATPase; K06865
GPL_13374_0052	hypothetical protein
GPL_13374_0047	glutamate decarboxylase; K01580 glutamate decarboxylase [EC:4.1.1.15]
GPL_13374_0045	bcp-1; peroxiredoxin; K03564 peroxiredoxin Q/BCP [EC:1.11.1.15]
GPL_13374_0033	translation initiation factor IF-5A; K03263 translation initiation factor eIF-5A
GPL_13374_0032	agmatinase; K01480 agmatinase [EC:3.5.3.11]
GPL_13374_0030	rpl10e; 50S ribosomal protein L10e; K02866 large subunit ribosomal protein L10e
GPL_13374_0027	hypothetical protein; K07050
GPL_13374_0026	tetrahydrofolylpolyglutamate synthase related protein; K11754 dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12 6.3.2.17]
GPL_13374_0024	metal-dependent hydrolase

GPL_13374_0022	pyridoxal biosynthesis lyase PdxS; K06215 pyridoxine biosynthesis protein [EC:4.-.-.-]
GPL_13374_0020	enoyl-CoA hydratase
GPL_13374_0018	Rieske Fe-S protein
GPL_13374_0014	cysteine desulfurase (EC:4.4.1.-)
GPL_13374_0011	hypothetical protein
GPL_13374_0008	aldo/keto reductase (EC:1.1.1.91)
GPL_13334_0195	transposase, IS4
GPL_13334_0193	NADH oxidoreductase (EC:1.-.-.-); K00540 [EC:1.-.-.-]
GPL_13334_0191	ribose-phosphate pyrophosphokinase (EC:2.7.6.1); K00948 ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
GPL_13334_0190	crt; 3-hydroxybutyryl-CoA dehydratase
GPL_13334_0187	iron-dependent transcription repressor related protein
GPL_13334_0184	multidrug resistance ABC transporter ATP-binding and permease protein; K06147 ATP-binding cassette, subfamily B, bacterial
GPL_13334_0183	domain of unknown function DUF1731; K07071
GPL_13334_0182	acetyl-CoA acetyltransferase (EC:2.3.1.16); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
GPL_13334_0166	universal stress protein UspA-like protein
GPL_13334_0165	aspA; aspartate ammonia-lyase (EC:4.3.1.1); K01679 fumarate hydratase, class II [EC:4.2.1.2]
GPL_13334_0164	methyltransferase type 11
GPL_13334_0163	amidohydrolase
GPL_13334_0158	6-phosphogluconate dehydrogenase NAD-binding; K00020 3-hydroxyisobutyrate dehydrogenase [EC:1.1.1.31]
GPL_13334_0156	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase (EC:4.1.1.36 6.3.2.5); K13038 phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase [EC:4.1.1.36 6.3.2.5]
GPL_13334_0145	SoxB-like sarcosine oxidase, beta subunit related
GPL_13334_0141	metal-binding protein
GPL_13334_0139	tryptophanyl-tRNA synthetase (EC:6.1.1.2); K01867 tryptophanyl-tRNA synthetase [EC:6.1.1.2]
GPL_13334_0138	ornithine cyclodeaminase (EC:4.3.1.12); K01750 ornithine cyclodeaminase [EC:4.3.1.12]
GPL_13334_0135	hypothetical protein
GPL_13334_0133	cbiA-2; cobyrinic acid a,c-diamide synthase (EC:6.3.5.9); K02224 cobyrinic acid a,c-diamide synthase [EC:6.3.5.9 6.3.1.-]
GPL_13334_0132	ilvE; branched-chain amino acid aminotransferase (EC:2.6.1.42); K00826 branched-chain amino acid aminotransferase [EC:2.6.1.42]
GPL_13334_0129	electron transfer flavoprotein subunit alpha; K03522 electron transfer flavoprotein alpha subunit
GPL_13334_0128	electron transfer flavoprotein subunit beta; K03521 electron transfer flavoprotein beta subunit

GPL_13334_0127	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
GPL_13334_0125	acyl-CoA dehydrogenase; K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
GPL_13334_0124	acyl-CoA dehydrogenase-like protein
GPL_13334_0120	trehalose synthase (EC:5.4.99.16); K05343 maltose alpha-D-glucosyltransferase [EC:5.4.99.16]
GPL_13334_0118	1,4-alpha-glucan branching enzyme (EC:2.4.1.18); K00700 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]
GPL_13334_0116	chromosome partitioning ATPase; K03593 ATP-binding protein involved in chromosome partitioning
GPL_13334_0112	transcriptional regulatory protein
GPL_13334_0108	citrate synthase; K01647 citrate synthase [EC:2.3.3.1]
GPL_13334_0107	PadR family transcriptional regulator
GPL_13334_0105	sugar kinase
GPL_13334_0104	glutamine synthetase; K01915 glutamine synthetase [EC:6.3.1.2]
GPL_13334_0103	30S ribosomal protein S19e; K02966 small subunit ribosomal protein S19e
GPL_13334_0102	hypothetical protein; K06875
GPL_13334_0100	50S ribosomal protein L31e; K02910 large subunit ribosomal protein L31e
GPL_13334_0098	pyrE; orotate phosphoribosyltransferase (EC:2.4.2.10); K00762 orotate phosphoribosyltransferase [EC:2.4.2.10]
GPL_13334_0097	fumarylacetoacetate (FAA) hydrolase
GPL_13334_0094	hypothetical protein
GPL_13334_0093	mannose-1-phosphate guanyltransferase (EC:2.7.7.13); K00966 mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
GPL_13334_0092	hutU; urocanate hydratase (EC:4.2.1.49); K01712 urocanate hydratase [EC:4.2.1.49]
GPL_13334_0090	acylaminoacyl-peptidase
GPL_13334_0079	aldo/keto reductase
GPL_13334_0078	acetyl-coenzyme-A synthetase; K01895 acetyl-CoA synthetase [EC:6.2.1.1]
GPL_13334_0073	methionine synthase; K00549 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [EC:2.1.1.14]
GPL_13334_0072	hypothetical protein
GPL_13334_0069	hypothetical protein
GPL_13334_0067	tricorn protease interacting factor F2 (EC:3.4.11.-); K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
GPL_13334_0059	ribonucleotide-diphosphate reductase subunit alpha (EC:1.17.4.1); K00525 ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
GPL_13334_0057	aminomethyltransferase (glycine cleavage system T protein); K00605 aminomethyltransferase [EC:2.1.2.10]
GPL_13334_0055	glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]

GPL_13334_0054	RecA-superfamily ATPase implicated in signal transduction-like protein
GPL_13334_0053	galactonate dehydratase
GPL_13334_0052	DNA topoisomerase I (EC:5.99.1.2); K03168 DNA topoisomerase I [EC:5.99.1.2]
GPL_13334_0050	tricorn protease; K08676 tricorn protease [EC:3.4.21.-]
GPL_13334_0048	purH; bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (EC:3.5.4.10 2.1.2.3); K00602 phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]
GPL_13334_0047	S-adenosylmethionine synthetase (EC:2.5.1.6); K00789 S-adenosylmethionine synthetase [EC:2.5.1.6]
GPL_13334_0042	hypothetical protein
GPL_13334_0040	hypothetical protein; K09716 hypothetical protein
GPL_13334_0039	hypothetical protein
GPL_13334_0038	valS; valyl-tRNA synthetase (EC:6.1.1.9); K01873 valyl-tRNA synthetase [EC:6.1.1.9]
GPL_13334_0035	4-aminobutyrate aminotransferase (EC:2.6.1.19); K00823 4-aminobutyrate aminotransferase [EC:2.6.1.19]
GPL_13334_0034	hypothetical protein
GPL_13334_0033	acyl-coenzyme A synthetase; K01895 acetyl-CoA synthetase [EC:6.2.1.1]
GPL_13334_0028	pyrG; CTP synthetase (EC:6.3.4.2); K01937 CTP synthase [EC:6.3.4.2]
GPL_13334_0026	GTPase; K06883
GPL_13334_0024	hypothetical protein
GPL_13334_0022	superoxide dismutase; K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
GPL_13334_0021	phospholipase D
GPL_13334_0017	hypothetical protein
GPL_13334_0016	V-type ATP synthase subunit C (EC:3.6.3.14); K02119 V-type H+-transporting ATPase subunit C [EC:3.6.3.14]
GPL_13334_0015	V-type ATP synthase subunit F (EC:3.6.3.14); K02122 V-type H+-transporting ATPase subunit F [EC:3.6.3.14]
GPL_13334_0014	atpA; V-type ATP synthase subunit A (EC:3.6.3.14); K02117 V-type H+-transporting ATPase subunit A [EC:3.6.3.14]
GPL_13334_0013	V-type ATP synthase subunit B (EC:3.6.3.14); K02118 V-type H+-transporting ATPase subunit B [EC:3.6.3.14]
GPL_13334_0012	V-type ATP synthase subunit D (EC:3.6.3.14); K02120 V-type H+-transporting ATPase subunit D [EC:3.6.3.14]
GPL_13334_0011	hypothetical protein
GPL_13334_0010	V-type ATP synthase subunit I (EC:3.6.3.14); K02123 V-type H+-transporting ATPase subunit I [EC:3.6.3.14]
GPL_13334_0007	hypothetical protein
GPL_13334_0006	UDP-glucose 4-epimerase (EC:5.1.3.2); K01784 UDP-glucose 4-epimerase [EC:5.1.3.2]
GPL_13334_0004	isopentenyl pyrophosphate isomerase (EC:5.3.3.2); K01823 isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]

GPL_13327_0080	hypothetical protein
GPL_13327_0079	metal-dependent RNase; K07041
GPL_13327_0078	proteasome, beta chain; K03433 proteasome beta subunit [EC:3.4.25.1]
GPL_13327_0077	inosine-5'-monophosphate dehydrogenase related protein
GPL_13327_0075	hypothetical protein
GPL_13327_0074	hemH; phosphoribosylaminoimidazole-succinocarboxamide synthase (EC:6.3.2.6); K01923 phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2.6]
GPL_13327_0073	hypothetical protein; K07145
GPL_13327_0072	peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K01802 peptidylprolyl isomerase [EC:5.2.1.8]
GPL_13327_0071	nicotinate phosphoribosyltransferase (EC:2.4.2.11); K00763 nicotinate phosphoribosyltransferase [EC:2.4.2.11]
GPL_13327_0069	cysS; cysteinyl-tRNA synthetase (EC:6.1.1.16); K01883 cysteinyl-tRNA synthetase [EC:6.1.1.16]
GPL_13327_0068	hypothetical protein
GPL_13327_0067	hypothetical protein
GPL_13327_0066	hypothetical protein
GPL_13327_0064	NADH peroxidase related protein; K00359 NADH oxidase [EC:1.6.-.-]
GPL_13327_0060	hypothetical protein
GPL_13327_0058	hypothetical protein
GPL_13327_0057	hypothetical protein
GPL_13327_0056	hypothetical protein
GPL_13327_0055	hypothetical protein
GPL_13327_0054	hypothetical protein
GPL_13327_0053	ATPase of the AAA+ class involved in cell division
GPL_13327_0052	hypothetical protein
GPL_13327_0049	heat shock protein GrpE related protein; K03687 molecular chaperone GrpE
GPL_13327_0048	dnaK; molecular chaperone DnaK; K04043 molecular chaperone DnaK
GPL_13327_0047	chaperone protein DnaJ; K03686 molecular chaperone DnaJ
GPL_13327_0045	universal stress protein
GPL_13327_0037	rps17E; 30S ribosomal protein S17e; K02962 small subunit ribosomal protein S17e
GPL_13327_0034	ileS; isoleucyl-tRNA synthetase (EC:6.1.1.5); K01870 isoleucyl-tRNA synthetase [EC:6.1.1.5]
GPL_13327_0031	winged helix-turn-helix domain-containing protein/riboflavin kinase; K07732 riboflavin kinase, archaea type [EC:2.7.1.161]
GPL_13327_0029	phosphoribosylformylglycinamidine synthase II (EC:6.3.5.3); K01952 phosphoribosylformylglycinamidine synthase

	[EC:6.3.5.3]
GPL_13327_0028	phosphoribosylformylglycinamidine synthase (EC:6.3.5.3); K01952 phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]
GPL_13327_0027	geranylgeranylglyceryl phosphate synthase-like protein; K07094
GPL_13327_0024	putative NTPase; K06928
GPL_13327_0019	acyl-CoA hydrolase related protein
GPL_13327_0018	ribose-5-phosphate isomerase A (EC:5.3.1.6); K01807 ribose 5-phosphate isomerase A [EC:5.3.1.6]
GPL_13327_0017	AsnC family transcriptional regulator
GPL_13327_0015	hypothetical protein
GPL_13327_0014	glucoamylase (EC:3.2.1.3); K01178 glucoamylase [EC:3.2.1.3]
GPL_13327_0009	endoribonuclease L-PSP; K07567 TdcF protein
GPL_13327_0008	glutamate dehydrogenase; K00261 glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]
GPL_13327_0007	alcohol dehydrogenase (EC:1.1.1.1); K13953 alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]
GPL_13327_0006	hypothetical protein
GPL_13317_0005	sporulation protein (spo0KD) related protein; K02031 peptide/nickel transport system ATP-binding protein; K02032 peptide/nickel transport system ATP-binding protein
GPL_13317_0003	penicillin amidase (EC:3.5.1.11); K07116
GPL_13296_0125	thrS; threonyl-tRNA synthetase (EC:6.1.1.3); K01868 threonyl-tRNA synthetase [EC:6.1.1.3]
GPL_13296_0124	tricorn protease interacting factor F2 (EC:3.4.11.-); K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
GPL_13296_0123	exported protein
GPL_13296_0119	hypothetical protein
GPL_13296_0118	hypothetical protein
GPL_13296_0117	hypothetical protein
GPL_13296_0115	hypothetical protein
GPL_13296_0114	hutH; histidine ammonia-lyase (EC:4.3.1.3); K01745 histidine ammonia-lyase [EC:4.3.1.3]
GPL_13296_0110	amidohydrolase (EC:3.5.1.-); K01463 [EC:3.5.1.-]
GPL_13296_0109	hypothetical protein
GPL_13296_0103	triosephosphate isomerase (EC:5.3.1.1); K01803 triosephosphate isomerase (TIM) [EC:5.3.1.1]
GPL_13296_0101	(S)-2-hydroxy-acid oxidase chain D (EC:1.1.3.15); K00104 glycolate oxidase [EC:1.1.3.15]
GPL_13296_0100	heterodisulfide reductase related protein
GPL_13296_0099	isochorismatase hydrolase
GPL_13296_0098	hypothetical protein

GPL_13296_0096	rpl3p; 50S ribosomal protein L3P; K02906 large subunit ribosomal protein L3
GPL_13296_0095	rpl4lp; 50S ribosomal protein L4P; K02930 large subunit ribosomal protein L4e
GPL_13296_0094	rplW; 50S ribosomal protein L23P; K02892 large subunit ribosomal protein L23
GPL_13296_0093	rpl2p; 50S ribosomal protein L2P; K02886 large subunit ribosomal protein L2
GPL_13296_0092	rps19p; 30S ribosomal protein S19P; K02965 small subunit ribosomal protein S19
GPL_13296_0091	rpl22p; 50S ribosomal protein L22P; K02890 large subunit ribosomal protein L22
GPL_13296_0090	rps3p; 30S ribosomal protein S3P; K02982 small subunit ribosomal protein S3
GPL_13296_0086	rps17p; 30S ribosomal protein S17P; K02961 small subunit ribosomal protein S17
GPL_13296_0085	rpl14p; 50S ribosomal protein L14P; K02874 large subunit ribosomal protein L14
GPL_13296_0084	rpl24p; 50S ribosomal protein L24P; K02895 large subunit ribosomal protein L24
GPL_13296_0083	30S ribosomal protein S4e; K02987 small subunit ribosomal protein S4e
GPL_13296_0082	rpl5p; 50S ribosomal protein L5P; K02931 large subunit ribosomal protein L5
GPL_13296_0080	rps8p; 30S ribosomal protein S8P; K02994 small subunit ribosomal protein S8
GPL_13296_0079	rpl6p; 50S ribosomal protein L6P; K02933 large subunit ribosomal protein L6
GPL_13296_0078	rpl32e; 50S ribosomal protein L32e; K02912 large subunit ribosomal protein L32e
GPL_13296_0077	rpl19e; 50S ribosomal protein L19e; K02885 large subunit ribosomal protein L19e
GPL_13296_0075	rps5p; 30S ribosomal protein S5P; K02988 small subunit ribosomal protein S5
GPL_13296_0074	rpl30p; 50S ribosomal protein L30P; K02907 large subunit ribosomal protein L30
GPL_13296_0073	rpl15p; 50S ribosomal protein L15P; K02876 large subunit ribosomal protein L15
GPL_13296_0071	adenylate kinase (EC:2.7.4.3); K00939 adenylate kinase [EC:2.7.4.3]
GPL_13296_0068	H/ACA RNA-protein complex component Cbf5p; K03177 tRNA pseudouridine synthase B [EC:5.4.99.12]
GPL_13296_0065	small nuclear ribonucleoprotein; K04796 small nuclear ribonucleoprotein
GPL_13296_0064	hypothetical protein
GPL_13296_0062	rpl44e; 50S ribosomal protein L44e; K02929 large subunit ribosomal protein L44e
GPL_13296_0060	translation initiation factor IF-2 subunit alpha; K03237 translation initiation factor eIF-2 alpha subunit
GPL_13296_0058	hypothetical protein; K07159
GPL_13296_0055	nitrilase related protein
GPL_13296_0053	alpha, alpha-trehalose-phosphate synthase (UDP-forming) related protein; K00697 alpha,alpha-trehalose-phosphate synthase (UDP-forming) [EC:2.4.1.15]
GPL_13296_0050	translation initiation factor IF-2B subunit alpha; K03239 translation initiation factor eIF-2B alpha subunit
GPL_13296_0048	rpoH; DNA-directed RNA polymerase subunit H (EC:2.7.7.6); K03053 DNA-directed RNA polymerase subunit H [EC:2.7.7.6]

GPL_13296_0047	DNA-directed RNA polymerase subunit B (EC:2.7.7.6); K13798 DNA-directed RNA polymerase subunit B [EC:2.7.7.6]
GPL_13296_0046	DNA-directed RNA polymerase subunit A' (EC:2.7.7.6); K03041 DNA-directed RNA polymerase subunit A' [EC:2.7.7.6]
GPL_13296_0045	DNA-directed RNA polymerase subunit A'' (EC:2.7.7.6); K03042 DNA-directed RNA polymerase subunit A'' [EC:2.7.7.6]
GPL_13296_0044	nusA; transcription elongation factor NusA-like protein; K02600 N utilization substance protein A
GPL_13296_0043	TIF11; translation initiation factor IF-1A; K03236 translation initiation factor eIF-1A
GPL_13296_0036	hypothetical protein
GPL_13296_0034	rps13p; 30S ribosomal protein S13P; K02952 small subunit ribosomal protein S13
GPL_13296_0033	rps4p; 30S ribosomal protein S4P; K02986 small subunit ribosomal protein S4
GPL_13296_0031	DNA-directed RNA polymerase subunit D (EC:2.7.7.6); K03047 DNA-directed RNA polymerase subunit D [EC:2.7.7.6]
GPL_13296_0030	inositol-phosphate phosphatase (EC:3.1.3.25); K01092 myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]
GPL_13296_0027	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative (EC:2.1.1.14); K00549 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [EC:2.1.1.14]
GPL_13296_0026	carboxyphosphonoenolpyruvate phosphonomutase; K01003 carboxyvinyl-carboxyphosphonate phosphorylmutase [EC:2.7.8.23]
GPL_13296_0025	hypothetical protein; K01720 2-methylcitrate dehydratase [EC:4.2.1.79]
GPL_13296_0023	D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein
GPL_13296_0022	hypothetical protein
GPL_13296_0019	ubiquinone/menaquinone methyltransferase related protein; K03183 ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.-]
GPL_13296_0010	hypothetical protein; K06930
GPL_13296_0009	pyruvate kinase (EC:2.7.1.40); K00873 pyruvate kinase [EC:2.7.1.40]
GPL_13296_0008	FKBP-type peptidyl-prolyl cis-trans isomerase; K01802 peptidylprolyl isomerase [EC:5.2.1.8]
GPL_13296_0006	50S ribosomal protein L18e; K02883 large subunit ribosomal protein L18e
GPL_13296_0005	rpl13p; 50S ribosomal protein L13P; K02871 large subunit ribosomal protein L13
GPL_13296_0004	rps9p; 30S ribosomal protein S9P; K02996 small subunit ribosomal protein S9
GPL_13296_0003	DNA-directed RNA polymerase subunit N (EC:2.7.7.6); K03058 DNA-directed RNA polymerase subunit N [EC:2.7.7.6]
GPL_13290_0191	hypothetical protein
GPL_13290_0186	hypothetical protein
GPL_13290_0181	D-3-phosphoglycerate dehydrogenase; K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]

GPL_13290_0180	serine--pyruvate aminotransferase; K00839 aminotransferase [EC:2.6.1.-]
GPL_13290_0173	O-methyltransferase family 3
GPL_13290_0166	hypothetical protein
GPL_13290_0165	hypothetical protein
GPL_13290_0162	hypothetical protein
GPL_13290_0154	VAT-2 protein
GPL_13290_0153	hypothetical protein
GPL_13290_0151	AAA ATPase central domain protein
GPL_13290_0150	hypothetical protein
GPL_13290_0148	hsp 20 family small heat shock protein
GPL_13290_0146	GTPase; K07588 LAO/AO transport system kinase [EC:2.7.-.-]
GPL_13290_0145	methylmalonyl-CoA mutase alpha subunit (EC:5.4.99.2); K01849 methylmalonyl-CoA mutase, C-terminal domain [EC:5.4.99.2]
GPL_13290_0124	alcohol dehydrogenase GroES domain protein
GPL_13290_0123	oxidoreductase
GPL_13290_0121	hypothetical protein; K09129 hypothetical protein
GPL_13290_0120	ABC transporter related protein
GPL_13290_0119	hypothetical protein
GPL_13290_0118	rubrerythrin
GPL_13290_0114	peroxiredoxin
GPL_13290_0110	adenylosuccinate lyase (EC:4.3.2.2); K01756 adenylosuccinate lyase [EC:4.3.2.2]
GPL_13290_0106	hypothetical protein
GPL_13290_0105	hypothetical protein
GPL_13290_0101	tfb; transcription initiation factor IIB; K03124 transcription initiation factor TFIIB
GPL_13290_0098	hypothetical protein
GPL_13290_0094	putative oxidoreductase
GPL_13290_0092	thioredoxin; K03671 thioredoxin 1
GPL_13290_0091	trxB-2; thioredoxin reductase (TrxB-2); K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]
GPL_13290_0089	TPR repeat-containing protein
GPL_13290_0087	enoyl-CoA hydratase; K01692 enoyl-CoA hydratase [EC:4.2.1.17]
GPL_13290_0086	3-hydroxybutyryl-CoA dehydrogenase (EC:1.1.1.157); K00074 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]

GPL_13290_0085	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
GPL_13290_0084	rhodanese domain protein
GPL_13290_0081	hypothetical protein
GPL_13290_0080	sugar ABC transporter 1, extracellular binding protein; K02027 multiple sugar transport system substrate-binding protein
GPL_13290_0079	sugar ABC transporter 1, ATP binding protein; K02023 multiple sugar transport system ATP-binding protein
GPL_13290_0075	long-chain-fatty-acid--CoA ligase (EC:2.3.1.86); K00666 fatty-acyl-CoA synthase [EC:6.2.1.-]
GPL_13290_0074	ftsZ; cell division protein FtsZ; K03531 cell division protein FtsZ
GPL_13290_0073	transketolase; K00615 transketolase [EC:2.2.1.1]
GPL_13290_0072	transketolase; K00615 transketolase [EC:2.2.1.1]
GPL_13290_0071	putative translaldolase (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2]
GPL_13290_0069	hypothetical protein
GPL_13290_0068	malate oxidoreductase (malic enzyme); K00027 malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
GPL_13290_0067	hypothetical protein
GPL_13290_0066	hypothetical protein
GPL_13290_0063	asnC; asparaginyl-tRNA synthetase (EC:6.1.1.22); K01893 asparaginyl-tRNA synthetase [EC:6.1.1.22]
GPL_13290_0060	translation elongation factor (GTPase)
GPL_13290_0059	phosphoribosylamine--glycine ligase (EC:6.3.4.13); K01945 phosphoribosylamine--glycine ligase [EC:6.3.4.13]
GPL_13290_0055	ribonuclease Z (EC:3.1.26.11); K00784 ribonuclease Z [EC:3.1.26.11]
GPL_13290_0053	chromosome hypothetical proteinregation protein related ptotein; K03529 chromosome hypothetical proteinregation protein
GPL_13290_0049	tyrosyl-tRNA synthetase (EC:6.1.1.1); K01866 tyrosyl-tRNA synthetase [EC:6.1.1.1]
GPL_13290_0048	flap endonuclease-1; K04799 flap endonuclease-1 [EC:3.-.-.-]
GPL_13290_0045	prolyl-tRNA synthetase (EC:6.1.1.15); K01881 prolyl-tRNA synthetase [EC:6.1.1.15]
GPL_13290_0044	diaminopimelate aminotransferase; K01439 succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]
GPL_13290_0041	aspartate aminotransferase (EC:2.6.1.1); K00812 aspartate aminotransferase [EC:2.6.1.1]
GPL_13290_0040	transcriptional regulator
GPL_13290_0034	protein of unknown function DUF255; K06888
GPL_13290_0031	4-hydroxyphenylpyruvate dioxygenase (EC:1.13.11.27); K00457 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]
GPL_13290_0030	fumarylacetoacetate hydrolase family protein
GPL_13290_0029	homogentisate 1,2-dioxygenase (EC:1.13.11.5); K00451 homogentisate 1,2-dioxygenase [EC:1.13.11.5]

GPL_13290_0027	DNA-binding protein; K06934
GPL_13290_0024	TenA/THI-4 family protein
GPL_13290_0021	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
GPL_13290_0018	hypothetical protein; K09732 hypothetical protein
GPL_13290_0017	molybdopterin binding domain-containing protein; K03742 competence/damage-inducible protein CinA
GPL_13290_0015	isomerizing glucosamine--fructose-6-phosphate aminotransferase (EC:2.6.1.16); K00820 glucosamine--fructose-6-phosphate aminotransferase (isomerizing) [EC:2.6.1.16]
GPL_13290_0010	hypothetical protein
GPL_13290_0007	DNA helicase II; K03657 DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.1.-]
GPL_13290_0006	putative alcohol dehydrogenase; K00001 alcohol dehydrogenase [EC:1.1.1.1]
GPL_13287_0180	hypothetical protein
GPL_13287_0178	hypothetical protein
GPL_13287_0176	diphosphomevalonate decarboxylase (EC:4.1.1.33); K01597 diphosphomevalonate decarboxylase [EC:4.1.1.33]
GPL_13287_0175	hypothetical protein
GPL_13287_0173	single-stranded DNA-binding protein; K07466 replication factor A1
GPL_13287_0172	ATP-dependent DNA ligase (EC:6.5.1.1); K10747 DNA ligase 1 [EC:6.5.1.1]
GPL_13287_0168	sdhA; succinate dehydrogenase flavoprotein subunit (EC:1.3.5.1); K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
GPL_13287_0167	fumarate reductase iron-sulfur subunit (EC:1.3.5.1); K00240 succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]
GPL_13287_0159	pyruvate dehydrogenase (EC:1.2.2.2); K00156 pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]
GPL_13287_0157	phosphoribosylaminoimidazole carboxylase catalytic subunit; K01588 5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]
GPL_13287_0152	tricorn protease interacting factor F2 (EC:3.4.11.-); K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
GPL_13287_0151	PmbA protein; K03592 PmbA protein
GPL_13287_0150	zinc metalloprotease (EC:3.4.24.-); K03568 TldD protein
GPL_13287_0149	CBS domain-containing protein
GPL_13287_0148	glycine hydroxymethyltransferase related protein; K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]
GPL_13287_0146	DNA polymerase II (EC:2.7.7.7); K02319 DNA polymerase I [EC:2.7.7.7]
GPL_13287_0139	hypothetical protein
GPL_13287_0137	Fe2+ uptake regulation protein; K03711 Fur family transcriptional regulator, ferric uptake regulator
GPL_13287_0136	hisS; histidyl-tRNA synthetase (EC:6.1.1.21); K01892 histidyl-tRNA synthetase [EC:6.1.1.21]
GPL_13287_0134	transcription regulator

GPL_13287_0132	GMP synthase subunit B (EC:6.3.5.2); K01951 GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]
GPL_13287_0131	rps2P; 30S ribosomal protein S2; K02967 small subunit ribosomal protein S2
GPL_13287_0128	aspartate aminotransferase related protein
GPL_13287_0124	transcription factor; K03120 transcription initiation factor TFIID TATA-box-binding protein
GPL_13287_0119	inosine 5'-monophosphate dehydrogenase (EC:1.1.1.205); K00088 IMP dehydrogenase [EC:1.1.1.205]
GPL_13287_0116	pyruvate phosphate dikinase (EC:2.7.9.1); K01006 pyruvate,orthophosphate dikinase [EC:2.7.9.1]
GPL_13287_0115	alpha/beta superfamily hydrolase
GPL_13287_0113	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase (EC:4.1.1.36 6.3.2.5); K13038 phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase [EC:4.1.1.36 6.3.2.5]
GPL_13287_0108	transcriptional regulator
GPL_13287_0107	probable endonuclease IV (EC:3.1.21.2); K01151 deoxyribonuclease IV [EC:3.1.21.2]
GPL_13287_0102	hypothetical protein; K07062
GPL_13287_0099	alpha-mannosidase; K01191 alpha-mannosidase [EC:3.2.1.24]
GPL_13287_0098	methyltransferase
GPL_13287_0097	protein of unknown function DUF323
GPL_13287_0091	acetylornithine aminotransferase (EC:2.6.1.11); K05830 acetylornithine/acetyl-lysine aminotransferase [EC:2.6.1.11 2.6.1.-]
GPL_13287_0087	hypothetical protein
GPL_13287_0080	beta-hydroxybutyryl-CoA dehydrogenase related protein; K00074 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
GPL_13287_0078	aspC; aspartyl-tRNA synthetase (EC:6.1.1.12); K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]
GPL_13287_0076	glucokinase (EC:2.7.1.2); K00845 glucokinase [EC:2.7.1.2]
GPL_13287_0071	gyrB; DNA gyrase subunit B; K02470 DNA gyrase subunit B [EC:5.99.1.3]
GPL_13287_0070	DNA gyrase subunit A; K02469 DNA gyrase subunit A [EC:5.99.1.3]
GPL_13287_0069	homoserine dehydrogenase (EC:1.1.1.3); K00003 homoserine dehydrogenase [EC:1.1.1.3]
GPL_13287_0067	4-hydroxybenzoate decarboxylase; K03182 3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiD [EC:4.1.1.-]
GPL_13287_0060	putative nitrite reductase/sulfite reductase
GPL_13287_0057	hypothetical protein
GPL_13287_0054	tyrosine recombinase XerD; K04763 integrase/recombinase XerD
GPL_13287_0050	Putative uncharacterized protein
GPL_13287_0040	hypothetical protein
GPL_13287_0036	NAD-dependent aldehyde dehydrogenase; K00128 aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]

GPL_13287_0035	hypothetical protein
GPL_13287_0034	arsenite-transporting ATPase (EC:3.6.3.16); K01551 arsenite-transporting ATPase [EC:3.6.3.16]
GPL_13287_0032	DNA/RNA-binding protein AlbA; K03622 archaea-specific DNA-binding protein
GPL_13287_0030	hypothetical protein
GPL_13287_0028	isovaleryl-CoA dehydrogenase; K00253 isovaleryl-CoA dehydrogenase [EC:1.3.99.10]
GPL_13287_0026	arginine deiminase
GPL_13287_0025	bifunctional phosphoglucose/phosphomannose isomerase; K01809 mannose-6-phosphate isomerase [EC:5.3.1.8]; K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]
GPL_13287_0024	hypothetical protein
GPL_13287_0022	UDP-glucose 4-epimerase
GPL_13287_0020	iron-regulated ABC transporter ATPase subunit; K09013 Fe-S cluster assembly ATP-binding protein
GPL_13287_0018	hypothetical protein; K07033
GPL_13287_0017	csd1; cysteine desulfurase (EC:4.4.1.-); K11717 cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]
GPL_13287_0013	ATPase; K06915
GPL_13287_0011	N-acyl-L-amino acid amidohydrolase (EC:3.5.1.14); K01436 aminoacylase [EC:3.5.1.14]
GPL_12824_0011	hypothetical protein
GPL_12303_0037	X-Pro dipeptidase
GPL_12303_0031	hypothetical protein
GPL_12303_0026	nadE; NAD synthetase (EC:6.3.1.5); K01916 NAD+ synthase [EC:6.3.1.5]
GPL_12303_0025	bifunctional protein FolD; K01491 methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase [EC:1.5.1.5 3.5.4.9]
GPL_12303_0024	glucose-1-dehydrogenase (EC:1.1.1.47); K00034 glucose 1-dehydrogenase [EC:1.1.1.47]
GPL_12303_0023	ribA; GTP cyclohydrolase II (EC:3.5.4.25); K01497 GTP cyclohydrolase II [EC:3.5.4.25]
GPL_12303_0022	hypothetical protein
GPL_12303_0020	NADH-dependent oxidoreductase (EC:1.6.-.-); K00359 NADH oxidase [EC:1.6.-.-]
GPL_12303_0016	hypothetical protein; K01760 cystathionine beta-lyase [EC:4.4.1.8]
GPL_12303_0012	acyl-CoA dehydrogenase related protein
GPL_12302_0044	potassium-transporting ATPase subunit B (EC:3.6.3.12); K01547 K+-transporting ATPase ATPase B chain [EC:3.6.3.12]
GPL_12302_0042	hypothetical protein
GPL_12302_0039	dihydroorotate dehydrogenase 1B (EC:1.3.3.1); K00226 dihydroorotate oxidase [EC:1.3.3.1]
GPL_12302_0034	hypothetical protein

GPL_12302_0027	pheS; phenylalanyl-tRNA synthetase subunit alpha (EC:6.1.1.20); K01889 phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]
GPL_12302_0022	regulatory protein MoxR related protein; K03924 MoxR-like ATPase [EC:3.6.3.-]
GPL_12302_0010	proline dipeptidase related protein; K01271 X-Pro dipeptidase [EC:3.4.13.9]
GPL_12302_0009	gamma-glutamyltranspeptidase; K00681 gamma-glutamyltranspeptidase [EC:2.3.2.2]
GPL_12302_0006	30S ribosomal protein S8e; K02995 small subunit ribosomal protein S8e
GPL_12302_0002	X-Pro dipeptidase
GPL_12052_0012	ATPase; K06921
GPL_11753_0005	site-specific DNA-methyltransferase (adenine-specific) (EC:2.1.1.72); K00571 site-specific DNA-methyltransferase (adenine-specific) [EC:2.1.1.72]
GPL_11753_0004	type III restriction enzyme, res subunit family
Fer2_97_0015	isopentenyl pyrophosphate isomerase (EC:5.3.3.2); K01823 isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]
Fer2_97_0013	ABC transporter ATP-binding protein
Fer2_97_0011	DEXX-box atpase
Fer2_97_0005	atpA; V-type ATP synthase subunit A (EC:3.6.3.14); K02117 V-type H+-transporting ATPase subunit A [EC:3.6.3.14]
Fer2_97_0004	V-type ATP synthase subunit B (EC:3.6.3.14); K02118 V-type H+-transporting ATPase subunit B [EC:3.6.3.14]
Fer2_93_0023	D-3-phosphoglycerate dehydrogenase (EC:1.1.1.95); K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]
Fer2_93_0019	glutaredoxin related protein
Fer2_93_0017	hypothetical protein
Fer2_93_0014	putative protease La homolog type 2 (EC:3.4.21.-); K01362 [EC:3.4.21.-]
Fer2_93_0013	DNA primase (EC:2.7.7.-)
Fer2_93_0011	endonuclease IV (EC:3.1.21.2); K01151 deoxyribonuclease IV [EC:3.1.21.2]
Fer2_93_0008	spermidine synthase (EC:2.5.1.16); K00797 spermidine synthase [EC:2.5.1.16]
Fer2_93_0007	DNA-binding protein
Fer2_93_0001	translation initiation factor IF-2 subunit gamma; K03242 translation initiation factor eIF-2 gamma subunit
Fer2_90_0009	hypothetical protein
Fer2_90_0003	acyl-CoA synthetase
Fer2_9_0076	NAD-dependent aldehyde dehydrogenase; K00155 [EC:1.2.1.-]
Fer2_9_0075	mannose-1-phosphate guanyltransferase related protein
Fer2_9_0062	putative NTPase (EC:3.6.1.-); K06928
Fer2_9_0052	hypothetical protein

Fer2_9_0048	universal stress protein
Fer2_9_0026	hypothetical protein; K09700 hypothetical protein
Fer2_9_0017	thermosome beta chain
Fer2_9_0016	thermosome subunit
Fer2_9_0006	molybdenum cofactor biosynthesis protein A; K06937
Fer2_89_0016	FixC protein; K00313 electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]
Fer2_89_0015	electron transfer flavoprotein alpha and beta-subunit
Fer2_89_0013	CBS domain-containing protein
Fer2_89_0012	citrate synthase (EC:2.3.3.5); K01647 citrate synthase [EC:2.3.3.1]
Fer2_85_0017	hypothetical protein
Fer2_85_0008	alanyl-tRNA synthetase (EC:6.1.1.7); K07050
Fer2_85_0006	rpl10e; 50S ribosomal protein L10e; K02866 large subunit ribosomal protein L10e
Fer2_85_0005	putative arginase (EC:3.5.3.1); K01476 arginase [EC:3.5.3.1]
Fer2_85_0004	translation initiation factor IF-5A; K03263 translation initiation factor eIF-5A
Fer2_83_0009	putative translaldolase (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2]
Fer2_83_0007	cleavage and polyadenylation specificity factor, 100 kDa subunit; K07041
Fer2_83_0006	proteasome beta subunit (EC:3.4.25.1); K03433 proteasome beta subunit [EC:3.4.25.1]
Fer2_83_0002	single-stranded DNA-binding protein; K07466 replication factor A1
Fer2_82_0023	peroxiredoxin
Fer2_82_0018	hypothetical protein
Fer2_82_0017	3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC:1.1.1.34); K00021 3-hydroxy-3-methylglutaryl-CoA reductase [EC:1.1.1.34]
Fer2_72_0006	dihydroorotate dehydrogenase (EC:1.3.3.1); K00226 dihydroorotate oxidase [EC:1.3.3.1]
Fer2_70_0013	fumarylacetoacetase (EC:3.7.1.2)
Fer2_70_0011	TenA/THI-4 family protein
Fer2_671_0002	hypothetical protein
Fer2_64_0022	hypothetical protein
Fer2_64_0015	3-hydroxyacyl-CoA dehydrogenase (EC:1.1.1.35); K00074 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
Fer2_64_0010	oxidoreductase (EC:1.-.-.-); K00540 [EC:1.-.-.-]
Fer2_64_0005	carbon monoxide dehydrogenase beta subunit (EC:1.2.99.2); K03520 carbon-monoxide dehydrogenase large subunit [EC:1.2.99.2]
Fer2_60_0035	spermidine synthase (EC:2.5.1.16); K00797 spermidine synthase [EC:2.5.1.16]

Fer2_60_0034	DNA-binding protein
Fer2_60_0030	translation initiation factor IF-2 subunit gamma; K03242 translation initiation factor eIF-2 gamma subunit
Fer2_60_0027	hypothetical protein
Fer2_60_0009	rpl3p; 50S ribosomal protein L3P; K02906 large subunit ribosomal protein L3
Fer2_60_0008	rpl4lp; 50S ribosomal protein L4P; K02930 large subunit ribosomal protein L4e
Fer2_60_0005	rps19p; 30S ribosomal protein S19P; K02965 small subunit ribosomal protein S19
Fer2_60_0004	rpl22p; 50S ribosomal protein L22P; K02890 large subunit ribosomal protein L22
Fer2_60_0003	rps3p; 30S ribosomal protein S3P; K02982 small subunit ribosomal protein S3
Fer2_584_0004	oxidoreductase (EC:1.-.-.-)
Fer2_56_0028	DNA polymerase beta subunit; K07076
Fer2_56_0012	hsp 20 family small heat shock protein
Fer2_56_0011	ubiquione biosynthesis protein
Fer2_56_0009	zinc-binding alcohol dehydrogenase (EC:1.1.1.1); K00001 alcohol dehydrogenase [EC:1.1.1.1]
Fer2_56_0005	integrase/recombinase; K04763 integrase/recombinase XerD
Fer2_55_0031	CBS domain-containing protein
Fer2_55_0029	putative S1 family peptidase
Fer2_55_0009	glycosyltransferase (EC:2.4.-.-); K00786 [EC:2.4.-.-]
Fer2_50_0012	ATP-dependent protease Lon
Fer2_50_0011	eno; phosphopyruvate hydratase (EC:4.2.1.11); K01689 enolase [EC:4.2.1.11]
Fer2_5_0090	Xaa-Pro dipeptidase (EC:3.4.13.9); K01271 X-Pro dipeptidase [EC:3.4.13.9]
Fer2_5_0078	ABC transporter extracellular solute-binding protein
Fer2_5_0074	tfb; transcription initiation factor IIB; K03124 transcription initiation factor TFIIB
Fer2_5_0072	tfb; transcription initiation factor IIB; K03124 transcription initiation factor TFIIB
Fer2_5_0065	30S ribosomal protein S3Ae; K02984 small subunit ribosomal protein S3Ae
Fer2_5_0059	glutamate dehydrogenase (EC:1.4.1.3); K00261 glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]
Fer2_5_0056	DNA polymerase sliding clamp; K04802 proliferating cell nuclear antigen
Fer2_5_0043	hypothetical protein
Fer2_5_0035	glycine dehydrogenase subunit 2 (EC:1.4.4.2); K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2]
Fer2_5_0034	replication factor A; K07466 replication factor A1
Fer2_5_0020	phosphoribosylamine--glycine ligase (EC:6.3.4.13); K01945 phosphoribosylamine--glycine ligase [EC:6.3.4.13]
Fer2_5_0011	formate dehydrogenase subunit alpha; K00123 formate dehydrogenase, alpha subunit [EC:1.2.1.2]
Fer2_491_0007	amidohydrolase

Fer2_47_0030	anthranilate synthase component I (EC:4.1.3.27); K01657 anthranilate synthase component I [EC:4.1.3.27]
Fer2_47_0024	ribosomal protein
Fer2_47_0020	hypothetical protein
Fer2_47_0004	hypothetical protein; K06875
Fer2_47_0003	30S ribosomal protein S19e; K02966 small subunit ribosomal protein S19e
Fer2_40_0044	30S ribosomal protein S7P
Fer2_40_0036	aspC; aspartyl-tRNA synthetase (EC:6.1.1.12); K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]
Fer2_39_0046	aspartate aminotransferase (EC:2.6.1.1); K00812 aspartate aminotransferase [EC:2.6.1.1]
Fer2_39_0038	pantothenate kinase; K00867 type I pantothenate kinase [EC:2.7.1.33]
Fer2_39_0029	oxidoreductase
Fer2_39_0028	transposase IS4 family protein
Fer2_39_0014	thioredoxin; K03671 thioredoxin 1
Fer2_39_0004	transporter
Fer2_39_0003	hypothetical protein
Fer2_38_0042	transcriptional regulator
Fer2_38_0041	alkyl hydroperoxide reductase subunit C; K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
Fer2_38_0039	hypothetical protein
Fer2_38_0027	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
Fer2_38_0024	dihydroxy-acid dehydratase; K01687 dihydroxy-acid dehydratase [EC:4.2.1.9]
Fer2_38_0023	dihydroxy-acid dehydratase; K01687 dihydroxy-acid dehydratase [EC:4.2.1.9]
Fer2_38_0021	acetolactate synthase catalytic subunit (EC:2.2.1.6); K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
Fer2_38_0019	ketol-acid reductoisomerase (EC:1.1.1.86); K00053 ketol-acid reductoisomerase [EC:1.1.1.86]
Fer2_37_0037	hypothetical protein
Fer2_37_0033	hypothetical protein
Fer2_37_0005	hypothetical protein
Fer2_36_0046	S-adenosylmethionine synthetase (EC:2.5.1.6); K00789 S-adenosylmethionine synthetase [EC:2.5.1.6]
Fer2_36_0038	acetyl-coenzyme A synthetase (EC:6.2.1.1); K01895 acetyl-CoA synthetase [EC:6.2.1.1]
Fer2_36_0036	cytochrome P450 (EC:1.14.14.1); K00493 unspecific monooxygenase [EC:1.14.14.1]
Fer2_36_0021	mRNA 3'-end processing factor; K07577 putative mRNA 3-end processing factor
Fer2_310_0008	hypothetical protein
Fer2_31_0045	xanthine-guanine phosphoribosyltransferase (EC:2.4.2.22); K00769 xanthine phosphoribosyltransferase

	[EC:2.4.2.22]
Fer2_31_0042	FAD dependent oxidoreductase; K00313 electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]
Fer2_31_0032	ef1a, tuf; elongation factor 1-alpha (EC:3.6.5.3); K03231 elongation factor EF-1 alpha subunit [EC:3.6.5.3]
Fer2_31_0030	fusA; elongation factor EF-2; K03234 elongation factor EF-2 [EC:3.6.5.3]
Fer2_31_0019	aspA; aspartate ammonia-lyase (EC:4.3.1.1); K01679 fumarate hydratase, class II [EC:4.2.1.2]
Fer2_31_0018	AsnC family transcriptional regulator
Fer2_31_0015	thioredoxin reductase (EC:1.8.1.9); K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]
Fer2_31_0008	50S ribosomal protein L1P
Fer2_31_0007	rplP0; acidic ribosomal protein P0; K02864 large subunit ribosomal protein L10
Fer2_31_0006	rpl12p; 50S ribosomal protein L12P; K02869 large subunit ribosomal protein L12
Fer2_31_0004	peroxiredoxin; K03564 peroxiredoxin Q/BCP [EC:1.11.1.15]
Fer2_307_0007	hypothetical protein; K01126 glycerophosphoryl diester phosphodiesterase [EC:3.1.4.46]
Fer2_307_0004	transposase IS4 family protein
Fer2_29_0049	DNA/RNA-binding protein AlbA; K03622 archaea-specific DNA-binding protein
Fer2_29_0044	rps4p; 30S ribosomal protein S4P; K02986 small subunit ribosomal protein S4
Fer2_29_0043	rps11p; 30S ribosomal protein S11P; K02948 small subunit ribosomal protein S11
Fer2_29_0032	methionine synthase (EC:2.1.1.14); K00549 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [EC:2.1.1.14]
Fer2_29_0031	hypothetical protein; K00549 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [EC:2.1.1.14]
Fer2_29_0024	transposase IS4 family protein
Fer2_29_0023	multitransmembrane protein
Fer2_29_0011	hypothetical protein
Fer2_247_0008	2-hydroxyacid dehydrogenase
Fer2_247_0006	sterol carrier protein
Fer2_24_0050	glutamine synthetase; K01915 glutamine synthetase [EC:6.3.1.2]
Fer2_24_0045	ferredoxin
Fer2_24_0042	DNA-binding protein
Fer2_24_0040	putative peroxiredoxin (EC:1.11.1.15); K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
Fer2_24_0024	peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K01802 peptidylprolyl isomerase [EC:5.2.1.8]
Fer2_205_0009	3-isopropylmalate dehydratase large subunit (EC:4.2.1.33); K01703 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]

Fer2_205_0006	sulfide-quinone oxidoreductase (EC:1.8.5.-); K05908 [EC:1.8.5.-]
Fer2_205_0005	hypothetical protein
Fer2_205_0004	hypothetical protein
Fer2_205_0002	transposase IS4 family protein
Fer2_20_0042	N-methylhydantoinase (EC:3.5.2.14); K01473 N-methylhydantoinase A [EC:3.5.2.14]
Fer2_20_0041	hydantoinase_b/oxoprolinase (EC:3.5.2.9); K01474 N-methylhydantoinase B [EC:3.5.2.14]
Fer2_20_0036	putative RNA-associated protein; K07582 hypothetical protein
Fer2_20_0035	exosome complex RNA-binding protein Rrp4; K03679 exosome complex component RRP4
Fer2_20_0034	exosome complex exonuclease Rrp41 (EC:2.7.7.56); K11600 exosome complex component RRP41
Fer2_20_0033	exosome complex RNA-binding protein Rrp42 (EC:2.7.7.56); K12589 exosome complex component RRP42
Fer2_20_0028	hypothetical protein; K07572 putative nucleotide binding protein
Fer2_20_0026	band 7 integral membrane protein-like protein
Fer2_20_0024	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
Fer2_20_0022	hypothetical protein; K07083
Fer2_20_0013	hypothetical protein
Fer2_20_0006	4-aminobutyrate aminotransferase (EC:2.6.1.19); K00823 4-aminobutyrate aminotransferase [EC:2.6.1.19]
Fer2_20_0005	membrane associated serine protease
Fer2_19_0069	hypothetical protein
Fer2_19_0045	pyridoxal biosynthesis lyase PdxS; K06215 pyridoxine biosynthesis protein [EC:4.-.-.-]
Fer2_19_0044	malate dehydrogenase (EC:1.1.1.37); K00024 malate dehydrogenase [EC:1.1.1.37]
Fer2_19_0043	sdhA; succinate dehydrogenase flavoprotein subunit (EC:1.3.5.1); K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
Fer2_19_0042	succinate dehydrogenase iron-sulfur subunit (EC:1.3.99.1); K00240 succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]
Fer2_19_0040	succinate dehydrogenase, subunit D (EC:1.3.99.1)
Fer2_19_0038	2-oxoglutarate synthase, alpha chain (EC:1.2.7.3); K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
Fer2_19_0036	succinyl-CoA synthetase subunit alpha (EC:6.2.1.5); K01902 succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
Fer2_19_0035	sucC; succinyl-CoA synthetase subunit beta (EC:6.2.1.5); K01903 succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
Fer2_19_0023	aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]
Fer2_19_0022	acetyltransferase
Fer2_19_0021	malate oxidoreductase (malic enzyme); K00027 malate dehydrogenase (oxaloacetate-decarboxylating)

	[EC:1.1.1.38]
Fer2_19_0016	DNA gyrase subunit A (EC:5.99.1.3); K02469 DNA gyrase subunit A [EC:5.99.1.3]
Fer2_19_0015	gyrB; DNA gyrase subunit B (EC:5.99.1.3); K02470 DNA gyrase subunit B [EC:5.99.1.3]
Fer2_18_0018	geranylgeranyl hydrogenase
Fer2_18_0015	gamma-aminobutyraldehyde dehydrogenase (EC:1.2.1.8); K00130 betaine-aldehyde dehydrogenase [EC:1.2.1.8]
Fer2_18_0014	gamma-aminobutyraldehyde dehydrogenase; K00130 betaine-aldehyde dehydrogenase [EC:1.2.1.8]
Fer2_18_0013	1,3-propanediol dehydrogenase
Fer2_18_0012	inorganic pyrophosphatase; K01507 inorganic pyrophosphatase [EC:3.6.1.1]
Fer2_18_0005	threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
Fer2_177_0005	tricorn protease interacting factor F3 (EC:3.4.11.-); K01269 aminopeptidase [EC:3.4.11.-]
Fer2_17_0066	hypothetical protein
Fer2_17_0054	hypothetical protein
Fer2_17_0026	thiamine pyrophosphate-dependent dehydrogenase, E1 component beta subunit (EC:1.2.4.1); K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
Fer2_17_0021	isocitrate dehydrogenase (EC:1.1.1.41); K00031 isocitrate dehydrogenase [EC:1.1.1.42]
Fer2_166_0006	hypothetical protein
Fer2_163_0009	hypothetical protein; K07484 transposase
Fer2_163_0007	protoporphyrin IX magnesium chelatase related protein; K03404 magnesium chelatase subunit D [EC:6.6.1.1]
Fer2_163_0005	rpl7ae; 50S ribosomal protein L7Ae; K02936 large subunit ribosomal protein L7Ae
Fer2_163_0004	rps28e; 30S ribosomal protein S28e; K02979 small subunit ribosomal protein S28e
Fer2_154_0009	sterol binding protein
Fer2_15_0070	alanyl-tRNA synthetase
Fer2_15_0066	50S ribosomal protein L10e
Fer2_15_0064	translation initiation factor IF-5A; K03263 translation initiation factor eIF-5A
Fer2_15_0047	putative deoxyhypusine synthase (EC:2.5.1.46); K00809 deoxyhypusine synthase [EC:2.5.1.46]
Fer2_15_0044	translation initiation factor IF-2B subunit alpha
Fer2_15_0042	DNA-directed RNA polymerase subunit B (EC:2.7.7.6); K13798 DNA-directed RNA polymerase subunit B [EC:2.7.7.6]
Fer2_15_0041	DNA-directed RNA polymerase subunit A' (EC:2.7.7.6); K03041 DNA-directed RNA polymerase subunit A' [EC:2.7.7.6]
Fer2_15_0040	DNA-directed RNA polymerase subunit A'' (EC:2.7.7.6); K03042 DNA-directed RNA polymerase subunit A'' [EC:2.7.7.6]
Fer2_15_0032	glutamate-1-semialdehyde aminotransferase (EC:5.4.3.8); K01845 glutamate-1-semialdehyde 2,1-aminomutase

	[EC:5.4.3.8]
Fer2_15_0025	small nuclear ribonucleoprotein; K04796 small nuclear ribonucleoprotein
Fer2_15_0016	rpl30p; 50S ribosomal protein L30P; K02907 large subunit ribosomal protein L30
Fer2_15_0015	rps5p; 30S ribosomal protein S5P; K02988 small subunit ribosomal protein S5
Fer2_15_0013	rpl19e; 50S ribosomal protein L19e; K02885 large subunit ribosomal protein L19e
Fer2_15_0011	rpl6p; 50S ribosomal protein L6P; K02933 large subunit ribosomal protein L6
Fer2_15_0010	rps8p; 30S ribosomal protein S8P; K02994 small subunit ribosomal protein S8
Fer2_15_0008	30S ribosomal protein S4e; K02987 small subunit ribosomal protein S4e
Fer2_15_0007	rpl24p; 50S ribosomal protein L24P; K02895 large subunit ribosomal protein L24
Fer2_15_0006	rpl14p; 50S ribosomal protein L14P; K02874 large subunit ribosomal protein L14
Fer2_15_0001	rps3p; 30S ribosomal protein S3P; K02982 small subunit ribosomal protein S3
Fer2_138_0013	urocanate hydratase (EC:4.2.1.49); K01712 urocanate hydratase [EC:4.2.1.49]
Fer2_12_0058	sugar ABC transporter 1, ATP binding protein; K02023 multiple sugar transport system ATP-binding protein
Fer2_12_0054	sugar ABC transporter 1, extracellular binding protein; K02027 multiple sugar transport system substrate-binding protein
Fer2_12_0038	hypothetical protein
Fer2_12_0031	proteasome subunit alpha (EC:3.4.25.1); K03432 proteasome alpha subunit [EC:3.4.25.1]
Fer2_12_0018	rps9p; 30S ribosomal protein S9P; K02996 small subunit ribosomal protein S9
Fer2_12_0017	rpl13p; 50S ribosomal protein L13P; K02871 large subunit ribosomal protein L13
Fer2_12_0013	peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K01802 peptidylprolyl isomerase [EC:5.2.1.8]
Fer2_12_0012	succinate-semialdehyde dehydrogenase [NADP+] (EC:1.2.1.16); K00135 succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]
Fer2_118_0015	ornithine carbamoyltransferase (EC:2.1.3.3); K00611 ornithine carbamoyltransferase [EC:2.1.3.3]
Fer2_118_0014	thioredoxin reductase (EC:1.8.1.9); K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]
Fer2_118_0013	thermosome subunit
Fer2_118_0011	NADH-dependent oxidoreductase (EC:1.6.-.-); K00359 NADH oxidase [EC:1.6.-.-]
Fer2_118_0003	hypothetical protein
Fer2_11_0067	permease
Fer2_11_0061	pyruvate dehydrogenase E1 component beta subunit (EC:1.2.4.1); K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
Fer2_11_0047	rps2P; 30S ribosomal protein S2; K02967 small subunit ribosomal protein S2
Fer2_11_0044	GntR family transcriptional regulator (EC:2.6.1.-); K00837 [EC:2.6.1.-]

Fer2_11_0035	transcription factor; K03120 transcription initiation factor TFIID TATA-box-binding protein
Fer2_11_0032	inosine 5'-monophosphate dehydrogenase (EC:1.1.1.205); K00088 IMP dehydrogenase [EC:1.1.1.205]
Fer2_11_0013	cell division cycle protein 48; K13525 transitional endoplasmic reticulum ATPase
Fer2_11_0009	superoxide dismutase [Fe] (EC:1.15.1.1); K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
Fer2_11_0004	gluconate/galactonate dehydratase (EC:4.2.1.39); K05308 gluconate dehydratase [EC:4.2.1.39]
Fer2_107_0017	Putative uncharacterized protein
Fer2_107_0012	glucose-1-dehydrogenase (EC:1.1.1.47); K00034 glucose 1-dehydrogenase [EC:1.1.1.47]
Fer2_104_0007	CoA-transferase family III protein
Fer2_103_0007	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent; K00525 ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
Fer2_103_0005	electron transfer flavoprotein subunit beta
Fer2_10_0056	carbon monoxide dehydrogenase beta subunit (EC:1.2.99.2); K03520 carbon-monoxide dehydrogenase large subunit [EC:1.2.99.2]
Fer2_10_0054	carbon monoxide dehydrogenase, medium chain (EC:1.2.99.2); K03519 carbon-monoxide dehydrogenase medium subunit [EC:1.2.99.2]
Fer2_10_0039	inosine-5'-monophosphate dehydrogenase (EC:1.1.1.205)
Fer2_10_0011	thermopsin precursor (EC:3.4.23.42); K01385 thermopsin [EC:3.4.23.42]
Fer2_1_0131	2-oxoacid ferredoxin oxidoreductase subunit beta (EC:1.2.7.1); K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
Fer2_1_0130	2-oxoacid--ferredoxin oxidoreductase, alpha subunit
Fer2_1_0118	tyrosyl-tRNA synthetase (EC:6.1.1.1); K01866 tyrosyl-tRNA synthetase [EC:6.1.1.1]
Fer2_1_0112	radA; DNA repair and recombination protein RadA; K04483 DNA repair protein RadA
Fer2_1_0109	hypothetical protein; K07496 putative transposase
Fer2_1_0106	dnaK; molecular chaperone DnaK; K04043 molecular chaperone DnaK
Fer2_1_0105	GrpE protein; K03687 molecular chaperone GrpE
Fer2_1_0095	gabT-1; 4-aminobutyrate aminotransferase (GabT-1) (EC:2.6.1.19); K00823 4-aminobutyrate aminotransferase [EC:2.6.1.19]
Fer2_1_0066	acyl-CoA dehydrogenase, short-chain specific (EC:1.3.99.2); K00248 butyryl-CoA dehydrogenase [EC:1.3.99.2]
Fer2_1_0065	acyl-CoA dehydrogenase (EC:1.3.99.-); K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
Fer2_1_0063	long-chain-fatty-acid--CoA ligase (EC:2.3.1.86); K00666 fatty-acyl-CoA synthase [EC:6.2.1.-]
Fer2_1_0062	3-hydroxybutyryl-CoA dehydrogenase/3-hydroxybutyryl-CoA dehydratase (EC:4.2.1.55 1.1.1.157)
Fer2_1_0059	RimK-like protein; K05827 lysine biosynthesis protein LysX
Fer2_1_0030	hypothetical protein

Fer1_1_1845	glpK; glycerol kinase (EC:2.7.1.30); K00864 glycerol kinase [EC:2.7.1.30]
Fer1_1_1837	ISA0963-3 transposase
Fer1_1_1822	asparagine synthetase A (EC:6.1.1.22); K01893 asparaginyl-tRNA synthetase [EC:6.1.1.22]
Fer1_1_1818	CBS domain-containing protein
Fer1_1_1813	threonine synthase
Fer1_1_1810	cytochrome P450 (EC:1.14.14.1); K00493 unspecific monooxygenase [EC:1.14.14.1]
Fer1_1_1784	3-hydroxyacyl-CoA dehydrogenase
Fer1_1_1769	carbon monoxide dehydrogenase beta subunit
Fer1_1_1765	glucose 1-dehydrogenase, putative
Fer1_1_1748	putative DNA-binding protein; K06934
Fer1_1_1745	pyridoxal biosynthesis lyase PdxS; K06215 pyridoxine biosynthesis protein [EC:4.-.-.-]
Fer1_1_1744	malate dehydrogenase (EC:1.1.1.37); K00024 malate dehydrogenase [EC:1.1.1.37]
Fer1_1_1743	sdhA; succinate dehydrogenase flavoprotein subunit (EC:1.3.5.1); K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
Fer1_1_1742	succinate dehydrogenase iron-sulfur subunit (EC:1.3.99.1); K00240 succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]
Fer1_1_1739	2-oxoglutarate ferredoxin oxidoreductase subunit beta (EC:1.2.7.3); K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
Fer1_1_1738	2-oxoglutarate synthase, alpha chain (EC:1.2.7.3); K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
Fer1_1_1736	succinyl-CoA synthetase subunit alpha (EC:6.2.1.5); K01902 succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
Fer1_1_1735	sucC; succinyl-CoA synthetase subunit beta (EC:6.2.1.5); K01903 succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
Fer1_1_1730	malate oxidoreductase (malic enzyme)
Fer1_1_1729	acetyltransferase
Fer1_1_1728	aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]
Fer1_1_1719	tricorn protease; K08676 tricorn protease [EC:3.4.21.-]
Fer1_1_1689	hypothetical protein
Fer1_1_1676	carbon monoxide dehydrogenase beta subunit
Fer1_1_1675	carbon monoxide dehydrogenase alpha subunit
Fer1_1_1674	carbon monoxide dehydrogenase, medium chain
Fer1_1_1669	tricorn protease interacting factor F2
Fer1_1_1668	inosine-5''''-monophosphate dehydrogenase

Fer1_1_1634	isochorismatase
Fer1_1_1628	TPR repeat-containing protein
Fer1_1_1618	thiamine-phosphate pyrophosphorylase
Fer1_1_1611	rps28e; 30S ribosomal protein S28e; K02979 small subunit ribosomal protein S28e
Fer1_1_1588	2-oxoacid--ferredoxin oxidoreductase, alpha subunit; K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
Fer1_1_1577	tyrosyl-tRNA synthetase (EC:6.1.1.1); K01866 tyrosyl-tRNA synthetase [EC:6.1.1.1]
Fer1_1_1574	chromosome partition protein smc; K03529 chromosome hypothetical proteinregation protein
Fer1_1_1572	radA; DNA repair and recombination protein RadA; K04483 DNA repair protein RadA
Fer1_1_1564	transposase (04)
Fer1_1_1561	sterol carrier protein
Fer1_1_1557	aminotransferase class-III
Fer1_1_1553	dnaK; molecular chaperone DnaK; K04043 molecular chaperone DnaK
Fer1_1_1548	FeS oxidoreductase; K06936
Fer1_1_1534	acyl-CoA dehydrogenase, short-chain specific
Fer1_1_1533	acyl-CoA dehydrogenase (EC:1.3.99.-); K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
Fer1_1_1532	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
Fer1_1_1531	long-chain-fatty-acid--CoA ligase (EC:2.3.1.86); K00666 fatty-acyl-CoA synthase [EC:6.2.1.-]
Fer1_1_1530	3-hydroxybutyryl-CoA dehydrogenase/3-hydroxybutyryl-CoA dehydratase
Fer1_1_1526	acetylornithine aminotransferase (EC:2.6.1.11); K05830 acetylornithine/acetyl-lysine aminotransferase [EC:2.6.1.11 2.6.1.-]
Fer1_1_1502	hypothetical protein
Fer1_1_1495	hypothetical protein
Fer1_1_1491	DNA polymerase II (EC:2.7.7.7); K02319 DNA polymerase I [EC:2.7.7.7]
Fer1_1_1469	replication factor A; K07466 replication factor A1
Fer1_1_1468	glycine dehydrogenase subunit 2 (EC:1.4.4.2); K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2]
Fer1_1_1461	hypothetical protein
Fer1_1_1455	S-adenosyl-L-homocysteine hydrolase
Fer1_1_1454	DNA polymerase sliding clamp
Fer1_1_1453	glutamate dehydrogenase (EC:1.4.1.3); K00261 glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]
Fer1_1_1450	30S ribosomal protein S3Ae
Fer1_1_1418	DNA integration/recombination/invertion protein

Fer1_1_1416	HsdR family type I site-specific deoxyribonuclease; K01153 type I restriction enzyme, R subunit [EC:3.1.21.3]
Fer1_1_1414	type I restriction-modification system methylation subunit (EC:3.1.21.3); K03427 type I restriction enzyme M protein [EC:2.1.1.72]
Fer1_1_1407	Xaa-Pro dipeptidase (EC:3.4.13.9); K01271 X-Pro dipeptidase [EC:3.4.13.9]
Fer1_1_1367	homoserine dehydrogenase (EC:1.1.1.3); K00003 homoserine dehydrogenase [EC:1.1.1.3]
Fer1_1_1361	gyrB; DNA gyrase subunit B (EC:5.99.1.3); K02470 DNA gyrase subunit B [EC:5.99.1.3]
Fer1_1_1336	phosphopyruvate hydratase
Fer1_1_1334	seryl-tRNA synthetase (EC:6.1.1.11); K01875 seryl-tRNA synthetase [EC:6.1.1.11]
Fer1_1_1330	hypothetical protein
Fer1_1_1326	uroporphyrin-III C-methyltransferase
Fer1_1_1322	hypothetical protein
Fer1_1_1320	dihydroorotate dehydrogenase
Fer1_1_1303	tricorn protease interacting factor F3 (EC:3.4.11.-); K01269 aminopeptidase [EC:3.4.11.-]
Fer1_1_1295	molybdenum cofactor biosynthesis protein A; K06937
Fer1_1_1269	aspartyl-tRNA synthetase
Fer1_1_1263	hypothetical protein
Fer1_1_1252	DNA-directed RNA polymerase subunit D (EC:2.7.7.6); K03047 DNA-directed RNA polymerase subunit D [EC:2.7.7.6]
Fer1_1_1250	30S ribosomal protein S4
Fer1_1_1249	30S ribosomal protein S13P
Fer1_1_1218	CRISPR-associated Csh2 family protein
Fer1_1_1214	hypothetical protein
Fer1_1_1206	alanyl-tRNA synthetase (EC:6.1.1.7); K07050
Fer1_1_1179	DNA-directed RNA polymerase subunit B (EC:2.7.7.6); K13798 DNA-directed RNA polymerase subunit B [EC:2.7.7.6]
Fer1_1_1178	DNA-directed RNA polymerase subunit A''''
Fer1_1_1177	DNA-directed RNA polymerase subunit A'' (EC:2.7.7.6); K03042 DNA-directed RNA polymerase subunit A'' [EC:2.7.7.6]
Fer1_1_1169	glutamate-1-semialdehyde aminotransferase (EC:5.4.3.8); K01845 glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]
Fer1_1_1164	small nuclear ribonucleoprotein; K04796 small nuclear ribonucleoprotein
Fer1_1_1155	rpl30p; 50S ribosomal protein L30P; K02907 large subunit ribosomal protein L30
Fer1_1_1154	30S ribosomal protein S5P

Fer1_1_1153	50S ribosomal protein L18P
Fer1_1_1152	50S ribosomal protein L19e
Fer1_1_1150	50S ribosomal protein L6P
Fer1_1_1149	rps8p; 30S ribosomal protein S8P; K02994 small subunit ribosomal protein S8
Fer1_1_1147	30S ribosomal protein S4e
Fer1_1_1145	rpl14p; 50S ribosomal protein L14P; K02874 large subunit ribosomal protein L14
Fer1_1_1140	30S ribosomal protein S3P
Fer1_1_1139	50S ribosomal protein L22P
Fer1_1_1138	rps19p; 30S ribosomal protein S19P; K02965 small subunit ribosomal protein S19
Fer1_1_1137	rpl2p; 50S ribosomal protein L2P; K02886 large subunit ribosomal protein L2
Fer1_1_1135	50S ribosomal protein L4P
Fer1_1_1134	rpl3p; 50S ribosomal protein L3P; K02906 large subunit ribosomal protein L3
Fer1_1_1113	hypothetical protein
Fer1_1_1110	translation initiation factor IF-2 subunit gamma; K03242 translation initiation factor eIF-2 gamma subunit
Fer1_1_1106	DNA-binding protein
Fer1_1_1105	spermidine synthase (EC:2.5.1.16); K00797 spermidine synthase [EC:2.5.1.16]
Fer1_1_1103	hypothetical protein
Fer1_1_1102	endonuclease IV
Fer1_1_1101	DNA primase (EC:2.7.7.-)
Fer1_1_1100	putative protease La homolog type 2 (EC:3.4.21.-); K01362 [EC:3.4.21.-]
Fer1_1_1095	glutaredoxin related protein
Fer1_1_1091	D-3-phosphoglycerate dehydrogenase
Fer1_1_1082	triosephosphate isomerase
Fer1_1_1071	ribosomal protein
Fer1_1_1052	50S ribosomal protein L31e; K02910 large subunit ribosomal protein L31e
Fer1_1_1050	hypothetical protein; K06875
Fer1_1_1049	30S ribosomal protein S19e
Fer1_1_1045	4-aminobutyrate aminotransferase (EC:2.6.1.19); K00823 4-aminobutyrate aminotransferase [EC:2.6.1.19]
Fer1_1_1038	hypothetical protein
Fer1_1_1028	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
Fer1_1_1027	hypothetical protein
Fer1_1_1026	band 7 integral membrane protein-like protein

Fer1_1_1024	hypothetical protein
Fer1_1_1018	exosome complex RNA-binding protein Rrp42
Fer1_1_1017	exosome complex exonuclease Rrp41
Fer1_1_1016	exosome complex RNA-binding protein Rrp4
Fer1_1_1015	putative RNA-associated protein
Fer1_1_0982	peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K01802 peptidylprolyl isomerase [EC:5.2.1.8]
Fer1_1_0968	phosphoribosylaminoimidazole synthetase
Fer1_1_0967	ferredoxin
Fer1_1_0960	glutamine synthetase (EC:6.3.1.2); K01915 glutamine synthetase [EC:6.3.1.2]
Fer1_1_0955	hypothetical protein
Fer1_1_0954	sulfide-quinone oxidoreductase (EC:1.8.5.-); K05908 [EC:1.8.5.-]
Fer1_1_0950	3-isopropylmalate dehydratase large subunit
Fer1_1_0936	V-type ATP synthase subunit A (EC:3.6.3.14); K02117 V-type H+-transporting ATPase subunit A [EC:3.6.3.14]
Fer1_1_0935	V-type ATP synthase subunit B (EC:3.6.3.14); K02118 V-type H+-transporting ATPase subunit B [EC:3.6.3.14]
Fer1_1_0930	gluconate/galactonate dehydratase
Fer1_1_0925	superoxide dismutase [Fe] (EC:1.15.1.1); K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
Fer1_1_0919	cell division cycle protein 48; K13525 transitional endoplasmic reticulum ATPase
Fer1_1_0917	peptide chain release factor 1
Fer1_1_0898	inosine 5'""-monophosphate dehydrogenase
Fer1_1_0895	transcription factor; K03120 transcription initiation factor TFIID TATA-box-binding protein
Fer1_1_0891	GntR family transcriptional regulator
Fer1_1_0888	30S ribosomal protein S2
Fer1_1_0883	hisS; histidyl-tRNA synthetase (EC:6.1.1.21); K01892 histidyl-tRNA synthetase [EC:6.1.1.21]
Fer1_1_0869	dihydrolipoamide dehydrogenase (EC:1.8.1.4); K00382 dihydrolipoamide dehydrogenase [EC:1.8.1.4]
Fer1_1_0867	pyruvate dehydrogenase E1 component beta subunit (EC:1.2.4.1); K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
Fer1_1_0852	Bacterio-opsin activator HTH domain protein
Fer1_1_0843	ribose-5-phosphate isomerase A
Fer1_1_0837	acyl-CoA synthetase
Fer1_1_0833	sterol binding protein
Fer1_1_0828	hypothetical protein
Fer1_1_0823	glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]

Fer1_1_0822	hypothetical protein
Fer1_1_0811	hypothetical protein; K09700 hypothetical protein
Fer1_1_0810	putative peroxiredoxin (EC:1.11.1.15); K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
Fer1_1_0785	N-acyl-L-amino acid amidohydrolase (EC:3.5.1.14); K01436 aminoacylase [EC:3.5.1.14]
Fer1_1_0773	acyl-CoA dehydrogenase (EC:1.3.99.-); K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
Fer1_1_0766	hypothetical protein
Fer1_1_0764	hypothetical protein
Fer1_1_0755	ef1a, tuf; elongation factor 1-alpha (EC:3.6.5.3); K03231 elongation factor EF-1 alpha subunit [EC:3.6.5.3]
Fer1_1_0754	rps10p; 30S ribosomal protein S10P; K02946 small subunit ribosomal protein S10
Fer1_1_0751	transposase (04); K07493 putative transposase
Fer1_1_0746	fusA; elongation factor EF-2; K03234 elongation factor EF-2 [EC:3.6.5.3]
Fer1_1_0742	heat shock protein
Fer1_1_0734	aspA; aspartate ammonia-lyase (EC:4.3.1.1); K01679 fumarate hydratase, class II [EC:4.2.1.2]
Fer1_1_0733	AsnC family transcriptional regulator
Fer1_1_0730	thioredoxin reductase (EC:1.8.1.9); K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]
Fer1_1_0722	rpl11p; 50S ribosomal protein L11P; K02867 large subunit ribosomal protein L11
Fer1_1_0721	rpl1P; 50S ribosomal protein L1P; K02863 large subunit ribosomal protein L1
Fer1_1_0720	acidic ribosomal protein P0
Fer1_1_0719	rpl12p; 50S ribosomal protein L12P; K02869 large subunit ribosomal protein L12
Fer1_1_0718	peroxiredoxin
Fer1_1_0706	succinate-semialdehyde dehydrogenase [NADP+] (EC:1.2.1.16); K00135 succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]
Fer1_1_0705	peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K01802 peptidylprolyl isomerase [EC:5.2.1.8]
Fer1_1_0701	rpl13p; 50S ribosomal protein L13P; K02871 large subunit ribosomal protein L13
Fer1_1_0700	rps9p; 30S ribosomal protein S9P; K02996 small subunit ribosomal protein S9
Fer1_1_0688	proteasome subunit alpha (EC:3.4.25.1); K03432 proteasome alpha subunit [EC:3.4.25.1]
Fer1_1_0651	ribonucleotide-diphosphate reductase subunit alpha (EC:1.17.4.1); K00525 ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
Fer1_1_0649	electron transfer flavoprotein subunit beta; K03521 electron transfer flavoprotein beta subunit
Fer1_1_0635	NADH-dependent oxidoreductase
Fer1_1_0633	thermosome subunit

Fer1_1_0632	thioredoxin reductase (EC:1.8.1.9); K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]
Fer1_1_0631	ornithine carbamoyltransferase
Fer1_1_0626	DNA/RNA-binding protein AlbA; K03622 archaea-specific DNA-binding protein
Fer1_1_0618	Fe-S oxidoreductase
Fer1_1_0611	single-stranded DNA-binding protein; K07466 replication factor A1
Fer1_1_0556	transketolase subunit A
Fer1_1_0554	putative translaldolase
Fer1_1_0551	proteasome beta subunit (EC:3.4.25.1); K03433 proteasome beta subunit [EC:3.4.25.1]
Fer1_1_0546	chaperonin GroEL
Fer1_1_0540	hypothetical protein; K09700 hypothetical protein
Fer1_1_0520	universal stress protein
Fer1_1_0506	putative NTPase
Fer1_1_0482	hypothetical protein
Fer1_1_0464	urocanate hydratase
Fer1_1_0419	cytochrome P450 (EC:1.14.14.1); K00493 unspecific monooxygenase [EC:1.14.14.1]
Fer1_1_0410	S-adenosylmethionine synthetase (EC:2.5.1.6); K00789 S-adenosylmethionine synthetase [EC:2.5.1.6]
Fer1_1_0383	hypothetical protein
Fer1_1_0371	dehydrogenase, E1 component
Fer1_1_0368	isocitrate dehydrogenase
Fer1_1_0330	dihydroxy-acid dehydratase; K01687 dihydroxy-acid dehydratase [EC:4.2.1.9]
Fer1_1_0323	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
Fer1_1_0311	hypothetical protein
Fer1_1_0309	alkyl hydroperoxide reductase subunit c
Fer1_1_0285	putative peroxiredoxin
Fer1_1_0272	hypothetical protein
Fer1_1_0271	3-hydroxy-3-methylglutaryl-coenzyme A reductase
Fer1_1_0250	long-chain-fatty-acid-CoA ligase
Fer1_1_0249	citrate synthase (EC:2.3.3.5); K01647 citrate synthase [EC:2.3.3.1]
Fer1_1_0248	CBS domain-containing protein
Fer1_1_0246	electron transfer flavoprotein alpha and beta-subunit
Fer1_1_0245	FixC protein; K00313 electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]
Fer1_1_0235	hypothetical protein

Fer1_1_0232	phosphoribosylaminoimidazole carboxylase catalytic subunit; K01588 5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]
Fer1_1_0229	gamma-glutamyltranspeptidase (EC:2.3.2.2); K00681 gamma-glutamyltranspeptidase [EC:2.3.2.2]
Fer1_1_0201	oxidoreductase
Fer1_1_0199	3-ketoacyl-(acyl-carrier-protein) reductase
Fer1_1_0188	hypothetical protein
Fer1_1_0183	aspartate aminotransferase
Fer1_1_0167	pyruvate dehydrogenase (EC:1.2.2.2); K00156 pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]
Fer1_1_0166	geranylgeranyl hydrogenase
Fer1_1_0158	alcohol dehydrogenase ; K00001 alcohol dehydrogenase [EC:1.1.1.1]
Fer1_1_0158	alcohol dehydrogenase ; K00001 alcohol dehydrogenase [EC:1.1.1.1]
Fer1_1_0157	inorganic pyrophosphatase
Fer1_1_0143	TenA/THI-4 family protein
Fer1_1_0139	peptide ABC transporter ATP-binding protein; K02032 peptide/nickel transport system ATP-binding protein
Fer1_1_0139	peptide ABC transporter ATP-binding protein; K02032 peptide/nickel transport system ATP-binding protein
Fer1_1_0117	glutamine synthetase (EC:6.3.1.2); K01915 glutamine synthetase [EC:6.3.1.2]
Fer1_1_0101	acetyl-coenzyme A synthetase (EC:6.2.1.1); K01895 acetyl-CoA synthetase [EC:6.2.1.1]
Fer1_1_0089	transposase (04); K07493 putative transposase
Fer1_1_0080	cellulose synthase (UDP-forming)
EPL_17965_0565	transferase hexapeptide domain protein
EPL_17965_0560	integrase/recombinase
EPL_17965_0557	rfc; replication factor C small subunit; K04801 replication factor C small subunit
EPL_17965_0549	hypothetical protein
EPL_17965_0547	argS; arginyl-tRNA synthetase (EC:6.1.1.19); K01887 arginyl-tRNA synthetase [EC:6.1.1.19]
EPL_17965_0538	Fe-S oxidoreductase (EC:1.8.-.-); K03423 [EC:1.8.-.-]
EPL_17965_0531	transcription regulator
EPL_17965_0528	rps2P; 30S ribosomal protein S2; K02967 small subunit ribosomal protein S2
EPL_17965_0526	GTPase; K06883
EPL_17965_0525	transcription regulator
EPL_17965_0522	transcription factor; K03120 transcription initiation factor TFIID TATA-box-binding protein
EPL_17965_0517	inosine 5'-monophosphate dehydrogenase (EC:1.1.1.205); K00088 IMP dehydrogenase [EC:1.1.1.205]
EPL_17965_0516	thermopsin precursor related protein

EPL_17965_0512	putative nitrite reductase/sulfite reductase
EPL_17965_0511	formyltetrahydrofolate synthetase; K01938 formate--tetrahydrofolate ligase [EC:6.3.4.3]
EPL_17965_0505	aromatic acid decarboxylase; K03186 3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiX [EC:4.1.1.-]
EPL_17965_0500	signal recognition particle protein SRP54; K03106 signal recognition particle subunit SRP54
EPL_17965_0498	CoA-binding protein; K06929
EPL_17965_0495	protein tyrosine phosphatase
EPL_17965_0491	NAD-dependent aldehyde dehydrogenase; K00130 betaine-aldehyde dehydrogenase [EC:1.2.1.8]
EPL_17965_0490	alcohol dehydrogenase IV; K00001 alcohol dehydrogenase [EC:1.1.1.1]
EPL_17965_0489	sterol carrier protein
EPL_17965_0466	hypothetical protein
EPL_17965_0459	hypothetical protein
EPL_17965_0456	small heat shock protein (HSP20) related protein
EPL_17965_0455	ABC transporter related protein
EPL_17965_0453	ef1B; elongation factor 1-beta; K03232 elongation factor EF-1 beta subunit
EPL_17965_0451	phosphomannomutase; K01835 phosphoglucomutase [EC:5.4.2.2]; K01840 phosphomannomutase [EC:5.4.2.8]
EPL_17965_0441	S-adenosyl-L-homocysteine hydrolase (EC:3.3.1.1); K01251 adenosylhomocysteinase [EC:3.3.1.1]
EPL_17965_0440	cofactor-independent phosphoglycerate mutase (EC:5.4.2.1); K01834 phosphoglycerate mutase [EC:5.4.2.1]
EPL_17965_0438	seryl-tRNA synthetase (EC:6.1.1.11); K01875 seryl-tRNA synthetase [EC:6.1.1.11]
EPL_17965_0437	putative oxidoreductase; K00266 glutamate synthase (NADPH/NADH) small chain [EC:1.4.1.13 1.4.1.14]
EPL_17965_0431	glpQ; putative phosphodiesterase (EC:3.1.4.46); K01126 glycerophosphoryl diester phosphodiesterase [EC:3.1.4.46]
EPL_17965_0429	NADH-dependent oxidoreductase (EC:1.6.-.-); K00359 NADH oxidase [EC:1.6.-.-]
EPL_17965_0428	hypothetical protein
EPL_17965_0427	DNA polymerase sliding clamp; K04802 proliferating cell nuclear antigen
EPL_17965_0424	hypothetical protein
EPL_17965_0423	malate dehydrogenase (EC:1.1.1.37); K00024 malate dehydrogenase [EC:1.1.1.37]
EPL_17965_0419	protein of unknown function DUF835
EPL_17965_0418	ATPase
EPL_17965_0416	peptidase M61 domain-containing protein
EPL_17965_0414	hypothetical protein
EPL_17965_0410	hypothetical protein
EPL_17965_0403	protein of unknown function DUF1621; K09152 hypothetical protein

EPL_17965_0402	regulator of amino acid metabolism; K07103
EPL_17965_0401	radA; DNA repair and recombination protein RADA; K04483 DNA repair protein RadA
EPL_17965_0400	glyceraldehyde-3-phosphate dehydrogenase (EC:1.2.1.59); K00150 glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]
EPL_17965_0395	proteasome subunit alpha (EC:3.4.25.1); K03432 proteasome alpha subunit [EC:3.4.25.1]
EPL_17965_0393	putative RNA-associated protein; K07582 hypothetical protein
EPL_17965_0392	exosome complex RNA-binding protein Rrp4; K03679 exosome complex component RRP4
EPL_17965_0391	exosome complex exonuclease Rrp41; K11600 exosome complex component RRP41
EPL_17965_0390	exosome complex RNA-binding protein Rrp42; K12589 exosome complex component RRP42
EPL_17965_0389	rpl37ae; 50S ribosomal protein L37Ae; K02921 large subunit ribosomal protein L37Ae
EPL_17965_0386	hypothetical protein
EPL_17965_0385	RNA-binding protein; K07572 putative nucleotide binding protein
EPL_17965_0383	band 7 integral membrane protein-like protein
EPL_17965_0378	hypothetical protein
EPL_17965_0375	hypothetical protein
EPL_17965_0353	Methylmalonyl-CoA mutase
EPL_17965_0352	methylmalonyl-CoA mutase alpha subunit (EC:5.4.99.2); K01849 methylmalonyl-CoA mutase, C-terminal domain [EC:5.4.99.2]
EPL_17965_0349	cystathionine beta-synthase; K01697 cystathionine beta-synthase [EC:4.2.1.22]
EPL_17965_0348	cystathionine gamma-lyase (EC:4.4.1.1); K01758 cystathionine gamma-lyase [EC:4.4.1.1]
EPL_17965_0345	succinate dehydrogenase and fumarate reductase iron-sulfur protein; K00240 succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]
EPL_17965_0344	sdhA; succinate dehydrogenase flavoprotein subunit; K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
EPL_17965_0342	hypothetical protein
EPL_17965_0334	gliding motility protein related; K01990 ABC-2 type transport system ATP-binding protein
EPL_17965_0333	methyltransferase
EPL_17965_0332	cysS; cysteinyl-tRNA synthetase (EC:6.1.1.16); K01883 cysteinyl-tRNA synthetase [EC:6.1.1.16]
EPL_17965_0330	nicotinate phosphoribosyltransferase (EC:2.4.2.11); K00763 nicotinate phosphoribosyltransferase [EC:2.4.2.11]
EPL_17965_0327	hypothetical protein
EPL_17965_0324	glutamate dehydrogenase; K00261 glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]
EPL_17965_0320	1,4-alpha-glucan branching enzyme (EC:2.4.1.18); K00700 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]
EPL_17965_0319	trehalose synthase (EC:5.4.99.16); K05343 maltose alpha-D-glucosyltransferase [EC:5.4.99.16]

EPL_17965_0313	tfb; transcription initiation factor IIB; K03124 transcription initiation factor TFIIB
EPL_17965_0311	tfb; transcription initiation factor IIB; K03124 transcription initiation factor TFIIB
EPL_17965_0303	DNA gyrase subunit B (Fragment)
EPL_17965_0302	DNA gyrase subunit A; K02469 DNA gyrase subunit A [EC:5.99.1.3]
EPL_17965_0301	homoserine dehydrogenase (EC:1.1.1.3); K00003 homoserine dehydrogenase [EC:1.1.1.3]
EPL_17965_0300	hypothetical protein
EPL_17965_0297	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
EPL_17965_0296	hypothetical protein; K07068
EPL_17965_0293	chaperonin GroEL
EPL_17965_0292	sucC; succinyl-CoA synthetase subunit beta (EC:6.2.1.5); K01903 succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
EPL_17965_0291	succinyl-CoA synthetase subunit alpha (EC:6.2.1.5); K01902 succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
EPL_17965_0290	ornithine carbamoyltransferase (EC:2.1.3.3); K00611 ornithine carbamoyltransferase [EC:2.1.3.3]
EPL_17965_0288	hypothetical protein
EPL_17965_0282	hypothetical protein; K07327 archaeal flagellar protein FlaD
EPL_17965_0281	flagellar protein C; K07822 archaeal flagellar protein FlaC
EPL_17965_0280	flagellin; K07325 archaeal flagellin FlaB
EPL_17965_0278	pheT; phenylalanyl-tRNA synthetase subunit beta (EC:6.1.1.20); K01890 phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]
EPL_17965_0271	rps15p; 30S ribosomal protein S15P; K02956 small subunit ribosomal protein S15
EPL_17965_0270	Molybdenum cofactor biosynthesis protein
EPL_17965_0266	short chain dehydrogenase
EPL_17965_0262	hypothetical protein
EPL_17965_0261	fabG; 3-ketoacyl-(acyl-carrier-protein) reductase (EC:1.1.1.100); K00059 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]
EPL_17965_0260	NAD-dependent aldehyde dehydrogenase; K00294 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]
EPL_17965_0258	phosphoenolpyruvate carboxykinase (EC:4.1.1.32); K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
EPL_17965_0254	translation initiation factor IF-2; K03243 translation initiation factor IF-2 unclassified subunit
EPL_17965_0253	ndk; nucleoside diphosphate kinase; K00940 nucleoside-diphosphate kinase [EC:2.7.4.6]
EPL_17965_0251	rps28e; 30S ribosomal protein S28e; K02979 small subunit ribosomal protein S28e
EPL_17965_0250	rpl7ae; 50S ribosomal protein L7Ae; K02936 large subunit ribosomal protein L7Ae
EPL_17965_0249	dihydrodipicolinate synthetase; K01714 dihydrodipicolinate synthase [EC:4.2.1.52]

EPL_17965_0236	hypothetical protein
EPL_17965_0228	hypothetical protein
EPL_17965_0222	hypothetical protein
EPL_17965_0220	metal-dependent hydrolase
EPL_17965_0219	hypothetical protein
EPL_17965_0216	alanyl-tRNA synthetase (EC:6.1.1.7); K07050
EPL_17965_0211	rpl10e; 50S ribosomal protein L10e; K02866 large subunit ribosomal protein L10e
EPL_17965_0210	agmatinase; K01480 agmatinase [EC:3.5.3.11]
EPL_17965_0209	translation initiation factor IF-5A; K03263 translation initiation factor eIF-5A
EPL_17965_0206	small nuclear ribonucleoprotein; K04796 small nuclear ribonucleoprotein
EPL_17965_0194	2-oxoglutarate synthase, alpha chain (EC:1.2.7.3); K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
EPL_17965_0193	2-oxoglutarate ferredoxin oxidoreductase subunit beta; K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
EPL_17965_0191	peptide chain release factor 1; K03265 peptide chain release factor eRF subunit 1
EPL_17965_0190	hypothetical protein
EPL_17965_0189	tricorn protease interacting factor F2 (EC:3.4.11.-); K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
EPL_17965_0187	VAT ATPase (VCP-like ATPase); K13525 transitional endoplasmic reticulum ATPase
EPL_17965_0179	acetyl-CoA acetyltransferase
EPL_17965_0175	2-phosphoglycerate kinase; K05715 2-phosphoglycerate kinase [EC:2.7.2.-]
EPL_17965_0174	amidohydrolase
EPL_17965_0165	carboxymethylenebutenolidase (EC:3.1.1.45); K01061 carboxymethylenebutenolidase [EC:3.1.1.45]
EPL_17965_0160	beta-hydroxybutyryl-CoA dehydrogenase related protein; K00074 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
EPL_17965_0158	aspC; aspartyl-tRNA synthetase (EC:6.1.1.12); K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]
EPL_17965_0155	transcription regulator; K00845 glucokinase [EC:2.7.1.2]
EPL_17965_0147	Rieske Fe-S protein
EPL_17965_0144	3-oxoacyl-[acyl-carrier-protein] reductase (EC:1.1.1.100); K00059 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]
EPL_17965_0138	phosphoribosylformylglycinamidine synthase II (EC:6.3.5.3); K01952 phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]
EPL_17965_0137	purS; phosphoribosylformylglycinamidine synthase (EC:6.3.5.3); K01952 phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]

EPL_17965_0133	putative NTPase; K06928
EPL_17965_0126	acyl-CoA hydrolase
EPL_17965_0124	hypothetical protein
EPL_17965_0123	hypothetical protein; K09721 hypothetical protein
EPL_17965_0119	ATP-dependent protease Lon; K04076 Lon-like ATP-dependent protease [EC:3.4.21.-]
EPL_17965_0116	hypothetical protein
EPL_17965_0113	ATPase; K03924 MoxR-like ATPase [EC:3.6.3.-]
EPL_17965_0112	hypothetical protein
EPL_17965_0102	hypothetical protein; K09732 hypothetical protein
EPL_17965_0099	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
EPL_17965_0096	TenA/THI-4 family protein
EPL_17965_0094	putative DNA-binding protein; K06934
EPL_17965_0092	homogentisate 1,2-dioxygenase (EC:1.13.11.5); K00451 homogentisate 1,2-dioxygenase [EC:1.13.11.5]
EPL_17965_0091	fumarylacetoacetase (EC:3.7.1.2)
EPL_17965_0090	4-hydroxyphenylpyruvate dioxygenase (EC:1.13.11.27); K00457 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]
EPL_17965_0085	hypothetical protein
EPL_17965_0081	chromosome partition protein smc; K03529 chromosome hypothetical proteinregation protein
EPL_17965_0078	dcd; deoxycytidine triphosphate deaminase (EC:3.5.4.13); K01494 dCTP deaminase [EC:3.5.4.13]
EPL_17965_0075	phosphoribosylamine--glycine ligase (EC:6.3.4.13); K01945 phosphoribosylamine--glycine ligase [EC:6.3.4.13]
EPL_17965_0068	hypothetical protein
EPL_17965_0058	single-stranded DNA-binding protein; K07466 replication factor A1
EPL_17965_0057	cobalamin periplasmic binding protein
EPL_17965_0050	glucoamylase (EC:3.2.1.3); K01178 glucoamylase [EC:3.2.1.3]
EPL_17965_0048	acetyltransferase
EPL_17965_0047	eno; phosphopyruvate hydratase (EC:4.2.1.11); K01689 enolase [EC:4.2.1.11]
EPL_17965_0045	hypothetical protein
EPL_17965_0044	heat shock protein GrpE related protein; K03687 molecular chaperone GrpE
EPL_17965_0043	dnaK; molecular chaperone DnaK; K04043 molecular chaperone DnaK
EPL_17965_0040	transposase IS4 family protein
EPL_17965_0039	universal stress protein
EPL_17965_0038	rps17E; 30S ribosomal protein S17e; K02962 small subunit ribosomal protein S17e

EPL_17965_0037	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
EPL_17965_0035	enoyl-CoA hydratase; K01692 enoyl-CoA hydratase [EC:4.2.1.17]
EPL_17965_0031	pyrB; aspartate carbamoyltransferase catalytic subunit (EC:2.1.3.2); K00609 aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]
EPL_17965_0030	aspartate carbamoyltransferase regulatory subunit (EC:2.1.3.2); K00610 aspartate carbamoyltransferase regulatory subunit
EPL_17965_0016	hypothetical protein
EPL_17965_0015	NDP-hexose 2,3-enoyl reductase TylCII related protein
EPL_17965_0014	DNA repair helicase
EPL_15833_0088	hypothetical protein
EPL_15833_0087	aldo/keto reductase
EPL_15833_0083	domain of unknown function DUF1731; K07071
EPL_15833_0076	acyl-coenzyme A synthetase; K01895 acetyl-CoA synthetase [EC:6.2.1.1]
EPL_15833_0073	4-aminobutyrate aminotransferase (EC:2.6.1.19); K00823 4-aminobutyrate aminotransferase [EC:2.6.1.19]
EPL_15833_0072	hypothetical protein
EPL_15833_0069	30S ribosomal protein S19e; K02966 small subunit ribosomal protein S19e
EPL_15833_0066	50S ribosomal protein L31e; K02910 large subunit ribosomal protein L31e
EPL_15833_0064	pyrE; orotate phosphoribosyltransferase (EC:2.4.2.10); K00762 orotate phosphoribosyltransferase [EC:2.4.2.10]
EPL_15833_0061	hypothetical protein
EPL_15833_0059	hutU; urocanate hydratase (EC:4.2.1.49); K01712 urocanate hydratase [EC:4.2.1.49]
EPL_15833_0058	adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]
EPL_15833_0057	isocitrate dehydrogenase; K00031 isocitrate dehydrogenase [EC:1.1.1.42]
EPL_15833_0054	hypothetical protein
EPL_15833_0051	hypothetical protein
EPL_15833_0050	acyl-CoA dehydrogenase-like protein
EPL_15833_0049	acyl-CoA dehydrogenase; K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
EPL_15833_0048	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
EPL_15833_0046	electron transfer flavoprotein subunit beta; K03521 electron transfer flavoprotein beta subunit
EPL_15833_0045	electron transfer flavoprotein subunit alpha related protein; K03522 electron transfer flavoprotein alpha subunit
EPL_15833_0041	hypothetical protein
EPL_15833_0040	branched-chain amino acid aminotransferase; K00826 branched-chain amino acid aminotransferase [EC:2.6.1.42]
EPL_15833_0038	3-methyl-2-oxobutanoate dehydrogenase alpha chain precursor; K00161 pyruvate dehydrogenase E1 component

	subunit alpha [EC:1.2.4.1]
EPL_15833_0037	3-methyl-2-oxobutanoate dehydrogenase chain E1-beta; K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
EPL_15251_0046	pyrG; CTP synthetase (EC:6.3.4.2); K01937 CTP synthase [EC:6.3.4.2]
EPL_15251_0043	superoxide dismutase; K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
EPL_15251_0041	aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]
EPL_15251_0040	galactonate dehydratase
EPL_15251_0039	RecA-superfamily ATPase implicated in signal transduction-like protein
EPL_15251_0037	glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]
EPL_15251_0035	aminomethyltransferase (glycine cleavage system T protein); K00605 aminomethyltransferase [EC:2.1.2.10]
EPL_15251_0028	SMC domain-containing protein
EPL_15251_0009	hypothetical protein
EPL_15251_0008	hypothetical protein
EPL_15251_0006	helicase domain-containing protein
EPL_15251_0003	hypothetical protein
EPL_15243_0827	peroxiredoxin
EPL_15243_0821	long-chain-fatty-acid--CoA ligase (EC:2.3.1.86); K00666 fatty-acyl-CoA synthase [EC:6.2.1.-]
EPL_15243_0819	putative translaldolase (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2]
EPL_15243_0818	transketolase; K00615 transketolase [EC:2.2.1.1]
EPL_15243_0817	transketolase subunit A (EC:2.2.1.1); K00615 transketolase [EC:2.2.1.1]
EPL_15243_0816	cell division protein FtsZ; K03531 cell division protein FtsZ
EPL_15243_0811	malate oxidoreductase (malic enzyme); K00027 malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
EPL_15243_0810	acetyltransferase
EPL_15243_0807	aspartate aminotransferase (EC:2.6.1.1); K00812 aspartate aminotransferase [EC:2.6.1.1]
EPL_15243_0804	diaminopimelate aminotransferase; K01439 succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]
EPL_15243_0803	hypothetical protein; K01881 prolyl-tRNA synthetase [EC:6.1.1.15]; K01885 glutamyl-tRNA synthetase [EC:6.1.1.17]
EPL_15243_0797	hypothetical protein
EPL_15243_0793	ileS; isoleucyl-tRNA synthetase (EC:6.1.1.5); K01870 isoleucyl-tRNA synthetase [EC:6.1.1.5]
EPL_15243_0788	hypothetical protein
EPL_15243_0772	phosphoheptose isomerase; K03271 phosphoheptose isomerase [EC:5.-.-.-]

EPL_15243_0767	Alcohol dehydrogenase (NADP(+))
EPL_15243_0766	zinc metalloprotease (EC:3.4.24.-); K07386 putative endopeptidase [EC:3.4.24.-]
EPL_15243_0765	nucleoside-diphosphate-sugar epimerase; K01795 [EC:5.1.3.-]
EPL_15243_0764	kinase related to galactokinase and mevalonate kinase; K07031
EPL_15243_0763	NAD-dependent epimerase/dehydratase
EPL_15243_0758	NADH ubiquinone oxidoreductase, 20 kDa subunit
EPL_15243_0750	thioredoxin; K03671 thioredoxin 1
EPL_15243_0745	NAD-dependent aldehyde dehydrogenase; K00155 [EC:1.2.1.-]
EPL_15243_0744	alsS; acetolactate synthase; K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
EPL_15243_0737	30S ribosomal protein S3Ae; K02984 small subunit ribosomal protein S3Ae
EPL_15243_0734	isovaleryl-CoA dehydrogenase; K00253 isovaleryl-CoA dehydrogenase [EC:1.3.99.10]
EPL_15243_0733	DNA-directed RNA polymerase subunit E'; K03049 DNA-directed RNA polymerase subunit E' [EC:2.7.7.6]
EPL_15243_0731	rps24e; 30S ribosomal protein S24e; K02974 small subunit ribosomal protein S24e
EPL_15243_0723	hypothetical protein
EPL_15243_0711	hypothetical protein
EPL_15243_0710	hypothetical protein; K07114
EPL_15243_0691	prefoldin subunit beta; K04798 prefoldin beta subunit
EPL_15243_0689	6,7-dimethyl-8-ribityllumazine synthase (EC:2.5.1.9); K00794 riboflavin synthase beta chain [EC:2.5.1.-]
EPL_15243_0681	TPR repeat-containing protein
EPL_15243_0680	proline dipeptidase related protein; K01271 X-Pro dipeptidase [EC:3.4.13.9]
EPL_15243_0675	metal-dependent RNase; K07041
EPL_15243_0674	proteasome protease subunit beta; K03433 proteasome beta subunit [EC:3.4.25.1]
EPL_15243_0673	inosine-5'-monophosphate dehydrogenase related protein
EPL_15243_0671	hypothetical protein
EPL_15243_0670	hypothetical protein
EPL_15243_0669	hemH; phosphoribosylaminoimidazole-succinocarboxamide synthase (EC:6.3.2.6); K01923 phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2.6]
EPL_15243_0649	hypothetical protein
EPL_15243_0647	Oxidoreductase, zinc-binding
EPL_15243_0643	malate synthase; K01638 malate synthase [EC:2.3.3.9]
EPL_15243_0634	putative alcohol dehydrogenase; K00001 alcohol dehydrogenase [EC:1.1.1.1]
EPL_15243_0626	indolepyruvate ferredoxin oxidoreductase, alpha subunit; K00179 indolepyruvate ferredoxin oxidoreductase, alpha

	subunit [EC:1.2.7.8]
EPL_15243_0623	pyridoxal biosynthesis lyase PdxS; K06215 pyridoxine biosynthesis protein [EC:4.-.-.-]
EPL_15243_0619	HTH DNA-binding protein
EPL_15243_0618	peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K01802 peptidylprolyl isomerase [EC:5.2.1.8]
EPL_15243_0615	type II secretion system protein E
EPL_15243_0613	type II secretion system F domain protein
EPL_15243_0608	glucose-1-dehydrogenase (EC:1.1.1.47); K00034 glucose 1-dehydrogenase [EC:1.1.1.47]
EPL_15243_0607	glucose 1-dehydrogenase; K00034 glucose 1-dehydrogenase [EC:1.1.1.47]
EPL_15243_0597	regulatory protein MoxR related protein; K03924 MoxR-like ATPase [EC:3.6.3.-]
EPL_15243_0595	hypothetical protein
EPL_15243_0592	exosome complex RNA-binding protein Csl4; K07573 exosome complex component CSL4
EPL_15243_0590	small nuclear ribonucleoprotein (snRNP)-like protein
EPL_15243_0586	dihydroorotate dehydrogenase (EC:1.3.3.1); K00226 dihydroorotate oxidase [EC:1.3.3.1]
EPL_15243_0583	DNA-directed RNA polymerase subunit L (EC:2.7.7.6); K03056 DNA-directed RNA polymerase subunit L [EC:2.7.7.6]
EPL_15243_0580	molecular chaperone (small heat shock protein, HSP20-related)
EPL_15243_0577	sulfide dehydrogenase related protein
EPL_15243_0576	hypothetical protein
EPL_15243_0575	OsmC-like protein; K07397 putative redox protein
EPL_15243_0573	fusA; elongation factor EF-2; K03234 elongation factor EF-2 [EC:3.6.5.3]
EPL_15243_0572	rps10p; 30S ribosomal protein S10P; K02946 small subunit ribosomal protein S10
EPL_15243_0571	ef1a, tuf; elongation factor 1-alpha (EC:3.6.5.3); K03231 elongation factor EF-1 alpha subunit [EC:3.6.5.3]
EPL_15243_0569	hypothetical protein
EPL_15243_0568	bifunctional phosphoglucose/phosphomannose isomerase; K01809 mannose-6-phosphate isomerase [EC:5.3.1.8]; K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]
EPL_15243_0541	pyruvate kinase (EC:2.7.1.40); K00873 pyruvate kinase [EC:2.7.1.40]
EPL_15243_0538	potassium channel protein
EPL_15243_0534	rps9p; 30S ribosomal protein S9P; K02996 small subunit ribosomal protein S9
EPL_15243_0533	rpl13p; 50S ribosomal protein L13P; K02871 large subunit ribosomal protein L13
EPL_15243_0532	50S ribosomal protein L18e; K02883 large subunit ribosomal protein L18e
EPL_15243_0531	rRNA methylase
EPL_15243_0530	FKBP-type peptidyl-prolyl cis-trans isomerase; K01802 peptidylprolyl isomerase [EC:5.2.1.8]

EPL_15243_0528	hypothetical protein; K01720 2-methylcitrate dehydratase [EC:4.2.1.79]
EPL_15243_0527	carboxyphosphonoenolpyruvate phosphonomutase; K01003 carboxyvinyl-carboxyphosphonate phosphorylmutase [EC:2.7.8.23]
EPL_15243_0526	citA; citrate synthase I (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]
EPL_15243_0524	ppnK; inorganic polyphosphate/ATP-NAD kinase (EC:2.7.1.23); K00858 NAD+ kinase [EC:2.7.1.23]
EPL_15243_0520	DNA-directed RNA polymerase subunit D (EC:2.7.7.6); K03047 DNA-directed RNA polymerase subunit D [EC:2.7.7.6]
EPL_15243_0519	rps11p; 30S ribosomal protein S11P; K02948 small subunit ribosomal protein S11
EPL_15243_0518	rps4p; 30S ribosomal protein S4P; K02986 small subunit ribosomal protein S4
EPL_15243_0517	rps13p; 30S ribosomal protein S13P; K02952 small subunit ribosomal protein S13
EPL_15243_0514	otsB; trehalose-6-phosphatase; K01087 trehalose-phosphatase [EC:3.1.3.12]
EPL_15243_0508	Putative uncharacterized protein
EPL_15243_0501	DNA-directed RNA polymerase subunit A'' (EC:2.7.7.6); K03042 DNA-directed RNA polymerase subunit A'' [EC:2.7.7.6]
EPL_15243_0500	DNA-directed RNA polymerase subunit A' (EC:2.7.7.6); K03041 DNA-directed RNA polymerase subunit A' [EC:2.7.7.6]
EPL_15243_0499	DNA-directed RNA polymerase subunit B (EC:2.7.7.6); K13798 DNA-directed RNA polymerase subunit B [EC:2.7.7.6]
EPL_15243_0466	rpl6p; 50S ribosomal protein L6P; K02933 large subunit ribosomal protein L6
EPL_15243_0465	rps8p; 30S ribosomal protein S8P; K02994 small subunit ribosomal protein S8
EPL_15243_0464	rpl5p; 50S ribosomal protein L5P; K02931 large subunit ribosomal protein L5
EPL_15243_0463	30S ribosomal protein S4e; K02987 small subunit ribosomal protein S4e
EPL_15243_0462	rpl24p; 50S ribosomal protein L24P; K02895 large subunit ribosomal protein L24
EPL_15243_0461	rpl14p; 50S ribosomal protein L14P; K02874 large subunit ribosomal protein L14
EPL_15243_0456	rps3p; 30S ribosomal protein S3P; K02982 small subunit ribosomal protein S3
EPL_15243_0455	rpl22p; 50S ribosomal protein L22P; K02890 large subunit ribosomal protein L22
EPL_15243_0454	rps19p; 30S ribosomal protein S19P; K02965 small subunit ribosomal protein S19
EPL_15243_0453	rpl2p; 50S ribosomal protein L2P; K02886 large subunit ribosomal protein L2
EPL_15243_0452	rplW; 50S ribosomal protein L23P; K02892 large subunit ribosomal protein L23
EPL_15243_0451	rpl4lp; 50S ribosomal protein L4P; K02930 large subunit ribosomal protein L4e
EPL_15243_0450	rpl3p; 50S ribosomal protein L3P; K02906 large subunit ribosomal protein L3
EPL_15243_0444	acetyl-CoA synthetase (ADP forming), beta chain (AcdB)
EPL_15243_0442	triosephosphate isomerase (EC:5.3.1.1); K01803 triosephosphate isomerase (TIM) [EC:5.3.1.1]

EPL_15243_0439	hutH; histidine ammonia-lyase (EC:4.3.1.3); K01745 histidine ammonia-lyase [EC:4.3.1.3]
EPL_15243_0438	Acyl-CoA synthetase
EPL_15243_0437	thrS; threonyl-tRNA synthetase (EC:6.1.1.3); K01868 threonyl-tRNA synthetase [EC:6.1.1.3]
EPL_15243_0436	electron transfer flavoprotein subunit alpha; K03522 electron transfer flavoprotein alpha subunit
EPL_15243_0435	electron transfer flavoprotein subunit beta; K03521 electron transfer flavoprotein beta subunit
EPL_15243_0433	dehydrogenase (flavoprotein); K00313 electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]
EPL_15243_0432	spermidine synthase (EC:2.5.1.16); K00797 spermidine synthase [EC:2.5.1.16]
EPL_15243_0427	translation initiation factor IF-2 subunit gamma; K03242 translation initiation factor eIF-2 gamma subunit
EPL_15243_0425	nucleoid DNA-binding protein (HB-related)
EPL_15243_0424	hypothetical protein
EPL_15243_0423	hypothetical protein; K01151 deoxyribonuclease IV [EC:3.1.21.2]
EPL_15243_0421	DNA primase
EPL_15243_0420	hypothetical protein; K01338 ATP-dependent Lon protease [EC:3.4.21.53]
EPL_15243_0418	putative peroxiredoxin (EC:1.11.1.15)
EPL_15243_0413	hypothetical protein
EPL_15243_0403	NADH dehydrogenase subunit D (EC:1.6.5.3); K00333 NADH dehydrogenase I subunit D [EC:1.6.5.3]
EPL_15243_0396	acyl-CoA dehydrogenase, short-chain specific (EC:1.3.99.2); K00248 butyryl-CoA dehydrogenase [EC:1.3.99.2]
EPL_15243_0391	hypothetical protein
EPL_15243_0388	NAD-dependent aldehyde dehydrogenase; K00128 aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]
EPL_15243_0386	DNA/RNA-binding protein AlbA; K03622 archaea-specific DNA-binding protein
EPL_15243_0377	aldehyde dehydrogenase; K07248 lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase [EC:1.2.1.22 1.2.1.21]
EPL_15243_0376	hypothetical protein
EPL_15243_0363	hypothetical protein
EPL_15243_0357	hypothetical protein
EPL_15243_0351	glycine dehydrogenase subunit 1 (EC:1.4.4.2); K00282 glycine dehydrogenase subunit 1 [EC:1.4.4.2]
EPL_15243_0350	glycine dehydrogenase subunit 2 (EC:1.4.4.2); K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2]
EPL_15243_0348	hypothetical protein; K09746 hypothetical protein
EPL_15243_0347	replication factor A; K07466 replication factor A1
EPL_15243_0340	hypothetical protein
EPL_15243_0335	aminopeptidase N; K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
EPL_15243_0334	CBS domain-containing protein

EPL_15243_0333	glycine hydroxymethyltransferase related protein; K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]
EPL_15243_0319	hypothetical protein
EPL_15243_0317	Fe2+ uptake regulation protein; K03711 Fur family transcriptional regulator, ferric uptake regulator
EPL_15243_0306	alcohol dehydrogenase related protein
EPL_15243_0304	TPR repeat-containing protein
EPL_15243_0296	mannose-1-phosphate guanyltransferase related protein
EPL_15243_0295	2-amino-3-ketobutyrate coenzyme A ligase (EC:2.3.1.29); K00639 glycine C-acetyltransferase [EC:2.3.1.29]
EPL_15243_0294	NAD-dependent epimerase/dehydratase
EPL_15243_0291	geranylgeranyl reductase
EPL_15243_0285	pyruvate phosphate dikinase (EC:2.7.9.1); K01006 pyruvate,orthophosphate dikinase [EC:2.7.9.1]
EPL_15243_0275	hypothetical protein
EPL_15243_0267	leucyl aminopeptidase (EC:3.4.11.1); K01255 leucyl aminopeptidase [EC:3.4.11.1]
EPL_15243_0261	RPL15; 50S ribosomal protein L15e; K02877 large subunit ribosomal protein L15e
EPL_15243_0256	hypothetical protein
EPL_15243_0255	chaperonin GroEL
EPL_15243_0253	acyl-CoA dehydrogenase; K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
EPL_15243_0249	inorganic pyrophosphatase; K01507 inorganic pyrophosphatase [EC:3.6.1.1]
EPL_15243_0239	acetyl-coenzyme-A synthetase; K01895 acetyl-CoA synthetase [EC:6.2.1.1]
EPL_15243_0235	hypothetical protein
EPL_15243_0231	prefoldin subunit alpha
EPL_15243_0230	pgk; phosphoglycerate kinase (EC:2.7.2.3); K00927 phosphoglycerate kinase [EC:2.7.2.3]
EPL_15243_0224	carbamate kinase (EC:2.7.2.2); K00926 carbamate kinase [EC:2.7.2.2]
EPL_15243_0213	putative deoxyhypusine synthase (EC:2.5.1.46); K00809 deoxyhypusine synthase [EC:2.5.1.46]
EPL_15243_0207	long-chain-fatty-acid--CoA ligase (EC:6.2.1.3)
EPL_15243_0205	hypothetical protein
EPL_15243_0204	hypothetical protein; K07068
EPL_15243_0203	AMP-dependent synthetase and ligase; K01897 long-chain acyl-CoA synthetase [EC:6.2.1.3]
EPL_15243_0198	hypothetical protein
EPL_15243_0194	30S ribosomal protein S7P; K02992 small subunit ribosomal protein S7
EPL_15243_0193	rps12P; 30S ribosomal protein S12P; K02950 small subunit ribosomal protein S12
EPL_15243_0180	acyl-CoA synthetase related protein
EPL_15243_0179	acyl-CoA dehydrogenase related protein

EPL_15243_0158	hypothetical protein
EPL_15243_0157	CRISPR-associated protein
EPL_15243_0156	hypothetical protein
EPL_15243_0155	hypothetical protein
EPL_15243_0146	CRISPR-associated protein Csc2
EPL_15243_0145	hypothetical protein
EPL_15243_0131	aspA; aspartate ammonia-lyase (EC:4.3.1.1); K01679 fumarate hydratase, class II [EC:4.2.1.2]
EPL_15243_0130	pyruvate ferredoxin oxidoreductase, alpha chain (EC:1.2.7.1); K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
EPL_15243_0129	2-oxoacid ferredoxin oxidoreductase subunit beta (EC:1.2.7.1); K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
EPL_15243_0126	ABC-type peptide transport system, solute-binding component
EPL_15243_0118	ABC-type peptide transporter, ATPase component; K02032 peptide/nickel transport system ATP-binding protein
EPL_15243_0117	ABC-type peptide transport system, ATPase component
EPL_15243_0114	rpl12p; 50S ribosomal protein L12P; K02869 large subunit ribosomal protein L12
EPL_15243_0113	rplP0; acidic ribosomal protein P0; K02864 large subunit ribosomal protein L10
EPL_15243_0112	rpl1P; 50S ribosomal protein L1P; K02863 large subunit ribosomal protein L1
EPL_15243_0111	rpl11p; 50S ribosomal protein L11P; K02867 large subunit ribosomal protein L11
EPL_15243_0107	hypothetical protein
EPL_15243_0106	hypothetical protein
EPL_15243_0105	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
EPL_15243_0104	nucleic-acid-binding protein; K07068
EPL_15243_0103	peroxiredoxin; K03564 peroxiredoxin Q/BCP [EC:1.11.1.15]
EPL_15243_0101	putative RNA-binding protein; K07575 PUA domain protein
EPL_15243_0100	hypothetical protein
EPL_15243_0099	nusG; transcription antitermination protein NusG; K02601 transcriptional antiterminator NusG
EPL_15243_0097	rpoK; DNA-directed RNA polymerase subunit K (EC:2.7.7.6); K03055 DNA-directed RNA polymerase subunit K [EC:2.7.7.6]
EPL_15243_0095	lysK; lysyl-tRNA synthetase (EC:6.1.1.6); K04566 lysyl-tRNA synthetase, class I [EC:6.1.1.6]
EPL_15243_0092	chromosome partitioning ATPase; K03593 ATP-binding protein involved in chromosome partitioning
EPL_15243_0086	phosphoribosylaminoimidazole synthetase (EC:6.3.3.1); K01933 phosphoribosylformylglycinamidine cyclo-ligase [EC:6.3.3.1]
EPL_15243_0069	phosphate uptake regulator

EPL_15243_0068	metal dependent hydrolase (EC:3.-.-.-); K01567 [EC:3.-.-.-]
EPL_15243_0067	S-adenosylmethionine synthetase (EC:2.5.1.6); K00789 S-adenosylmethionine synthetase [EC:2.5.1.6]
EPL_15243_0066	purH; bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (EC:3.5.4.10 2.1.2.3); K00602 phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]
EPL_15243_0064	DNA topoisomerase I (EC:5.99.1.2); K03168 DNA topoisomerase I [EC:5.99.1.2]
EPL_15243_0061	hypothetical protein
EPL_15243_0060	L-3-hydroxyacyl-CoA dehydrogenase precursor related protein
EPL_15243_0058	ABC transporter related protein
EPL_15243_0051	mercuric reductase (EC:1.16.1.1); K00520 mercuric reductase [EC:1.16.1.1]
EPL_15243_0045	metallo-beta-lactamase family protein
EPL_15243_0044	alkyl hydroperoxide reductase subunit f related protein
EPL_15243_0039	formiminotransferase cyclodeaminase related protein
EPL_15243_0038	glutamate formiminotransferase; K01746 formiminotetrahydrofolate cyclodeaminase [EC:4.3.1.4]
EPL_15243_0037	ribonucleotide-diphosphate reductase subunit alpha (EC:1.17.4.1); K00525 ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
EPL_15243_0030	predicted succinyl-CoA:3-ketoacid-CoA ligase
EPL_15243_0021	hypothetical protein
EPL_15243_0018	2-methylcitrate synthase/citrate synthase II (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]
EPL_15243_0014	glutamine synthetase; K01915 glutamine synthetase [EC:6.3.1.2]
EPL_15243_0012	metal-binding protein containing
EPL_12876_0003	transferase hexapeptide domain protein
ARMAN5:or1105	Arginyl-tRNA synthetase (Fragment)
ARMAN5:or1100	Putative uncharacterized protein (Fragment)
ARMAN5:or1083	fusA; elongation factor EF-2; K03234 elongation factor EF-2 [EC:3.6.5.3]
ARMAN5:or1073	Putative uncharacterized protein
ARMAN5:or1053	Sulfatase
ARMAN5:or1046	Heat shock protein Hsp20
ARMAN5:or1045	Putative uncharacterized protein
ARMAN5:or1025	Heavy metal translocating P-type ATPase
ARMAN5:or1022	aconitate hydratase; K01681 aconitate hydratase 1 [EC:4.2.1.3]
ARMAN5:or0993	Translation initiation factor 2, alpha subunit

ARMAN5:or0991a	Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein
ARMAN5:or0990a	trxA; TrxA protein; K03671 thioredoxin 1
ARMAN5:or0988	Methionine adenosyltransferase
ARMAN5:or0951	H+transporting two-sector ATPase alpha/beta subunit domain protein
ARMAN5:or0944	AAA family ATPase, CDC48 subfamily
ARMAN5:or0937	Isoleucyl-tRNA synthetase
ARMAN5:or0935	transcription factor; K03120 transcription initiation factor TFIID TATA-box-binding protein
ARMAN5:or0915	Proliferating cell nuclear antigen PcnA
ARMAN5:or0910	Putative uncharacterized protein
ARMAN5:or0886	top6A; DNA topoisomerase VI subunit A (EC:5.99.1.3); K03166 DNA topoisomerase VI subunit A [EC:5.99.1.3]
ARMAN5:or0859	Putative uncharacterized protein
ARMAN5:or0857	Chaperone protein DnaK
ARMAN5:or0843	Aspartate/glutamate/uridylate kinase
ARMAN5:or0825	V-type ATPase 116 kDa subunit
ARMAN5:or0822	V-type ATP synthase subunit B (EC:3.6.3.14); K02118 V-type H+-transporting ATPase subunit B [EC:3.6.3.14]
ARMAN5:or0821	ATP synthase, A subunit (EC:3.6.3.14); K02117 V-type H+-transporting ATPase subunit A [EC:3.6.3.14]
ARMAN5:or0815	Superoxide dismutase
ARMAN5:or0795	Proteasome endopeptidase complex
ARMAN5:or0785	Asparagine synthase
ARMAN5:or0764	Putative uncharacterized protein
ARMAN5:or0761	PrkA AAA domain protein
ARMAN5:or0755	putative RNA-processing protein; K06961
ARMAN5:or0731	Putative uncharacterized protein
ARMAN5:or0728	Putative uncharacterized protein
ARMAN5:or0714	Putative uncharacterized protein
ARMAN5:or0708	Elongation factor Tu domain protein (Fragment)
ARMAN5:or0679	KH type 2 domain protein
ARMAN5:or0668	Transcriptional regulator TrmB
ARMAN5:or0663	ATP-dependent protease; K13525 transitional endoplasmic reticulum ATPase
ARMAN5:or0656	H+transporting two-sector ATPase alpha/beta subunit central region
ARMAN5:or0655	V-type ATP synthase subunit B (EC:3.6.3.14); K02118 V-type H+-transporting ATPase subunit B [EC:3.6.3.14]
ARMAN5:or0652	V-type ATP synthase subunit I (EC:3.6.3.14); K02123 V-type H+-transporting ATPase subunit I [EC:3.6.3.14]

ARMAN5:or0649	hypothetical protein
ARMAN5:or0648	ATP-dependent protease Lon; K04076 Lon-like ATP-dependent protease [EC:3.4.21.-]
ARMAN5:or0597	Succinate dehydrogenase
ARMAN5:or0590	Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein
ARMAN5:or0520	TOPRIM domain protein
ARMAN5:or0513	cation transport ATPase; K01533 Cu2+-exporting ATPase [EC:3.6.3.4]
ARMAN5:or0510	Aconitate hydratase 1
ARMAN5:or0502	GatB-like protein
ARMAN5:or0483	cell division protein FtsZ; K03531 cell division protein FtsZ
ARMAN5:or0475	Zinc-binding alcohol dehydrogenase family protein
ARMAN5:or0472	Putative uncharacterized protein
ARMAN5:or0461	Beta-lactamase domain protein
ARMAN5:or0439	rpl12p; 50S ribosomal protein L12P; K02869 large subunit ribosomal protein L12
ARMAN5:or0434	Fructose-bisphosphate aldolase
ARMAN5:or0432	Putative uncharacterized protein
ARMAN5:or0421	ribosomal protein S27E
ARMAN5:or0414	ArsR family transcriptional regulator
ARMAN5:or0405	DNA repair and recombination protein RadA
ARMAN5:or0373	Putative uncharacterized protein
ARMAN5:or0349	Phosphoadenosine phosphosulfate reductase
ARMAN5:or0346	Putative uncharacterized protein
ARMAN5:or0342	hypothetical protein
ARMAN5:or0341	Chaperonin Cpn60/TCP-1
ARMAN5:or0297	tfb; transcription initiation factor IIB; K03124 transcription initiation factor TFIIB
ARMAN5:or0291	Nucleoside diphosphate kinase
ARMAN5:or0288	Selenocysteine-specific translation elongation factor-like protein
ARMAN5:or0277	DNA polymerase II, large subunit DP2
ARMAN5:or0276	CBS domain containing protein
ARMAN5:or0255	Glucose-6-phosphate isomerase
ARMAN5:or0223	Deoxyribose-phosphate aldolase
ARMAN5:or0160	Putative uncharacterized protein
ARMAN5:or0147	fusA; elongation factor EF-2; K03234 elongation factor EF-2 [EC:3.6.5.3]

ARMAN5:or0132	Serine protease-like protein
ARMAN5:or0130	glycyl-tRNA synthetase (EC:6.1.1.14); K01880 glycyl-tRNA synthetase [EC:6.1.1.14]
ARMAN5:or0111	RNA polymerase Rpb7 domain protein
ARMAN5:or0104	Regulatory protein ArsR
ARMAN5:or0053	aspC; aspartyl-tRNA synthetase (EC:6.1.1.12); K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]
ARMAN5:or0016	tRNA synthetase valyl/leucyl anticodon-binding
ARMAN4:or1007	CRISPR-associated protein (Fragment)
ARMAN4:or0984	Glycine hydroxymethyltransferase
ARMAN4:or0956	TATA-box binding family protein
ARMAN4:or0951	CBS domain containing membrane protein
ARMAN4:or0947	Elongation factor 1-alpha
ARMAN4:or0945	Transposase, IS605 OrfB family
ARMAN4:or0929	hypothetical protein
ARMAN4:or0926	Aminoacyl-tRNA synthetase class Ia
ARMAN4:or0920	Putative circadian clock protein, KaiC
ARMAN4:or0919	Putative uncharacterized protein
ARMAN4:or0895	putative NADPH:quinone oxidoreductase
ARMAN4:or0876	Putative uncharacterized protein
ARMAN4:or0871	Putative uncharacterized protein
ARMAN4:or0868	Putative uncharacterized protein
ARMAN4:or0838	hypothetical protein; K07133
ARMAN4:or0835	Peptidase S16, Lon protease
ARMAN4:or0834	hypothetical protein
ARMAN4:or0833	Acyl-CoA synthetase (NDP forming)-like protein
ARMAN4:or0776	Putative uncharacterized protein
ARMAN4:or0767	Ribosomal protein L3
ARMAN4:or0761	non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (GAPN) (EC:1.2.1.9)
ARMAN4:or0755	Proteasome endopeptidase complex
ARMAN4:or0753	KH type 1 domain protein
ARMAN4:or0751	Putative uncharacterized protein
ARMAN4:or0728	Putative uncharacterized protein
ARMAN4:or0709	rps5p; 30S ribosomal protein S5P; K02988 small subunit ribosomal protein S5

ARMAN4:or0706	Elongation factor G domain IV
ARMAN4:or0700	Metallophosphoesterase
ARMAN4:or0692	RNA polymerase beta subunit
ARMAN4:or0691	RNA polymerase Rpb2 domain 6
ARMAN4:or0690	RNA polymerase Rpb1 domain 1
ARMAN4:or0687	RNA polymerase Rpb1 domain 4
ARMAN4:or0686	RNA polymerase Rpb1 domain 5
ARMAN4:or0662	Small GTP-binding protein
ARMAN4:or0648	Deoxyhypusine synthase
ARMAN4:or0599	Seryl-tRNA synthetase
ARMAN4:or0592	DNA polymerase sliding clamp
ARMAN4:or0587	Putative uncharacterized protein
ARMAN4:or0570	Succinate dehydrogenase
ARMAN4:or0563	pyruvate flavodoxin/ferredoxin oxidoreductase domain-containing protein; K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
ARMAN4:or0562	trxA; TrxA protein; K03671 thioredoxin 1
ARMAN4:or0556	Succinate--CoA ligase (ADP-forming)
ARMAN4:or0551	TOPRIM domain protein
ARMAN4:or0543	Nucleotidyl transferase
ARMAN4:or0536	Aconitate hydratase 1
ARMAN4:or0513	transcriptional regulator, XRE family; K10726 replicative DNA helicase Mcm [EC:3.6.1.-]
ARMAN4:or0509	rps10p; 30S ribosomal protein S10P; K02946 small subunit ribosomal protein S10
ARMAN4:or0508	rpl7ae; 50S ribosomal protein L7Ae; K02936 large subunit ribosomal protein L7Ae
ARMAN4:or0507	rps28e; 30S ribosomal protein S28e; K02979 small subunit ribosomal protein S28e
ARMAN4:or0504	Putative uncharacterized protein
ARMAN4:or0501	Putative uncharacterized protein
ARMAN4:or0495	Phosphoenolpyruvate synthase
ARMAN4:or0489	Nucleotidyl transferase
ARMAN4:or0449	Cell division protein ftsZ
ARMAN4:or0395	aspC; aspartyl-tRNA synthetase (EC:6.1.1.12); K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]
ARMAN4:or0391	Putative uncharacterized protein
ARMAN4:or0379	Phosphoglycerate mutase 1 family

ARMAN4:or0360	DNA repair and recombination protein RadA
ARMAN4:or0327	Transcriptional regulator, ArsR family
ARMAN4:or0315	Ribosomal protein L10
ARMAN4:or0314	rpl12p; 50S ribosomal protein L12P; K02869 large subunit ribosomal protein L12
ARMAN4:or0308	Fructose-bisphosphate aldolase 1
ARMAN4:or0288	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen
ARMAN4:or0283	aspA; aspartate ammonia-lyase (EC:4.3.1.1); K01744 aspartate ammonia-lyase [EC:4.3.1.1]
ARMAN4:or0277	Beta-lactamase domain protein
ARMAN4:or0252	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
ARMAN4:or0249	Serine protease-like protein
ARMAN4:or0245	Beta-lactamase domain protein
ARMAN4:or0234	Translation elongation factor aEF-2
ARMAN4:or0224	Putative uncharacterized protein
ARMAN4:or0219	Putative uncharacterized protein
ARMAN4:or0210	Glycosyl transferase group 1
ARMAN4:or0201	Putative methyl-accepting chemotaxis sensory transducer
ARMAN4:or0186	Lysyl-tRNA synthetase
ARMAN4:or0182	Phosphoadenosine phosphosulfate reductase
ARMAN4:or0178	like-Sm ribonucleoprotein core; K04796 small nuclear ribonucleoprotein
ARMAN4:or0177	Thermosome
ARMAN4:or0159	Putative uncharacterized protein
ARMAN4:or0143	Type III restriction protein res subunit
ARMAN4:or0137	Putative uncharacterized protein
ARMAN4:or0136	Putative uncharacterized protein
ARMAN4:or0132	Transcription factor TFIIB cyclin-related protein
ARMAN4:or0124	Selenocysteine-specific translation elongation factor-like protein
ARMAN4:or0109	Putative uncharacterized protein
ARMAN4:or0108	KH type 2 domain protein
ARMAN4:or0107	50S ribosomal protein L22P
ARMAN4:or0098	Transcriptional regulator, TrmB
ARMAN4:or0093	Microtubule-severing ATPase
ARMAN4:or0086	H+transporting two-sector ATPase alpha/beta subunit central region

ARMAN4:or0085	H+transporting two-sector ATPase alpha/beta subunit central region
ARMAN4:or0064	Superoxide dismutase
ARMAN4:or0046	Putative uncharacterized protein
ARMAN4:or0037	Putative serine protein kinase, PrkA
ARMAN4:or0030	Putative uncharacterized protein
ARMAN4:or0025	Chaperone protein dnaK
ARMAN4:or0024	CoA-binding domain protein
ARMAN2_15008_980	Ribosomal protein S8
ARMAN2_15008_973	Putative uncharacterized protein
ARMAN2_15008_935	Putative uncharacterized protein
ARMAN2_15008_921	Ribosomal protein S2
ARMAN2_15008_918	Putative uncharacterized protein
ARMAN2_15008_917	Type II secretion system protein E
ARMAN2_15008_892	Putative uncharacterized protein
ARMAN2_15008_858	Peptidase U61 LD-carboxypeptidase A
ARMAN2_15008_841	SpoVT/AbrB domain protein
ARMAN2_15008_838	NADP oxidoreductase coenzyme F420-dependent
ARMAN2_15008_837	deoxyribonuclease
ARMAN2_15008_836	DNA polymerase sliding clamp
ARMAN2_15008_830	Putative uncharacterized protein
ARMAN2_15008_814	Ribosomal protein S3-domain protein
ARMAN2_15008_804	DNA gyrase, A subunit
ARMAN2_15008_803	DNA topoisomerase (ATP-hydrolyzing)
ARMAN2_15008_780	Thermosome
ARMAN2_15008_778	hypothetical protein; K07466 replication factor A1
ARMAN2_15008_769	2-oxoacid--ferredoxin oxidoreductase subunit alpha; K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
ARMAN2_15008_762	Aconitate hydratase 1
ARMAN2_15008_752	hypothetical protein
ARMAN2_15008_750	aldehyde dehydrogenase; K00294 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]
ARMAN2_15008_739	geranylgeranyl reductase
ARMAN2_15008_735	SMC domain protein

ARMAN2_15008_731	Ribosomal protein S7
ARMAN2_15008_718	succinyl-CoA synthetase alpha subunit related protein
ARMAN2_15008_701	thioredoxin; K03671 thioredoxin 1
ARMAN2_15008_692	Proteasome subunit alpha
ARMAN2_15008_689	Putative uncharacterized protein
ARMAN2_15008_682	Glu/Leu/Phe/Val dehydrogenase
ARMAN2_15003_652	Ribosomal protein S13
ARMAN2_15003_644	inorganic pyrophosphatase; K01507 inorganic pyrophosphatase [EC:3.6.1.1]
ARMAN2_15003_637	rpl12p; 50S ribosomal protein L12P; K02869 large subunit ribosomal protein L12
ARMAN2_15003_611	Putative uncharacterized protein
ARMAN2_15003_564	sdhA; succinate dehydrogenase flavoprotein subunit (EC:1.3.99.1); K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
ARMAN2_15003_559	Malate dehydrogenase (Oxaloacetate-decarboxylating) (NADP(+))
ARMAN2_15003_558	Putative uncharacterized protein
ARMAN2_15003_521	Putative uncharacterized protein
ARMAN2_15003_493	Putative uncharacterized protein
ARMAN2_15003_472	RNA polymerase beta subunit
ARMAN2_15003_471	RNA polymerase Rpb2 domain 6
ARMAN2_15003_470	RNA polymerase alpha subunit
ARMAN2_15003_469	RNA polymerase Rpb1 domain 5
ARMAN2_15003_459	Heat shock protein Hsp20
ARMAN2_15003_456	Chaperone protein dnaK
ARMAN2_15003_455	chaperone protein DnaJ; K03686 molecular chaperone DnaJ
ARMAN2_15003_453	Proteasome endopeptidase complex
ARMAN2_15003_450	Transcription factor TFIIB cyclin-related
ARMAN2_15003_418	Glycosyl transferase family 2
ARMAN2_15003_416	Short-chain dehydrogenase/reductase SDR
ARMAN2_15003_406	Dihydroxy-acid dehydratase
ARMAN2_15003_403	Aldehyde Dehydrogenase
ARMAN2_15003_400	hypothetical protein
ARMAN2_15003_350	Histidine ammonia-lyase
ARMAN2_15003_335	Glycosyl transferase group 1 (Fragment)

ARMAN2_15002_308	Putative uncharacterized protein
ARMAN2_15002_301	ATP-dependent protease Lon; K04076 Lon-like ATP-dependent protease [EC:3.4.21.-]
ARMAN2_15002_297	ribonucleoside-diphosphate reductase; K00525 ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
ARMAN2_15001_250	Elongation factor 1-alpha
ARMAN2_15001_235	DNA polymerase II, large subunit DP2 (EC:2.7.7.7); K02322 DNA polymerase II large subunit [EC:2.7.7.7]
ARMAN2_15001_224	Putative signal transduction protein with CBS domains
ARMAN2_15001_218	tRNA/rRNA methyltransferase (SpoU)
ARMAN2_15001_214	cell division protein FtsZ
ARMAN2_15001_204	ATP synthase, A subunit (EC:3.6.3.14); K02117 V-type H+-transporting ATPase subunit A [EC:3.6.3.14]
ARMAN2_15001_203	H+transporting two-sector ATPase alpha/beta subunit central region
ARMAN2_15001_177	hypothetical protein; K06937
ARMAN2_13246_120	cell division protein CDC48; K13525 transitional endoplasmic reticulum ATPase
ARMAN2_13246_116	Transcriptional regulator, TrmB
ARMAN2_13235_40	Putative uncharacterized protein
APL_17518_0017	gamma-glutamyltransferase related protein; K00681 gamma-glutamyltranspeptidase [EC:2.3.2.2]
APL_17518_0010	sterol carrier protein
APL_17518_0009	alcohol dehydrogenase IV; K00001 alcohol dehydrogenase [EC:1.1.1.1]
APL_17518_0006	ABC transporter ATP-binding protein; K01990 ABC-2 type transport system ATP-binding protein
APL_17500_0037	sdhB; succinate dehydrogenase iron-sulfur subunit (EC:1.3.99.1); K00240 succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]
APL_17500_0036	sdhA; succinate dehydrogenase flavoprotein subunit (EC:1.3.5.1); K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]
APL_17500_0034	small heat shock protein (HSP20) related protein
APL_17500_0031	eno; phosphopyruvate hydratase (EC:4.2.1.11); K01689 enolase [EC:4.2.1.11]
APL_17500_0030	acetyltransferase
APL_17500_0027	ATP-dependent protease Lon; K04076 Lon-like ATP-dependent protease [EC:3.4.21.-]
APL_17500_0021	alaS; alanyl-tRNA synthetase (EC:6.1.1.7); K01872 alanyl-tRNA synthetase [EC:6.1.1.7]
APL_17500_0018	transcription factor; K03627 putative transcription factor
APL_17500_0016	beta-hydroxybutyryl-CoA dehydrogenase related protein; K00074 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
APL_17500_0012	aspC; aspartyl-tRNA synthetase (EC:6.1.1.12); K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]
APL_17500_0003	type I restriction-modification enzyme, M subunit; K03427 type I restriction enzyme M protein [EC:2.1.1.72]

APL_17500_0001	HsdR family type I site-specific deoxyribonuclease; K01153 type I restriction enzyme, R subunit [EC:3.1.21.3]
APL_17498_0017	transcription regulator; K00845 glucokinase [EC:2.7.1.2]
APL_17498_0009	pyruvate kinase (EC:2.7.1.40); K00873 pyruvate kinase [EC:2.7.1.40]
APL_17498_0008	peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K01802 peptidylprolyl isomerase [EC:5.2.1.8]
APL_17498_0006	50S ribosomal protein L18e; K02883 large subunit ribosomal protein L18e
APL_17498_0004	rps9p; 30S ribosomal protein S9P; K02996 small subunit ribosomal protein S9
APL_17498_0003	DNA-directed RNA polymerase subunit N (EC:2.7.7.6); K03058 DNA-directed RNA polymerase subunit N [EC:2.7.7.6]
APL_17493_0013	4-hydroxybenzoate transporter
APL_17487_0019	signal recognition particle receptor FtsY; K03110 fused signal recognition particle receptor
APL_17487_0018	prefoldin subunit alpha; K04797 prefoldin alpha subunit
APL_17487_0017	Phosphoglycerate kinase
APL_17487_0016	pgk; phosphoglycerate kinase (EC:2.7.2.3); K00927 phosphoglycerate kinase [EC:2.7.2.3]
APL_17487_0015	glucose-1-phosphate thymidylyltransferase related protein; K00973 glucose-1-phosphate thymidylyltransferase [EC:2.7.7.24]
APL_17487_0014	sulfolipid biosynthesis protein
APL_17487_0010	hypothetical protein; K07577 putative mRNA 3-end processing factor
APL_17487_0009	RNA processing exonuclease; K07577 putative mRNA 3-end processing factor
APL_17487_0008	5'-methylthioadenosine phosphorylase II (EC:2.4.2.28); K00772 5'-methylthioadenosine phosphorylase [EC:2.4.2.28]
APL_17481_0009	2-amino-3-ketobutyrate coenzyme A ligase (EC:2.3.1.29); K00639 glycine C-acetyltransferase [EC:2.3.1.29]
APL_17481_0008	hypothetical protein
APL_17481_0006	carbamoyl phosphate synthase small subunit (EC:6.3.5.5); K01956 carbamoyl-phosphate synthase small subunit [EC:6.3.5.5]
APL_17481_0005	carB; carbamoyl phosphate synthase large subunit (EC:6.3.5.5); K01955 carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]
APL_17481_0003	geranylgeranyl reductase
APL_17472_0049	metal-dependent hydrolase
APL_17472_0048	metal-dependent hydrolase
APL_17472_0047	mannose-1-phosphate guanyltransferase related protein
APL_17472_0039	CBS domain-containing protein
APL_17472_0038	glycyl-tRNA synthetase (EC:6.1.1.14); K01880 glycyl-tRNA synthetase [EC:6.1.1.14]
APL_17472_0033	ABC transporter ATP-binding protein

APL_17472_0026	aldehyde dehydrogenase family protein; K00155 [EC:1.2.1.-]
APL_17472_0025	isocitrate dehydrogenase; K00031 isocitrate dehydrogenase [EC:1.1.1.42]
APL_17472_0023	purA; adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]
APL_17472_0021	urocanate hydratase (EC:4.2.1.49); K01712 urocanate hydratase [EC:4.2.1.49]
APL_17472_0018	mannose-1-phosphate guanyltransferase (EC:2.7.7.13); K00966 mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
APL_17472_0017	hypothetical protein
APL_17472_0013	orotidine 5'-phosphate decarboxylase (EC:4.1.1.23); K01591 orotidine-5'-phosphate decarboxylase [EC:4.1.1.23]
APL_17472_0010	pyrE; orotate phosphoribosyltransferase (EC:2.4.2.10); K00762 orotate phosphoribosyltransferase [EC:2.4.2.10]
APL_17472_0009	TIF6; translation initiation factor IF-6; K03264 translation initiation factor eIF-6
APL_17472_0008	50S ribosomal protein L31e; K02910 large subunit ribosomal protein L31e
APL_17472_0006	hypothetical protein; K06875
APL_17472_0005	30S ribosomal protein S19e; K02966 small subunit ribosomal protein S19e
APL_17472_0003	gliding motility protein related
APL_17466_0017	nicotinate phosphoribosyltransferase (EC:2.4.2.11); K00763 nicotinate phosphoribosyltransferase [EC:2.4.2.11]
APL_17466_0005	pepQ-like3; prolidase (Xaa-Pro dipeptidase) (PepQ-like3) (EC:3.4.13.9)
APL_17462_0060	NAD-dependent aldehyde dehydrogenase; K00130 betaine-aldehyde dehydrogenase [EC:1.2.1.8]
APL_17462_0058	2-hydroxyacid dehydrogenase
APL_17462_0032	hypothetical protein
APL_17462_0023	glucose 1-dehydrogenase; K04708 3-dehydrosphinganine reductase [EC:1.1.1.102]
APL_17462_0014	hypothetical protein
APL_17454_0010	putative alcohol dehydrogenase; K00001 alcohol dehydrogenase [EC:1.1.1.1]
APL_17452_0021	30S ribosomal protein S3Ae; K02984 small subunit ribosomal protein S3Ae
APL_17452_0020	arginine deiminase
APL_17452_0017	DNA-directed RNA polymerase subunit E'; K03049 DNA-directed RNA polymerase subunit E' [EC:2.7.7.6]
APL_17452_0016	rpoE; DNA-directed RNA polymerase subunit E'' (EC:2.7.7.6); K03050 DNA-directed RNA polymerase subunit E'' [EC:2.7.7.6]
APL_17452_0014	rps24e; 30S ribosomal protein S24e; K02974 small subunit ribosomal protein S24e
APL_17452_0010	hypothetical protein; K03724 ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.1.-]
APL_17452_0004	putative alcohol dehydrogenase; K00001 alcohol dehydrogenase [EC:1.1.1.1]
APL_17449_0026	ribonuclease Z (EC:3.1.26.11); K00784 ribonuclease Z [EC:3.1.26.11]
APL_17449_0022	thiosulfate sulfurtransferase (EC:2.8.1.1); K01010 thiosulfate sulfurtransferase [EC:2.8.1.1]

APL_17449_0021	phosphoribosylamine--glycine ligase (EC:6.3.4.13); K01945 phosphoribosylamine--glycine ligase [EC:6.3.4.13]
APL_17449_0020	protein translation elongation factor
APL_17449_0017	hypothetical protein
APL_17449_0015	asnC; asparaginyl-tRNA synthetase (EC:6.1.1.22); K01893 asparaginyl-tRNA synthetase [EC:6.1.1.22]
APL_17445_0046	cysteine synthase (EC:2.5.1.47); K01738 cysteine synthase A [EC:2.5.1.47]
APL_17445_0044	VAT ATPase (VCP-like ATPase); K13525 transitional endoplasmic reticulum ATPase
APL_17445_0041	peptide chain release factor 1; K03265 peptide chain release factor eRF subunit 1
APL_17445_0040	pyrH; uridylate kinase (EC:2.7.4.-); K09903 uridylate kinase [EC:2.7.4.22]
APL_17445_0039	Fe-S oxidoreductase
APL_17445_0036	ABC transporter related protein; K09687 antibiotic transport system ATP-binding protein
APL_17445_0030	hypothetical protein
APL_17445_0029	hypothetical protein; K00123 formate dehydrogenase, alpha subunit [EC:1.2.1.2]
APL_17445_0024	moaC; putative molybdenum cofactor biosynthesis protein MoaC; K03637 molybdenum cofactor biosynthesis protein C
APL_17445_0019	hypothetical protein
APL_17445_0013	hypothetical protein
APL_17442_0020	aldehyde dehydrogenase; K07248 lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase [EC:1.2.1.22 1.2.1.21]
APL_17442_0019	molybdenum cofactor biosynthesis protein A; K06937
APL_17442_0018	Fe-S oxidoreductase; K06937
APL_17442_0016	pyruvoyl-dependent arginine decarboxylase (EC:4.1.1.19); K02626 arginine decarboxylase [EC:4.1.1.19]
APL_17442_0015	leuS; leucyl-tRNA synthetase (EC:6.1.1.4); K01869 leucyl-tRNA synthetase [EC:6.1.1.4]
APL_17442_0014	short chain dehydrogenase
APL_17442_0010	ATP-dependent DNA ligase (EC:6.5.1.1); K10747 DNA ligase 1 [EC:6.5.1.1]
APL_17442_0009	single-stranded DNA-binding protein; K07466 replication factor A1
APL_17439_0035	hypothetical protein
APL_17439_0031	methylmalonyl-CoA mutase alpha subunit (EC:5.4.99.2); K01849 methylmalonyl-CoA mutase, C-terminal domain [EC:5.4.99.2]
APL_17439_0030	GTPase; K07588 LAO/AO transport system kinase [EC:2.7.-.-]
APL_17439_0028	ABC transporter related protein
APL_17439_0022	proteasome subunit alpha (EC:3.4.25.1); K03432 proteasome alpha subunit [EC:3.4.25.1]
APL_17439_0021	putative RNA-associated protein; K07582 hypothetical protein

APL_17439_0020	exosome complex RNA-binding protein Rrp4; K03679 exosome complex component RRP4
APL_17439_0019	exosome complex exonuclease Rrp41; K11600 exosome complex component RRP41
APL_17439_0018	exosome complex RNA-binding protein Rrp42; K12589 exosome complex component RRP42
APL_17439_0017	rpl37ae; 50S ribosomal protein L37Ae; K02921 large subunit ribosomal protein L37Ae
APL_17439_0013	RNA-binding protein; K07572 putative nucleotide binding protein
APL_17439_0011	band 7 integral membrane protein-like protein
APL_17439_0009	pyruvate phosphate dikinase (EC:2.7.9.1); K01006 pyruvate,orthophosphate dikinase [EC:2.7.9.1]
APL_17439_0008	pyruvate phosphate dikinase (EC:2.7.9.1); K01006 pyruvate,orthophosphate dikinase [EC:2.7.9.1]
APL_17439_0007	purine phosphoribosyltransferase related protein; K07101
APL_17439_0005	solute-binding protein; K07083
APL_17433_0053	ornithine carbamoyltransferase (EC:2.1.3.3); K00611 ornithine carbamoyltransferase [EC:2.1.3.3]
APL_17433_0052	succinyl-CoA synthetase subunit alpha (EC:6.2.1.5); K01902 succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
APL_17433_0051	sucC; succinyl-CoA synthetase subunit beta (EC:6.2.1.5); K01903 succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
APL_17433_0050	thioredoxin reductase; K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]
APL_17433_0048	thermosome, alpha chain
APL_17433_0046	hypothetical protein; K07068
APL_17433_0045	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
APL_17433_0044	NADH-dependent oxidoreductase (EC:1.6.-.-); K00359 NADH oxidase [EC:1.6.-.-]
APL_17433_0039	hypothetical protein
APL_17433_0029	homoserine dehydrogenase (EC:1.1.1.3); K00003 homoserine dehydrogenase [EC:1.1.1.3]
APL_17433_0028	DNA gyrase subunit A; K02469 DNA gyrase subunit A [EC:5.99.1.3]
APL_17433_0027	gyrB; DNA gyrase subunit B; K02470 DNA gyrase subunit B [EC:5.99.1.3]
APL_17433_0021	gltX; glutamyl-tRNA synthetase (EC:6.1.1.17); K01885 glutamyl-tRNA synthetase [EC:6.1.1.17]
APL_17433_0020	gltX; glutamyl-tRNA synthetase (EC:6.1.1.17); K01885 glutamyl-tRNA synthetase [EC:6.1.1.17]
APL_17433_0018	GMP synthase subunit A (EC:6.3.5.2); K01951 GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]
APL_17433_0017	tfb; transcription initiation factor IIB; K03124 transcription initiation factor TFIIB
APL_17433_0015	tfb; transcription initiation factor IIB; K03124 transcription initiation factor TFIIB
APL_17433_0013	2-methylcitrate synthase/citrate synthase II (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]
APL_17433_0010	threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]
APL_17433_0007	metB; hypothetical protein; K01739 cystathionine gamma-synthase [EC:2.5.1.48]
APL_17433_0004	FAD-dependent pyridine nucleotide-disulfide oxidoreductase

APL_17433_0003	acetyl-coenzyme-A synthetase; K01895 acetyl-CoA synthetase [EC:6.2.1.1]
APL_17433_0002	acetyl-coenzyme-A synthetase; K01895 acetyl-CoA synthetase [EC:6.2.1.1]
APL_17428_0041	DNA polymerase sliding clamp; K04802 proliferating cell nuclear antigen
APL_17428_0038	malate dehydrogenase (EC:1.1.1.37); K00024 malate dehydrogenase [EC:1.1.1.37]
APL_17428_0036	ATPase
APL_17428_0033	putative peroxiredoxin (EC:1.11.1.15); K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
APL_17428_0031	sec-independent protein translocase protein TatA; K03116 sec-independent protein translocase protein TatA
APL_17428_0017	NADH dehydrogenase subunit D (EC:1.6.5.3); K00333 NADH dehydrogenase I subunit D [EC:1.6.5.3]
APL_17428_0013	glutamyl-tRNA(Gln) amidotransferase subunit E; K03330 glutamyl-tRNA(Gln) amidotransferase subunit E [EC:6.3.5.7]
APL_17428_0012	glutamyl-tRNA(Gln) amidotransferase subunit D; K09482 glutamyl-tRNA(Gln) amidotransferase subunit D [EC:6.3.5.7]
APL_17428_0009	acyl-CoA dehydrogenase; K00257 [EC:1.3.99.-]
APL_17428_0007	rubrerythrin
APL_17393_0043	hypothetical protein
APL_17393_0038	glycine dehydrogenase subunit 2 (EC:1.4.4.2); K00283 glycine dehydrogenase subunit 2 [EC:1.4.4.2]
APL_17393_0035	replication factor A; K07466 replication factor A1
APL_17393_0034	hypothetical protein
APL_17393_0032	hypothetical protein
APL_17393_0029	adhP; Zn-dependent alcohol dehydrogenase; K13953 alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]
APL_17393_0020	transcriptional regulator
APL_17393_0010	inorganic pyrophosphatase (EC:3.6.1.1); K01507 inorganic pyrophosphatase [EC:3.6.1.1]
APL_17393_0007	hypothetical protein
APL_17393_0006	chaperonin GroEL
APL_17393_0003	acyl-CoA dehydrogenase; K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
APL_17387_0044	hypothetical protein
APL_17387_0042	hydroxymethylglutaryl-CoA reductase, degradative (EC:1.1.1.88); K00054 hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]
APL_17387_0041	pyrB; aspartate carbamoyltransferase catalytic subunit (EC:2.1.3.2); K00609 aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]
APL_17387_0040	aspartate carbamoyltransferase regulatory subunit (EC:2.1.3.2); K00610 aspartate carbamoyltransferase regulatory subunit

APL_17387_0037	translation initiation factor IF-2 subunit beta; K03238 translation initiation factor eIF-2 beta subunit
APL_17387_0035	winged helix-turn-helix domain-containing protein/riboflavin kinase; K07732 riboflavin kinase, archaea type [EC:2.7.1.161]
APL_17387_0031	geranylgeranylglyceryl phosphate synthase-like protein; K07094
APL_17387_0026	putative NTPase; K06928
APL_17387_0025	hypothetical protein; K09739 hypothetical protein
APL_17387_0017	acyl-CoA hydrolase related protein
APL_17387_0016	ribose-5-phosphate isomerase A (EC:5.3.1.6); K01807 ribose 5-phosphate isomerase A [EC:5.3.1.6]
APL_17387_0015	ArsR family transcriptional regulator
APL_17387_0013	AsnC family transcriptional regulator
APL_17387_0006	6,7-dimethyl-8-ribityllumazine synthase (EC:2.5.1.9); K00794 riboflavin synthase beta chain [EC:2.5.1.-]
APL_17365_0050	hypothetical protein
APL_17365_0048	zinc metalloprotease (EC:3.4.24.-); K07386 putative endopeptidase [EC:3.4.24.-]
APL_17365_0047	protease (PspA) related protein
APL_17365_0044	universal stress protein
APL_17365_0032	hypothetical protein; K09129 hypothetical protein
APL_17365_0026	hypothetical protein
APL_17365_0018	putative signal recognition particle; K03105 signal recognition particle subunit SRP19
APL_17365_0016	proline dipeptidase related protein; K01271 X-Pro dipeptidase [EC:3.4.13.9]
APL_17365_0015	Xaa-Pro dipeptidase (EC:3.4.13.9); K01271 X-Pro dipeptidase [EC:3.4.13.9]
APL_17365_0009	dihydroorotase (EC:3.5.2.3); K01465 dihydroorotase [EC:3.5.2.3]
APL_17365_0006	hypothetical protein
APL_17357_0093	hypothetical protein; K03564 peroxiredoxin Q/BCP [EC:1.11.1.15]
APL_17357_0091	hypothetical protein
APL_17357_0090	hypothetical protein; K01720 2-methylcitrate dehydratase [EC:4.2.1.79]
APL_17357_0088	carboxyphosphonoenolpyruvate phosphonomutase; K01003 carboxyvinyl-carboxyphosphonate phosphorylmutase [EC:2.7.8.23]
APL_17357_0084	DNA-directed RNA polymerase subunit D (EC:2.7.7.6); K03047 DNA-directed RNA polymerase subunit D [EC:2.7.7.6]
APL_17357_0083	rps11p; 30S ribosomal protein S11P; K02948 small subunit ribosomal protein S11
APL_17357_0082	rps4p; 30S ribosomal protein S4P; K02986 small subunit ribosomal protein S4
APL_17357_0081	rps13p; 30S ribosomal protein S13P; K02952 small subunit ribosomal protein S13

APL_17357_0067	DNA-directed RNA polymerase subunit A'' (EC:2.7.7.6); K03042 DNA-directed RNA polymerase subunit A'' [EC:2.7.7.6]
APL_17357_0066	DNA-directed RNA polymerase subunit A' (EC:2.7.7.6); K03041 DNA-directed RNA polymerase subunit A' [EC:2.7.7.6]
APL_17357_0065	DNA-directed RNA polymerase subunit B (EC:2.7.7.6); K13798 DNA-directed RNA polymerase subunit B [EC:2.7.7.6]
APL_17357_0064	rpoH; DNA-directed RNA polymerase subunit H (EC:2.7.7.6); K03053 DNA-directed RNA polymerase subunit H [EC:2.7.7.6]
APL_17357_0062	ABC transporter-like protein; K01990 ABC-2 type transport system ATP-binding protein
APL_17357_0060	translation initiation factor IF-2B subunit alpha; K03239 translation initiation factor eIF-2B alpha subunit
APL_17357_0041	translation initiation factor IF-2 subunit alpha; K03237 translation initiation factor eIF-2 alpha subunit
APL_17357_0036	small nuclear ribonucleoprotein; K04796 small nuclear ribonucleoprotein
APL_17357_0032	H/ACA RNA-protein complex component Cbf5p; K03177 tRNA pseudouridine synthase B [EC:5.4.99.12]
APL_17357_0029	adenylate kinase (EC:2.7.4.3); K00939 adenylate kinase [EC:2.7.4.3]
APL_17357_0026	rpl30p; 50S ribosomal protein L30P; K02907 large subunit ribosomal protein L30
APL_17357_0025	rps5p; 30S ribosomal protein S5P; K02988 small subunit ribosomal protein S5
APL_17357_0024	rpl18p; 50S ribosomal protein L18P; K02881 large subunit ribosomal protein L18
APL_17357_0023	rpl19e; 50S ribosomal protein L19e; K02885 large subunit ribosomal protein L19e
APL_17357_0022	rpl32e; 50S ribosomal protein L32e; K02912 large subunit ribosomal protein L32e
APL_17357_0021	rpl6p; 50S ribosomal protein L6P; K02933 large subunit ribosomal protein L6
APL_17357_0020	rps8p; 30S ribosomal protein S8P; K02994 small subunit ribosomal protein S8
APL_17357_0018	rpl5p; 50S ribosomal protein L5P; K02931 large subunit ribosomal protein L5
APL_17357_0017	30S ribosomal protein S4e; K02987 small subunit ribosomal protein S4e
APL_17357_0016	rpl24p; 50S ribosomal protein L24P; K02895 large subunit ribosomal protein L24
APL_17357_0015	rpl14p; 50S ribosomal protein L14P; K02874 large subunit ribosomal protein L14
APL_17357_0014	rps17p; 30S ribosomal protein S17P; K02961 small subunit ribosomal protein S17
APL_17357_0011	rps3p; 30S ribosomal protein S3P; K02982 small subunit ribosomal protein S3
APL_17357_0010	rpl22p; 50S ribosomal protein L22P; K02890 large subunit ribosomal protein L22
APL_17357_0009	rps19p; 30S ribosomal protein S19P; K02965 small subunit ribosomal protein S19
APL_17357_0008	rpl2p; 50S ribosomal protein L2P; K02886 large subunit ribosomal protein L2
APL_17357_0007	rplW; 50S ribosomal protein L23P; K02892 large subunit ribosomal protein L23
APL_17357_0006	rpl4lp; 50S ribosomal protein L4P; K02930 large subunit ribosomal protein L4e
APL_17357_0005	rpl3p; 50S ribosomal protein L3P; K02906 large subunit ribosomal protein L3

APL_17346_0015	aminotransferase, class V; K00839 aminotransferase [EC:2.6.1.-]
APL_17346_0014	TPR domain-containing protein
APL_17346_0007	multitransmembrane protein
APL_17346_0003	hypothetical protein
APL_17336_0059	4-hydroxyphenylpyruvate dioxygenase (EC:1.13.11.27); K00457 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]
APL_17336_0052	hypothetical protein
APL_17336_0051	molybdopterin binding domain-containing protein; K03742 competence/damage-inducible protein CinA
APL_17336_0035	hypothetical protein; K09732 hypothetical protein
APL_17336_0029	nucleoside-diphosphate-sugar epimerase; K01795 [EC:5.1.3.-]
APL_17336_0022	hypothetical protein
APL_17336_0018	hypothetical protein
APL_17336_0017	D-3-phosphoglycerate dehydrogenase (EC:1.1.1.95); K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]
APL_17336_0016	D-3-phosphoglycerate dehydrogenase; K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]
APL_17336_0015	serine--pyruvate aminotransferase; K00839 aminotransferase [EC:2.6.1.-]
APL_17336_0013	TPR domain-containing protein
APL_17325_0017	Rieske iron-sulfur protein SoxF related protein
APL_17325_0008	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
APL_17314_0003	hypothetical protein
APL_17306_0034	regulator of amino acid metabolism; K07103
APL_17306_0027	SoxB-like sarcosine oxidase, beta subunit related
APL_17306_0025	hypothetical protein; K01338 ATP-dependent Lon protease [EC:3.4.21.53]
APL_17306_0024	DNA primase (EC:2.7.7.-)
APL_17306_0023	endonuclease IV; K01151 deoxyribonuclease IV [EC:3.1.21.2]
APL_17306_0021	DNA-binding protein HTa
APL_17306_0019	spermidine synthase (EC:2.5.1.16); K00797 spermidine synthase [EC:2.5.1.16]
APL_17306_0015	NADH dehydrogenase (quinone) (EC:1.6.99.5)
APL_17306_0014	formate dehydrogenase, alpha subunit; K00123 formate dehydrogenase, alpha subunit [EC:1.2.1.2]
APL_17306_0013	RPS6; 30S ribosomal protein S6e; K02991 small subunit ribosomal protein S6e
APL_17306_0012	translation initiation factor IF-2 subunit gamma; K03242 translation initiation factor eIF-2 gamma subunit
APL_17306_0010	dehydrogenase (flavoprotein); K00313 electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]
APL_17306_0009	FixC protein related; K00313 electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]

APL_17306_0008	ferredoxin-like protein
APL_17306_0007	electron transfer flavoprotein subunit beta; K03521 electron transfer flavoprotein beta subunit
APL_17306_0006	electron transfer flavoprotein subunit alpha; K03522 electron transfer flavoprotein alpha subunit
APL_17306_0004	thrS; threonyl-tRNA synthetase (EC:6.1.1.3); K01868 threonyl-tRNA synthetase [EC:6.1.1.3]
APL_17300_0022	UDP-glucose 4-epimerase related protein; K01784 UDP-glucose 4-epimerase [EC:5.1.3.2]
APL_17300_0017	V-type ATP synthase subunit I (EC:3.6.3.14); K02123 V-type H+-transporting ATPase subunit I [EC:3.6.3.14]
APL_17300_0016	hypothetical protein
APL_17300_0013	V-type ATP synthase subunit B (EC:3.6.3.14); K02118 V-type H+-transporting ATPase subunit B [EC:3.6.3.14]
APL_17300_0012	V-type ATP synthase subunit B (EC:3.6.3.14); K02118 V-type H+-transporting ATPase subunit B [EC:3.6.3.14]
APL_17300_0011	ntpA; V-type ATP synthase subunit A (EC:3.6.3.14); K02117 V-type H+-transporting ATPase subunit A [EC:3.6.3.14]
APL_17300_0005	isopentenyl pyrophosphate isomerase (EC:5.3.3.2); K01823 isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]
APL_17298_0106	hypothetical protein
APL_17298_0105	Rieske Fe-S protein
APL_17298_0100	pyridoxal biosynthesis lyase PdxS; K06215 pyridoxine biosynthesis protein [EC:4.-.-.-]
APL_17298_0094	putative oxidoreductase; K00266 glutamate synthase (NADPH/NADH) small chain [EC:1.4.1.13 1.4.1.14]
APL_17298_0093	seryl-tRNA synthetase (EC:6.1.1.11); K01875 seryl-tRNA synthetase [EC:6.1.1.11]
APL_17298_0091	cofactor-independent phosphoglycerate mutase (EC:5.4.2.1); K01834 phosphoglycerate mutase [EC:5.4.2.1]
APL_17298_0090	S-adenosyl-L-homocysteine hydrolase (EC:3.3.1.1); K01251 adenosylhomocysteinase [EC:3.3.1.1]
APL_17298_0081	phosphomannomutase; K01835 phosphoglucomutase [EC:5.4.2.2]; K01840 phosphomannomutase [EC:5.4.2.8]
APL_17298_0069	hypothetical protein; K07327 archaeal flagellar protein FlaD
APL_17298_0068	flagellar protein C; K07822 archaeal flagellar protein FlaC
APL_17298_0065	acetyltransferase
APL_17298_0063	pheT; phenylalanyl-tRNA synthetase subunit beta (EC:6.1.1.20); K01890 phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]
APL_17298_0060	hypothetical protein; K07151 dolichyl-diphosphooligosaccharide--protein glycosyltransferase [EC:2.4.1.119]
APL_17298_0054	rps15p; 30S ribosomal protein S15P; K02956 small subunit ribosomal protein S15
APL_17298_0047	peroxiredoxin
APL_17298_0042	long-chain-fatty-acid--CoA ligase (EC:2.3.1.86); K00666 fatty-acyl-CoA synthase [EC:6.2.1.-]
APL_17298_0039	cell division protein FtsZ; K03531 cell division protein FtsZ
APL_17298_0037	transketolase; K00615 transketolase [EC:2.2.1.1]
APL_17298_0036	putative translaldolase (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2]

APL_17298_0034	cleavage and polyadenylation specificity factor, 100 kDa subunit; K07041
APL_17298_0033	proteasome, beta chain; K03433 proteasome beta subunit [EC:3.4.25.1]
APL_17298_0032	inosine-5'-monophosphate dehydrogenase related protein
APL_17298_0029	hemH; phosphoribosylaminoimidazole-succinocarboxamide synthase (EC:6.3.2.6); K01923 phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2.6]
APL_17298_0016	hypothetical protein
APL_17298_0009	asparagine synthetase A (EC:6.1.1.22); K01893 asparaginyl-tRNA synthetase [EC:6.1.1.22]
APL_17298_0006	aldehyde dehydrogenase related protein; K00294 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]
APL_17298_0001	translation initiation factor IF-2; K03243 translation initiation factor IF-2 unclassified subunit
APL_17112_0058	aspA; aspartate ammonia-lyase (EC:4.3.1.1); K01679 fumarate hydratase, class II [EC:4.2.1.2]
APL_17112_0057	2-oxoacid--ferredoxin oxidoreductase, alpha subunit; K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
APL_17112_0056	2-oxoacid ferredoxin oxidoreductase subunit beta (EC:1.2.7.1); K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
APL_17112_0054	ABC-type peptide transport system, solute-binding component
APL_17112_0052	amidohydrolase (EC:3.5.-.-)
APL_17112_0049	ABC-type peptide transporter, ATPase component; K02032 peptide/nickel transport system ATP-binding protein
APL_17112_0048	ABC-type peptide transport system, ATPase component
APL_17112_0043	hypothetical protein
APL_17112_0041	hypothetical protein
APL_17112_0039	hypothetical protein
APL_17112_0038	hypothetical protein
APL_17112_0036	aroB; 3-dehydroquinate synthase (EC:4.2.3.4); K01735 3-dehydroquinate synthase [EC:4.2.3.4]
APL_17112_0033	ATP-binding protein; K02023 multiple sugar transport system ATP-binding protein
APL_17112_0030	hypothetical protein; K02027 multiple sugar transport system substrate-binding protein
APL_17112_0024	Fe-S oxidoreductase
APL_17112_0022	proline iminopeptidase; K01259 proline iminopeptidase [EC:3.4.11.5]
APL_17112_0018	hypothetical protein
APL_17112_0017	alpha/beta superfamily hydrolase
APL_17112_0014	hypothetical protein
APL_17112_0007	aldehyde ferredoxin oxidoreductase; K03738 aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]
APL_17112_0003	oxidoreductase; K03738 aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]

APL_17112_0002	oxidoreductase; K03738 aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]
APL_17087_0077	hypothetical protein
APL_17087_0075	glyceraldehyde-3-phosphate dehydrogenase (EC:1.2.1.59); K00150 glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]
APL_17087_0074	radA; DNA repair and recombination protein RadA; K04483 DNA repair protein RadA
APL_17087_0073	hypothetical protein; K07103
APL_17087_0071	purE; phosphoribosylaminoimidazole carboxylase catalytic subunit (EC:4.1.1.21); K01588 5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]
APL_17087_0069	ilvB-5; pyruvate dehydrogenase (EC:1.2.2.2); K00156 pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]
APL_17087_0068	aminopeptidase N; K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
APL_17087_0067	tricorn protease interacting factor F2; K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
APL_17087_0066	aminopeptidase N; K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
APL_17087_0065	tricorn protease interacting factor F2 (EC:3.4.11.-); K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
APL_17087_0064	PmbA protein; K03592 PmbA protein
APL_17087_0061	inosine-5'-monophosphate dehydrogenase (EC:1.1.1.205)
APL_17087_0060	glycine hydroxymethyltransferase; K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]
APL_17087_0058	glycerate dehydrogenase (EC:1.1.1.29); K00018 glycerate dehydrogenase [EC:1.1.1.29]
APL_17087_0057	HTH DNA-binding protein
APL_17087_0042	hisS; histidyl-tRNA synthetase (EC:6.1.1.21); K01892 histidyl-tRNA synthetase [EC:6.1.1.21]
APL_17087_0041	transcription regulator
APL_17087_0036	glutamate-1-semialdehyde aminotransferase (EC:5.4.3.8); K01845 glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]
APL_17087_0035	GMP synthase subunit B (EC:6.3.5.2); K01951 GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]
APL_17087_0034	rps2P; 30S ribosomal protein S2; K02967 small subunit ribosomal protein S2
APL_17087_0032	GTPase; K06883
APL_17087_0031	transcription regulator
APL_17087_0028	transcription factor; K03120 transcription initiation factor TFIID TATA-box-binding protein
APL_17087_0021	inosine 5'-monophosphate dehydrogenase (EC:1.1.1.205); K00088 IMP dehydrogenase [EC:1.1.1.205]
APL_17087_0014	isocitrate dehydrogenase (EC:1.1.1.42); K00031 isocitrate dehydrogenase [EC:1.1.1.42]
APL_17087_0010	hypothetical protein
APL_17087_0006	serine/threonine protein phosphatase
APL_17087_0002	hypothetical protein

APL_17082_0070	yycN; GNAT family acetyltransferase (EC:2.3.1.-)
APL_17082_0027	phospho-2-dehydro-3-deoxyheptonate aldolase; K03856 3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]
APL_17082_0014	long-chain fatty-acid-CoA ligase; K01897 long-chain acyl-CoA synthetase [EC:6.2.1.3]
APL_17082_0009	electron transfer flavoprotein, alpha and beta subunits related protein; K03522 electron transfer flavoprotein alpha subunit
APL_17079_0009	acetyl-CoA synthetase related protein; K01895 acetyl-CoA synthetase [EC:6.2.1.1]
APL_17079_0004	4-aminobutyrate aminotransferase (EC:2.6.1.19); K00823 4-aminobutyrate aminotransferase [EC:2.6.1.19]
APL_17068_0087	heterodisulfide reductase related protein
APL_17068_0086	L-3-hydroxyacyl-CoA dehydrogenase precursor related protein
APL_17068_0085	L-3-hydroxyacyl-CoA dehydrogenase precursor related protein
APL_17068_0084	sterol carrier protein
APL_17068_0082	alkyl hydroperoxide reductase subunit f related protein
APL_17068_0081	metal-dependent hydrolase related to alanyl-tRNA synthetase; K07050
APL_17068_0076	dihydrolipoamide dehydrogenase (EC:1.8.1.4); K00382 dihydrolipoamide dehydrogenase [EC:1.8.1.4]
APL_17068_0075	branched-chain alpha-keto acid dehydrogenase subunit E2; K00627 pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
APL_17068_0074	thiamine pyrophosphate-dependent dehydrogenase, E1 component beta subunit; K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
APL_17068_0073	3-methyl-2-oxobutanoate dehydrogenase alpha chain precursor; K00161 pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
APL_17068_0067	electron transfer flavoprotein subunit alpha; K03522 electron transfer flavoprotein alpha subunit
APL_17068_0066	electron transfer flavoprotein subunit beta
APL_17068_0064	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
APL_17068_0063	acyl-CoA dehydrogenase; K00249 acyl-CoA dehydrogenase [EC:1.3.99.3]
APL_17068_0062	acyl-CoA dehydrogenase-like protein
APL_17068_0040	formate-tetrahydrofolate ligase; K01938 formate--tetrahydrofolate ligase [EC:6.3.4.3]
APL_17068_0035	ferredoxin
APL_17068_0034	phosphoribosylaminoimidazole synthetase (EC:6.3.3.1); K01933 phosphoribosylformylglycinamidine cyclo-ligase [EC:6.3.3.1]
APL_17068_0029	mrp; chromosome partitioning ATPase; K03593 ATP-binding protein involved in chromosome partitioning
APL_17068_0027	orotate phosphoribosyltransferase-like protein; K00762 orotate phosphoribosyltransferase [EC:2.4.2.10]
APL_17068_0026	lysK; lysyl-tRNA synthetase (EC:6.1.1.6); K04566 lysyl-tRNA synthetase, class I [EC:6.1.1.6]
APL_17068_0021	nusG; transcription antitermination protein NusG; K02601 transcriptional antiterminator NusG

APL_17068_0018	thiol-specific antioxidant related protein; K03564 peroxiredoxin Q/BCP [EC:1.11.1.15]
APL_17068_0015	rpl1P; 50S ribosomal protein L1P; K02863 large subunit ribosomal protein L1
APL_17068_0014	rplP0; acidic ribosomal protein P0; K02864 large subunit ribosomal protein L10
APL_17068_0013	rpl12p; 50S ribosomal protein L12P; K02869 large subunit ribosomal protein L12
APL_17068_0008	hypothetical protein
APL_17068_0007	hypothetical protein
APL_17068_0006	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
APL_17068_0003	rfc; replication factor C small subunit; K04801 replication factor C small subunit
APL_14887_0077	yycN; GNAT family acetyltransferase (EC:2.3.1.-)
APL_14887_0067	gluconate/galactonate dehydratase (EC:4.2.1.39); K05308 gluconate dehydratase [EC:4.2.1.39]
APL_14887_0066	aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]
APL_14887_0063	glutamine synthetase; K01915 glutamine synthetase [EC:6.3.1.2]
APL_14887_0061	valS; valyl-tRNA synthetase (EC:6.1.1.9); K01873 valyl-tRNA synthetase [EC:6.1.1.9]
APL_14887_0060	hypothetical protein
APL_14887_0058	hypothetical protein; K09716 hypothetical protein
APL_14887_0056	hypothetical protein
APL_14887_0051	pyrG; CTP synthetase (EC:6.3.4.2); K01937 CTP synthase [EC:6.3.4.2]
APL_14887_0046	superoxide dismutase [Fe] (EC:1.15.1.1); K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
APL_14887_0040	sugar kinase
APL_14887_0039	ribose-phosphate pyrophosphokinase (EC:2.7.6.1); K00948 ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
APL_14887_0034	nonspecific lipid-transfer protein; K00632 acetyl-CoA acyltransferase [EC:2.3.1.16]
APL_14887_0032	carnitine dehydratase
APL_14887_0029	glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]
APL_14887_0028	glutamine amidotransferase subunit PdxT; K08681 glutamine amidotransferase [EC:2.6.-.-]
APL_14887_0027	aminomethyltransferase (glycine cleavage system T protein); K00605 aminomethyltransferase [EC:2.1.2.10]
APL_14887_0024	hypothetical protein
APL_13214_0061	putative peroxiredoxin (EC:1.11.1.15); K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
APL_13214_0060	small nuclear ribonucleoprotein (snRNP)-like protein
APL_13214_0058	exosome complex RNA-binding protein Csl4; K07573 exosome complex component CSL4
APL_13214_0055	hypothetical protein
APL_13214_0053	regulatory protein MoxR related protein; K03924 MoxR-like ATPase [EC:3.6.3.-]

APL_13214_0050	ssnA; metal-dependent hydrolase
APL_13214_0049	translation initiation factor IF-5A; K03263 translation initiation factor eIF-5A
APL_13214_0048	agmatinase; K01480 agmatinase [EC:3.5.3.11]
APL_13214_0046	rpl10e; 50S ribosomal protein L10e; K02866 large subunit ribosomal protein L10e
APL_13214_0042	hypothetical protein; K07050
APL_13214_0037	2-oxoglutarate ferredoxin oxidoreductase subunit beta; K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]
APL_13214_0036	2-oxoacid ferredoxin oxidoreductase subunit alpha; K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]
APL_13214_0030	dihydroorotate dehydrogenase (EC:1.3.3.1); K00226 dihydroorotate oxidase [EC:1.3.3.1]
APL_13214_0029	hypothetical protein
APL_13214_0022	protoheme IX farnesyltransferase (EC:2.5.1.-); K02301 protoheme IX farnesyltransferase [EC:2.5.1.-]
APL_13214_0018	carbon monoxide dehydrogenase subunit G; K09386 hypothetical protein
APL_13214_0016	bifunctional phosphoglucose/phosphomannose isomerase; K01809 mannose-6-phosphate isomerase [EC:5.3.1.8]; K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]
APL_13214_0013	ef1a, tuf; elongation factor 1-alpha (EC:3.6.5.3); K03231 elongation factor EF-1 alpha subunit [EC:3.6.5.3]
APL_13214_0012	rps10p; 30S ribosomal protein S10P; K02946 small subunit ribosomal protein S10
APL_13214_0011	fusA; elongation factor EF-2; K03234 elongation factor EF-2 [EC:3.6.5.3]
APL_13214_0007	hypothetical protein
APL_13214_0006	NAD(FAD)-dependent dehydrogenase
APL_13214_0003	GrpE protein; K03687 molecular chaperone GrpE
APL_13214_0002	dnaK; molecular chaperone DnaK; K04043 molecular chaperone DnaK
APL_13186_0041	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
APL_13186_0040	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
APL_13186_0039	3-hydroxybutyryl-CoA dehydrogenase (EC:1.1.1.157); K00074 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
APL_13186_0038	3-hydroxybutyryl-CoA dehydratase; K01692 enoyl-CoA hydratase [EC:4.2.1.17]
APL_13186_0037	chromosome partition protein smc; K03529 chromosome hypothetical proteinregation protein
APL_13186_0033	tyrosyl-tRNA synthetase (EC:6.1.1.1); K01866 tyrosyl-tRNA synthetase [EC:6.1.1.1]
APL_13186_0028	prolyl-tRNA synthetase (EC:6.1.1.15); K01881 prolyl-tRNA synthetase [EC:6.1.1.15]
APL_13186_0027	diaminopimelate aminotransferase; K01439 succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]
APL_13186_0026	nicotinamide-nucleotide adenylyltransferase (EC:2.7.7.1); K00952 nicotinamide-nucleotide adenylyltransferase [EC:2.7.7.1]

APL_13186_0019	aspartate aminotransferase (EC:2.6.1.1); K00812 aspartate aminotransferase [EC:2.6.1.1]
APL_13186_0018	hypothetical protein
APL_13186_0010	NAD(FAD)-dependent dehydrogenase
APL_13083_0007	chromosome hypothetical proteinregation protein; K03546 exonuclease SbcC
APL_12979_0010	hypothetical protein
APL_12979_0005	acetyl-CoA synthetase; K09181 hypothetical protein
APL_12979_0002	aldo/keto reductase
APL_12840_0002	aldehyde dehydrogenase; K07248 lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase [EC:1.2.1.22 1.2.1.21]
APL_12840_0001	molybdenum cofactor biosynthesis protein A; K06937
APL_12463_0002	thiI; thiamine biosynthesis protein ThiI; K03151 thiamine biosynthesis protein ThiI
APL_12102_0002	hypothetical protein
APL_12042_0003	oxidoreductase; K03738 aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]
APL_11661_0006	chaperonin GroEL
APL_11661_0005	thermosome, alpha chain
APL_11661_0004	chaperonin GroEL
APL_11661_0003	thermosome, alpha chain
APL_10622_0001	hypothetical protein; K03724 ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.1.-]
APL_10144_0001	D-3-phosphoglycerate dehydrogenase; K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]
APL_00419_0005	rpl7ae; 50S ribosomal protein L7Ae; K02936 large subunit ribosomal protein L7Ae
APL_00419_0004	rps28e; 30S ribosomal protein S28e; K02979 small subunit ribosomal protein S28e
APL_00419_0002	ndk; nucleoside diphosphate kinase; K00940 nucleoside-diphosphate kinase [EC:2.7.4.6]

Table S4: Proteins detected in central metabolic pathways and pathways associated with carbon-acquisition and breakdown

EC number	Gene name	Aplasma	Eplasma	Gplasma	Fer1	Fer2	Iplasma	ARMAN2	ARMAN4	ARMAN5
Electron transport chain										
NADH dehydrogenase										
1.6.5.3	NuoA									
	NuoB									
	NuoC			13455_0041						
	NuoD	17428_0017	15243_0403	13455_0042						
	NuoF	17306_0015								
	NuoI			13455_0044						
	NuoL									
	NuoM									
Succinate dehydrogenase										
1.3.99.1	Succinate dehydrogenase	17500_0036	17965_0344	13287_0168	1743	19_0043				
	SdhA	17500_0037	17965_0345	13287_0167	1742	19_0042				
	SdhC									
	SdhD			13334_0105		19_0040				
Cytochrome bc complex										

1.10.2.2	CytB/PetB									
	Rieske/PetA		17965_0147	13374_0018						
Cytochrome C oxidase										
1.9.3.1	CoxAC (catalytic subunit)			13374_0156						
Cytochrome bd complex										
1.10.3.-	CydA									
	CydA									
ATPase A-type										
3.6.3.14	NtpD/AhaD			13334_0012						
	NtpB/AhaB	17300_0012		13334_0013		97_0004	13606_0200			
		17300_0013								
	NtpA/AtpA	17300_0011		13334_0014	936	97_0005	13606_0201			
	NtpG/AhaF			13334_0015						
	AhaC/NtpC			13334_0016						
	NtpE/AhaE			13334_0017						
	NtpI/AhaI	17300_0017		13334_0010						
	AhaH	17300_0016								
Entner Doudoroff pathway										
1.1.1.47	Glucose dehydrogenase		15243_0608	12303_0024		107_0012				
4.2.1.39	Gluconate dehydratase	14887_0067	15251_0040	13334_0053	930	11_0004				
4.1.2.-	KDG aldolase		17965_0249	13374_0117						
1.2.1.3	GADH	12840_0002	15243_0377	13374_0164	706	12_0012	13624_0267			
2.7.1.165	Glycerate kinase									
4.2.1.11	Enolase	17500_0031	17965_0047	13374_0178	1336	50_0011				
2.7.1.40	Pyruvate kinase	17498_0009	15243_0541	13296_0009						

Embden-Meyerhoff Glycolysis										
2.7.1.2	Glucokinase		17965_155	13287_0076						
5.3.1.9	Glucose-6-phosphate isomerase (archaeal bifunctional enzyme)	13214_0016	EPL_15243_0568	13287_0025						255
4.2.1.13	Fructose 1,6-bisphosphate aldolase/phosphatase (archaeal type)	13214_0029	15243_0586	13374_0081	1320				308	434
		13214_0030								
5.3.1.1	Triosephosphate isomerase (TIM)		15243_0442	13296_0103	1082					
1.2.1.59	Glyceraldehyde-3-phosphate dehydrogenase (NAD(P))	17087_0075	17965_0400	13459_0136						
2.7.2.3	Phosphoglycerate kinase	17487_0016	15243_0230	13459_0014						
5.4.2.1	Phosphoglycerate mutase	17298_0091	17965_0440						379	
5.4.2.1				13459_0073						
4.2.1.11	Enolase	17500_0031	17965_0047	13374_0178	1336	50_0011				
2.7.1.40	Pyruvate kinase	17498_0009	15243_0541	13296_0009						
Pyruvate dehydrogenase complex										
1.2.4.1	Pyruvate dehydrogenase E1 component subunit alpha	17068_0073	15833_38	13459_0211						
1.2.4.1	Pyruvate dehydrogenase E1 component subunit beta	17068_0074	15833_37	13459_0212	867	11_0061				
					371					

2.3.1.12	Pyruvate dehydrogenase E2 component	17068_0075		13459_0213						
1.8.1.4	Pyruvate dehydrogenase E3/dihydrolipoamide dehydrogenase	17068_0076		13459_0214	869					
TCA cycle										
2.3.3.1	Citrate synthase	17433_0013	15243_18	13334_0108		89_0012				
2.3.3.1			15243_526	13459_0255	249					
4.2.1.3	Aconitase	14887_0066	15251_41	13459_0162	1728	19_0023	13606_0363		536	1022
1.1.1.42	Isocitrate dehydrogenase		15833_0057	13459_0219	368		15911_0558			
1.2.7.3	2-oxoacid:ferredoxin oxidoreductase a/g-subunit		15243_0130	13374_0086	1588	1_0130	13606_0265	15008_769	563	
1.2.7.3			17965_0194	13459_0183	1738		15911_0268			
1.2.7.3	2-oxoacid:ferredoxin oxidoreductase b-subunit		15243_129	13374_0087		1_0131				
1.2.7.3			17965_0193	13459_0182	1739					
6.2.1.5	Succinyl-CoA synthetase alpha subunit		17965_0291	13374_0106	1736	19_0036		15008_718		
6.2.1.5	Succinyl-CoA synthetase beta subunit		17965_0292	13374_0105	1735	19_0035				
1.3.99.1	Succinate dehydrogenase flavoprotein subunit			13287_0168	1743	19_0043				
							13606_0110			
1.3.99.1	Succinate dehydrogenase iron-sulfur protein			13287_0167	1742					

1.3.5.1	Succinate dehydrogenase (ubiquinone) cytochrome b subunit									
1.3.5.1	Succinate dehydrogenase cytochrome b small subunit			13334_0105		19_0040				
4.2.1.2	Fumarate hydratase		15243_0131	13334_0165	734	31_0019				
1.1.1.37	Malate dehydrogenase		17965_0423	13459_0040	1744	19_0044		15003_559		
Glyoxylate shunt enzymes not found in the TCA cycle										
2.3.3.9	Malate synthase		15243_0643							
4.1.3.1	Isocitrate lyase									
Polysaccharide catabolism										
3.2.1.3	Glucoamylase		17965_0050	13327_0014						
3.2.1.3	Glucan 1,4-alpha-glucosidase									
3.2.1.20	Alpha-glucosidase									
3.2.1.20	Alpha-glucosidase			13374_0167						
	Beta-galactosidase									
3.2.1.133	Glucan 1,4-α-maltohydrolase									
2.4.1.25, 3.2.1.33	GlgX: glycogen debranching enzyme isoform 1						15911_0569			
2.4.1.21	GlgA: glycogen synthase									
	Oligosaccharide amylase									

Fatty acid oxidation										
6.2.1.3	Fatty acyl-CoA synthetase	17298_0042	15243_0438	13477_0036	250					
			15243_0203			1_0063				
		17082_0014	15243_0207	13459_0328						
				13334_0078						
				13290_0075						
				13334_0033						
1.3.8.-	Acyl-CoA dehydrogenase	17393_0003	15243_0396	13455_0035						
		17428_0009								
	Delta-3-cis-delta-2-trans-enoyl-CoA isomerase	13186_0039	15243_0060	13459_0259	1530	1_0062				
		17500_0016		13287_0080	1784	64_0015	13249_0160			
		17068_0085		13290_0086						
				13290_0087						
4.2.1.17	Enoyl-CoA hydratase		15243_0377	13374_0164	706		13624_0267			
		12840_0002		13287_0036		12_0012				
		17462_0060								
2.3.1.16	3-ketoacyl-CoA thiolase	17068_0064	15833_0048	13334_0182						
		13186_0040	17965_0179	13290_0085	1532					
		14887_0034	17965_0037	13334_0127	323	38_0027				
Protein transport/ catabolism										
	ABC-type peptide transport system, ATPase	17112_0048	15243_0117							
		17112_0049	15243_0118							
	ABC-type peptide transport system, solute-binding component	17112_0054	15243_0126							
	Acylaminoacyl-peptidase			13334_0090						

3.5.-.-	Amidohydrolase	17112_0052								
	Aminopeptidase N	17087_0068	15243_0335							
		17087_0066								
3.4.21.-	Lon-like ATP-dependent protease	17500_0027	17965_0119	13374_0182		50_0012				
		17306_0025	15243_0420	13455_0062						
	ATP-dependent protease									
2.3.2.2	Gamma-glutamyltranspeptidase			12302_0009	229					
3.4.11.1	Leucyl aminopeptidase		15243_0267							
	Membrane associated serine protease					20_0005				
	Membrane metalloprotease						13624_0044			
3.4.11.18	Methionine aminopeptidase			13475_0012						
				13459_0265						
3.4.24.11	M13 family endopeptidase			13459_0310						
	Oligopeptide ABC transporter Opp1, ATP binding protein			13459_0128			15911_0573			
	Oligopeptide ABC transporter Opp1, extracellular binding protein			13459_0131						
	Oligopeptide ABC transporter Opp1, permease protein			13459_0129						

	Oligopeptide/dipeptide ABC transporter, ATPase subunit						13606_0059			
3.4.13.9	PepQ-like3; prolidase (Xaa-Pro dipeptidase)	17466_0005								
	Peptidase M61 domain-containing protein		17965_0416	13459_0043						
3.4.21.-	Peptidase S16, Lon-like protease						15911_0222			
	Peptidase S8/S53 subtilisin kexin sedolisin			13459_0026						
	Peptidase U61 LD-carboxypeptidase A									
K02032	Peptide ABC transporter ATP-binding protein				139					
3.4.13.9	Proline dipeptidase related protein	17365_0016	15243_0680	13459_0323						
				12302_0010						
3.4.11.5	Proline iminopeptidase	17112_0022								
3.4.21.26	Prolyl endopeptidase			13459_0206						
	Protease (PspA) related protein	17365_0047								
	Proteasome endopeptidase complex									
3.4.25.1	Proteasome endopeptidase complex, alpha subunit						13624_0064			

3.4.25.1	Proteasome protease subunit beta		15243_0674							
3.4.21.-	Putative protease La homolog type 2				1100	93_0014				
	Putative S1 family peptidase					55_0029				
	Serine protease-like protein									
3.4.11.-	Tricorn protease interacting factor F2	17087_0065	17965_0189	13287_0152	1669					
		17087_0067		13296_0124	1669					
				13334_0067						
3.4.11.-	Tricorn protease interacting factor F3				1303	177_0005				
3.4.21.-	Tricorn protease			13334_0050	1719					
				13459_0161						
	X-Pro dipeptidase			12303_0037						
				12302_0002						
3.4.13.9	Xaa-Pro dipeptidase	17365_0015			1407	5_0090				
3.4.24.-	Zinc metalloprotease TldD protein	17365_0048	15243_0766	13287_0150						
Sugar transporters										
	Trehalose/maltose transport ATP-hydrolyzing subunit			13455_0097						
	Trehalose/maltose binding protein			13455_0094						
	Sugar ABC transporter extracellular solute binding protein			13374_0100						

	Sugar ABC transporter ATP binding protein			13374_0098						
	Sugar ABC transporter 1, extracellular binding protein			13290_0080		12_0054				
	Sugar ABC transporter 1, ATP binding protein			13290_0079		12_0058				
	Multiple sugar transport system ATP-binding-like protein	17112_0033								
	Multiple sugar transport system substrate-binding protein	17112_0030								

Table S5: Gplasma proteins in higher relative abundance in sunken samples

Protein	Annotation
13455_0013	hypothetical protein
13327_0045	universal stress protein
13459_0287	hypothetical protein
13459_0282	hypothetical protein
13327_0057	hypothetical protein
13327_0055	hypothetical protein
13459_0100	band 7 integral membrane protein-like protein
13455_0058	hypothetical protein
13459_0041	ATPase
13287_0011	N-acyl-L-amino acid amidohydrolase (EC:3.5.1.14); K01436 aminoacylase [EC:3.5.1.14]
13477_0077	aldo/keto reductase
13374_0102	hypothetical protein; K07068
13374_0072	NAD(FAD)-dependent dehydrogenase
13290_0173	O-methyltransferase family 3
13334_0022	superoxide dismutase; K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
13334_0053	galactonate dehydratase
13459_0036	DNA polymerase sliding clamp; K04802 proliferating cell nuclear antigen
13287_0124	transcription factor; K03120 transcription initiation factor TFIID TATA-box-binding protein
13374_0118	rpl7ae; 50S ribosomal protein L7Ae; K02936 large subunit ribosomal protein L7Ae
13374_0101	acetyl-CoA acetyltransferase (EC:2.3.1.9); K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
13455_0035	acyl-CoA dehydrogenase; K00257 [EC:1.3.99.-]
12303_0024	glucose-1-dehydrogenase (EC:1.1.1.47); K00034 glucose 1-dehydrogenase [EC:1.1.1.47]
13287_0116	pyruvate phosphate dikinase (EC:2.7.9.1); K01006 pyruvate,orthophosphate dikinase [EC:2.7.9.1]
13290_0080	sugar ABC transporter 1, extracellular binding protein; K02027 multiple sugar transport system substrate-binding protein
13290_0071	putative translaldolase (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2]
13374_0117	dihydrodipicolinate synthetase; K01714 dihydrodipicolinate synthase [EC:4.2.1.52]
13459_0095	acetolactate synthase (EC:2.2.1.6); K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
13334_0132	ilvE; branched-chain amino acid aminotransferase (EC:2.6.1.42); K00826 branched-chain amino acid aminotransferase [EC:2.6.1.42]
13287_0159	pyruvate dehydrogenase (EC:1.2.2.2); K00156 pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]

13290_0041	aspartate aminotransferase (EC:2.6.1.1); K00812 aspartate aminotransferase [EC:2.6.1.1]
13287_0148	glycine hydroxymethyltransferase related protein; K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]
13459_0263	cystathionine gamma-lyase (EC:4.4.1.1); K01739 cystathionine gamma-synthase [EC:2.5.1.48]
13334_0067	tricorn protease interacting factor F2 (EC:3.4.11.-); K13722 tricorn protease interacting factor F2/3 [EC:3.4.11.-]
13287_0036	NAD-dependent aldehyde dehydrogenase; K00128 aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]
13477_0019	oxidoreductase
13459_0040	malate dehydrogenase (EC:1.1.1.37); K00024 malate dehydrogenase [EC:1.1.1.37]
13455_0087	electron transfer flavoprotein subunit beta; K03521 electron transfer flavoprotein beta subunit
13459_0214	dihydrolipoamide dehydrogenase (EC:1.8.1.4); K00382 dihydrolipoamide dehydrogenase [EC:1.8.1.4]
13459_0213	branched-chain alpha-keto acid dehydrogenase subunit E2; K00627 pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
13459_0212	thiamine pyrophosphate-dependent dehydrogenase, E1 component beta subunit; K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
13459_0162	aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]
13459_0183	pyruvate ferredoxin oxidoreductase, alpha chain (EC:1.2.7.1); K00174 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]

Table S6. Results of pair-wise comparisons of deamidation frequencies between archaea and bacteria in early growth stage (GS1), late growth-stage (GS2) and sunken biofilms using Tukey's honestly significant difference test. NS = not significant; * = *p* < 0.05; ** = *p* <0.01; * *p* = <.001.**

	Archaea GS1	Archaea GS2	Archaea Sunken	Bacteria GS1	Bacteria GS2	Bacteria Sunken
Archaea GS1		NS	***	NS	***	***
Archaea GS2	NS		**	NS	***	***
Archaea Sunken	NS	NS		NS	NS	**
Bacteria GS1	NS	NS	NS		***	***
Bacteria GS2	*	NS	NS	*		*
Bacteria Sunken	***	***	***	***	**	