Metagenomic insights into the microbial diversity in Manganese-contaminated mine tailings and their role in biogeochemical cycling of Manganese

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COG ID	Sequence count	COG domain		
COG0001	58	Glutamate-1-semialdehyde aminotransferase		
COG0002	44	Acetylglutamate semialdehyde dehydrogenase		
COG0003	43	Oxyanion-translocating ATPase		
COG0004	59	Ammonia permease		
COG0005	48	Purine nucleoside phosphorylase		
COG0006	114	Xaa-Pro aminopeptidase		
COG0007	23	Uroporphyrinogen-III methylase		
COG0008	99	Glutamyl- and glutaminyl-tRNA synthetases		
COG0009	33	Putative translation factor (SUA5)		
COG0010	51	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family		
COG0011	7	Uncharacterized conserved protein		
COG0012	29	Predicted GTPase, probable translation factor		
COG0013	69	Alanyl-tRNA synthetase		
COG0014	25	Gamma-glutamyl phosphate reductase		
COG0015	56	Adenylosuccinate lyase		
COG0016	40	Phenylalanyl-tRNA synthetase alpha subunit		
COG0017	26	Aspartyl/asparaginyl-tRNA synthetases		
COG0018	64	Arginyl-tRNA synthetase		
COG0019	71	Diaminopimelate decarboxylase		
COG0020	25	Undecaprenyl pyrophosphate synthase		
COG0021	77	Transketolase		
COG0022	82	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit		
COG0023	3	Translation initiation factor 1 (eIF-1/SUI1) and related proteins		
COG0024	30	Methionine aminopeptidase		
COG0025	23	NhaP-type Na+/H+ and K+/H+ antiporters		
COG0026	16	Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)		
COG0027	2	Formate-dependent phosphoribosylglycinamide formyltransferase (GAR transformylase)		
COG0028	232	Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phospl		
COG0029	29	Aspartate oxidase		
COG0030	34	Dimethyladenosine transferase (rRNA methylation)		
COG0031	88	Cysteine synthase		
COG0033	21	Phosphoglucomutase		
COG0034	52	Glutamine phosphoribosylpyrophosphate amidotransferase		
COG0035	13	Uracil phosphoribosyltransferase		
COG0036	19	Pentose-5-phosphate-3-epimerase		
COG0037	46	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control		
COG0038	26	Chloride channel protein EriC		
COG0039	27	Malate/lactate dehydrogenases		
COG0040	26	ATP phosphoribosyltransferase		
COG0041	19	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase		
COG0042	37	tRNA-dihydrouridine synthase		
COG0043	89	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases		
COG0044	98	Dihydroorotase and related cyclic amidohydrolases		
COG0045	30	Succinyl-CoA synthetase, beta subunit		
COG0046	57	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain		
COG0047	18	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain		
COG0048	5	Ribosomal protein S12		
COG0049	11	Ribosomal protein S7		
COG0050	10	GTPases - translation elongation factors		
COG0051	5	Ribosomal protein S10		
COG0052	18	Ribosomal protein S2		
COG0053	75	Predicted Co/Zn/Cd cation transporters		
COG0054	15	Riboflavin synthase beta-chain		
COG0055	19	F0F1-type ATP synthase, beta subunit		
COG0056	32	F0F1-type ATP synthase, alpha subunit		
COG0057	29	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase		
COG0058	90	Glucan phosphorylase		
COG0059	16	Ketol-acid reductoisomerase		
COG0060	83	Isoleucyl-tRNA synthetase		
COG0061	30	Predicted sugar kinase		
COG0062	16	Uncharacterized conserved protein		
COG0063	23	Predicted sugar kinase		
COG0064	50	Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)		
COG0065	48	3-isopropylmalate dehydratase large subunit		
COG0066	20	3-isopropylmalate dehydratase small subunit		
COG0067	20	Glutamate synthase domain 1		
COG0068	44	Hydrogenase maturation factor		
COG0069	56	Glutamate synthase domain 2		
COG0070	20	Glutamate synthase domain 3		
COG0071	60	Molecular chaperone (small heat shock protein)		
COG0072	65	Phenylalanyl-tRNA synthetase beta subunit		
COG0073	22	EMAP domain		
COG0074	25	Succinyl-CoA synthetase, alpha subunit		
COG0075	64	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase		
COG0076	83	Glutamate decarboxylase and related PLP-dependent proteins		
COG0077	25	Prephenate dehydratase		
COG0078	43	Ornithine carbamoyltransferase		
COG0079	56	Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase		
COG0080	10	Ribosomal protein L11		
COG0081	16	Ribosomal protein L1		
COG0082	34	Chorismate synthase		
COG0083	7	Homoserine kinase		
COG0084	27	Mg-dependent DNase		

COG0085	74	DNA-directed RNA polymerase, beta subunit/140 kD subunit		
COG0086	82	DNA-directed RNA polymerase, beta' subunit/160 kD subunit		
COG0087	32	Ribosomal protein L3		
COG0088	27	Ribosomal protein L4		
COG0089	17	Ribosomal protein L23		
COG0090	28	Ribosomal protein L2		
COG0091	19	Ribosomal protein L22		
COG0092	19	Ribosomal protein S3		
COG0093	11	Ribosomal protein L14		
COG0094	15	Ribosomal protein L5		
COG0095	12	Lipoate-protein ligase A		
COG0096	21	Ribosomal protein S8		
COG0097	26	Ribosomal protein L6P/L9E		
COG0098	13	Ribosomal protein S5		
COG0099	14	Ribosomal protein S13		
COG0100	7	Ribosomal protein S11		
COG0101	23	Pseudouridylate synthase		
COG0102	15	Ribosomal protein L13		
COG0103	15	Ribosomal protein S9		
COG0104	43	Adenylosuccinate synthase		
COG0105	15	Nucleoside diphosphate kinase		
COG0106	18	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase		
COG0107	23	Imidazoleglycerol-phosphate synthase		
COG0108	17	3,4-dihydroxy-2-butanone 4-phosphate synthase		
COG0109	30	Polyprenyltransferase (cytochrome oxidase assembly factor)		
COG0110	53	Acetyltransferase (isoleucine patch superfamily)		
COG0111	147	Phosphoglycerate dehydrogenase and related dehydrogenases		
COG0112	47	Glycine/serine hydroxymethyltransferase		
COG0113	18	Delta-aminolevulinic acid dehydratase		
COG0114	24	Fumarase		
COG0115	78	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase		
COG0116	17	Predicted N6-adenine-specific DNA methylase		
COG0117	6	Pyrimidine deaminase		
COG0118	27	Glutamine amidotransferase		
COG0119	109	Isopropylmalate/homocitrate/citramalate synthases		
COG0120	7	Ribose 5-phosphate isomerase		
COG0121	22	Predicted glutamine amidotransferase		
COG0122	26	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase		
COG0123	46	Deacetylases, including yeast histone deacetylase and acetoin utilization protein		
COG0124	46	Histidyl-tRNA synthetase		
COG0125	32	Thymidylate kinase		
COG0126	35	3-phosphoglycerate kinase		
COG0127	20	Xanthosine triphosphate pyrophosphatase		
COG0128	58	5-enolpyruvylshikimate-3-phosphate synthase		
COG0129	75	Dihydroxyacid dehydratase/phosphogluconate dehydratase		
COG0130	37	Pseudouridine synthase		
COG0131	14	Imidazoleglycerol-phosphate dehydratase		
COG0132	5	Dethiobiotin synthetase		
COG0133	21	Tryptophan synthase beta chain		
COG0134	19	Indole-3-glycerol phosphate synthase		
COG0135	21	Phosphoribosylanthranilate isomerase		
COG0136	34	Aspartate-semialdehyde dehydrogenase		
COG0137	30	Argininosuccinate synthase		
COG0138	27	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)		
COG0139	8	Phosphoribosyl-AMP cyclohydrolase		
COG0140	5	Phosphoribosyl-ATP pyrophosphohydrolase		
COG0141	43	Histidinol dehydrogenase		
COG0142	48	Geranylgeranyl pyrophosphate synthase		
COG0143	54	Methionyl-tRNA synthetase		
COG0144	55	tRNA and rRNA cytosine-C5-methylases		
COG0145	76	N-methylhydantoinase A/acetone carboxylase, beta subunit		
COG0146	86	N-methylhydantoinase B/acetone carboxylase, alpha subunit		
COG0147	73	Anthranilate/para-aminobenzoate synthases component I		
COG0148	31	Enolase		
COG0149	17	Triosephosphate isomerase		
COG0150	31	Phosphoribosylaminoimidazole (AIR) synthetase		
COG0151	30	Phosphoribosylamine-glycine ligase		
COG0152	27	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase		
COG0153	11	Galactokinase		
COG0154	178	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases		
COG0155	37	Sulfite reductase, beta subunit (hemoprotein)		
COG0156	67	7-keto-8-aminopelargonate synthetase and related enzymes		
COG0157	30	Nicotinate-nucleotide pyrophosphorylase		
COG0158	11	Fructose-1,6-bisphosphatase		
COG0159	29	Tryptophan synthase alpha chain		
COG0160	73	4-aminobutyrate aminotransferase and related aminotransferases		
COG0161	77	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase		
COG0162	50	Tyrosyl-tRNA synthetase		
COG0163	18	3-polyprenyl-4-hydroxybenzoate decarboxylase		
COG0164	26	Ribonuclease HII		
COG0165	42	Argininosuccinate lyase		
COG0166	51	Glucose-6-phosphate isomerase		
COG0167	59	Dihydroorotate dehydrogenase		
COG0168	9	Trk-type K+ transport systems, membrane components		

COG0169	37	Shikimate 5-dehydrogenase		
COG0170	2	Dolichol kinase		
COG0171	37	NAD synthase		
COG0172	56	Seryl-tRNA synthetase		
COG0173	53	Aspartyl-tRNA synthetase		
COG0174	104	Glutamine synthetase		
COG0175	26	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes		
COG0176	40	Transaldolase		
COG0177	24	Predicted EndoIII-related endonuclease		
COG0178	109	Excinuclease ATPase subunit		
COG0179	80	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)		
COG0180	46	Tryptophanyl-tRNA synthetase		
COG0181	27	Porphobilinogen deaminase		
COG0182	23	Predicted translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family		
COG0183	228	Acetyl-CoA acetyltransferase		
COG0184	7	Ribosomal protein S15P/S13E		
COG0185	4	Ribosomal protein S19		
COG0186	11	Ribosomal protein S17		
COG0187	52	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit		
COG0188	84	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit		
COG0189	30	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)		
COG0190	31	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase		
COG0191	8	Fructose/tagatose bisphosphate aldolase		
COG0192	19	S-adenosylmethionine synthetase		
COG0193	24	Peptidyl-tRNA hydrolase		
COG0194	19	Guanylate kinase		
COG0195	28	Transcription elongation factor		
COG0196	28	FAD synthase		
COG0197	9	Ribosomal protein L16/L10E		
COG0198	16	Ribosomal protein L24		
COG0199	3	Ribosomal protein S14		
COG0200	13	Ribosomal protein L15		
COG0201	30	Preprotein translocase subunit SecY		
COG0202	30	DNA-directed RNA polymerase, alpha subunit/40 kD subunit		
COG0203	19	Ribosomal protein L17		
COG0204	126	1-acyl-sn-glycerol-3-phosphate acyltransferase		
COG0205	53	6-phosphofructokinase		
COG0206	37	Cell division GTPase		
COG0207	9	Thymidylate synthase		
COG0208	14	Ribonucleotide reductase, beta subunit		
COG0209	81	Ribonucleotide reductase, alpha subunit		
COG0210	123	Superfamily I DNA and RNA helicases		
COG0211	12	Ribosomal protein L27		
COG0212	11	5-formyltetrahydrofolate cyclo-ligase		
COG0213	22	Thymidine phosphorylase		
COG0214	8	Pyridoxine biosynthesis enzyme		
COG0215	43	Cysteinyl-tRNA synthetase		
COG0216	21	Protein chain release factor A		
COG0217	21	Uncharacterized conserved protein		
COG0218	18	Predicted GTPase		
COG0219	14	Predicted rRNA methylase (SpoU class)		
COG0220	7	Predicted S-adenosylmethionine-dependent methyltransferase		
COG0221	20	Inorganic pyrophosphatase		
COG0222	5	Ribosomal protein L7/L12		
COG0223	50	Methionyl-tRNA formyltransferase		
COG0224	35	F0F1-type ATP synthase, gamma subunit		
COG0225	33	Peptide methionine sulfoxide reductase		
COG0226	59	ABC-type phosphate transport system, periplasmic component		
COG0227	6	Ribosomal protein L28		
COG0228	12	Ribosomal protein S16		
COG0229	15	Conserved domain frequently associated with peptide methionine sulfoxide reductase		
COG0230	1	Ribosomal protein L34		
COG0231	30	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)		
COG0232	23	dGTP triphosphohydrolase		
COG0233	25	Ribosome recycling factor		
COG0234	9	Co-chaperonin GroES (HSP10)		
COG0235	58	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases		
COG0236	19	Acyl carrier protein		
COG0237	19	Dephospho-CoA kinase		
COG0238	10	Ribosomal protein S18		
COG0239	16	Integral membrane protein possibly involved in chromosome condensation		
COG0240	37	Glycerol-3-phosphate dehydrogenase		
COG0241	12	Histidinol phosphatase and related phosphatases		
COG0242	35	N-formylmethionyl-tRNA deformylase		
COG0243	306	Anaerobic dehydrogenases, typically selenocysteine-containing		
COG0244	19	Ribosomal protein L10		
COG0245	18	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase		
COG0246	9	Mannitol-1-phosphate/altronate dehydrogenases		
COG0247	153	Fe-S oxidoreductase		
COG0248	56	Exopolyphosphatase		
COG0249	78	Mismatch repair ATPase (MutS family)		
COG0250	16	Transcription antiterminator		
COG0251	94	Putative translation initiation inhibitor, yjgF family		
COG0252	12	L-asparaginase/archaeal Glu-tRNAGln amidotransferase subunit D		

COG0253	26	Diaminopimelate epimerase		
COG0254	6	Ribosomal protein L31		
COG0255	7	Ribosomal protein L29		
COG0256	11	Ribosomal protein L18		
COG0257	1	Ribosomal protein L36		
COG0258	43	5'-3' exonuclease (including N-terminal domain of PolI)		
COG0259	18	Pyridoxamine-phosphate oxidase		
COG0260	52	Leucyl aminopeptidase		
COG0261	15	Ribosomal protein L21		
COG0262	77	Dihydrofolate reductase		
COG0263	22	Glutamate 5-kinase		
COG0264	31	Translation elongation factor Ts		
COG0265	171	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain		
COG0266	64	Formamidopyrimidine-DNA glycosylase		
COG0267	5	Ribosomal protein L33		
COG0268	10	Ribosomal protein S20		
COG0269	1	3-hexulose-6-phosphate synthase and related proteins		
COG0270	14	Site-specific DNA methylase		
COG0271	4	Stress-induced morphogen (activity unknown)		
COG0272	63	NAD-dependent DNA ligase (contains BRCT domain type II)		
COG0274	13	Deoxyribose-phosphate aldolase		
COG0275	31	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis		
COG0276	32	Protoheme ferro-lyase (ferrochelatase)		
COG0277	253	FAD/FMN-containing dehydrogenases		
COG0278	3	Glutaredoxin-related protein		
COG0279	11	Phosphoheptose isomerase		
COG0280	44	Phosphotransacetylase		
COG0281	47	Malic enzyme		
COG0282	26	Acetate kinase		
COG0283	18	Cytidylate kinase		
COG0284	27	Orotidine-5'-phosphate decarboxylase		
COG0285	47	Folylpolyglutamate synthase		
COG0286	44	Type I restriction-modification system methyltransferase subunit		
COG0287	21	Prephenate dehydrogenase		
COG0288	24	Carbonic anhydrase		
COG0289	21	Dihydrodipicolinate reductase		
COG0290	24	Translation initiation factor 3 (IF-3)		
COG0291	3	Ribosomal protein L35		
COG0292	5	Ribosomal protein L20		
COG0293	13	23S rRNA methylase		
COG0294	34	Dihydropteroate synthase and related enzymes		
COG0295	8	Cytidine deaminase		
COG0296	59	1,4-alpha-glucan branching enzyme		
COG0297	22	Glycogen synthase		
COG0298	11	Hydrogenase maturation factor		
COG0299	27	Folate-dependent phosphoribosylglycinamide formyltransferase PurN		
COG0300	25	Short-chain dehydrogenases of various substrate specificities		
COG0301	4	Thiamine biosynthesis ATP pyrophosphatase		
COG0302	25	GTP cyclohydrolase I		
COG0303	61	Molybdopterin biosynthesis enzyme		
COG0304	88	3-oxoacyl-(acyl-carrier-protein) synthase		
COG0305	59	Replicative DNA helicase		
COG0306	31	Phosphate/sulphate permeases		
COG0307	29	Riboflavin synthase alpha chain		
COG0308	100	Aminopeptidase N		
COG0309	20	Hydrogenase maturation factor		
COG0310	6	ABC-type Co2+ transport system, permease component		
COG0311	4	Predicted glutamine amidotransferase involved in pyridoxine biosynthesis		
COG0312	93	Predicted Zn-dependent proteases and their inactivated homologs		
COG0313	34	Predicted methyltransferases		
COG0314	14	Molybdopterin converting factor, large subunit		
COG0315	14	Molybdenum cofactor biosynthesis enzyme		
COG0316	24	Uncharacterized conserved protein		
COG0317	92	Guanosine polyphosphate pyrophosphohydrolases/synthetases		
COG0318	370	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II		
COG0319	14	Predicted metal-dependent hydrolase		
COG0320	32	Lipoate synthase		
COG0321	22	Lipoate-protein ligase B		
COG0322	58	Nuclease subunit of the excinuclease complex		
COG0323	43	DNA mismatch repair enzyme (predicted ATPase)		
COG0324	28	tRNA delta(2)-isopentenylpyrophosphate transferase		
COG0325	22	Predicted enzyme with a TIM-barrel fold		
COG0326	11	Molecular chaperone, HSP90 family		
COG0327	8	Uncharacterized conserved protein		
COG0328	18	Ribonuclease HI		
COG0329	68	Dihydrodipicolinate synthase/N-acetylneuraminate lyase		
COG0330	81	Membrane protease subunits, stomatin/prohibitin homologs		
COG0331	37	(acyl-carrier-protein) S-malonyltransferase		
COG0332	71	3-oxoacyl-[acyl-carrier-protein] synthase III		
COG0333	2	Ribosomal protein L32		
COG0334	66	Glutamate dehydrogenase/leucine dehydrogenase		
COG0335	11	Ribosomal protein L19		
COG0336	26	tRNA-(guanine-N1)-methyltransferase		
COG0337	29	3-dehydroquinate synthetase		

COG0338	1	Site-specific DNA methylase		
COG0339	48	Zn-dependent oligopeptidases		
COG0340	28	Biotin-(acetyl-CoA carboxylase) ligase		
COG0341	31	Preprotein translocase subunit SecF		
COG0342	42	Preprotein translocase subunit SecD		
COG0343	25	Queuine/archaeosine tRNA-ribosyltransferase		
COG0344	21	Predicted membrane protein		
COG0345	27	Pyrroline-5-carboxylate reductase		
COG0346	152	Lactoylglutathione lyase and related lyases		
COG0347	14	Nitrogen regulatory protein PII		
COG0348	27	Polyferredoxin		
COG0349	17	Ribonuclease D		
COG0350	29	Methylated DNA-protein cysteine methyltransferase		
COG0351	25	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase		
COG0352	20	Thiamine monophosphate synthase		
COG0353	17	Recombinational DNA repair protein (RecF pathway)		
COG0354	27	Predicted aminomethyltransferase related to GcvT		
COG0355	7	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit)		
COG0356	46	F0F1-type ATP synthase, subunit a		
COG0357	23	Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division		
COG0358	48	DNA primase (bacterial type)		
COG0359	22	Ribosomal protein L9		
COG0360	18	Ribosomal protein S6		
COG0361	12	Translation initiation factor 1 (IF-1)		
COG0362	12	6-phosphogluconate dehydrogenase		
COG0363	25	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase		
COG0364	39	Glucose-6-phosphate 1-dehydrogenase		
COG0365	191	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases		
COG0366	99	Glycosidases		
COG0367	152	Asparagine synthase (glutamine-hydrolyzing)		
COG0369	8	Sulfite reductase, alpha subunit (flavoprotein)		
COG0370	35	Fe2+ transport system protein B		
COG0371	3	Glycerol dehydrogenase and related enzymes		
COG0372	54	Citrate synthase		
COG0373	42	Glutamyl-tRNA reductase		
COG0374	37	Ni,Fe-hydrogenase I large subunit		
COG0375	3	Zn finger protein HypA/HybF (possibly regulating hydrogenase expression)		
COG0376	17	Catalase (peroxidase I)		
COG0377	12	NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases		
COG0378	12	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase		
COG0379	23	Quinolinate synthase		
COG0380	44	Trehalose-6-phosphate synthase		
COG0381	42	UDP-N-acetylglucosamine 2-epimerase		
COG0382	49	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases		
COG0383	19	Alpha-mannosidase		
COG0384	42	Predicted epimerase, PhzC/PhzF homolog		
COG0385	2	Predicted Na+-dependent transporter		
COG0386	7	Glutathione peroxidase		
COG0387	22	Ca2+/H+ antiporter		
COG0388	121	Predicted amidohydrolase		
COG0389	63	Nucleotidyltransferase/DNA polymerase involved in DNA repair		
COG0390	1	ABC-type uncharacterized transport system, permease component		
COG0391	41	Uncharacterized conserved protein		
COG0392	25	Predicted integral membrane protein		
COG0393	10	Uncharacterized conserved protein		
COG0394	34	Protein-tyrosine-phosphatase		
COG0395	139	ABC-type sugar transport system, permease component		
COG0396	14	ABC-type transport system involved in Fe-S cluster assembly, ATPase component		
COG0397	11	Uncharacterized conserved protein		
COG0398	13	Uncharacterized conserved protein		
COG0399	131	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis		
COG0400	14	Predicted esterase		
COG0402	95	Cytosine deaminase and related metal-dependent hydrolases		
COG0403	27	Glycine cleavage system protein P (pyridoxal-binding), N-terminal domain		
COG0404	96	Glycine cleavage system T protein (aminomethyltransferase)		
COG0405	136	Gamma-glutamyltransferase		
COG0406	50	Fructose-2,6-bisphosphatase		
COG0407	38	Uroporphyrinogen-III decarboxylase		
COG0408	7	Coproporphyrinogen III oxidase		
COG0409	11	Hydrogenase maturation factor		
COG0410	110	ABC-type branched-chain amino acid transport systems, ATPase component		
COG0411	124	ABC-type branched-chain amino acid transport systems, ATPase component		
COG0412	71	Dienelactone hydrolase and related enzymes		
COG0413	26	Ketopantoate hydroxymethyltransferase		
COG0414	21	Panthothenate synthetase		
COG0415	28	Deoxyribodipyrimidine photolyase		
COG0416	30	Fatty acid/phospholipid biosynthesis enzyme		
COG0417	16	DNA polymerase elongation subunit (family B)		
COG0418	9	Dihydroorotase		
COG0419	14	ATPase involved in DNA repair		
COG0420	5	DNA repair exonuclease		
COG0421	30	Spermidine synthase		
COG0422	10	Thiamine biosynthesis protein ThiC		
COG0423	14	Glycyl-tRNA synthetase (class II)		

COG0424	26	Nucleotide-binding protein implicated in inhibition of septum formation		
COG0425	12	Predicted redox protein, regulator of disulfide bond formation		
COG0426	2	Uncharacterized flavoproteins		
COG0427	15	Acetyl-CoA hydrolase		
COG0428	8	Predicted divalent heavy-metal cations transporter		
COG0429	16	Predicted hydrolase of the alpha/beta-hydrolase fold		
COG0430	6	RNA 3'-terminal phosphate cyclase		
COG0431	31	Predicted flavoprotein		
COG0432	26	Uncharacterized conserved protein		
COG0433	45	Predicted ATPase		
COG0434	6	Predicted TIM-barrel enzyme		
COG0435	11	Predicted glutathione S-transferase		
COG0436	188	Aspartate/tyrosine/aromatic aminotransferase		
COG0437	73	Fe-S-cluster-containing hydrogenase components 1		
COG0438	517	Glycosyltransferase		
COG0439	49	Biotin carboxylase		
COG0440	12	Acetolactate synthase, small (regulatory) subunit		
COG0441	66	Threonyl-tRNA synthetase		
COG0442	44	Prolyl-tRNA synthetase		
COG0443	81	Molecular chaperone		
COG0444	36	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component		
COG0445	38	NAD/FAD-utilizing enzyme apparently involved in cell division		
COG0446	106	Uncharacterized NAD(FAD)-dependent dehydrogenases		
COG0447	12	Dihydroxynaphthoic acid synthase		
COG0448	42	ADP-glucose pyrophosphorylase		
COG0449	54	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains		
COG0450	15	Peroxiredoxin		
COG0451	352	Nucleoside-diphosphate-sugar epimerases		
COG0452	38	Phosphopantothenoylcysteine synthetase/decarboxylase		
COG0454	165	Histone acetyltransferase HPA2 and related acetyltransferases		
COG0455	9	ATPases involved in chromosome partitioning		
COG0456	37	Acetyltransferases		
COG0457	393	FOG: TPR repeat		
COG0458	60	Carbamoylphosphate synthase large subunit (split gene in MJ)		
COG0459	39	Chaperonin GroEL (HSP60 family)		
COG0460	37	Homoserine dehydrogenase		
COG0461	21	Orotate phosphoribosyltransferase		
COG0462	50	Phosphoribosylpyrophosphate synthetase		
COG0463	336	Glycosyltransferases involved in cell wall biogenesis		
COG0464	59	ATPases of the AAA+ class		
COG0465	71	ATP-dependent Zn proteases		
COG0466	92	ATP-dependent Lon protease, bacterial type		
COG0467	37	RecA-superfamily ATPases implicated in signal transduction		
COG0468	31	RecA/RadA recombinase		
COG0469	41	Pyruvate kinase		
COG0470	20	ATPase involved in DNA replication		
COG0471	24	Di- and tricarboxylate transporters		
COG0472	57	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase		
COG0473	58	Isocitrate/isopropylmalate dehydrogenase		
COG0474	159	Cation transport ATPase		
COG0475	59	Kef-type K+ transport systems, membrane components		
COG0476	39	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2		
COG0477	941	Permeases of the major facilitator superfamily		
COG0479	35	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit		
COG0480	130	Translation elongation factors (GTPases)		
COG0481	45	Membrane GTPase LepA		
COG0482	46	Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains the PP-loop ATPase domain		
COG0483	52	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family		
COG0484	50	DnaJ-class molecular chaperone with C-terminal Zn finger domain		
COG0486	35	Predicted GTPase		
COG0488	66	ATPase components of ABC transporters with duplicated ATPase domains		
COG0489	76	ATPases involved in chromosome partitioning		
COG0490	2	Putative regulatory, ligand-binding protein related to C-terminal domains of K+ channels		
COG0491	230	Zn-dependent hydrolases, including glyoxylases		
COG0492	96	Thioredoxin reductase		
COG0493	110	NADPH-dependent glutamate synthase beta chain and related oxidoreductases		
COG0494	80	NTP pyrophosphohydrolases including oxidative damage repair enzymes		
COG0495	73	Leucyl-tRNA synthetase		
COG0496	25	Predicted acid phosphatase		
COG0497	48	ATPase involved in DNA repair		
COG0498	65	Threonine synthase		
COG0499	28	S-adenosylhomocysteine hydrolase		
COG0500	502	SAM-dependent methyltransferases		
COG0501	88	Zn-dependent protease with chaperone function		
COG0502	20	Biotin synthase and related enzymes		
COG0503	10	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins		
COG0504	32	CTP synthase (UTP-ammonia lyase)		
COG0505	39	Carbamoylphosphate synthase small subunit		
COG0506	28	Proline dehydrogenase		
COG0507	44	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member		
COG0508	99	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes		
COG0509	28	Glycine cleavage system H protein (lipoate-binding)		
COG0510	6	Predicted choline kinase involved in LPS biosynthesis		
COG0511	11	Biotin carboxyl carrier protein		

COG0512	16	Anthranilate/para-aminobenzoate synthases component II		
COG0513	60	Superfamily II DNA and RNA helicases		
COG0514	40	Superfamily II DNA helicase		
COG0515	365	Serine/threonine protein kinase		
COG0516	52	IMP dehydrogenase/GMP reductase		
COG0517	103	FOG: CBS domain		
COG0518	25	GMP synthase - Glutamine amidotransferase domain		
COG0519	21	GMP synthase, PP-ATPase domain/subunit		
COG0520	111	Selenocysteine lyase		
COG0521	18	Molybdopterin biosynthesis enzymes		
COG0522	18	Ribosomal protein S4 and related proteins		
COG0523	19	Putative GTPases (G3E family)		
COG0524	73	Sugar kinases, ribokinase family		
COG0525	84	Valyl-tRNA synthetase		
COG0526	147	Thiol-disulfide isomerase and thioredoxins		
COG0527	35	Aspartokinases		
COG0528	18	Uridylate kinase		
COG0529	15	Adenylylsulfate kinase and related kinases		
COG0530	18	Ca2+/Na+ antiporter		
COG0531	252	Amino acid transporters		
COG0532	40	Translation initiation factor 2 (IF-2; GTPase)		
COG0533	28	Metal-dependent proteases with possible chaperone activity		
COG0534	48	Na+-driven multidrug efflux pump		
COG0535	97	Predicted Fe-S oxidoreductases		
COG0536	33	Predicted GTPase		
COG0537	49	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases		
COG0538	19	Isocitrate dehydrogenases		
COG0539	43	Ribosomal protein S1		
COG0540	35	Aspartate carbamoyltransferase, catalytic chain		
COG0541	40	Signal recognition particle GTPase		
COG0542	110	ATPases with chaperone activity, ATP-binding subunit		
COG0543	57	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases		
COG0544	51	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)		
COG0545	11	FKBP-type peptidyl-prolyl cis-trans isomerases 1		
COG0546	41	Predicted phosphatases		
COG0547	29	Anthranilate phosphoribosyltransferase		
COG0548	28	Acetylglutamate kinase		
COG0549	16	Carbamate kinase		
COG0550	61	Topoisomerase IA		
COG0551	15	Zn-finger domain associated with topoisomerase type I		
COG0552	18	Signal recognition particle GTPase		
COG0553	56	Superfamily II DNA/RNA helicases, SNF2 family		
COG0554	40	Glycerol kinase		
COG0555	17	ABC-type sulfate transport system, permease component		
COG0556	41	Helicase subunit of the DNA excision repair complex		
COG0557	64	Exoribonuclease R		
COG0558	54	Phosphatidylglycerophosphate synthase		
COG0559	153	Branched-chain amino acid ABC-type transport system, permease components		
COG0560	28	Phosphoserine phosphatase		
COG0561	33	Predicted hydrolases of the HAD superfamily		
COG0562	11	UDP-galactopyranose mutase		
COG0563	35	Adenylate kinase and related kinases		
COG0564	55	Pseudouridylate synthases, 23S RNA-specific		
COG0565	19	rRNA methylase		
COG0566	55	rRNA methylases		
COG0567	38	2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes		
COG0568	82	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)		
COG0569	23	K+ transport systems, NAD-binding component		
COG0571	26	dsRNA-specific ribonuclease		
COG0572	18	Uridine kinase		
COG0573	38	ABC-type phosphate transport system, permease component		
COG0574	126	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase		
COG0575	22	CDP-diglyceride synthetase		
COG0576	21	Molecular chaperone GrpE (heat shock protein)		
COG0577	187	ABC-type antimicrobial peptide transport system, permease component		
COG0578	47	Glycerol-3-phosphate dehydrogenase		
COG0579	30	Predicted dehydrogenase		
COG0580	30	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)		
COG0581	38	ABC-type phosphate transport system, permease component		
COG0582	118	Integrase		
COG0583	248	Transcriptional regulator		
COG0584	36	Glycerophosphoryl diester phosphodiesterase		
COG0585	3	Uncharacterized conserved protein		
COG0586	59	Uncharacterized membrane-associated protein		
COG0587	186	DNA polymerase III, alpha subunit		
COG0588	7	Phosphoglycerate mutase 1		
COG0589	79	Universal stress protein UspA and related nucleotide-binding proteins		
COG0590	25	Cytosine/adenosine deaminases		
COG0591	61	Na+/proline symporter		
COG0592	48	DNA polymerase sliding clamp subunit (PCNA homolog)		
COG0593	48	ATPase involved in DNA replication initiation		
COG0594	18	RNase P protein component		
COG0595	45	Predicted hydrolase of the metallo-beta-lactamase superfamily		
COG0596	521	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)		

COG0597	15	Lipoprotein signal peptidase		
COG0598	50	Mg2+ and Co2+ transporters		
COG0599	27	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit		
COG0600	80	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component		
COG0601	184	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components		
COG0602	15	Organic radical activating enzymes		
COG0603	21	Predicted PP-loop superfamily ATPase		
COG0604	194	NADPH:quinone reductase and related Zn-dependent oxidoreductases		
COG0605	21	Superoxide dismutase		
COG0606	60	Predicted ATPase with chaperone activity		
COG0607	78	Rhodanese-related sulfurtransferase		
COG0608	41	Single-stranded DNA-specific exonuclease		
COG0609	13	ABC-type Fe3+-siderophore transport system, permease component		
COG0610	35	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases		
COG0611	25	Thiamine monophosphate kinase		
COG0612	209	Predicted Zn-dependent peptidases		
COG0613	28	Predicted metal-dependent phosphoesterases (PHP family)		
COG0614	35	ABC-type Fe3+-hydroxamate transport system, periplasmic component		
COG0616	42	Periplasmic serine proteases (ClpP class)		
COG0617	51	tRNA nucleotidyltransferase/poly(A) polymerase		
COG0618	31	Exopolyphosphatase-related proteins		
COG0619	13	ABC-type cobalt transport system, permease component CbiQ and related transporters		
COG0620	72	Methionine synthase II (cobalamin-independent)		
COG0621	77	2-methylthioadenine synthetase		
COG0622	18	Predicted phosphoesterase		
COG0623	35	Enoyl-[acyl-carrier-protein] reductase (NADH)		
COG0624	226	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases		
COG0625	133	Glutathione S-transferase		
COG0626	84	Cystathionine beta-lyases/cystathionine gamma-synthases		
COG0627	17	Predicted esterase		
COG0628	65	Predicted permease		
COG0629	24	Single-stranded DNA-binding protein		
COG0630	2	Type IV secretory pathway, VirB11 components, and related ATPases involved in archaeal flagella biosynthesis		
COG0631	43	Serine/threonine protein phosphatase		
COG0632	21	Holliday junction resolvasome, DNA-binding subunit		
COG0633	13	Ferredoxin		
COG0634	26	Hypoxanthine-guanine phosphoribosyltransferase		
COG0635	52	Coproporphyrinogen III oxidase and related Fe-S oxidoreductases		
COG0636	8	F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K		
COG0637	26	Predicted phosphatase/phosphohexomutase		
COG0638	11	20S proteasome, alpha and beta subunits		
COG0639	59	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases		
COG0640	86	Predicted transcriptional regulators		
COG0641	10	Arylsulfatase regulator (Fe-S oxidoreductase)		
COG0642	750	Signal transduction histidine kinase		
COG0643	80	Chemotaxis protein histidine kinase and related kinases		
COG0644	62	Dehydrogenases (flavoproteins)		
COG0645	3	Predicted kinase		
COG0646	41	Methionine synthase I (cobalamin-dependent), methyltransferase domain		
COG0647	19	Predicted sugar phosphatases of the HAD superfamily		
COG0648	34	Endonuclease IV		
COG0649	70	NADH:ubiquinone oxidoreductase 49 kD subunit 7		
COG0650	13	Formate hydrogenlyase subunit 4		
COG0651	54	Formate hydrogenlyase subunit 3/Multisubunit Na+/H+ antiporter, MnhD subunit		
COG0652	34	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family		
COG0653	73	Preprotein translocase subunit SecA (ATPase, RNA helicase)		
COG0654	127	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases		
COG0655	28	Multimeric flavodoxin WrbA		
COG0656	39	Aldo/keto reductases, related to diketogulonate reductase		
COG0657	49	Esterase/lipase		
COG0658	23	Predicted membrane metal-binding protein		
COG0659	53	Sulfate permease and related transporters (MFS superfamily)		
COG0661	57	Predicted unusual protein kinase		
COG0662	20	Mannose-6-phosphate isomerase		
COG0663	31	Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily		
COG0664	150	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases		
COG0665	190	Glycine/D-amino acid oxidases (deaminating)		
COG0666	38	FOG: Ankyrin repeat		
COG0667	157	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)		
COG0668	45	Small-conductance mechanosensitive channel		
COG0669	22	Phosphopantetheine adenylyltransferase		
COG0670	10	Integral membrane protein, interacts with FtsH		
COG0671	14	Membrane-associated phospholipid phosphatase		
COG0672	13	High-affinity Fe2+/Pb2+ permease		
COG0673	224	Predicted dehydrogenases and related proteins		
COG0674	108	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit		
COG0675	10	Transposase and inactivated derivatives		
COG0676	1	Uncharacterized enzymes related to aldose 1-epimerase		
COG0677	49	UDP-N-acetyl-D-mannosaminuronate dehydrogenase		
COG0678	3	Peroxiredoxin		
COG0679	11	Predicted permeases		
COG0680	15	Ni,Fe-hydrogenase maturation factor		
COG0681	47	Signal peptidase I		
COG0682	26	Prolipoprotein diacylglyceryltransferase		

COG0683	253	ABC-type branched-chain amino acid transport systems, periplasmic component		
COG0684	27	Demethylmenaquinone methyltransferase		
COG0685	56	5,10-methylenetetrahydrofolate reductase		
COG0686	27	Alanine dehydrogenase		
COG0687	35	Spermidine/putrescine-binding periplasmic protein		
COG0688	14	Phosphatidylserine decarboxylase		
COG0689	19	RNase PH		
COG0690	2	Preprotein translocase subunit SecE		
COG0691	26	tmRNA-binding protein		
COG0692	6	Uracil DNA glycosylase		
COG0693	39	Putative intracellular protease/amidase		
COG0694	6	Thioredoxin-like proteins and domains		
COG0695	13	Glutaredoxin and related proteins		
COG0696	22	Phosphoglyceromutase		
COG0697	200	Permeases of the drug/metabolite transporter (DMT) superfamily		
COG0698	25	Ribose 5-phosphate isomerase RpiB		
COG0699	12	Predicted GTPases (dynamin-related)		
COG0700	4	Uncharacterized membrane protein		
COG0701	18	Predicted permeases		
COG0702	72	Predicted nucleoside-diphosphate-sugar epimerases		
COG0703	22	Shikimate kinase		
COG0704	22	Phosphate uptake regulator		
COG0705	46	Uncharacterized membrane protein (homolog of Drosophila rhomboid)		
COG0706	54	Preprotein translocase subunit YidC		
COG0707	37	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase		
COG0708	29	Exonuclease III		
COG0709	27	Selenophosphate synthase		
COG0710	3	3-dehydroquinate dehydratase		
COG0711	9	F0F1-type ATP synthase, subunit b		
COG0712	19	F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein)		
COG0713	10	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)		
COG0714	92	MoxR-like ATPases		
COG0715	105	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components		
COG0716	3	Flavodoxins		
COG0717	20	Deoxycytidine deaminase		
COG0718	10	Uncharacterized protein conserved in bacteria		
COG0719	48	ABC-type transport system involved in Fe-S cluster assembly, permease component		
COG0720	21	6-pyruvoyl-tetrahydropterin synthase		
COG0721	7	Asp-tRNAAsn/Glu-tRNAGln amidotransferase C subunit		
COG0722	11	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase		
COG0723	31	Rieske Fe-S protein		
COG0724	10	RNA-binding proteins (RRM domain)		
COG0725	58	ABC-type molybdate transport system, periplasmic component		
COG0726	106	Predicted xylanase/chitin deacetylase		
COG0727	5	Predicted Fe-S-cluster oxidoreductase		
COG0728	46	Uncharacterized membrane protein, putative virulence factor		
COG0729	23	Outer membrane protein		
COG0730	86	Predicted permeases		
COG0731	2	Fe-S oxidoreductases		
COG0732	13	Restriction endonuclease S subunits		
COG0733	5	Na+-dependent transporters of the SNF family		
COG0735	32	Fe2+/Zn2+ uptake regulation proteins		
COG0736	14	Phosphopantetheinyl transferase (holo-ACP synthase)		
COG0737	42	5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases		
COG0738	2	Fucose permease		
COG0739	116	Membrane proteins related to metalloendopeptidases		
COG0740	26	Protease subunit of ATP-dependent Clp proteases		
COG0741	103	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)		
COG0742	23	N6-adenine-specific methylase		
COG0743	33	1-deoxy-D-xylulose 5-phosphate reductoisomerase		
COG0744	106	Membrane carboxypeptidase (penicillin-binding protein)		
COG0745	284	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain		
COG0746	9	Molybdopterin-guanine dinucleotide biosynthesis protein A		
COG0747	349	ABC-type dipeptide transport system, periplasmic component		
COG0748	4	Putative heme iron utilization protein		
COG0749	48	DNA polymerase I - 3'-5' exonuclease and polymerase domains		
COG0750	48	Predicted membrane-associated Zn-dependent proteases 1		
COG0751	33	Glycyl-tRNA synthetase, beta subunit		
COG0752	12	Glycyl-tRNA synthetase, alpha subunit		
COG0753	10	Catalase		
COG0754	9	Glutathionylspermidine synthase		
COG0755	47	ABC-type transport system involved in cytochrome c biogenesis, permease component		
COG0756	13	dUTPase		
COG0757	17	3-dehydroquinate dehydratase II		
COG0758	32	Predicted Rossmann fold nucleotide-binding protein involved in DNA uptake		
COG0759	13	Uncharacterized conserved protein		
COG0760	86	Parvulin-like peptidyl-prolyl isomerase		
COG0761	29	Penicillin tolerance protein		
COG0762	10	Predicted integral membrane protein		
COG0763	27	Lipid A disaccharide synthetase		
COG0764	23	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases		
COG0765	49	ABC-type amino acid transport system, permease component		
COG0766	49	UDP-N-acetylglucosamine enolpyruvyl transferase		
COG0767	50	ABC-type transport system involved in resistance to organic solvents, permease component		

COG0768	159	Cell division protein FtsI/penicillin-binding protein 2		
COG0769	56	UDP-N-acetylmuramyl tripeptide synthase		
COG0770	34	UDP-N-acetylmuramyl pentapeptide synthase		
COG0771	31	UDP-N-acetylmuramoylalanine-D-glutamate ligase		
COG0772	84	Bacterial cell division membrane protein		
COG0773	50	UDP-N-acetylmuramate-alanine ligase		
COG0774	25	UDP-3-O-acyl-N-acetylglucosamine deacetylase		
COG0775	6	Nucleoside phosphorylase		
COG0776	32	Bacterial nucleoid DNA-binding protein		
COG0777	22	Acetyl-CoA carboxylase beta subunit		
COG0778	57	Nitroreductase		
COG0779	22	Uncharacterized protein conserved in bacteria		
COG0780	11	Enzyme related to GTP cyclohydrolase I		
COG0781	19	Transcription termination factor		
COG0782	35	Transcription elongation factor		
COG0783	10	DNA-binding ferritin-like protein (oxidative damage protectant)		
COG0784	286	FOG: CheY-like receiver		
COG0785	18	Cytochrome c biogenesis protein		
COG0786	1	Na+/glutamate symporter		
COG0787	36	Alanine racemase		
COG0788	6	Formyltetrahydrofolate hydrolase		
COG0789	54	Predicted transcriptional regulators		
COG0790	25	FOG: TPR repeat, SEL1 subfamily		
COG0791	33	Cell wall-associated hydrolases (invasion-associated proteins)		
COG0792	13	Predicted endonuclease distantly related to archaeal Holliday junction resolvase		
COG0793	84	Periplasmic protease		
COG0794	12	Predicted sugar phosphate isomerase involved in capsule formation		
COG0795	41	Predicted permeases		
COG0796	15	Glutamate racemase		
COG0797	13	Lipoproteins		
COG0798	22	Arsenite efflux pump ACR3 and related permeases		
COG0799	15	Uncharacterized homolog of plant Iojap protein		
COG0800	8	2-keto-3-deoxy-6-phosphogluconate aldolase		
COG0801	17	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase		
COG0802	17	Predicted ATPase or kinase		
COG0803	33	ABC-type metal ion transport system, periplasmic component/surface adhesin		
COG0804	11	Urea amidohydrolase (urease) alpha subunit		
COG0805	33	Sec-independent protein secretion pathway component TatC		
COG0806	16	RimM protein, required for 16S rRNA processing		
COG0807	25	GTP cyclohydrolase II		
COG0809	34	S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)		
COG0810	28	Periplasmic protein TonB, links inner and outer membranes		
COG0811	29	Biopolymer transport proteins		
COG0812	30	UDP-N-acetylmuramate dehydrogenase		
COG0813	4	Purine-nucleoside phosphorylase		
COG0815	31	Apolipoprotein N-acyltransferase		
COG0816	18	Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis)		
COG0817	18	Holliday junction resolvasome, endonuclease subunit		
COG0818	5	Diacylglycerol kinase		
COG0819	4	Putative transcription activator		
COG0820	39	Predicted Fe-S-cluster redox enzyme		
COG0821	24	Enzyme involved in the deoxyxylulose pathway of isoprenoid biosynthesis		
COG0822	15	NifU homolog involved in Fe-S cluster formation		
COG0823	109	Periplasmic component of the Tol biopolymer transport system		
COG0824	48	Predicted thioesterase		
COG0825	20	Acetyl-CoA carboxylase alpha subunit		
COG0826	29	Collagenase and related proteases		
COG0827	5	Adenine-specific DNA methylase		
COG0828	4	Ribosomal protein S21		
COG0829	2	Urease accessory protein UreH		
COG0830	1	Urease accessory protein UreF		
COG0831	4	Urea amidohydrolase (urease) gamma subunit		
COG0832	3	Urea amidohydrolase (urease) beta subunit		
COG0834	78	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain		
COG0835	24	Chemotaxis signal transduction protein		
COG0836	36	Mannose-1-phosphate guanylyltransferase		
COG0837	9	Glucokinase		
COG0838	18	NADH:ubiquinone oxidoreductase subunit 3 (chain A)		
COG0839	20	NADH:ubiquinone oxidoreductase subunit 6 (chain J)		
COG0840	90	Methyl-accepting chemotaxis protein		
COG0841	410	Cation/multidrug efflux pump		
COG0842	141	ABC-type multidrug transport system, permease component		
COG0843	81	Heme/copper-type cytochrome/quinol oxidases, subunit 1		
COG0845	326	Membrane-fusion protein		
COG0846	28	NAD-dependent protein deacetylases, SIR2 family		
COG0847	26	DNA polymerase III, epsilon subunit and related 3'-5' exonucleases		
COG0848	18	Biopolymer transport protein		
COG0849	32	Actin-like ATPase involved in cell division		
COG0850	2	Septum formation inhibitor		
COG0851	2	Septum formation topological specificity factor		
COG0852	21	NADH:ubiquinone oxidoreductase 27 kD subunit		
COG0853	6	Aspartate 1-decarboxylase		
COG0854	19	Pyridoxal phosphate biosynthesis protein		
COG0855	47	Polyphosphate kinase		

COG0857	4	BioD-like N-terminal domain of phosphotransacetylase		
COG0858	16	Ribosome-binding factor A		
COG0859	52	ADP-heptose:LPS heptosyltransferase		
COG0860	42	N-acetylmuramoyl-L-alanine amidase		
COG0861	43	Membrane protein TerC, possibly involved in tellurium resistance		
COG0863	35	DNA modification methylase		
COG1001	14	Adenine deaminase		
COG1002	28	Type II restriction enzyme, methylase subunits		
COG1003	36	Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain		
COG1004	50	Predicted UDP-glucose 6-dehydrogenase		
COG1005	55	NADH:ubiquinone oxidoreductase subunit 1 (chain H)		
COG1006	3	Multisubunit Na+/H+ antiporter, MnhC subunit		
COG1007	59	NADH:ubiquinone oxidoreductase subunit 2 (chain N)		
COG1008	63	NADH:ubiquinone oxidoreductase subunit 4 (chain M)		
COG1009	64	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, MnhA subunit		
COG1010	6	Precorrin-3B methylase		
COG1011	76	Predicted hydrolase (HAD superfamily)		
COG1012	358	NAD-dependent aldehyde dehydrogenases		
COG1013	65	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit		
COG1014	74	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit		
COG1015	18	Phosphopentomutase		
COG1017	1	Hemoglobin-like flavoprotein		
COG1018	37	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1		
COG1019	1	Predicted nucleotidyltransferase		
COG1020	110	Non-ribosomal peptide synthetase modules and related proteins		
COG1021	10	Peptide arylation enzymes		
COG1022	95	Long-chain acyl-CoA synthetases (AMP-forming)		
COG1023	19	Predicted 6-phosphogluconate dehydrogenase		
COG1024	292	Enoyl-CoA hydratase/carnithine racemase		
COG1026	1	Predicted Zn-dependent peptidases, insulinase-like		
COG1027	19	Aspartate ammonia-lyase		
COG1028	682	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)		
COG1029	1	Formylmethanofuran dehydrogenase subunit B		
COG1030	31	Membrane-bound serine protease (ClpP class)		
COG1032	154	Fe-S oxidoreductase		
COG1033	18	Predicted exporters of the RND superfamily		
COG1034	38	NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)		
COG1035	4	Coenzyme F420-reducing hydrogenase, beta subunit		
COG1036	1	Archaeal flavoproteins		
COG1038	22	Pyruvate carboxylase		
COG1039	3	Ribonuclease HIII		
COG1040	22	Predicted amidophosphoribosyltransferases		
COG1042	111	Acyl-CoA synthetase (NDP forming)		
COG1043	31	Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase		
COG1044	31	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase		
COG1045	18	Serine acetyltransferase		
COG1047	9	FKBP-type peptidyl-prolyl cis-trans isomerases 2		
COG1048	69	Aconitase A		
COG1049	7	Aconitase B		
COG1051	39	ADP-ribose pyrophosphatase		
COG1052	38	Lactate dehydrogenase and related dehydrogenases		
COG1053	117	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit		
COG1054	1	Predicted sulfurtransferase		
COG1055	29	Na+/H+ antiporter NhaD and related arsenite permeases		
COG1057	22	Nicotinic acid mononucleotide adenylyltransferase		
COG1058	34	Predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA		
COG1060	51	Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes		
COG1061	38	DNA or RNA helicases of superfamily II		
COG1062	49	Zn-dependent alcohol dehydrogenases, class III		
COG1063	157	Threonine dehydrogenase and related Zn-dependent dehydrogenases		
COG1064	51	Zn-dependent alcohol dehydrogenases		
COG1066	37	Predicted ATP-dependent serine protease		
COG1067	32	Predicted ATP-dependent protease		
COG1069	7	Ribulose kinase		
COG1070	44	Sugar (pentulose and hexulose) kinases		
COG1071	92	Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit		
COG1072	4	Panthothenate kinase		
COG1073	69	Hydrolases of the alpha/beta superfamily		
COG1074	24	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)		
COG1075	20	Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold		
COG1076	10	DnaJ-domain-containing proteins 1		
COG1077	34	Actin-like ATPase involved in cell morphogenesis		
COG1078	7	HD superfamily phosphohydrolases		
COG1079	28	Uncharacterized ABC-type transport system, permease component		
COG1080	33	Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)		
COG1082	64	Sugar phosphate isomerases/epimerases		
COG1083	2	CMP-N-acetylneuraminic acid synthetase		
COG1085	25	Galactose-1-phosphate uridylyltransferase		
COG1086	39	Predicted nucleoside-diphosphate sugar epimerases		
COG1087	28	UDP-glucose 4-epimerase		
COG1088	25	dTDP-D-glucose 4,6-dehydratase		
COG1089	29	GDP-D-mannose dehydratase		
COG1090	17	Predicted nucleoside-diphosphate sugar epimerase		
COG1091	36	dTDP-4-dehydrorhamnose reductase		

COG1092	37	Predicted SAM-dependent methyltransferases		
COG1099	5	Predicted metal-dependent hydrolases with the TIM-barrel fold		
COG1100	13	GTPase SAR1 and related small G proteins		
COG1102	1	Cytidylate kinase		
COG1104	54	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes		
COG1105	14	Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB)		
COG1108	22	ABC-type Mn2+/Zn2+ transport systems, permease components		
COG1109	100	Phosphomannomutase		
COG1112	22	Superfamily I DNA and RNA helicases and helicase subunits		
COG1113	2	Gamma-aminobutyrate permease and related permeases		
COG1116	33	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component		
COG1117	14	ABC-type phosphate transport system, ATPase component		
COG1118	11	ABC-type sulfate/molybdate transport systems, ATPase component		
COG1119	6	ABC-type molybdenum transport system, ATPase component/photorepair protein PhrA		
COG1120	12	ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components		
COG1121	11	ABC-type Mn/Zn transport systems, ATPase component		
COG1122	25	ABC-type cobalt transport system, ATPase component		
COG1123	25	ATPase components of various ABC-type transport systems, contain duplicated ATPase		
COG1125	6	ABC-type proline/glycine betaine transport systems, ATPase components		
COG1126	11	ABC-type polar amino acid transport system, ATPase component		
COG1127	37	ABC-type transport system involved in resistance to organic solvents, ATPase component		
COG1129	41	ABC-type sugar transport system, ATPase component		
COG1131	163	ABC-type multidrug transport system, ATPase component		
COG1132	290	ABC-type multidrug transport system, ATPase and permease components		
COG1134	29	ABC-type polysaccharide/polyol phosphate transport system, ATPase component		
COG1135	3	ABC-type metal ion transport system, ATPase component		
COG1136	86	ABC-type antimicrobial peptide transport system, ATPase component		
COG1137	13	ABC-type (unclassified) transport system, ATPase component		
COG1138	47	Cytochrome c biogenesis factor		
COG1139	21	Uncharacterized conserved protein containing a ferredoxin-like domain		
COG1140	12	Nitrate reductase beta subunit		
COG1141	2	Ferredoxin		
COG1142	3	Fe-S-cluster-containing hydrogenase components 2		
COG1143	30	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)		
COG1144	13	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit		
COG1145	48	Ferredoxin		
COG1146	19	Ferredoxin		
COG1148	53	Heterodisulfide reductase, subunit A and related polyferredoxins		
COG1150	12	Heterodisulfide reductase, subunit C		
COG1151	6	6Fe-6S prismane cluster-containing protein		
COG1152	2	CO dehydrogenase/acetyl-CoA synthase alpha subunit		
COG1154	40	Deoxyxylulose-5-phosphate synthase		
COG1155	14	Archaeal/vacuolar-type H+-ATPase subunit A		
COG1156	9	Archaeal/vacuolar-type H+-ATPase subunit B		
COG1157	11	Flagellar biosynthesis/type III secretory pathway ATPase		
COG1158	30	Transcription termination factor		
COG1159	30	GTPase		
COG1160	53	Predicted GTPases		
COG1162	36	Predicted GTPases		
COG1163	9	Predicted GTPase		
COG1164	43	Oligoendopeptidase F		
COG1165	23	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase		
COG1166	21	Arginine decarboxylase (spermidine biosynthesis)		
COG1167	74	Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic c		
COG1168	11	Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities		
COG1169	16	Isochorismate synthase		
COG1171	83	Threonine dehydratase		
COG1172	54	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components		
COG1173	156	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components		
COG1174	11	ABC-type proline/glycine betaine transport systems, permease component		
COG1175	133	ABC-type sugar transport systems, permease components		
COG1176	29	ABC-type spermidine/putrescine transport system, permease component I		
COG1177	41	ABC-type spermidine/putrescine transport system, permease component II		
COG1178	72	ABC-type Fe3+ transport system, permease component		
COG1179	3	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 1		
COG1180	30	Pyruvate-formate lyase-activating enzyme		
COG1181	75	D-alanine-D-alanine ligase and related ATP-grasp enzymes		
COG1182	1	Acyl carrier protein phosphodiesterase		
COG1183	19	Phosphatidylserine synthase		
COG1185	39	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)		
COG1186	27	Protein chain release factor B		
COG1187	46	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases		
COG1188	7	Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)		
COG1189	16	Predicted rRNA methylase		
COG1190	35	Lysyl-tRNA synthetase (class II)		
COG1191	43	DNA-directed RNA polymerase specialized sigma subunit		
COG1192	59	ATPases involved in chromosome partitioning		
COG1193	30	Mismatch repair ATPase (MutS family)		
COG1194	33	A/G-specific DNA glycosylase		
COG1195	17	Recombinational DNA repair ATPase (RecF pathway)		
COG1196	51	Chromosome segregation ATPases		
COG1197	72	Transcription-repair coupling factor (superfamily II helicase)		
COG1198	56	Primosomal protein N' (replication factor Y) - superfamily II helicase		
COG1199	57	Rad3-related DNA helicases		

COG1200	50	RecG-like helicase		
COG1201	91	Lhr-like helicases		
COG1202	1	Superfamily II helicase, archaea-specific		
COG1203	6	Predicted helicases		
COG1204	2	Superfamily II helicase		
COG1205	42	Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster		
COG1206	26	NAD(FAD)-utilizing enzyme possibly involved in translation		
COG1207	49	N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)		
COG1208	77	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/eps		
COG1209	33	dTDP-glucose pyrophosphorylase		
COG1210	17	UDP-glucose pyrophosphorylase		
COG1211	19	4-diphosphocytidyl-2-methyl-D-erithritol synthase		
COG1212	20	CMP-2-keto-3-deoxyoctulosonic acid synthetase		
COG1213	1	Predicted sugar nucleotidyltransferases		
COG1214	19	Inactive homolog of metal-dependent proteases, putative molecular chaperone		
COG1215	82	Glycosyltransferases, probably involved in cell wall biogenesis		
COG1216	63	Predicted glycosyltransferases		
COG1217	32	Predicted membrane GTPase involved in stress response		
COG1218	8	3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase		
COG1219	19	ATP-dependent protease Clp, ATPase subunit		
COG1220	20	ATP-dependent protease HslVU (ClpYQ), ATPase subunit		
COG1221	7	Transcriptional regulators containing an AAA-type ATPase domain and a DNA-binding domain		
COG1222	4	ATP-dependent 26S proteasome regulatory subunit		
COG1223	1	Predicted ATPase (AAA+ superfamily)		
COG1225	49	Peroxiredoxin		
COG1226	56	Kef-type K+ transport systems, predicted NAD-binding component		
COG1227	4	Inorganic pyrophosphatase/exopolyphosphatase		
COG1228	155	Imidazolonepropionase and related amidohydrolases		
COG1229	8	Formylmethanofuran dehydrogenase subunit A		
COG1230	33	Co/Zn/Cd efflux system component		
COG1231	20	Monoamine oxidase		
COG1232	52	Protoporphyrinogen oxidase		
COG1233	93	Phytoene dehydrogenase and related proteins		
COG1234	43	Metal-dependent hydrolases of the beta-lactamase superfamily III		
COG1235	67	Metal-dependent hydrolases of the beta-lactamase superfamily I		
COG1236	59	Predicted exonuclease of the beta-lactamase fold involved in RNA processing		
COG1237	12	Metal-dependent hydrolases of the beta-lactamase superfamily II		
COG1238	4	Predicted membrane protein		
COG1239	31	Mg-chelatase subunit ChlI		
COG1240	4	Mg-chelatase subunit ChlD		
COG1242	2	Predicted Fe-S oxidoreductase		
COG1243	4	Histone acetyltransferase		
COG1244	2	Predicted Fe-S oxidoreductase		
COG1246	14	N-acetylglutamate synthase and related acetyltransferases		
COG1247	21	Sortase and related acyltransferases		
COG1249	142	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes		
COG1250	96	3-hydroxyacyl-CoA dehydrogenase		
COG1251	23	NAD(P)H-nitrite reductase		
COG1252	52	NADH dehydrogenase, FAD-containing subunit		
COG1253	66	Hemolysins and related proteins containing CBS domains		
COG1254	16	Acylphosphatases		
COG1256	6	Flagellar hook-associated protein		
COG1257	17	Hydroxymethylglutaryl-CoA reductase		
COG1259	18	Uncharacterized conserved protein		
COG1260	12	Myo-inositol-1-phosphate synthase		
COG1261	1	Flagellar basal body P-ring biosynthesis protein		
COG1262	78	Uncharacterized conserved protein		
COG1263	3	Phosphotransferase system IIC components, glucose/maltose/N-acetylglucosamine-specific		
COG1264	1	Phosphotransferase system IIB components		
COG1266	30	Predicted metal-dependent membrane protease		
COG1267	8	Phosphatidylglycerophosphatase A and related proteins		
COG1268	5	Uncharacterized conserved protein		
COG1269	4	Archaeal/vacuolar-type H+-ATPase subunit I		
COG1270	8	Cobalamin biosynthesis protein CobD/CbiB		
COG1271	33	Cytochrome bd-type quinol oxidase, subunit 1		
COG1272	15	Predicted membrane protein, hemolysin III homolog		
COG1273	36	Uncharacterized conserved protein		
COG1274	30	Phosphoenolpyruvate carboxykinase (GTP)		
COG1275	5	Tellurite resistance protein and related permeases		
COG1277	29	ABC-type transport system involved in multi-copper enzyme maturation, permease component		
COG1278	28	Cold shock proteins		
COG1280	22	Putative threonine efflux protein		
COG1281	5	Disulfide bond chaperones of the HSP33 family		
COG1282	18	NAD/NADP transhydrogenase beta subunit		
COG1283	10	Na+/phosphate symporter		
COG1284	2	Uncharacterized conserved protein		
COG1285	11	Uncharacterized membrane protein		
COG1286	2	Uncharacterized membrane protein, required for colicin V production		
COG1288	3	Predicted membrane protein		
COG1289	1	Predicted membrane protein		
COG1290	55	Cytochrome b subunit of the bc complex		
COG1291	5	Flagellar motor component		
COG1292	4	Choline-glycine betaine transporter		
COG1293	6	Predicted RNA-binding protein homologous to eukaryotic snRNP		

COG1294	19	Cytochrome bd-type quinol oxidase, subunit 2		
COG1295	45	Predicted membrane protein		
COG1296	10	Predicted branched-chain amino acid permease (azaleucine resistance)		
COG1297	43	Predicted membrane protein		
COG1298	16	Flagellar biosynthesis pathway, component FlhA		
COG1299	1	Phosphotransferase system, fructose-specific IIC component		
COG1300	14	Uncharacterized membrane protein		
COG1301	31	Na+/H+-dicarboxylate symporters		
COG1302	2	Uncharacterized protein conserved in bacteria		
COG1304	58	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases		
COG1305	63	Transglutaminase-like enzymes, putative cysteine proteases		
COG1306	11	Uncharacterized conserved protein		
COG1307	21	Uncharacterized protein conserved in bacteria		
COG1308	1	Transcription factor homologous to NACalpha-BTF3		
COG1309	219	Transcriptional regulator		
COG1310	4	Predicted metal-dependent protease of the PAD1/JAB1 superfamily		
COG1312	7	D-mannonate dehydratase		
COG1313	12	Uncharacterized Fe-S protein PflX, homolog of pyruvate formate lyase activating proteins		
COG1314	2	Preprotein translocase subunit SecG		
COG1316	31	Transcriptional regulator		
COG1317	3	Flagellar biosynthesis/type III secretory pathway protein		
COG1318	1	Predicted transcriptional regulators		
COG1319	72	Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs		
COG1320	1	Multisubunit Na+/H+ antiporter, MnhG subunit		
COG1321	25	Mn-dependent transcriptional regulator		
COG1322	28	Uncharacterized protein conserved in bacteria		
COG1324	9	Uncharacterized protein involved in tolerance to divalent cations		
COG1327	6	Predicted transcriptional regulator, consists of a Zn-ribbon and ATP-cone domains		
COG1328	5	Oxygen-sensitive ribonucleoside-triphosphate reductase		
COG1329	12	Transcriptional regulators, similar to M. xanthus CarD		
COG1330	10	Exonuclease V gamma subunit		
COG1331	42	Highly conserved protein containing a thioredoxin domain		
COG1333	12	ResB protein required for cytochrome c biosynthesis		
COG1334	1	Uncharacterized flagellar protein FlaG		
COG1335	60	Amidases related to nicotinamidase		
COG1338	6	Flagellar biosynthesis pathway, component FliP		
COG1341	1	Predicted GTPase or GTP-binding protein		
COG1343	1	Uncharacterized protein predicted to be involved in DNA repair		
COG1344	18	Flagellin and related hook-associated proteins		
COG1345	9	Flagellar capping protein		
COG1346	1	Putative effector of murein hydrolase		
COG1347	2	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrD		
COG1348	1	Nitrogenase subunit NifH (ATPase)		
COG1349	22	Transcriptional regulators of sugar metabolism		
COG1350	18	Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB)		
COG1351	21	Predicted alternative thymidylate synthase		
COG1352	58	Methylase of chemotaxis methyl-accepting proteins		
COG1354	19	Uncharacterized conserved protein		
COG1355	16	Predicted dioxygenase		
COG1357	13	Uncharacterized low-complexity proteins		
COG1358	4	Ribosomal protein HS6-type (S12/L30/L7a)		
COG1359	5	Uncharacterized conserved protein		
COG1360	17	Flagellar motor protein		
COG1362	2	Aspartyl aminopeptidase		
COG1363	27	Cellulase M and related proteins		
COG1364	31	N-acetylglutamate synthase (N-acetylornithine aminotransferase)		
COG1366	40	Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor)		
COG1368	13	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily		
COG1371	5	Uncharacterized conserved protein		
COG1372	13	Intein/homing endonuclease		
COG1373	11	Predicted ATPase (AAA+ superfamily)		
COG1376	47	Uncharacterized protein conserved in bacteria		
COG1377	6	Flagellar biosynthesis pathway, component FlhB		
COG1378	1	Predicted transcriptional regulators		
COG1379	2	Uncharacterized conserved protein		
COG1380	2	Putative effector of murein hydrolase LrgA		
COG1381	23	Recombinational DNA repair protein (RecF pathway)		
COG1384	4	Lysyl-tRNA synthetase (class I)		
COG1385	18	Uncharacterized protein conserved in bacteria		
COG1386	16	Predicted transcriptional regulator containing the HTH domain		
COG1387	25	Histidinol phosphatase and related hydrolases of the PHP family		
COG1388	8	FOG: LysM repeat		
COG1389	4	DNA topoisomerase VI, subunit B		
COG1390	1	Archaeal/vacuolar-type H+-ATPase subunit E		
COG1391	54	Glutamine synthetase adenylyltransferase		
COG1392	19	Phosphate transport regulator (distant homolog of PhoU)		
COG1393	7	Arsenate reductase and related proteins, glutaredoxin family		
COG1394	3	Archaeal/vacuolar-type H+-ATPase subunit D		
COG1396	49	Predicted transcriptional regulators		
COG1397	7	ADP-ribosylglycohydrolase		
COG1398	40	Fatty-acid desaturase		
COG1399	22	Predicted metal-binding, possibly nucleic acid-binding protein		
COG1401	2	GTPase subunit of restriction endonuclease		
COG1402	24	Uncharacterized protein, putative amidase		

COG1403	52	Restriction endonuclease		
COG1404	158	Subtilisin-like serine proteases		
COG1407	2	Predicted ICC-like phosphoesterases		
COG1408	25	Predicted phosphohydrolases		
COG1409	59	Predicted phosphohydrolases		
COG1410	63	Methionine synthase I, cobalamin-binding domain		
COG1411	1	Uncharacterized protein related to proFAR isomerase (HisA)		
COG1413	31	FOG: HEAT repeat		
COG1414	60	Transcriptional regulator		
COG1415	8	Uncharacterized conserved protein		
COG1416	3	Uncharacterized conserved protein		
COG1418	25	Predicted HD superfamily hydrolase		
COG1419	6	Flagellar GTP-binding protein		
COG1420	36	Transcriptional regulator of heat shock gene		
COG1426	15	Uncharacterized protein conserved in bacteria		
COG1427	7	Predicted periplasmic solute-binding protein		
COG1428	23	Deoxynucleoside kinases		
COG1429	17	Cobalamin biosynthesis protein CobN and related Mg-chelatases		
COG1430	14	Uncharacterized conserved protein		
COG1432	10	Uncharacterized conserved protein		
COG1434	13	Uncharacterized conserved protein		
COG1435	7	Thymidine kinase		
COG1437	1	Adenylate cyclase, class 2 (thermophilic)		
COG1438	7	Arginine repressor		
COG1443	3	Isopentenyldiphosphate isomerase		
COG1446	19	Asparaginase		
COG1448	8	Aspartate/tyrosine/aromatic aminotransferase		
COG1449	34	Alpha-amylase/alpha-mannosidase		
COG1450	53	Type II secretory pathway, component PulD		
COG1451	12	Predicted metal-dependent hydrolase		
COG1452	27	Organic solvent tolerance protein OstA		
COG1453	4	Predicted oxidoreductases of the aldo/keto reductase family		
COG1454	36	Alcohol dehydrogenase, class IV		
COG1456	5	CO dehydrogenase/acetyl-CoA synthase gamma subunit (corrinoid Fe-S protein)		
COG1457	13	Purine-cytosine permease and related proteins		
COG1459	106	Type II secretory pathway, component PulF		
COG1461	18	Predicted kinase related to dihydroxyacetone kinase		
COG1462	9	Uncharacterized protein involved in formation of curli polymers		
COG1463	58	ABC-type transport system involved in resistance to organic solvents, periplasmic component		
COG1464	2	ABC-type metal ion transport system, periplasmic component/surface antigen		
COG1465	2	Predicted alternative 3-dehydroquinate synthase		
COG1466	11	DNA polymerase III, delta subunit		
COG1467	1	Eukaryotic-type DNA primase, catalytic (small) subunit		
COG1468	3	RecB family exonuclease		
COG1469	8	Uncharacterized conserved protein		
COG1470	4	Predicted membrane protein		
COG1471	1	Ribosomal protein S4E		
COG1472	105	Beta-glucosidase-related glycosidases		
COG1473	80	Metal-dependent amidase/aminoacylase/carboxypeptidase		
COG1474	2	Cdc6-related protein, AAA superfamily ATPase		
COG1475	44	Predicted transcriptional regulators		
COG1476	1	Predicted transcriptional regulators		
COG1477	31	Membrane-associated lipoprotein involved in thiamine biosynthesis		
COG1478	8	Uncharacterized conserved protein		
COG1479	9	Uncharacterized conserved protein		
COG1480	11	Predicted membrane-associated HD superfamily hydrolase		
COG1481	4	Uncharacterized protein conserved in bacteria		
COG1482	11	Phosphomannose isomerase		
COG1483	4	Predicted ATPase (AAA+ superfamily)		
COG1484	48	DNA replication protein		
COG1485	7	Predicted ATPase		
COG1486	16	Alpha-galactosidases/6-phospho-beta-glucosidases, family 4 of glycosyl hydrolases		
COG1487	8	Predicted nucleic acid-binding protein, contains PIN domain		
COG1488	46	Nicotinic acid phosphoribosyltransferase		
COG1489	2	DNA-binding protein, stimulates sugar fermentation		
COG1490	17	D-Tyr-tRNAtyr deacylase		
COG1492	9	Cobyric acid synthase		
COG1493	16	Serine kinase of the HPr protein, regulates carbohydrate metabolism		
COG1494	19	Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisphosphatase and related proteins		
COG1495	8	Disulfide bond formation protein DsbB		
COG1496	25	Uncharacterized conserved protein		
COG1501	24	Alpha-glucosidases, family 31 of glycosyl hydrolases		
COG1502	72	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes		
COG1503	1	Peptide chain release factor 1 (eRF1)		
COG1504	1	Uncharacterized conserved protein		
COG1505	59	Serine proteases of the peptidase family S9A		
COG1506	217	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases		
COG1507	2	Uncharacterized conserved protein		
COG1508	40	DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog		
COG1509	25	Lysine 2,3-aminomutase		
COG1510	5	Predicted transcriptional regulators		
COG1511	2	Predicted membrane protein		
COG1512	14	Beta-propeller domains of methanol dehydrogenase type		
COG1513	1	Cyanate lyase		

COG1514	8	2'-5' RNA ligase		
COG1515	3	Deoxyinosine 3'endonuclease (endonuclease V)		
COG1516	3	Flagellin-specific chaperone FliS		
COG1518	9	Uncharacterized protein predicted to be involved in DNA repair		
COG1519	16	3-deoxy-D-manno-octulosonic-acid transferase		
COG1520	51	FOG: WD40-like repeat		
COG1521	30	Putative transcriptional regulator, homolog of Bvg accessory factor		
COG1522	54	Transcriptional regulators		
COG1523	36	Type II secretory pathway, pullulanase PulA and related glycosidases		
COG1524	34	Uncharacterized proteins of the AP superfamily		
COG1525	9	Micrococcal nuclease (thermonuclease) homologs		
COG1526	16	Uncharacterized protein required for formate dehydrogenase activity		
COG1528	6	Ferritin-like protein		
COG1529	482	Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs		
COG1530	43	Ribonucleases G and E		
COG1533	27	DNA repair photolyase		
COG1534	3	Predicted RNA-binding protein containing KH domain, possibly ribosomal protein		
COG1536	14	Flagellar motor switch protein		
COG1538	123	Outer membrane protein		
COG1539	13	Dihydroneopterin aldolase		
COG1540	7	Uncharacterized proteins, homologs of lactam utilization protein B		
COG1541	72	Coenzyme F390 synthetase		
COG1543	18	Uncharacterized conserved protein		
COG1544	17	Ribosome-associated protein Y (PSrp-1)		
COG1545	20	Predicted nucleic-acid-binding protein containing a Zn-ribbon		
COG1546	24	Uncharacterized protein (competence- and mitomycin-induced)		
COG1547	3	Uncharacterized conserved protein		
COG1548	2	Predicted transcriptional regulator/sugar kinase		
COG1550	6	Uncharacterized protein conserved in bacteria		
COG1551	5	Carbon storage regulator (could also regulate swarming and quorum sensing)		
COG1553	2	Uncharacterized conserved protein involved in intracellular sulfur reduction		
COG1554	12	Trehalose and maltose hydrolases (possible phosphorylases)		
COG1555	12	DNA uptake protein and related DNA-binding proteins		
COG1556	10	Uncharacterized conserved protein		
COG1558	6	Flagellar basal body rod protein		
COG1559	28	Predicted periplasmic solute-binding protein		
COG1560	27	Lauroyl/myristoyl acyltransferase		
COG1561	19	Uncharacterized stress-induced protein		
COG1562	43	Phytoene/squalene synthetase		
COG1565	13	Uncharacterized conserved protein		
COG1566	22	Multidrug resistance efflux pump		
COG1568	1	Predicted methyltransferases		
COG1569	2	Predicted nucleic acid-binding protein, contains PIN domain		
COG1570	44	Exonuclease VII, large subunit		
COG1573	55	Uracil-DNA glycosylase		
COG1574	88	Predicted metal-dependent hydrolase with the TIM-barrel fold		
COG1575	10	1,4-dihydroxy-2-naphthoate octaprenyltransferase		
COG1576	10	Uncharacterized conserved protein		
COG1577	1	Mevalonate kinase		
COG1578	3	Uncharacterized conserved protein		
COG1579	10	Zn-ribbon protein, possibly nucleic acid-binding		
COG1584	6	Predicted membrane protein		
COG1585	2	Membrane protein implicated in regulation of membrane protease activity		
COG1586	3	S-adenosylmethionine decarboxylase		
COG1587	22	Uroporphyrinogen-III synthase		
COG1589	14	Cell division septal protein		
COG1592	10	Rubrerythrin		
COG1593	129	TRAP-type C4-dicarboxylate transport system, large permease component		
COG1595	311	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog		
COG1596	49	Periplasmic protein involved in polysaccharide export		
COG1597	38	Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase		
COG1598	6	Uncharacterized conserved protein		
COG1600	28	Uncharacterized Fe-S protein		
COG1601	1	Translation initiation factor 2, beta subunit (eIF-2beta)/eIF-5 N-terminal domain		
COG1605	3	Chorismate mutase		
COG1606	13	ATP-utilizing enzymes of the PP-loop superfamily		
COG1607	18	Acyl-CoA hydrolase		
COG1608	1	Predicted archaeal kinase		
COG1609	73	Transcriptional regulators		
COG1610	10	Uncharacterized conserved protein		
COG1611	34	Predicted Rossmann fold nucleotide-binding protein		
COG1612	27	Uncharacterized protein required for cytochrome oxidase assembly		
COG1613	16	ABC-type sulfate transport system, periplasmic component		
COG1614	6	CO dehydrogenase/acetyl-CoA synthase beta subunit		
COG1615	29	Uncharacterized conserved protein		
COG1619	10	Uncharacterized proteins, homologs of microcin C7 resistance protein MccF		
COG1620	13	L-lactate permease		
COG1621	5	Beta-fructosidases (levanase/invertase)		
COG1622	56	Heme/copper-type cytochrome/quinol oxidases, subunit 2		
COG1623	10	Predicted nucleic-acid-binding protein (contains the HHH domain)		
COG1624	21	Uncharacterized conserved protein		
COG1625	8	Fe-S oxidoreductase, related to NifB/MoaA family		
COG1626	3	Neutral trehalase		
COG1628	2	Uncharacterized conserved protein		

COG1629	191	Outer membrane receptor proteins, mostly Fe transport		
COG1632	1	Ribosomal protein L15E		
COG1633	10	Uncharacterized conserved protein		
COG1635	1	Flavoprotein involved in thiazole biosynthesis		
COG1636	1	Uncharacterized protein conserved in bacteria		
COG1637	3	Predicted nuclease of the RecB family		
COG1638	107	TRAP-type C4-dicarboxylate transport system, periplasmic component		
COG1639	7	Predicted signal transduction protein		
COG1640	51	4-alpha-glucanotransferase		
COG1641	25	Uncharacterized conserved protein		
COG1643	53	HrpA-like helicases		
COG1646	1	Predicted phosphate-binding enzymes, TIM-barrel fold		
COG1647	7	Esterase/lipase		
COG1648	9	Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain)		
COG1649	12	Uncharacterized protein conserved in bacteria		
COG1651	46	Protein-disulfide isomerase		
COG1652	15	Uncharacterized protein containing LysM domain		
COG1653	166	ABC-type sugar transport system, periplasmic component		
COG1654	2	Biotin operon repressor		
COG1656	9	Uncharacterized conserved protein		
COG1657	23	Squalene cyclase		
COG1659	3	Uncharacterized protein, linocin/CFP29 homolog		
COG1660	19	Predicted P-loop-containing kinase		
COG1661	3	Predicted DNA-binding protein with PD1-like DNA-binding motif		
COG1662	1	Transposase and inactivated derivatives, IS1 family		
COG1663	10	Tetraacyldisaccharide-1-P 4'-kinase		
COG1664	24	Integral membrane protein CcmA involved in cell shape determination		
COG1666	13	Uncharacterized protein conserved in bacteria		
COG1668	20	ABC-type Na+ efflux pump, permease component		
COG1669	6	Predicted nucleotidyltransferases		
COG1670	69	Acetyltransferases, including N-acetylases of ribosomal proteins		
COG1671	5	Uncharacterized protein conserved in bacteria		
COG1672	5	Predicted ATPase (AAA+ superfamily)		
COG1674	58	DNA segregation ATPase FtsK/SpoIIIE and related proteins		
COG1677	1	Flagellar hook-basal body protein		
COG1678	24	Putative transcriptional regulator		
COG1679	10	Uncharacterized conserved protein		
COG1680	170	Beta-lactamase class C and other penicillin binding proteins		
COG1682	49	ABC-type polysaccharide/polyol phosphate export systems, permease component		
COG1683	8	Uncharacterized conserved protein		
COG1684	2	Flagellar biosynthesis pathway, component FliR		
COG1686	36	D-alanyl-D-alanine carboxypeptidase		
COG1690	47	Uncharacterized conserved protein		
COG1691	15	NCAIR mutase (PurE)-related proteins		
COG1692	19	Uncharacterized protein conserved in bacteria		
COG1694	25	Predicted pyrophosphatase		
COG1695	32	Predicted transcriptional regulators		
COG1696	19	Predicted membrane protein involved in D-alanine export		
COG1697	6	DNA topoisomerase VI, subunit A		
COG1702	19	Phosphate starvation-inducible protein PhoH, predicted ATPase		
COG1703	27	Putative periplasmic protein kinase ArgK and related GTPases of G3E family		
COG1704	31	Uncharacterized conserved protein		
COG1705	2	Muramidase (flagellum-specific)		
COG1706	4	Flagellar basal-body P-ring protein		
COG1707	1	ACT domain-containing protein		
COG1708	3	Predicted nucleotidyltransferases		
COG1712	7	Predicted dinucleotide-utilizing enzyme		
COG1714	18	Predicted membrane protein/domain		
COG1715	1	Restriction endonuclease		
COG1716	58	FOG: FHA domain		
COG1718	2	Serine/threonine protein kinase involved in cell cycle control		
COG1720	10	Uncharacterized conserved protein		
COG1721	74	Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)		
COG1722	5	Exonuclease VII small subunit		
COG1724	2	Predicted periplasmic or secreted lipoprotein		
COG1725	8	Predicted transcriptional regulators		
COG1726	2	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrA		
COG1727	1	Ribosomal protein L18E		
COG1729	12	Uncharacterized protein conserved in bacteria		
COG1732	25	Periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein)		
COG1733	38	Predicted transcriptional regulators		
COG1734	34	DnaK suppressor protein		
COG1735	10	Predicted metal-dependent hydrolase with the TIM-barrel fold		
COG1737	8	Transcriptional regulators		
COG1738	5	Uncharacterized conserved protein		
COG1740	22	Ni,Fe-hydrogenase I small subunit		
COG1741	40	Pirin-related protein		
COG1743	12	Adenine-specific DNA methylase containing a Zn-ribbon		
COG1744	28	Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein		
COG1746	1	tRNA nucleotidyltransferase (CCA-adding enzyme)		
COG1747	1	Uncharacterized N-terminal domain of the transcription elongation factor GreA		
COG1748	17	Saccharopine dehydrogenase and related proteins		
COG1749	7	Flagellar hook protein FlgE		
COG1750	1	Archaeal serine proteases		

COG1752	81	Predicted esterase of the alpha-beta hydrolase superfamily		
COG1754	11	Uncharacterized C-terminal domain of topoisomerase IA		
COG1755	2	Uncharacterized protein conserved in bacteria		
COG1758	3	DNA-directed RNA polymerase, subunit K/omega		
COG1760	8	L-serine deaminase		
COG1762	17	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)		
COG1763	6	Molybdopterin-guanine dinucleotide biosynthesis protein		
COG1764	28	Predicted redox protein, regulator of disulfide bond formation		
COG1765	21	Predicted redox protein, regulator of disulfide bond formation		
COG1766	14	Flagellar biosynthesis/type III secretory pathway lipoprotein		
COG1770	24	Protease II		
COG1773	3	Rubredoxin		
COG1774	12	Uncharacterized homolog of PSP1		
COG1775	19	Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB		
COG1776	4	Chemotaxis protein CheC, inhibitor of MCP methylation		
COG1778	14	Low specificity phosphatase (HAD superfamily)		
COG1781	1	Aspartate carbamoyltransferase, regulatory subunit		
COG1782	1	Predicted metal-dependent RNase, consists of a metallo-beta-lactamase domain and an RNA-binding KH domain		
COG1783	2	Phage terminase large subunit		
COG1785	10	Alkaline phosphatase		
COG1786	5	Uncharacterized conserved protein		
COG1788	35	Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit		
COG1791	1	Uncharacterized conserved protein, contains double-stranded beta-helix domain		
COG1792	23	Cell shape-determining protein		
COG1793	111	ATP-dependent DNA ligase		
COG1794	15	Aspartate racemase		
COG1795	1	Uncharacterized conserved protein		
COG1796	25	DNA polymerase IV (family X)		
COG1797	16	Cobyrinic acid a,c-diamide synthase		
COG1799	3	Uncharacterized protein conserved in bacteria		
COG1801	61	Uncharacterized conserved protein		
COG1802	40	Transcriptional regulators		
COG1803	5	Methylglyoxal synthase		
COG1804	195	Predicted acyl-CoA transferases/carnitine dehydratase		
COG1805	6	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrB		
COG1806	9	Uncharacterized protein conserved in bacteria		
COG1807	54	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family		
COG1809	6	Uncharacterized conserved protein		
COG1810	2	Uncharacterized protein conserved in archaea		
COG1811	2	Uncharacterized membrane protein, possible Na+ channel or pump		
COG1812	9	Archaeal S-adenosylmethionine synthetase		
COG1814	22	Uncharacterized membrane protein		
COG1815	5	Flagellar basal body protein		
COG1816	34	Adenosine deaminase		
COG1817	3	Uncharacterized protein conserved in archaea		
COG1819	23	Glycosyl transferases, related to UDP-glucuronosyltransferase		
COG1820	12	N-acetylglucosamine-6-phosphate deacetylase		
COG1824	3	Permease, similar to cation transporters		
COG1825	28	Ribosomal protein L25 (general stress protein Ctc)		
COG1826	9	Sec-independent protein secretion pathway components		
COG1828	4	Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component		
COG1830	13	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes		
COG1832	31	Predicted CoA-binding protein		
COG1833	1	Uncharacterized conserved protein		
COG1834	18	N-Dimethylarginine dimethylaminohydrolase		
COG1835	31	Predicted acyltransferases		
COG1836	1	Predicted membrane protein		
COG1837	8	Predicted RNA-binding protein (contains KH domain)		
COG1838	10	Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal domain		
COG1839	5	Uncharacterized conserved protein		
COG1840	57	ABC-type Fe3+ transport system, periplasmic component		
COG1841	5	Ribosomal protein L30/L7E		
COG1842	16	Phage shock protein A (IM30), suppresses sigma54-dependent transcription		
COG1843	6	Flagellar hook capping protein		
COG1845	36	Heme/copper-type cytochrome/quinol oxidase, subunit 3		
COG1846	95	Transcriptional regulators		
COG1847	7	Predicted RNA-binding protein		
COG1848	11	Predicted nucleic acid-binding protein, contains PIN domain		
COG1850	7	Ribulose 1,5-bisphosphate carboxylase, large subunit		
COG1852	2	Uncharacterized conserved protein		
COG1853	41	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family		
COG1856	3	Uncharacterized homolog of biotin synthetase		
COG1858	50	Cytochrome c peroxidase		
COG1859	1	RNA:NAD 2'-phosphotransferase		
COG1861	5	Spore coat polysaccharide biosynthesis protein F, CMP-KDO synthetase homolog		
COG1862	8	Preprotein translocase subunit YajC		
COG1864	5	DNA/RNA endonuclease G, NUC1		
COG1866	20	Phosphoenolpyruvate carboxykinase (ATP)		
COG1868	11	Flagellar motor switch protein		
COG1869	1	ABC-type ribose transport system, auxiliary component		
COG1871	6	Chemotaxis protein; stimulates methylation of MCP proteins		
COG1872	12	Uncharacterized conserved protein		
COG1874	14	Beta-galactosidase		
COG1875	18	Predicted ATPase related to phosphate starvation-inducible protein PhoH		

COG1876	5	D-alanyl-D-alanine carboxypeptidase		
COG1877	13	Trehalose-6-phosphatase		
COG1878	24	Predicted metal-dependent hydrolase		
COG1879	53	ABC-type sugar transport system, periplasmic component		
COG1881	25	Phospholipid-binding protein		
COG1882	20	Pyruvate-formate lyase		
COG1883	5	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit		
COG1884	72	Methylmalonyl-CoA mutase, N-terminal domain/subunit		
COG1886	4	Flagellar motor switch/type III secretory pathway protein		
COG1887	12	Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC		
COG1890	1	Ribosomal protein S3AE		
COG1893	42	Ketopantoate reductase		
COG1894	82	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit		
COG1895	1	Uncharacterized conserved protein related to C-terminal domain of eukaryotic chaperone, SACSIN		
COG1896	1	Predicted hydrolases of HD superfamily		
COG1897	1	Homoserine trans-succinylase		
COG1898	34	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes		
COG1899	18	Deoxyhypusine synthase		
COG1902	70	NADH:flavin oxidoreductases, Old Yellow Enzyme family		
COG1903	4	Cobalamin biosynthesis protein CbiD		
COG1904	6	Glucuronate isomerase		
COG1905	29	NADH:ubiquinone oxidoreductase 24 kD subunit		
COG1908	12	Coenzyme F420-reducing hydrogenase, delta subunit		
COG1910	6	Periplasmic molybdate-binding protein/domain		
COG1911	1	Ribosomal protein L30E		
COG1912	29	Uncharacterized conserved protein		
COG1913	7	Predicted Zn-dependent proteases		
COG1914	49	Mn2+ and Fe2+ transporters of the NRAMP family		
COG1915	10	Uncharacterized conserved protein		
COG1916	2	Uncharacterized homolog of PrgY (pheromone shutdown protein)		
COG1917	29	Uncharacterized conserved protein, contains double-stranded beta-helix domain		
COG1918	2	Fe2+ transport system protein A		
COG1920	5	Uncharacterized conserved protein		
COG1921	35	Selenocysteine synthase [seryl-tRNASer selenium transferase]		
COG1922	15	Teichoic acid biosynthesis proteins		
COG1923	6	Uncharacterized host factor I protein		
COG1924	34	Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)		
COG1925	8	Phosphotransferase system, HPr-related proteins		
COG1926	31	Predicted phosphoribosyltransferases		
COG1928	6	Dolichyl-phosphate-mannose--protein O-mannosyl transferase		
COG1929	12	Glycerate kinase		
COG1932	17	Phosphoserine aminotransferase		
COG1933	1	Archaeal DNA polymerase II, large subunit		
COG1934	8	Uncharacterized protein conserved in bacteria		
COG1937	8	Uncharacterized protein conserved in bacteria		
COG1940	76	Transcriptional regulator/sugar kinase		
COG1941	17	Coenzyme F420-reducing hydrogenase, gamma subunit		
COG1942	5	Uncharacterized protein, 4-oxalocrotonate tautomerase homolog		
COG1943	39	Transposase and inactivated derivatives		
COG1945	5	Uncharacterized conserved protein		
COG1946	12	Acyl-CoA thioesterase		
COG1947	22	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synthase		
COG1949	10	Oligoribonuclease (3'->5' exoribonuclease)		
COG1950	5	Predicted membrane protein		
COG1951	17	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain		
COG1952	7	Preprotein translocase subunit SecB		
COG1953	10	Cytosine/uracil/thiamine/allantoin permeases		
COG1956	7	GAF domain-containing protein		
COG1957	11	Inosine-uridine nucleoside N-ribohydrolase		
COG1959	37	Predicted transcriptional regulator		
COG1960	474	Acyl-CoA dehydrogenases		
COG1961	26	Site-specific recombinases, DNA invertase Pin homologs		
COG1962	1	Tetrahydromethanopterin S-methyltransferase, subunit H		
COG1963	4	Uncharacterized protein conserved in bacteria		
COG1964	18	Predicted Fe-S oxidoreductases		
COG1965	1	Protein implicated in iron transport, frataxin homolog		
COG1966	25	Carbon starvation protein, predicted membrane protein		
COG1968	36	Uncharacterized bacitracin resistance protein		
COG1969	8	Ni,Fe-hydrogenase I cytochrome b subunit		
COG1970	15	Large-conductance mechanosensitive channel		
COG1971	2	Predicted membrane protein		
COG1972	17	Nucleoside permease		
COG1974	28	SOS-response transcriptional repressors (RecA-mediated autopeptidases)		
COG1975	44	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family		
COG1977	10	Molybdopterin converting factor, small subunit		
COG1979	1	Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family		
COG1980	8	Archaeal fructose 1,6-bisphosphatase		
COG1981	5	Predicted membrane protein		
COG1982	36	Arginine/lysine/ornithine decarboxylases		
COG1983	9	Putative stress-responsive transcriptional regulator		
COG1984	10	Allophanate hydrolase subunit 2		
COG1985	27	Pyrimidine reductase, riboflavin biosynthesis		
COG1988	1	Predicted membrane-bound metal-dependent hydrolases		
COG1989	24	Type II secretory pathway, prepilin signal peptidase PulO and related peptidases		

COG1990	3	Uncharacterized conserved protein		
COG1993	20	Uncharacterized conserved protein		
COG1994	29	Zn-dependent proteases		
COG1995	31	Pyridoxal phosphate biosynthesis protein		
COG1997	1	Ribosomal protein L37AE/L43A		
COG1999	47	Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems		
COG2000	1	Predicted Fe-S protein		
COG2001	24	Uncharacterized protein conserved in bacteria		
COG2002	3	Regulators of stationary/sporulation gene expression		
COG2003	28	DNA repair proteins		
COG2004	1	Ribosomal protein S24E		
COG2005	8	N-terminal domain of molybdenum-binding protein		
COG2006	12	Uncharacterized conserved protein		
COG2007	3	Ribosomal protein S8E		
COG2008	30	Threonine aldolase		
COG2009	12	Succinate dehydrogenase/fumarate reductase, cytochrome b subunit		
COG2010	100	Cytochrome c, mono- and diheme variants		
COG2013	16	Uncharacterized conserved protein		
COG2015	3	Alkyl sulfatase and related hydrolases		
COG2017	23	Galactose mutarotase and related enzymes		
COG2018	5	Uncharacterized distant relative of homeotic protein bithoraxoid		
COG2020	46	Putative protein-S-isoprenylcysteine methyltransferase		
COG2021	30	Homoserine acetyltransferase		
COG2022	21	Uncharacterized enzyme of thiazole biosynthesis		
COG2025	29	Electron transfer flavoprotein, alpha subunit		
COG2026	6	Cytotoxic translational repressor of toxin-antitoxin stability system		
COG2027	25	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 4)		
COG2030	76	Acyl dehydratase		
COG2031	4	Short chain fatty acids transporter		
COG2032	3	Cu/Zn superoxide dismutase		
COG2036	1	Histones H3 and H4		
COG2037	6	Formylmethanofuran:tetrahydromethanopterin formyltransferase		
COG2038	5	NaMN:DMB phosphoribosyltransferase		
COG2039	3	Pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)		
COG2040	12	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)		
COG2041	73	Sulfite oxidase and related enzymes		
COG2043	3	Uncharacterized protein conserved in archaea		
COG2044	2	Predicted peroxiredoxins		
COG2045	11	Phosphosulfolactate phosphohydrolase and related enzymes		
COG2046	16	ATP sulfurylase (sulfate adenylyltransferase)		
COG2048	22	Heterodisulfide reductase, subunit B		
COG2049	6	Allophanate hydrolase subunit 1		
COG2050	52	Uncharacterized protein, possibly involved in aromatic compounds catabolism		
COG2054	1	Uncharacterized archaeal kinase related to aspartokinases, uridylate kinases		
COG2055	37	Malate/L-lactate dehydrogenases		
COG2057	28	Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit		
COG2059	47	Chromate transport protein ChrA		
COG2060	18	K+-transporting ATPase, A chain		
COG2062	12	Phosphohistidine phosphatase SixA		
COG2063	2	Flagellar basal body L-ring protein		
COG2064	16	Flp pilus assembly protein TadC		
COG2065	13	Pyrimidine operon attenuation protein/uracil phosphoribosyltransferase		
COG2066	6	Glutaminase		
COG2067	22	Long-chain fatty acid transport protein		
COG2068	12	Uncharacterized MobA-related protein		
COG2069	1	CO dehydrogenase/acetyl-CoA synthase delta subunit (corrinoid Fe-S protein)		
COG2070	67	Dioxygenases related to 2-nitropropane dioxygenase		
COG2071	19	Predicted glutamine amidotransferases		
COG2072	90	Predicted flavoprotein involved in K+ transport		
COG2073	1	Cobalamin biosynthesis protein CbiG		
COG2074	6	2-phosphoglycerate kinase		
COG2075	1	Ribosomal protein L24E		
COG2076	4	Membrane transporters of cations and cationic drugs		
COG2077	6	Peroxiredoxin		
COG2078	9	Uncharacterized conserved protein		
COG2079	82	Uncharacterized protein involved in propionate catabolism		
COG2080	43	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs		
COG2081	9	Predicted flavoproteins		
COG2082	4	Precorrin isomerase		
COG2084	106	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases		
COG2085	27	Predicted dinucleotide-binding enzymes		
COG2086	32	Electron transfer flavoprotein, beta subunit		
COG2087	7	Adenosyl cobinamide kinase/adenosyl cobinamide phosphate guanylyltransferase		
COG2088	4	Uncharacterized protein, involved in the regulation of septum location		
COG2089	14	Sialic acid synthase		
COG2091	3	Phosphopantetheinyl transferase		
COG2094	14	3-methyladenine DNA glycosylase		
COG2095	18	Multiple antibiotic transporter		
COG2096	16	Uncharacterized conserved protein		
COG2097	1	Ribosomal protein L31E		
COG2099	2	Precorrin-6x reductase		
COG2102	3	Predicted ATPases of PP-loop superfamily		
COG2103	17	Predicted sugar phosphate isomerase		
COG2104	5	Sulfur transfer protein involved in thiamine biosynthesis		

COG2107	18	Predicted periplasmic solute-binding protein		
COG2109	8	ATP:corrinoid adenosyltransferase		
COG2110	22	Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1		
COG2113	1	ABC-type proline/glycine betaine transport systems, periplasmic components		
COG2114	173	Adenylate cyclase, family 3 (some proteins contain HAMP domain)		
COG2115	9	Xylose isomerase		
COG2116	16	Formate/nitrite family of transporters		
COG2119	9	Predicted membrane protein		
COG2120	59	Uncharacterized proteins, LmbE homologs		
COG2121	5	Uncharacterized protein conserved in bacteria		
COG2122	1	Uncharacterized conserved protein		
COG2124	150	Cytochrome P450		
COG2125	1	Ribosomal protein S6E (S10)		
COG2127	6	Uncharacterized conserved protein		
COG2128	38	Uncharacterized conserved protein		
COG2129	25	Predicted phosphoesterases, related to the Icc protein		
COG2130	19	Putative NADP-dependent oxidoreductases		
COG2131	11	Deoxycytidylate deaminase		
COG2132	103	Putative multicopper oxidases		
COG2133	66	Glucose/sorbosone dehydrogenases		
COG2135	14	Uncharacterized conserved protein		
COG2137	9	Uncharacterized protein conserved in bacteria		
COG2138	6	Uncharacterized conserved protein		
COG2139	2	Ribosomal protein L21E		
COG2140	3	Thermophilic glucose-6-phosphate isomerase and related metalloenzymes		
COG2141	256	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases		
COG2142	5	Succinate dehydrogenase, hydrophobic anchor subunit		
COG2143	1	Thioredoxin-related protein		
COG2145	2	Hydroxyethylthiazole kinase, sugar kinase family		
COG2146	35	Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases		
COG2147	1	Ribosomal protein L19E		
COG2148	42	Sugar transferases involved in lipopolysaccharide synthesis		
COG2149	3	Predicted membrane protein		
COG2151	28	Predicted metal-sulfur cluster biosynthetic enzyme		
COG2152	9	Predicted glycosylase		
COG2153	2	Predicted acyltransferase		
COG2154	19	Pterin-4a-carbinolamine dehydratase		
COG2155	1	Uncharacterized conserved protein		
COG2156	10	K+-transporting ATPase, c chain		
COG2159	131	Predicted metal-dependent hydrolase of the TIM-barrel fold		
COG2160	7	L-arabinose isomerase		
COG2161	1	Antitoxin of toxin-antitoxin stability system		
COG2162	10	Arylamine N-acetyltransferase		
COG2163	2	Ribosomal protein L14E/L6E/L27E		
COG2164	3	Uncharacterized conserved protein		
COG2165	25	Type II secretory pathway, pseudopilin PulG		
COG2166	3	SufE protein probably involved in Fe-S center assembly		
COG2168	2	Uncharacterized conserved protein involved in oxidation of intracellular sulfur		
COG2169	17	Adenosine deaminase		
COG2170	23	Uncharacterized conserved protein		
COG2171	18	Tetrahydrodipicolinate N-succinyltransferase		
COG2172	28	Anti-sigma regulatory factor (Ser/Thr protein kinase)		
COG2173	4	D-alanyl-D-alanine dipeptidase		
COG2175	45	Probable taurine catabolism dioxygenase		
COG2176	10	DNA polymerase III, alpha subunit (gram-positive type)		
COG2177	15	Cell division protein		
COG2178	1	Predicted RNA-binding protein of the translin family		
COG2179	1	Predicted hydrolase of the HAD superfamily		
COG2180	4	Nitrate reductase delta subunit		
COG2181	4	Nitrate reductase gamma subunit		
COG2182	6	Maltose-binding periplasmic proteins/domains		
COG2183	10	Transcriptional accessory protein		
COG2184	1	Protein involved in cell division		
COG2185	14	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-binding)		
COG2186	22	Transcriptional regulators		
COG2187	14	Uncharacterized protein conserved in bacteria		
COG2188	31	Transcriptional regulators		
COG2189	16	Adenine specific DNA methylase Mod		
COG2190	3	Phosphotransferase system IIA components		
COG2191	3	Formylmethanofuran dehydrogenase subunit E		
COG2192	37	Predicted carbamoyl transferase, NodU family		
COG2193	19	Bacterioferritin (cytochrome b1)		
COG2194	1	Predicted membrane-associated, metal-dependent hydrolase		
COG2195	34	Di- and tripeptidases		
COG2197	245	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain		
COG2198	4	FOG: HPt domain		
COG2199	189	FOG: GGDEF domain		
COG2200	127	FOG: EAL domain		
COG2201	63	Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain		
COG2202	390	FOG: PAS/PAC domain		
COG2203	147	FOG: GAF domain		
COG2204	282	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains		
COG2205	54	Osmosensitive K+ channel histidine kinase		
COG2206	101	HD-GYP domain		

COG2207	57	AraC-type DNA-binding domain-containing proteins		
COG2208	77	Serine phosphatase RsbU, regulator of sigma subunit		
COG2209	1	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrE		
COG2210	12	Uncharacterized conserved protein		
COG2211	12	Na+/melibiose symporter and related transporters		
COG2212	1	Multisubunit Na+/H+ antiporter, MnhF subunit		
COG2213	3	Phosphotransferase system, mannitol-specific IIBC component		
COG2214	23	DnaJ-class molecular chaperone		
COG2215	5	ABC-type uncharacterized transport system, permease component		
COG2216	19	High-affinity K+ transport system, ATPase chain B		
COG2217	145	Cation transport ATPase		
COG2220	63	Predicted Zn-dependent hydrolases of the beta-lactamase fold		
COG2221	7	Dissimilatory sulfite reductase (desulfoviridin), alpha and beta subunits		
COG2222	15	Predicted phosphosugar isomerases		
COG2223	27	Nitrate/nitrite transporter		
COG2224	12	Isocitrate lyase		
COG2225	22	Malate synthase		
COG2226	49	Methylase involved in ubiquinone/menaquinone biosynthesis		
COG2227	20	2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1,4-benzoquinol methylase		
COG2230	41	Cyclopropane fatty acid synthase and related methyltransferases		
COG2231	3	Uncharacterized protein related to Endonuclease III		
COG2232	3	Predicted ATP-dependent carboligase related to biotin carboxylase		
COG2233	17	Xanthine/uracil permeases		
COG2234	110	Predicted aminopeptidases		
COG2235	10	Arginine deiminase		
COG2236	4	Predicted phosphoribosyltransferases		
COG2239	42	Mg/Co/Ni transporter MgtE (contains CBS domain)		
COG2240	1	Pyridoxal/pyridoxine/pyridoxamine kinase		
COG2241	4	Precorrin-6B methylase 1		
COG2242	2	Precorrin-6B methylase 2		
COG2243	1	Precorrin-2 methylase		
COG2244	30	Membrane protein involved in the export of O-antigen and teichoic acid		
COG2246	11	Predicted membrane protein		
COG2249	7	Putative NADPH-quinone reductase (modulator of drug activity B)		
COG2251	8	Predicted nuclease (RecB family)		
COG2252	24	Permeases		
COG2253	1	Uncharacterized conserved protein		
COG2255	31	Holliday junction resolvasome, helicase subunit		
COG2256	29	ATPase related to the helicase subunit of the Holliday junction resolvase		
COG2257	1	Uncharacterized homolog of the cytoplasmic domain of flagellar protein FhlB		
COG2258	11	Uncharacterized protein conserved in bacteria		
COG2259	35	Predicted membrane protein		
COG2261	8	Predicted membrane protein		
COG2262	24	GTPases		
COG2263	1	Predicted RNA methylase		
COG2264	21	Ribosomal protein L11 methylase		
COG2265	48	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase		
COG2267	17	Lysophospholipase		
COG2268	17	Uncharacterized protein conserved in bacteria		
COG2269	4	Truncated, possibly inactive, lysyl-tRNA synthetase (class II)		
COG2270	19	Permeases of the major facilitator superfamily		
COG2271	3	Sugar phosphate permease		
COG2272	16	Carboxylesterase type B		
COG2273	13	Beta-glucanase/Beta-glucan synthetase		
COG2274	26	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain		
COG2301	34	Citrate lyase beta subunit		
COG2303	190	Choline dehydrogenase and related flavoproteins		
COG2304	61	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain		
COG2306	2	Uncharacterized conserved protein		
COG2307	13	Uncharacterized protein conserved in bacteria		
COG2308	19	Uncharacterized conserved protein		
COG2309	39	Leucyl aminopeptidase (aminopeptidase T)		
COG2311	3	Predicted membrane protein		
COG2312	11	Erythromycin esterase homolog		
COG2313	13	Uncharacterized enzyme involved in pigment biosynthesis		
COG2314	3	Predicted membrane protein		
COG2315	2	Uncharacterized protein conserved in bacteria		
COG2316	7	Predicted hydrolase (HD superfamily)		
COG2317	20	Zn-dependent carboxypeptidase		
COG2318	13	Uncharacterized protein conserved in bacteria		
COG2319	81	FOG: WD40 repeat		
COG2320	4	Uncharacterized conserved protein		
COG2321	12	Predicted metalloprotease		
COG2323	13	Predicted membrane protein		
COG2324	3	Predicted membrane protein		
COG2326	31	Uncharacterized conserved protein		
COG2327	2	Uncharacterized conserved protein		
COG2329	9	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides		
COG2331	8	Uncharacterized protein conserved in bacteria		
COG2332	10	Cytochrome c-type biogenesis protein CcmE		
COG2333	29	Predicted hydrolase (metallo-beta-lactamase superfamily)		
COG2334	15	Putative homoserine kinase type II (protein kinase fold)		
COG2335	10	Secreted and surface protein containing fasciclin-like repeats		
COG2336	1	Growth regulator		

COG2337	5	Growth inhibitor		
COG2339	4	Predicted membrane protein		
COG2340	14	Uncharacterized protein with SCP/PR1 domains		
COG2343	15	Uncharacterized protein conserved in bacteria		
COG2344	7	AT-rich DNA-binding protein		
COG2345	16	Predicted transcriptional regulator		
COG2346	12	Truncated hemoglobins		
COG2348	5	Uncharacterized protein involved in methicillin resistance		
COG2350	1	Uncharacterized protein conserved in bacteria		
COG2351	5	Transthyretin-like protein		
COG2352	39	Phosphoenolpyruvate carboxylase		
COG2353	47	Uncharacterized conserved protein		
COG2354	2	Uncharacterized protein conserved in bacteria		
COG2355	44	Zn-dependent dipeptidase, microsomal dipeptidase homolog		
COG2356	2	Endonuclease I		
COG2358	41	TRAP-type uncharacterized transport system, periplasmic component		
COG2360	12	Leu/Phe-tRNA-protein transferase		
COG2361	2	Uncharacterized conserved protein		
COG2362	13	D-aminopeptidase		
COG2363	5	Uncharacterized small membrane protein		
COG2364	4	Predicted membrane protein		
COG2365	4	Protein tyrosine/serine phosphatase		
COG2366	78	Protein related to penicillin acylase		
COG2367	14	Beta-lactamase class A		
COG2368	31	Aromatic ring hydroxylase		
COG2369	1	Uncharacterized protein, homolog of phage Mu protein gp30		
COG2370	1	Hydrogenase/urease accessory protein		
COG2371	2	Urease accessory protein UreE		
COG2372	4	Uncharacterized protein, homolog of Cu resistance protein CopC		
COG2373	31	Large extracellular alpha-helical protein		
COG2374	15	Predicted extracellular nuclease		
COG2375	2	Siderophore-interacting protein		
COG2376	13	Dihydroxyacetone kinase		
COG2377	23	Predicted molecular chaperone distantly related to HSP70-fold metalloproteases		
COG2378	24	Predicted transcriptional regulator		
COG2379	29	Putative glycerate kinase		
COG2382	7	Enterochelin esterase and related enzymes		
COG2385	22	Sporulation protein and related proteins		
COG2386	15	ABC-type transport system involved in cytochrome c biogenesis, permease component		
COG2388	3	Predicted acetyltransferase		
COG2389	1	Uncharacterized metal-binding protein		
COG2390	1	Transcriptional regulator, contains sigma factor-related N-terminal domain		
COG2391	17	Predicted transporter component		
COG2402	3	Predicted nucleic acid-binding protein, contains PIN domain		
COG2403	14	Predicted GTPase		
COG2407	10	L-fucose isomerase and related proteins		
COG2409	80	Predicted drug exporters of the RND superfamily		
COG2411	1	Uncharacterized conserved protein		
COG2414	69	Aldehyde:ferredoxin oxidoreductase		
COG2421	36	Predicted acetamidase/formamidase		
COG2423	39	Predicted ornithine cyclodeaminase, mu-crystallin homolog		
COG2425	3	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain		
COG2442	12	Uncharacterized conserved protein		
COG2445	1	Uncharacterized conserved protein		
COG2452	3	Predicted site-specific integrase-resolvase		
COG2453	3	Predicted protein-tyrosine phosphatase		
COG2461	3	Uncharacterized conserved protein		
COG2502	6	Asparagine synthetase A		
COG2503	2	Predicted secreted acid phosphatase		
COG2508	16	Regulator of polyketide synthase expression		
COG2509	10	Uncharacterized FAD-dependent dehydrogenases		
COG2513	56	PEP phosphonomutase and related enzymes		
COG2514	17	Predicted ring-cleavage extradiol dioxygenase		
COG2515	12	1-aminocyclopropane-1-carboxylate deaminase		
COG2516	5	Biotin synthase-related enzyme		
COG2518	39	Protein-L-isoaspartate carboxylmethyltransferase		
COG2519	6	tRNA(1-methyladenosine) methyltransferase and related methyltransferases		
COG2521	1	Predicted archaeal methyltransferase		
COG2602	1	Beta-lactamase class D		
COG2603	3	Predicted ATPase		
COG2605	8	Predicted kinase related to galactokinase and mevalonate kinase		
COG2606	27	Uncharacterized conserved protein		
COG2607	9	Predicted ATPase (AAA+ superfamily)		
COG2608	8	Copper chaperone		
COG2609	43	Pyruvate dehydrogenase complex, dehydrogenase (E1) component		
COG2610	7	H+/gluconate symporter and related permeases		
COG2703	11	Hemerythrin		
COG2704	4	Anaerobic C4-dicarboxylate transporter		
COG2706	9	3-carboxymuconate cyclase		
COG2710	6	Nitrogenase molybdenum-iron protein, alpha and beta chains		
COG2715	6	Uncharacterized membrane protein, required for spore maturation in B.subtilis.		
COG2716	1	Glycine cleavage system regulatory protein		
COG2717	7	Predicted membrane protein		
COG2718	7	Uncharacterized conserved protein		

COG2719	10	Uncharacterized conserved protein		
COG2720	11	Uncharacterized vancomycin resistance protein		
COG2721	27	Altronate dehydratase		
COG2723	34	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase		
COG2730	8	Endoglucanase		
COG2733	9	Predicted membrane protein		
COG2738	3	Predicted Zn-dependent protease		
COG2739	1	Uncharacterized protein conserved in bacteria		
COG2740	5	Predicted nucleic-acid-binding protein implicated in transcription termination		
COG2746	3	Aminoglycoside N3'-acetyltransferase		
COG2755	28	Lysophospholipase L1 and related esterases		
COG2759	22	Formyltetrahydrofolate synthetase		
COG2761	14	Predicted dithiol-disulfide isomerase involved in polyketide biosynthesis		
COG2764	25	Uncharacterized protein conserved in bacteria		
COG2766	31	Putative Ser protein kinase		
COG2768	3	Uncharacterized Fe-S center protein		
COG2770	23	FOG: HAMP domain		
COG2771	54	DNA-binding HTH domain-containing proteins		
COG2801	230	Transposase and inactivated derivatives		
COG2802	11	Uncharacterized protein, similar to the N-terminal domain of Lon protease		
COG2804	84	Type II secretory pathway, ATPase PulE/Tfp pilus assembly pathway, ATPase PilB		
COG2805	62	Tfp pilus assembly protein, pilus retraction ATPase PilT		
COG2807	6	Cyanate permease		
COG2808	8	Transcriptional regulator		
COG2812	40	DNA polymerase III, gamma/tau subunits		
COG2813	2	16S RNA G1207 methylase RsmC		
COG2814	6	Arabinose efflux permease		
COG2815	14	Uncharacterized protein conserved in bacteria		
COG2816	13	NTP pyrophosphohydrolases containing a Zn-finger, probably nucleic-acid-binding		
COG2818	10	3-methyladenine DNA glycosylase		
COG2819	5	Predicted hydrolase of the alpha/beta superfamily		
COG2820	3	Uridine phosphorylase		
COG2821	13	Membrane-bound lytic murein transglycosylase		
COG2822	2	Predicted periplasmic lipoprotein involved in iron transport		
COG2823	18	Predicted periplasmic or secreted lipoprotein		
COG2825	4	Outer membrane protein		
COG2826	17	Transposase and inactivated derivatives, IS30 family		
COG2827	8	Predicted endonuclease containing a URI domain		
COG2828	9	Uncharacterized protein conserved in bacteria		
COG2829	8	Outer membrane phospholipase A		
COG2831	20	Hemolysin activation/secretion protein		
COG2832	1	Uncharacterized protein conserved in bacteria		
COG2833	1	Uncharacterized protein conserved in bacteria		
COG2834	11	Outer membrane lipoprotein-sorting protein		
COG2835	2	Uncharacterized conserved protein		
COG2836	7	Uncharacterized conserved protein		
COG2837	17	Predicted iron-dependent peroxidase		
COG2838	10	Monomeric isocitrate dehydrogenase		
COG2840	4	Uncharacterized protein conserved in bacteria		
COG2843	26	Putative enzyme of poly-gamma-glutamate biosynthesis (capsule formation)		
COG2844	45	UTP:GlnB (protein PII) uridylyltransferase		
COG2845	1	Uncharacterized protein conserved in bacteria		
COG2846	4	Regulator of cell morphogenesis and NO signaling		
COG2847	6	Uncharacterized protein conserved in bacteria		
COG2848	3	Uncharacterized conserved protein		
COG2849	4	Uncharacterized protein conserved in bacteria		
COG2850	10	Uncharacterized conserved protein		
COG2852	3	Uncharacterized protein conserved in bacteria		
COG2853	6	Surface lipoprotein		
COG2854	15	ABC-type transport system involved in resistance to organic solvents, auxiliary component		
COG2855	8	Predicted membrane protein		
COG2856	3	Predicted Zn peptidase		
COG2857	13	Cytochrome c1		
COG2860	12	Predicted membrane protein		
COG2861	2	Uncharacterized protein conserved in bacteria		
COG2862	3	Predicted membrane protein		
COG2863	61	Cytochrome c553		
COG2864	16	Cytochrome b subunit of formate dehydrogenase		
COG2865	4	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafe		
COG2866	20	Predicted carboxypeptidase		
COG2867	3	Oligoketide cyclase/lipid transport protein		
COG2869	2	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrC		
COG2870	43	ADP-heptose synthase, bifunctional sugar kinase/adenylyltransferase		
COG2871	3	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrF		
COG2872	14	Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain		
COG2873	29	O-acetylhomoserine sulfhydrylase		
COG2875	4	Precorrin-4 methylase		
COG2876	30	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase		
COG2877	19	3-deoxy-D-manno-octulosonic acid (KDO) 8-phosphate synthase		
COG2878	6	Predicted NADH:ubiquinone oxidoreductase, subunit RnfB		
COG2884	8	Predicted ATPase involved in cell division		
COG2885	71	Outer membrane protein and related peptidoglycan-associated (lipo)proteins		
COG2887	16	RecB family exonuclease		
COG2890	36	Methylase of polypeptide chain release factors		

COG2891	3	Cell shape-determining protein		
COG2893	10	Phosphotransferase system, mannose/fructose-specific component IIA		
COG2894	5	Septum formation inhibitor-activating ATPase		
COG2895	28	GTPases - Sulfate adenylate transferase subunit 1		
COG2896	28	Molybdenum cofactor biosynthesis enzyme		
COG2897	38	Rhodanese-related sulfurtransferase		
COG2898	28	Uncharacterized conserved protein		
COG2899	2	Uncharacterized protein conserved in bacteria		
COG2901	1	Factor for inversion stimulation Fis, transcriptional activator		
COG2902	36	NAD-specific glutamate dehydrogenase		
COG2905	26	Predicted signal-transduction protein containing cAMP-binding and CBS domains		
COG2907	16	Predicted NAD/FAD-binding protein		
COG2908	9	Uncharacterized protein conserved in bacteria		
COG2909	49	ATP-dependent transcriptional regulator		
COG2910	1	Putative NADH-flavin reductase		
COG2911	9	Uncharacterized protein conserved in bacteria		
COG2912	18	Uncharacterized conserved protein		
COG2913	6	Small protein A (tmRNA-binding)		
COG2914	2	Uncharacterized protein conserved in bacteria		
COG2917	8	Intracellular septation protein A		
COG2918	6	Gamma-glutamylcysteine synthetase		
COG2919	3	Septum formation initiator		
COG2920	14	Dissimilatory sulfite reductase (desulfoviridin), gamma subunit		
COG2921	2	Uncharacterized conserved protein		
COG2922	1	Uncharacterized protein conserved in bacteria		
COG2923	1	Uncharacterized protein involved in the oxidation of intracellular sulfur		
COG2924	3	Fe-S cluster protector protein		
COG2927	6	DNA polymerase III, chi subunit		
COG2928	8	Uncharacterized conserved protein		
COG2929	7	Uncharacterized protein conserved in bacteria		
COG2930	11	Uncharacterized conserved protein		
COG2931	80	RTX toxins and related Ca2+-binding proteins		
COG2933	3	Predicted SAM-dependent methyltransferase		
COG2935	7	Putative arginyl-tRNA:protein arginylyltransferase		
COG2936	97	Predicted acyl esterases		
COG2937	12	Glycerol-3-phosphate O-acyltransferase		
COG2938	2	Uncharacterized conserved protein		
COG2939	19	Carboxypeptidase C (cathepsin A)		
COG2940	6	Proteins containing SET domain		
COG2941	3	Ubiquinone biosynthesis protein COQ7		
COG2942	3	N-acyl-D-glucosamine 2-epimerase		
COG2943	4	Membrane glycosyltransferase		
COG2944	2	Predicted transcriptional regulator		
COG2945	12	Predicted hydrolase of the alpha/beta superfamily		
COG2946	1	Putative phage replication protein RstA		
COG2947	12	Uncharacterized conserved protein		
COG2949	1	Uncharacterized membrane protein		
COG2951	21	Membrane-bound lytic murein transglycosylase B		
COG2954	2	Uncharacterized protein conserved in bacteria		
COG2956	9	Predicted N-acetylglucosaminyl transferase		
COG2957	12	Peptidylarginine deiminase and related enzymes		
COG2959	3	Uncharacterized enzyme of heme biosynthesis		
COG2960	1	Uncharacterized protein conserved in bacteria		
COG2961	2	Protein involved in catabolism of external DNA		
COG2962	10	Predicted permeases		
COG2963	18	Transposase and inactivated derivatives		
COG2965	4	Primosomal replication protein N		
COG2966	5	Uncharacterized conserved protein		
COG2967	4	Uncharacterized protein affecting Mg2+/Co2+ transport		
COG2968	9	Uncharacterized conserved protein		
COG2969	4	Stringent starvation protein B		
COG2971	7	Predicted N-acetylglucosamine kinase		
COG2972	13	Predicted signal transduction protein with a C-terminal ATPase domain		
COG2975	1	Uncharacterized protein conserved in bacteria		
COG2976	4	Uncharacterized protein conserved in bacteria		
COG2977	2	Phosphopantetheinyl transferase component of siderophore synthetase		
COG2978	2	Putative p-aminobenzoyl-glutamate transporter		
COG2980	5	Rare lipoprotein B		
COG2982	17	Uncharacterized protein involved in outer membrane biogenesis		
COG2983	3	Uncharacterized conserved protein		
COG2984	46	ABC-type uncharacterized transport system, periplasmic component		
COG2985	4	Predicted permease		
COG2986	31	Histidine ammonia-lyase		
COG2987	17	Urocanate hydratase		
COG2989	20	Uncharacterized protein conserved in bacteria		
COG2993	10	Cbb3-type cytochrome oxidase, cytochrome c subunit		
COG2995	5	Uncharacterized paraquat-inducible protein A		
COG2998	8	ABC-type tungstate transport system, permease component		
COG3000	25	Sterol desaturase		
COG3001	4	Fructosamine-3-kinase		
COG3002	6	Uncharacterized protein conserved in bacteria		
COG3004	15	Na+/H+ antiporter		
COG3005	9	Nitrate/TMAO reductases, membrane-bound tetraheme cytochrome c subunit		
COG3008	8	Paraquat-inducible protein B		

COG3011	1	Uncharacterized protein conserved in bacteria		
COG3012	1	Uncharacterized protein conserved in bacteria		
COG3014	1	Uncharacterized protein conserved in bacteria		
COG3016	6	Uncharacterized iron-regulated protein		
COG3017	3	Outer membrane lipoprotein involved in outer membrane biogenesis		
COG3019	7	Predicted metal-binding protein		
COG3021	1	Uncharacterized protein conserved in bacteria		
COG3023	9	Negative regulator of beta-lactamase expression		
COG3024	2	Uncharacterized protein conserved in bacteria		
COG3025	5	Uncharacterized conserved protein		
COG3026	9	Negative regulator of sigma E activity		
COG3027	7	Uncharacterized protein conserved in bacteria		
COG3028	2	Uncharacterized protein conserved in bacteria		
COG3029	5	Fumarate reductase subunit C		
COG3030	5	Protein affecting phage T7 exclusion by the F plasmid		
COG3031	1	Type II secretory pathway, component PulC		
COG3033	15	Tryptophanase		
COG3034	10	Uncharacterized protein conserved in bacteria		
COG3037	1	Uncharacterized protein conserved in bacteria		
COG3038	4	Cytochrome B561		
COG3039	19	Transposase and inactivated derivatives, IS5 family		
COG3040	2	Bacterial lipocalin		
COG3041	1	Uncharacterized protein conserved in bacteria		
COG3043	6	Nitrate reductase cytochrome c-type subunit		
COG3046	2	Uncharacterized protein related to deoxyribodipyrimidine photolyase		
COG3051	1	Citrate lyase, alpha subunit		
COG3058	5	Uncharacterized protein involved in formate dehydrogenase formation		
COG3063	9	Tfp pilus assembly protein PilF		
COG3065	2	Starvation-inducible outer membrane lipoprotein		
COG3069	1	C4-dicarboxylate transporter		
COG3070	3	Regulator of competence-specific genes		
COG3071	3	Uncharacterized enzyme of heme biosynthesis		
COG3073	1	Negative regulator of sigma E activity		
COG3075	1	Anaerobic glycerol-3-phosphate dehydrogenase		
COG3080	5	Fumarate reductase subunit D		
COG3081	1	Nucleoid-associated protein		
COG3083	4	Predicted hydrolase of alkaline phosphatase superfamily		
COG3087	1	Cell division protein		
COG3088	11	Uncharacterized protein involved in biosynthesis of c-type cytochromes		
COG3090	28	TRAP-type C4-dicarboxylate transport system, small permease component		
COG3093	11	Plasmid maintenance system antidote protein		
COG3094	2	Uncharacterized protein conserved in bacteria		
COG3103	1	SH3 domain protein		
COG3104	27	Dipeptide/tripeptide permease		
COG3107	4	Putative lipoprotein		
COG3108	4	Uncharacterized protein conserved in bacteria		
COG3113	1	Predicted NTP binding protein (contains STAS domain)		
COG3116	1	Cell division protein		
COG3117	2	Uncharacterized protein conserved in bacteria		
COG3118	10	Thioredoxin domain-containing protein		
COG3119	117	Arylsulfatase A and related enzymes		
COG3121	4	P pilus assembly protein, chaperone PapD		
COG3123	1	Uncharacterized protein conserved in bacteria		
COG3124	1	Uncharacterized protein conserved in bacteria		
COG3126	2	Uncharacterized protein conserved in bacteria		
COG3127	19	Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, permease component		
COG3128	1	Uncharacterized iron-regulated protein		
COG3131	3	Periplasmic glucans biosynthesis protein		
COG3132	12	Uncharacterized protein conserved in bacteria		
COG3134	1	Predicted outer membrane lipoprotein		
COG3135	6	Uncharacterized protein involved in benzoate metabolism		
COG3137	1	Putative salt-induced outer membrane protein		
COG3138	3	Arginine/ornithine N-succinyltransferase beta subunit		
COG3142	6	Uncharacterized protein involved in copper resistance		
COG3143	1	Chemotaxis protein		
COG3144	1	Flagellar hook-length control protein		
COG3145	10	Alkylated DNA repair protein		
COG3146	9	Uncharacterized protein conserved in bacteria		
COG3147	2	Uncharacterized protein conserved in bacteria		
COG3148	1	Uncharacterized conserved protein		
COG3150	5	Predicted esterase		
COG3152	1	Predicted membrane protein		
COG3153	5	Predicted acetyltransferase		
COG3154	2	Putative lipid carrier protein		
COG3155	2	Uncharacterized protein involved in an early stage of isoprenoid biosynthesis		
COG3156	10	Type II secretory pathway, component PulK		
COG3157	1	Hemolysin-coregulated protein (uncharacterized)		
COG3158	37	K+ transporter		
COG3159	5	Uncharacterized protein conserved in bacteria		
COG3162	2	Predicted membrane protein		
COG3164	22	Predicted membrane protein		
COG3165	5	Uncharacterized protein conserved in bacteria		
COG3166	6	Tfp pilus assembly protein PilN		
COG3167	9	Tfp pilus assembly protein PilO		

COG3168	4	Tfp pilus assembly protein PilP		
COG3169	3	Uncharacterized protein conserved in bacteria		
COG3170	17	Tfp pilus assembly protein FimV		
COG3172	1	Predicted ATPase/kinase involved in NAD metabolism		
COG3173	37	Predicted aminoglycoside phosphotransferase		
COG3174	8	Predicted membrane protein		
COG3175	6	Cytochrome oxidase assembly factor		
COG3176	7	Putative hemolysin		
COG3177	12	Uncharacterized conserved protein		
COG3178	16	Predicted phosphotransferase related to Ser/Thr protein kinases		
COG3179	1	Predicted chitinase		
COG3180	8	Putative ammonia monooxygenase		
COG3181	791	Uncharacterized protein conserved in bacteria		
COG3182	3	Uncharacterized iron-regulated membrane protein		
COG3184	2	Uncharacterized protein conserved in bacteria		
COG3185	14	4-hydroxyphenylpyruvate dioxygenase and related hemolysins		
COG3186	17	Phenylalanine-4-hydroxylase		
COG3187	2	Heat shock protein		
COG3188	10	P pilus assembly protein, porin PapC		
COG3189	9	Uncharacterized conserved protein		
COG3190	2	Flagellar biogenesis protein		
COG3191	23	L-aminopeptidase/D-esterase		
COG3193	20	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol		
COG3194	1	Ureidoglycolate hydrolase		
COG3195	4	Uncharacterized protein conserved in bacteria		
COG3198	2	Uncharacterized protein conserved in bacteria		
COG3199	5	Uncharacterized conserved protein		
COG3200	13	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase		
COG3201	2	Nicotinamide mononucleotide transporter		
COG3202	15	ATP/ADP translocase		
COG3203	11	Outer membrane protein (porin)		
COG3204	4	Uncharacterized protein conserved in bacteria		
COG3206	21	Uncharacterized protein involved in exopolysaccharide biosynthesis		
COG3208	2	Predicted thioesterase involved in non-ribosomal peptide biosynthesis		
COG3209	82	Rhs family protein		
COG3210	45	Large exoproteins involved in heme utilization or adhesion		
COG3211	7	Predicted phosphatase		
COG3213	7	Uncharacterized protein involved in response to NO		
COG3214	30	Uncharacterized protein conserved in bacteria		
COG3215	2	Tfp pilus assembly protein PilZ		
COG3216	3	Uncharacterized protein conserved in bacteria		
COG3217	12	Uncharacterized Fe-S protein		
COG3218	1	ABC-type uncharacterized transport system, auxiliary component		
COG3220	9	Uncharacterized protein conserved in bacteria		
COG3221	23	ABC-type phosphate/phosphonate transport system, periplasmic component		
COG3222	9	Uncharacterized protein conserved in bacteria		
COG3223	3	Predicted membrane protein		
COG3225	13	ABC-type uncharacterized transport system involved in gliding motility, auxiliary component		
COG3227	8	Zinc metalloprotease (elastase)		
COG3228	8	Uncharacterized protein conserved in bacteria		
COG3231	2	Aminoglycoside phosphotransferase		
COG3233	1	Predicted deacetylase		
COG3235	1	Predicted membrane protein		
COG3236	1	Uncharacterized protein conserved in bacteria		
COG3237	7	Uncharacterized protein conserved in bacteria		
COG3238	3	Uncharacterized protein conserved in bacteria		
COG3239	19	Fatty acid desaturase		
COG3240	2	Phospholipase/lecithinase/hemolysin		
COG3243	53	Poly(3-hydroxyalkanoate) synthetase		
COG3245	11	Cytochrome c5		
COG3246	24	Uncharacterized conserved protein		
COG3247	4	Uncharacterized conserved protein		
COG3250	34	Beta-galactosidase/beta-glucuronidase		
COG3251	1	Uncharacterized protein conserved in bacteria		
COG3252	3	Methenyltetrahydromethanopterin cyclohydrolase		
COG3253	15	Uncharacterized conserved protein		
COG3254	1	Uncharacterized conserved protein		
COG3255	5	Putative sterol carrier protein		
COG3256	21	Nitric oxide reductase large subunit		
COG3258	6	Cytochrome c		
COG3259	39	Coenzyme F420-reducing hydrogenase, alpha subunit		
COG3260	11	Ni,Fe-hydrogenase III small subunit		
COG3261	18	Ni,Fe-hydrogenase III large subunit		
COG3262	3	Ni,Fe-hydrogenase III component G		
COG3263	16	NhaP-type Na+/H+ and K+/H+ antiporters with a unique C-terminal domain		
COG3264	4	Small-conductance mechanosensitive channel		
COG3265	4	Gluconate kinase		
COG3267	23	Type II secretory pathway, component ExeA (predicted ATPase)		
COG3268	18	Uncharacterized conserved protein		
COG3271	1	Predicted double-glycine peptidase		
COG3272	1	Uncharacterized conserved protein		
COG3273	1	Uncharacterized conserved protein		
COG3275	6	Putative regulator of cell autolysis		
COG3276	28	Selenocysteine-specific translation elongation factor		

COG3278	16	Cbb3-type cytochrome oxidase, subunit 1		
COG3279	42	Response regulator of the LytR/AlgR family		
COG3280	33	Maltooligosyl trehalose synthase		
COG3281	12	Uncharacterized protein, probably involved in trehalose biosynthesis		
COG3283	3	Transcriptional regulator of aromatic amino acids metabolism		
COG3284	20	Transcriptional activator of acetoin/glycerol metabolism		
COG3285	63	Predicted eukaryotic-type DNA primase		
COG3287	2	Uncharacterized conserved protein		
COG3288	34	NAD/NADP transhydrogenase alpha subunit		
COG3291	55	FOG: PKD repeat		
COG3292	22	Predicted periplasmic ligand-binding sensor domain		
COG3293	46	Transposase and inactivated derivatives		
COG3294	2	Uncharacterized conserved protein		
COG3298	8	Predicted 3'-5' exonuclease related to the exonuclease domain of PolB		
COG3300	1	MHYT domain (predicted integral membrane sensor domain)		
COG3301	1	Formate-dependent nitrite reductase, membrane component		
COG3302	1	DMSO reductase anchor subunit		
COG3303	9	Formate-dependent nitrite reductase, periplasmic cytochrome c552 subunit		
COG3304	2	Predicted membrane protein		
COG3305	5	Predicted membrane protein		
COG3307	8	Lipid A core - O-antigen ligase and related enzymes		
COG3310	1	Uncharacterized protein conserved in bacteria		
COG3311	1	Predicted transcriptional regulator		
COG3313	1	Predicted Fe-S protein		
COG3315	21	O-Methyltransferase involved in polyketide biosynthesis		
COG3316	2	Transposase and inactivated derivatives		
COG3317	7	Uncharacterized lipoprotein		
COG3318	1	Predicted metal-binding protein related to the C-terminal domain of SecA		
COG3319	5	Thioesterase domains of type I polyketide synthases or non-ribosomal peptide synthetases		
COG3320	11	Putative dehydrogenase domain of multifunctional non-ribosomal peptide synthetases and related enzymes		
COG3321	55	Polyketide synthase modules and related proteins		
COG3322	3	Predicted periplasmic ligand-binding sensor domain		
COG3324	29	Predicted enzyme related to lactoylglutathione lyase		
COG3325	3	Chitinase		
COG3327	4	Phenylacetic acid-responsive transcriptional repressor		
COG3328	61	Transposase and inactivated derivatives		
COG3329	2	Predicted permease		
COG3330	1	Uncharacterized protein conserved in bacteria		
COG3332	5	Uncharacterized conserved protein		
COG3333	90	Uncharacterized protein conserved in bacteria		
COG3334	1	Uncharacterized conserved protein		
COG3335	80	Transposase and inactivated derivatives		
COG3336	11	Predicted membrane protein		
COG3339	6	Uncharacterized conserved protein		
COG3340	9	Peptidase E		
COG3342	18	Uncharacterized conserved protein		
COG3344	56	Retron-type reverse transcriptase		
COG3345	10	Alpha-galactosidase		
COG3346	13	Uncharacterized conserved protein		
COG3347	18	Uncharacterized conserved protein		
COG3349	10	Uncharacterized conserved protein		
COG3350	1	Uncharacterized conserved protein		
COG3357	2	Predicted transcriptional regulator containing an HTH domain fused to a Zn-ribbon		
COG3358	7	Uncharacterized conserved protein		
COG3359	7	Predicted exonuclease		
COG3360	6	Uncharacterized conserved protein		
COG3361	8	Uncharacterized conserved protein		
COG3363	1	Archaeal IMP cyclohydrolase		
COG3367	9	Uncharacterized conserved protein		
COG3369	10	Uncharacterized conserved protein		
COG3375	6	Uncharacterized conserved protein		
COG3376	10	High-affinity nickel permease		
COG3378	3	Predicted ATPase		
COG3379	13	Uncharacterized conserved protein		
COG3380	2	Predicted NAD/FAD-dependent oxidoreductase		
COG3381	5	Uncharacterized component of anaerobic dehydrogenases		
COG3382	5	Uncharacterized conserved protein		
COG3383	46	Uncharacterized anaerobic dehydrogenase		
COG3384	13	Uncharacterized conserved protein		
COG3385	33	FOG: Transposase and inactivated derivatives		
COG3386	70	Gluconolactonase		
COG3387	78	Glucoamylase and related glycosyl hydrolases		
COG3391	254	Uncharacterized conserved protein		
COG3392	3	Adenine-specific DNA methylase		
COG3393	4	Predicted acetyltransferase		
COG3394	5	Uncharacterized protein conserved in bacteria		
COG3395	8	Uncharacterized protein conserved in bacteria		
COG3396	23	Uncharacterized conserved protein		
COG3397	1	Uncharacterized protein conserved in bacteria		
COG3401	3	Fibronectin type 3 domain-containing protein		
COG3402	1	Uncharacterized conserved protein		
COG3404	4	Methenyl tetrahydrofolate cyclohydrolase		
COG3405	3	Endoglucanase Y		
COG3408	43	Glycogen debranching enzyme		

COG3409	16	Putative peptidoglycan-binding domain-containing protein		
COG3410	1	Uncharacterized conserved protein		
COG3411	8	Ferredoxin		
COG3412	1	Uncharacterized protein conserved in bacteria		
COG3415	13	Transposase and inactivated derivatives		
COG3417	3	Collagen-binding surface adhesin SpaP (antigen I/II family)		
COG3419	38	Tfp pilus assembly protein, tip-associated adhesin PilY1		
COG3420	9	Nitrous oxidase accessory protein		
COG3424	12	Predicted naringenin-chalcone synthase		
COG3425	4	3-hydroxy-3-methylglutaryl CoA synthase		
COG3426	3	Butyrate kinase		
COG3427	21	Uncharacterized conserved protein		
COG3428	1	Predicted membrane protein		
COG3429	3	Glucose-6-P dehydrogenase subunit		
COG3431	2	Predicted membrane protein		
COG3434	7	Predicted signal transduction protein containing EAL and modified HD-GYP domains		
COG3435	23	Gentisate 1,2-dioxygenase		
COG3436	48	Transposase and inactivated derivatives		
COG3437	64	Response regulator containing a CheY-like receiver domain and an HD-GYP domain		
COG3439	7	Uncharacterized conserved protein		
COG3440	6	Predicted restriction endonuclease		
COG3442	8	Predicted glutamine amidotransferase		
COG3444	3	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIB		
COG3447	4	Predicted integral membrane sensor domain		
COG3448	2	CBS-domain-containing membrane protein		
COG3451	9	Type IV secretory pathway, VirB4 components		
COG3452	1	Predicted periplasmic ligand-binding sensor domain		
COG3453	1	Uncharacterized protein conserved in bacteria		
COG3454	1	Metal-dependent hydrolase involved in phosphonate metabolism		
COG3455	6	Uncharacterized protein conserved in bacteria		
COG3456	3	Uncharacterized conserved protein, contains FHA domain		
COG3457	1	Predicted amino acid racemase		
COG3458	1	Acetyl esterase (deacetylase)		
COG3459	49	Cellobiose phosphorylase		
COG3460	4	Uncharacterized enzyme of phenylacetate metabolism		
COG3461	2	Uncharacterized conserved protein		
COG3463	2	Predicted membrane protein		
COG3464	26	Transposase and inactivated derivatives		
COG3467	7	Predicted flavin-nucleotide-binding protein		
COG3468	5	Type V secretory pathway, adhesin AidA		
COG3469	2	Chitinase		
COG3471	2	Predicted periplasmic/secreted protein		
COG3472	1	Uncharacterized conserved protein		
COG3473	14	Maleate cis-trans isomerase		
COG3474	5	Cytochrome c2		
COG3476	10	Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog)		
COG3480	5	Predicted secreted protein containing a PDZ domain		
COG3481	6	Predicted HD-superfamily hydrolase		
COG3482	1	Uncharacterized conserved protein		
COG3483	11	Tryptophan 2,3-dioxygenase (vermilion)		
COG3484	4	Predicted proteasome-type protease		
COG3485	28	Protocatechuate 3,4-dioxygenase beta subunit		
COG3486	1	Lysine/ornithine N-monooxygenase		
COG3488	6	Predicted thiol oxidoreductase		
COG3491	7	Isopenicillin N synthase and related dioxygenases		
COG3494	10	Uncharacterized protein conserved in bacteria		
COG3495	1	Uncharacterized protein conserved in bacteria		
COG3496	10	Uncharacterized conserved protein		
COG3497	21	Phage tail sheath protein FI		
COG3500	6	Phage protein D		
COG3501	13	Uncharacterized protein conserved in bacteria		
COG3503	12	Predicted membrane protein		
COG3505	5	Type IV secretory pathway, VirD4 components		
COG3507	8	Beta-xylosidase		
COG3508	27	Homogentisate 1,2-dioxygenase		
COG3509	13	Poly(3-hydroxybutyrate) depolymerase		
COG3510	3	Cephalosporin hydroxylase		
COG3511	33	Phospholipase C		
COG3513	4	Uncharacterized protein conserved in bacteria		
COG3514	1	Uncharacterized protein conserved in bacteria		
COG3515	7	Uncharacterized protein conserved in bacteria		
COG3516	8	Uncharacterized protein conserved in bacteria		
COG3517	9	Uncharacterized protein conserved in bacteria		
COG3518	3	Uncharacterized protein conserved in bacteria		
COG3519	7	Uncharacterized protein conserved in bacteria		
COG3520	4	Uncharacterized protein conserved in bacteria		
COG3521	1	Uncharacterized protein conserved in bacteria		
COG3522	8	Uncharacterized protein conserved in bacteria		
COG3523	8	Uncharacterized protein conserved in bacteria		
COG3525	20	N-acetyl-beta-hexosaminidase		
COG3526	1	Uncharacterized protein conserved in bacteria		
COG3528	2	Uncharacterized protein conserved in bacteria		
COG3531	1	Predicted protein-disulfide isomerase		
COG3533	22	Uncharacterized protein conserved in bacteria		

COG3534	19	Alpha-L-arabinofuranosidase		
COG3535	1	Uncharacterized conserved protein		
COG3536	3	Uncharacterized protein conserved in bacteria		
COG3537	15	Putative alpha-1,2-mannosidase		
COG3540	38	Phosphodiesterase/alkaline phosphatase D		
COG3541	1	Predicted nucleotidyltransferase		
COG3544	3	Uncharacterized protein conserved in bacteria		
COG3545	5	Predicted esterase of the alpha/beta hydrolase fold		
COG3546	1	Mn-containing catalase		
COG3547	167	Transposase and inactivated derivatives		
COG3548	14	Predicted integral membrane protein		
COG3549	3	Plasmid maintenance system killer protein		
COG3550	1	Uncharacterized protein related to capsule biosynthesis enzymes		
COG3551	1	Uncharacterized protein conserved in bacteria		
COG3552	33	Protein containing von Willebrand factor type A (vWA) domain		
COG3555	4	Aspartyl/asparaginyl beta-hydroxylase and related dioxygenases		
COG3556	1	Predicted membrane protein		
COG3557	1	Uncharacterized domain/protein associated with RNAses G and E		
COG3558	7	Uncharacterized protein conserved in bacteria		
COG3559	2	Putative exporter of polyketide antibiotics		
COG3562	3	Capsule polysaccharide export protein		
COG3563	2	Capsule polysaccharide export protein		
COG3565	3	Predicted dioxygenase of extradiol dioxygenase family		
COG3568	21	Metal-dependent hydrolase		
COG3569	18	Topoisomerase IB		
COG3571	7	Predicted hydrolase of the alpha/beta-hydrolase fold		
COG3572	10	Gamma-glutamylcysteine synthetase		
COG3573	9	Predicted oxidoreductase		
COG3575	1	Uncharacterized protein conserved in bacteria		
COG3576	13	Predicted flavin-nucleotide-binding protein structurally related to pyridoxine 5'-phosphate oxidase		
COG3577	5	Predicted aspartyl protease		
COG3579	2	Aminopeptidase C		
COG3580	14	Uncharacterized protein conserved in bacteria		
COG3581	7	Uncharacterized protein conserved in bacteria		
COG3583	3	Uncharacterized protein conserved in bacteria		
COG3584	1	Uncharacterized protein conserved in bacteria		
COG3585	2	Molybdopterin-binding protein		
COG3586	1	Uncharacterized conserved protein		
COG3587	2	Restriction endonuclease		
COG3588	16	Fructose-1,6-bisphosphate aldolase		
COG3590	53	Predicted metalloendopeptidase		
COG3591	1	V8-like Glu-specific endopeptidase		
COG3592	2	Uncharacterized conserved protein		
COG3593	2	Predicted ATP-dependent endonuclease of the OLD family		
COG3595	5	Uncharacterized conserved protein		
COG3597	1	Uncharacterized protein/domain associated with GTPases		
COG3598	1	RecA-family ATPase		
COG3599	12	Cell division initiation protein		
COG3603	3	Uncharacterized conserved protein		
COG3604	43	Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains		
COG3605	7	Signal transduction protein containing GAF and PtsI domains		
COG3607	4	Predicted lactoylglutathione lyase		
COG3608	5	Predicted deacylase		
COG3609	2	Predicted transcriptional regulators containing the CopG/Arc/MetJ DNA-binding domain		
COG3610	3	Uncharacterized conserved protein		
COG3614	2	Predicted periplasmic ligand-binding sensor domain		
COG3616	23	Predicted amino acid aldolase or racemase		
COG3617	1	Prophage antirepressor		
COG3618	32	Predicted metal-dependent hydrolase of the TIM-barrel fold		
COG3620	3	Predicted transcriptional regulator with C-terminal CBS domains		
COG3621	6	Patatin		
COG3622	10	Hydroxypyruvate isomerase		
COG3626	3	Uncharacterized enzyme of phosphonate metabolism		
COG3627	1	Uncharacterized enzyme of phosphonate metabolism		
COG3628	4	Phage baseplate assembly protein W		
COG3629	33	DNA-binding transcriptional activator of the SARP family		
COG3631	3	Ketosteroid isomerase-related protein		
COG3634	1	Alkyl hydroperoxide reductase, large subunit		
COG3635	12	Predicted phosphoglycerate mutase, AP superfamily		
COG3636	1	Predicted transcriptional regulator		
COG3637	4	Opacity protein and related surface antigens		
COG3638	6	ABC-type phosphate/phosphonate transport system, ATPase component		
COG3639	4	ABC-type phosphate/phosphonate transport system, permease component		
COG3640	9	CO dehydrogenase maturation factor		
COG3643	20	Glutamate formiminotransferase		
COG3647	7	Predicted membrane protein		
COG3648	5	Uricase (urate oxidase)		
COG3649	2	Uncharacterized protein predicted to be involved in DNA repair		
COG3651	6	Uncharacterized protein conserved in bacteria		
COG3652	6	Predicted outer membrane protein		
COG3653	83	N-acyl-D-aspartate/D-glutamate deacylase		
COG3654	6	Prophage maintenance system killer protein		
COG3655	1	Predicted transcriptional regulator		
COG3657	3	Uncharacterized protein conserved in bacteria		

COG3658	4	Cytochrome b		
COG3659	1	Carbohydrate-selective porin		
COG3660	2	Predicted nucleoside-diphosphate-sugar epimerase		
COG3661	3	Alpha-glucuronidase		
COG3662	8	Uncharacterized protein conserved in bacteria		
COG3663	5	G:T/U mismatch-specific DNA glycosylase		
COG3664	12	Beta-xylosidase		
COG3665	6	Uncharacterized conserved protein		
COG3666	45	Transposase and inactivated derivatives		
COG3667	1	Uncharacterized protein involved in copper resistance		
COG3668	6	Plasmid stabilization system protein		
COG3669	18	Alpha-L-fucosidase		
COG3670	4	Lignostilbene-alpha,beta-dioxygenase and related enzymes		
COG3671	2	Predicted membrane protein		
COG3672	1	Predicted periplasmic protein		
COG3673	6	Uncharacterized conserved protein		
COG3676	4	Transposase and inactivated derivatives		
COG3677	2	Transposase and inactivated derivatives		
COG3682	5	Predicted transcriptional regulator		
COG3684	10	Tagatose-1,6-bisphosphate aldolase		
COG3685	10	Uncharacterized protein conserved in bacteria		
COG3686	1	Predicted membrane protein		
COG3687	5	Predicted metal-dependent hydrolase		
COG3688	1	Predicted RNA-binding protein containing a PIN domain		
COG3689	1	Predicted membrane protein		
COG3693	3	Beta-1,4-xylanase		
COG3694	14	ABC-type uncharacterized transport system, permease component		
COG3695	7	Predicted methylated DNA-protein cysteine methyltransferase		
COG3696	179	Putative silver efflux pump		
COG3701	1	Type IV secretory pathway, TrbF components		
COG3702	1	Type IV secretory pathway, VirB3 components		
COG3703	6	Uncharacterized protein involved in cation transport		
COG3704	2	Type IV secretory pathway, VirB6 components		
COG3705	15	ATP phosphoribosyltransferase involved in histidine biosynthesis		
COG3706	40	Response regulator containing a CheY-like receiver domain and a GGDEF domain		
COG3707	14	Response regulator with putative antiterminator output domain		
COG3710	11	DNA-binding winged-HTH domains		
COG3712	1	Fe2+-dicitrate sensor, membrane component		
COG3713	6	Outer membrane protein V		
COG3714	2	Predicted membrane protein		
COG3715	2	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIC		
COG3716	6	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IID		
COG3718	2	Uncharacterized enzyme involved in inositol metabolism		
COG3719	1	Ribonuclease I		
COG3723	1	Recombinational DNA repair protein (RecE pathway)		
COG3724	1	Succinylarginine dihydrolase		
COG3726	1	Uncharacterized membrane protein affecting hemolysin expression		
COG3727	4	DNA G:T-mismatch repair endonuclease		
COG3729	1	General stress protein		
COG3733	10	Cu2+-containing amine oxidase		
COG3734	1	2-keto-3-deoxy-galactonokinase		
COG3735	6	Uncharacterized protein conserved in bacteria		
COG3737	4	Uncharacterized conserved protein		
COG3738	1	Uncharacterized protein conserved in bacteria		
COG3740	4	Phage head maturation protease		
COG3741	7	N-formylglutamate amidohydrolase		
COG3742	2	Uncharacterized protein conserved in bacteria		
COG3743	1	Uncharacterized conserved protein		
COG3744	3	Uncharacterized protein conserved in bacteria		
COG3745	5	Flp pilus assembly protein CpaB		
COG3746	1	Phosphate-selective porin		
COG3748	20	Predicted membrane protein		
COG3749	4	Uncharacterized protein conserved in bacteria		
COG3752	4	Predicted membrane protein		
COG3753	4	Uncharacterized protein conserved in bacteria		
COG3754	4	Lipopolysaccharide biosynthesis protein		
COG3755	1	Uncharacterized protein conserved in bacteria		
COG3757	4	Lyzozyme M1 (1,4-beta-N-acetylmuramidase)		
COG3759	2	Predicted membrane protein		
COG3761	3	NADH:ubiquinone oxidoreductase 17.2 kD subunit		
COG3762	7	Predicted membrane protein		
COG3764	9	Sortase (surface protein transpeptidase)		
COG3766	3	Predicted membrane protein		
COG3768	1	Predicted membrane protein		
COG3772	1	Phage-related lysozyme (muraminidase)		
COG3773	4	Cell wall hydrolyses involved in spore germination		
COG3774	1	Mannosyltransferase OCH1 and related enzymes		
COG3775	2	Phosphotransferase system, galactitol-specific IIC component		
COG3777	8	Uncharacterized conserved protein		
COG3779	1	Uncharacterized protein conserved in bacteria		
COG3780	1	DNA endonuclease related to intein-encoded endonucleases		
COG3784	1	Uncharacterized protein conserved in bacteria		
COG3785	2	Uncharacterized conserved protein		
COG3786	5	Uncharacterized protein conserved in bacteria		

COG3791	35	Uncharacterized conserved protein		
COG3794	17	Plastocyanin		
COG3795	27	Uncharacterized protein conserved in bacteria		
COG3797	6	Uncharacterized protein conserved in bacteria		
COG3800	3	Predicted transcriptional regulator		
COG3801	7	Uncharacterized protein conserved in bacteria		
COG3803	3	Uncharacterized protein conserved in bacteria		
COG3804	7	Uncharacterized conserved protein related to dihydrodipicolinate reductase		
COG3805	2	Aromatic ring-cleaving dioxygenase		
COG3806	1	Anti-sigma factor		
COG3807	1	Uncharacterized protein conserved in bacteria		
COG3808	28	Inorganic pyrophosphatase		
COG3809	4	Uncharacterized protein conserved in bacteria		
COG3812	6	Uncharacterized protein conserved in bacteria		
COG3813	4	Uncharacterized protein conserved in bacteria		
COG3815	2	Predicted membrane protein		
COG3816	2	Uncharacterized protein conserved in bacteria		
COG3818	1	Predicted acetyltransferase, GNAT superfamily		
COG3819	2	Predicted membrane protein		
COG3821	2	Predicted membrane protein		
COG3822	2	ABC-type sugar transport system, auxiliary component		
COG3823	3	Glutamine cyclotransferase		
COG3824	7	Uncharacterized protein conserved in bacteria		
COG3825	5	Uncharacterized protein conserved in bacteria		
COG3826	7	Uncharacterized protein conserved in bacteria		
COG3828	4	Uncharacterized protein conserved in bacteria		
COG3829	26	Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains		
COG3830	1	ACT domain-containing protein		
COG3832	49	Uncharacterized conserved protein		
COG3833	4	ABC-type maltose transport systems, permease component		
COG3835	2	Sugar diacid utilization regulator		
COG3836	38	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase		
COG3837	15	Uncharacterized conserved protein, contains double-stranded beta-helix domain		
COG3838	2	Type IV secretory pathway, VirB2 components (pilins)		
COG3839	35	ABC-type sugar transport systems, ATPase components		
COG3842	39	ABC-type spermidine/putrescine transport systems, ATPase components		
COG3843	3	Type IV secretory pathway, VirD2 components (relaxase)		
COG3844	16	Kynureninase		
COG3845	35	ABC-type uncharacterized transport systems, ATPase components		
COG3850	13	Signal transduction histidine kinase, nitrate/nitrite-specific		
COG3851	3	Signal transduction histidine kinase, glucose-6-phosphate specific		
COG3852	15	Signal transduction histidine kinase, nitrogen specific		
COG3853	5	Uncharacterized protein involved in tellurite resistance		
COG3854	4	Uncharacterized protein conserved in bacteria		
COG3856	2	Uncharacterized conserved protein (small basic protein)		
COG3857	2	ATP-dependent nuclease, subunit B		
COG3858	14	Predicted glycosyl hydrolase		
COG3860	2	Uncharacterized protein conserved in bacteria		
COG3861	1	Uncharacterized protein conserved in bacteria		
COG3864	1	Uncharacterized protein conserved in bacteria		
COG3865	21	Uncharacterized protein conserved in bacteria		
COG3866	1	Pectate lyase		
COG3867	2	Arabinogalactan endo-1,4-beta-galactosidase		
COG3868	3	Uncharacterized conserved protein		
COG3869	4	Arginine kinase		
COG3870	5	Uncharacterized protein conserved in bacteria		
COG3871	2	Uncharacterized stress protein (general stress protein 26)		
COG3872	15	Predicted metal-dependent enzyme		
COG3875	21	Uncharacterized conserved protein		
COG3876	26	Uncharacterized protein conserved in bacteria		
COG3877	1	Uncharacterized protein conserved in bacteria		
COG3878	1	Uncharacterized protein conserved in bacteria		
COG3879	5	Uncharacterized protein conserved in bacteria		
COG3880	2	Uncharacterized protein with conserved CXXC pairs		
COG3882	4	Predicted enzyme involved in methoxymalonyl-ACP biosynthesis		
COG3883	3	Uncharacterized protein conserved in bacteria		
COG3885	1	Uncharacterized conserved protein		
COG3886	3	Predicted HKD family nuclease		
COG3887	2	Predicted signaling protein consisting of a modified GGDEF domain and a DHH domain		
COG3892	1	Uncharacterized protein conserved in bacteria		
COG3893	4	Inactivated superfamily I helicase		
COG3894	25	Uncharacterized metal-binding protein		
COG3897	3	Predicted methyltransferase		
COG3899	98	Predicted ATPase		
COG3901	1	Regulator of nitric oxide reductase transcription		
COG3903	80	Predicted ATPase		
COG3907	1	PAP2 (acid phosphatase) superfamily protein		
COG3910	5	Predicted ATPase		
COG3911	1	Predicted ATPase		
COG3913	5	Uncharacterized protein conserved in bacteria		
COG3914	17	Predicted O-linked N-acetylglucosamine transferase, SPINDLY family		
COG3917	14	2-hydroxychromene-2-carboxylate isomerase		
COG3919	5	Predicted ATP-grasp enzyme		
COG3920	26	Signal transduction histidine kinase		

COG3921	1	Uncharacterized protein conserved in bacteria		
COG3926	2	Putative secretion activating protein		
COG3930	2	Uncharacterized protein conserved in bacteria		
COG3932	2	Uncharacterized ABC-type transport system, permease components		
COG3934	3	Endo-beta-mannanase		
COG3937	1	Uncharacterized conserved protein		
COG3938	12	Proline racemase		
COG3943	1	Virulence protein		
COG3944	1	Capsular polysaccharide biosynthesis protein		
COG3945	8	Uncharacterized conserved protein		
COG3946	5	Type IV secretory pathway, VirJ component		
COG3947	3	Response regulator containing CheY-like receiver and SARP domains		
COG3951	2	Rod binding protein		
COG3952	1	Predicted membrane protein		
COG3953	2	SLT domain proteins		
COG3954	7	Phosphoribulokinase		
COG3956	8	Protein containing tetrapyrrole methyltransferase domain and MazG-like (predicted pyrophosphatase) domain		
COG3957	21	Phosphoketolase		
COG3958	11	Transketolase, C-terminal subunit		
COG3959	14	Transketolase, N-terminal subunit		
COG3960	7	Glyoxylate carboligase		
COG3961	3	Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes		
COG3962	12	Acetolactate synthase		
COG3963	3	Phospholipid N-methyltransferase		
COG3964	8	Predicted amidohydrolase		
COG3967	1	Short-chain dehydrogenase involved in D-alanine esterification of lipoteichoic acid and wall teichoic acid (D-alanine transfer protein)		
COG3968	11	Uncharacterized protein related to glutamine synthetase		
COG3969	3	Predicted phosphoadenosine phosphosulfate sulfotransferase		
COG3970	10	Fumarylacetoacetate (FAA) hydrolase family protein		
COG3971	11	2-keto-4-pentenoate hydratase		
COG3972	4	Superfamily I DNA and RNA helicases		
COG3973	13	Superfamily I DNA and RNA helicases		
COG3975	35	Predicted protease with the C-terminal PDZ domain		
COG3979	35	Uncharacterized protein contain chitin-binding domain type 3		
COG3980	1	Spore coat polysaccharide biosynthesis protein, predicted glycosyltransferase		
COG3981	1	Predicted acetyltransferase		
COG4012	3	Uncharacterized protein conserved in archaea		
COG4032	5	Predicted thiamine-pyrophosphate-binding protein		
COG4034	1	Uncharacterized protein conserved in archaea		
COG4060	1	Tetrahydromethanopterin S-methyltransferase, subunit D		
COG4089	1	Predicted membrane protein		
COG4091	20	Predicted homoserine dehydrogenase		
COG4094	10	Predicted membrane protein		
COG4095	3	Uncharacterized conserved protein		
COG4096	27	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases		
COG4097	5	Predicted ferric reductase		
COG4099	4	Predicted peptidase		
COG4101	4	Predicted mannose-6-phosphate isomerase		
COG4102	19	Uncharacterized protein conserved in bacteria		
COG4103	1	Uncharacterized protein conserved in bacteria		
COG4105	17	DNA uptake lipoprotein		
COG4106	2	Trans-aconitate methyltransferase		
COG4107	1	ABC-type phosphonate transport system, ATPase component		
COG4108	18	Peptide chain release factor RF-3		
COG4109	1	Predicted transcriptional regulator containing CBS domains		
COG4111	2	Uncharacterized conserved protein		
COG4112	1	Predicted phosphoesterase (MutT family)		
COG4113	3	Predicted nucleic acid-binding protein, contains PIN domain		
COG4115	1	Uncharacterized protein conserved in bacteria		
COG4117	9	Thiosulfate reductase cytochrome B subunit (membrane anchoring protein)		
COG4118	2	Antitoxin of toxin-antitoxin stability system		
COG4119	7	Predicted NTP pyrophosphohydrolase		
COG4120	1	ABC-type uncharacterized transport system, permease component		
COG4121	3	Uncharacterized conserved protein		
COG4122	19	Predicted O-methyltransferase		
COG4123	1	Predicted O-methyltransferase		
COG4124	7	Beta-mannanase		
COG4126	6	Hydantoin racemase		
COG4132	6	ABC-type uncharacterized transport system, permease component		
COG4133	4	ABC-type transport system involved in cytochrome c biogenesis, ATPase component		
COG4134	5	ABC-type uncharacterized transport system, periplasmic component		
COG4137	3	ABC-type uncharacterized transport system, permease component		
COG4143	3	ABC-type thiamine transport system, periplasmic component		
COG4145	1	Na+/panthothenate symporter		
COG4146	11	Predicted symporter		
COG4147	25	Predicted symporter		
COG4148	5	ABC-type molybdate transport system, ATPase component		
COG4149	9	ABC-type molybdate transport system, permease component		
COG4152	11	ABC-type uncharacterized transport system, ATPase component		
COG4154	1	Fucose dissimilation pathway protein FucU		
COG4158	2	Predicted ABC-type sugar transport system, permease component		
COG4166	44	ABC-type oligopeptide transport system, periplasmic component		
COG4172	2	ABC-type uncharacterized transport system, duplicated ATPase component		
COG4174	2	ABC-type uncharacterized transport system, permease component		

COG4175	1	ABC-type proline/glycine betaine transport system, ATPase component		
COG4176	1	ABC-type proline/glycine betaine transport system, permease component		
COG4177	209	ABC-type branched-chain amino acid transport system, permease component		
COG4178	16	ABC-type uncharacterized transport system, permease and ATPase components		
COG4181	8	Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component		
COG4185	2	Uncharacterized protein conserved in bacteria		
COG4188	6	Predicted dienelactone hydrolase		
COG4190	2	Predicted transcriptional regulator		
COG4191	13	Signal transduction histidine kinase regulating C4-dicarboxylate transport system		
COG4195	1	Phage-related replication protein		
COG4196	10	Uncharacterized protein conserved in bacteria		
COG4198	11	Uncharacterized conserved protein		
COG4200	1	Uncharacterized protein conserved in bacteria		
COG4206	19	Outer membrane cobalamin receptor protein		
COG4208	8	ABC-type sulfate transport system, permease component		
COG4211	1	ABC-type glucose/galactose transport system, permease component		
COG4213	5	ABC-type xylose transport system, periplasmic component		
COG4214	14	ABC-type xylose transport system, permease component		
COG4219	3	Antirepressor regulating drug resistance, predicted signal transduction N-terminal membrane component		
COG4220	2	Phage DNA packaging protein, Nu1 subunit of terminase		
COG4221	21	Short-chain alcohol dehydrogenase of unknown specificity		
COG4222	2	Uncharacterized protein conserved in bacteria		
COG4225	1	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins		
COG4226	1	Uncharacterized protein encoded in hypervariable junctions of pilus gene clusters		
COG4227	3	Antirestriction protein		
COG4230	10	Delta 1-pyrroline-5-carboxylate dehydrogenase		
COG4231	66	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits		
COG4232	22	Thiol:disulfide interchange protein		
COG4233	5	Uncharacterized protein predicted to be involved in C-type cytochrome biogenesis		
COG4235	8	Cytochrome c biogenesis factor		
COG4237	6	Hydrogenase 4 membrane component (E)		
COG4239	4	ABC-type uncharacterized transport system, permease component		
COG4242	2	Cyanophycinase and related exopeptidases		
COG4243	1	Predicted membrane protein		
COG4244	6	Predicted membrane protein		
COG4248	2	Uncharacterized protein with protein kinase and helix-hairpin-helix DNA-binding domains		
COG4249	17	Uncharacterized protein containing caspase domain		
COG4250	1	Predicted sensor protein/domain		
COG4251	10	Bacteriophytochrome (light-regulated signal transduction histidine kinase)		
COG4252	25	Predicted transmembrane sensor domain		
COG4254	3	Uncharacterized protein conserved in bacteria		
COG4255	2	Uncharacterized protein conserved in bacteria		
COG4256	1	Hemin uptake protein		
COG4257	30	Streptogramin lyase		
COG4258	10	Predicted exporter		
COG4260	5	Putative virion core protein (lumpy skin disease virus)		
COG4261	2	Predicted acyltransferase		
COG4262	3	Predicted spermidine synthase with an N-terminal membrane domain		
COG4263	14	Nitrous oxide reductase		
COG4266	8	Allantoicase		
COG4267	2	Predicted membrane protein		
COG4269	7	Predicted membrane protein		
COG4271	3	Predicted nucleotide-binding protein containing TIR -like domain		
COG4274	2	Uncharacterized conserved protein		
COG4275	30	Uncharacterized conserved protein		
COG4276	3	Uncharacterized conserved protein		
COG4277	6	Predicted DNA-binding protein with the Helix-hairpin-helix motif		
COG4279	1	Uncharacterized conserved protein		
COG4280	6	Predicted membrane protein		
COG4281	2	Acyl-CoA-binding protein		
COG4283	1	Uncharacterized conserved protein		
COG4284	5	UDP-glucose pyrophosphorylase		
COG4286	1	Uncharacterized conserved protein related to MYG1 family		
COG4287	5	PhoPQ-activated pathogenicity-related protein		
COG4288	1	Uncharacterized protein conserved in bacteria		
COG4289	1	Uncharacterized protein conserved in bacteria		
COG4290	9	Guanyl-specific ribonuclease Sa		
COG4291	3	Predicted membrane protein		
COG4292	11	Predicted membrane protein		
COG4293	3	Uncharacterized protein conserved in bacteria		
COG4299	6	Uncharacterized conserved protein		
COG4301	21	Uncharacterized conserved protein		
COG4302	1	Ethanolamine ammonia-lyase, small subunit		
COG4303	4	Ethanolamine ammonia-lyase, large subunit		
COG4306	1	Uncharacterized protein conserved in bacteria		
COG4308	1	Limonene-1,2-epoxide hydrolase		
COG4309	1	Uncharacterized conserved protein		
COG4310	4	Uncharacterized protein conserved in bacteria with an aminopeptidase-like domain		
COG4311	2	Sarcosine oxidase delta subunit		
COG4312	25	Uncharacterized protein conserved in bacteria		
COG4313	4	Protein involved in meta-pathway of phenol degradation		
COG4315	10	Uncharacterized protein conserved in bacteria		
COG4319	3	Ketosteroid isomerase homolog		
COG4320	10	Uncharacterized protein conserved in bacteria		

COG4323	3	Predicted membrane protein		
COG4324	11	Predicted aminopeptidase		
COG4325	4	Predicted membrane protein		
COG4327	6	Predicted membrane protein		
COG4328	1	Uncharacterized protein conserved in bacteria		
COG4330	2	Predicted membrane protein		
COG4333	2	Uncharacterized protein conserved in bacteria		
COG4336	6	Uncharacterized conserved protein		
COG4338	1	Uncharacterized protein conserved in bacteria		
COG4339	1	Uncharacterized protein conserved in bacteria		
COG4340	1	Uncharacterized protein conserved in bacteria		
COG4346	1	Predicted membrane-bound dolichyl-phosphate-mannose-protein mannosyltransferase		
COG4352	1	Ribosomal protein L13E		
COG4354	1	Predicted bile acid beta-glucosidase		
COG4359	1	Uncharacterized conserved protein, possibly involved in methylthioadenosine recycling		
COG4362	2	Nitric oxide synthase, oxygenase domain		
COG4365	6	Uncharacterized protein conserved in bacteria		
COG4373	1	Mu-like prophage FluMu protein gp28		
COG4374	1	Uncharacterized protein conserved in bacteria		
COG4380	1	Uncharacterized protein conserved in bacteria		
COG4389	1	Site-specific recombinase		
COG4391	2	Uncharacterized protein conserved in bacteria		
COG4392	5	Predicted membrane protein		
COG4394	2	Uncharacterized protein conserved in bacteria		
COG4395	6	Uncharacterized protein conserved in bacteria		
COG4398	19	Uncharacterized protein conserved in bacteria		
COG4399	1	Uncharacterized protein conserved in bacteria		
COG4401	12	Chorismate mutase		
COG4402	5	Uncharacterized protein conserved in bacteria		
COG4409	1	Neuraminidase (sialidase)		
COG4412	5	Uncharacterized protein conserved in bacteria		
COG4420	12	Predicted membrane protein		
COG4422	11	Bacteriophage protein gp37		
COG4424	1	Uncharacterized protein conserved in bacteria		
COG4425	3	Predicted membrane protein		
COG4427	5	Uncharacterized protein conserved in bacteria		
COG4430	7	Uncharacterized protein conserved in bacteria		
COG4443	1	Uncharacterized protein conserved in bacteria		
COG4446	1	Uncharacterized protein conserved in bacteria		
COG4447	11	Uncharacterized protein related to plant photosystem II stability/assembly factor		
COG4448	15	L-asparaginase II		
COG4451	3	Ribulose bisphosphate carboxylase small subunit		
COG4452	10	Inner membrane protein involved in colicin E2 resistance		
COG4453	1	Uncharacterized protein conserved in bacteria		
COG4454	7	Uncharacterized copper-binding protein		
COG4455	1	Protein of avirulence locus involved in temperature-dependent protein secretion		
COG4459	1	Periplasmic nitrate reductase system, NapE component		
COG4464	12	Capsular polysaccharide biosynthesis protein		
COG4478	1	Predicted membrane protein		
COG4481	1	Uncharacterized protein conserved in bacteria		
COG4487	4	Uncharacterized protein conserved in bacteria		
COG4493	1	Uncharacterized protein conserved in bacteria		
COG4508	1	Uncharacterized protein conserved in bacteria		
COG4517	1	Uncharacterized protein conserved in bacteria		
COG4520	4	Surface antigen		
COG4521	3	ABC-type taurine transport system, periplasmic component		
COG4529	3	Uncharacterized protein conserved in bacteria		
COG4533	1	ABC-type uncharacterized transport system, periplasmic component		
COG4535	5	Putative Mg2+ and Co2+ transporter CorC		
COG4536	9	Putative Mg2+ and Co2+ transporter CorB		
COG4539	5	Predicted membrane protein		
COG4544	1	Uncharacterized conserved protein		
COG4547	6	Cobalamin biosynthesis protein CobT (nicotinate-mononucleotide:5, 6-dimethylbenzimidazole phosphoribosyltransferase)		
COG4548	3	Nitric oxide reductase activation protein		
COG4552	3	Predicted acetyltransferase involved in intracellular survival and related acetyltransferases		
COG4553	10	Poly-beta-hydroxyalkanoate depolymerase		
COG4555	4	ABC-type Na+ transport system, ATPase component		
COG4558	2	ABC-type hemin transport system, periplasmic component		
COG4559	1	ABC-type hemin transport system, ATPase component		
COG4564	15	Signal transduction histidine kinase		
COG4565	2	Response regulator of citrate/malate metabolism		
COG4566	20	Response regulator		
COG4567	7	Response regulator consisting of a CheY-like receiver domain and a Fis-type HTH domain		
COG4569	3	Acetaldehyde dehydrogenase (acetylating)		
COG4570	1	Holliday junction resolvase		
COG4572	1	Putative cation transport regulator		
COG4573	3	Predicted tagatose 6-phosphate kinase		
COG4575	4	Uncharacterized conserved protein		
COG4576	4	Carbon dioxide concentrating mechanism/carboxysome shell protein		
COG4577	9	Carbon dioxide concentrating mechanism/carboxysome shell protein		
COG4579	11	Isocitrate dehydrogenase kinase/phosphatase		
COG4580	1	Maltoporin (phage lambda and maltose receptor)		
COG4581	30	Superfamily II RNA helicase		
COG4582	2	Uncharacterized protein conserved in bacteria		

COG4583	1	Sarcosine oxidase gamma subunit		
COG4584	53	Transposase and inactivated derivatives		
COG4585	96	Signal transduction histidine kinase		
COG4586	7	ABC-type uncharacterized transport system, ATPase component		
COG4587	7	ABC-type uncharacterized transport system, permease component		
COG4589	4	Predicted CDP-diglyceride synthetase/phosphatidate cytidylyltransferase		
COG4590	6	ABC-type uncharacterized transport system, permease component		
COG4591	39	ABC-type transport system, involved in lipoprotein release, permease component		
COG4597	2	ABC-type amino acid transport system, permease component		
COG4603	29	ABC-type uncharacterized transport system, permease component		
COG4608	39	ABC-type oligopeptide transport system, ATPase component		
COG4618	8	ABC-type protease/lipase transport system, ATPase and permease components		
COG4623	8	Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein		
COG4624	2	Iron only hydrogenase large subunit, C-terminal domain		
COG4625	4	Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain		
COG4626	4	Phage terminase-like protein, large subunit		
COG4627	4	Uncharacterized protein conserved in bacteria		
COG4630	2	Xanthine dehydrogenase, iron-sulfur cluster and FAD-binding subunit A		
COG4631	10	Xanthine dehydrogenase, molybdopterin-binding subunit B		
COG4632	1	Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase		
COG4633	4	Uncharacterized protein conserved in bacteria		
COG4634	1	Uncharacterized protein conserved in bacteria		
COG4635	8	Flavodoxin		
COG4636	19	Uncharacterized protein conserved in cyanobacteria		
COG4637	5	Predicted ATPase		
COG4638	84	Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit		
COG4639	4	Predicted kinase		
COG4641	18	Uncharacterized protein conserved in bacteria		
COG4642	4	Uncharacterized protein conserved in bacteria		
COG4643	1	Uncharacterized protein conserved in bacteria		
COG4644	7	Transposase and inactivated derivatives, TnpA family		
COG4646	4	DNA methylase		
COG4648	2	Predicted membrane protein		
COG4650	1	Sigma54-dependent transcription regulator containing an AAA-type ATPase domain and a DNA-binding domain		
COG4651	5	Kef-type K+ transport system, predicted NAD-binding component		
COG4653	1	Predicted phage phi-C31 gp36 major capsid-like protein		
COG4654	7	Cytochrome c551/c552		
COG4656	8	Predicted NADH:ubiquinone oxidoreductase, subunit RnfC		
COG4657	2	Predicted NADH:ubiquinone oxidoreductase, subunit RnfA		
COG4658	3	Predicted NADH:ubiquinone oxidoreductase, subunit RnfD		
COG4659	2	Predicted NADH:ubiquinone oxidoreductase, subunit RnfG		
COG4660	2	Predicted NADH:ubiquinone oxidoreductase, subunit RnfE		
COG4662	8	ABC-type tungstate transport system, periplasmic component		
COG4663	14	TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component		
COG4664	36	TRAP-type mannitol/chloroaromatic compound transport system, large permease component		
COG4665	20	TRAP-type mannitol/chloroaromatic compound transport system, small permease component		
COG4666	32	TRAP-type uncharacterized transport system, fused permease components		
COG4669	3	Type III secretory pathway, lipoprotein EscJ		
COG4670	7	Acyl CoA:acetate/3-ketoacid CoA transferase		
COG4671	16	Predicted glycosyl transferase		
COG4674	3	Uncharacterized ABC-type transport system, ATPase component		
COG4675	5	Microcystin-dependent protein		
COG4676	3	Uncharacterized protein conserved in bacteria		
COG4677	2	Pectin methylesterase		
COG4678	1	Muramidase (phage lambda lysozyme)		
COG4679	8	Phage-related protein		
COG4680	1	Uncharacterized protein conserved in bacteria		
COG4681	4	Uncharacterized protein conserved in bacteria		
COG4682	1	Predicted membrane protein		
COG4683	2	Uncharacterized protein conserved in bacteria		
COG4684	1	Predicted membrane protein		
COG4690	6	Dipeptidase		
COG4692	6	Predicted neuraminidase (sialidase)		
COG4695	5	Phage-related protein		
COG4704	1	Uncharacterized protein conserved in bacteria		
COG4705	6	Uncharacterized membrane-anchored protein conserved in bacteria		
COG4706	1	Predicted 3-hydroxylacyl-(acyl carrier protein) dehydratase		
COG4712	1	Uncharacterized protein conserved in bacteria		
COG4714	1	Uncharacterized membrane-anchored protein conserved in bacteria		
COG4715	2	Uncharacterized conserved protein		
COG4716	1	Myosin-crossreactive antigen		
COG4717	1	Uncharacterized conserved protein		
COG4719	3	Uncharacterized protein conserved in bacteria		
COG4725	1	Transcriptional activator, adenine-specific DNA methyltransferase		
COG4726	3	Tfp pilus assembly protein PilX		
COG4727	1	Uncharacterized protein conserved in bacteria		
COG4728	1	Uncharacterized protein conserved in bacteria		
COG4729	1	Uncharacterized conserved protein		
COG4731	3	Uncharacterized protein conserved in bacteria		
COG4736	1	Cbb3-type cytochrome oxidase, subunit 3		
COG4741	1	Predicted secreted endonuclease distantly related to archaeal Holliday junction resolvase		
COG4745	5	Predicted membrane-bound mannosyltransferase		
COG4747	7	ACT domain-containing protein		
COG4749	1	Uncharacterized protein conserved in archaea		

COG4752	1	Uncharacterized protein conserved in bacteria		
COG4753	5	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain		
COG4754	1	Uncharacterized conserved protein		
COG4756	1	Predicted cation transporter		
COG4757	2	Predicted alpha/beta hydrolase		
COG4759	1	Uncharacterized protein conserved in bacteria containing thioredoxin-like domain		
COG4760	1	Predicted membrane protein		
COG4762	1	Uncharacterized protein conserved in bacteria		
COG4769	2	Predicted membrane protein		
COG4770	38	Acetyl/propionyl-CoA carboxylase, alpha subunit		
COG4771	5	Outer membrane receptor for ferrienterochelin and colicins		
COG4772	4	Outer membrane receptor for Fe3+-dicitrate		
COG4775	59	Outer membrane protein/protective antigen OMA87		
COG4778	2	ABC-type phosphonate transport system, ATPase component		
COG4779	2	ABC-type enterobactin transport system, permease component		
COG4782	3	Uncharacterized protein conserved in bacteria		
COG4783	26	Putative Zn-dependent protease, contains TPR repeats		
COG4784	18	Putative Zn-dependent protease		
COG4785	2	Lipoprotein NlpI, contains TPR repeats		
COG4786	16	Flagellar basal body rod protein		
COG4787	1	Flagellar basal body rod protein		
COG4789	2	Type III secretory pathway, component EscV		
COG4792	1	Type III secretory pathway, component EscU		
COG4795	2	Type II secretory pathway, component PulJ		
COG4796	49	Type II secretory pathway, component HofQ		
COG4798	5	Predicted methyltransferase		
COG4799	90	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)		
COG4802	2	Ferredoxin-thioredoxin reductase, catalytic subunit		
COG4803	1	Predicted membrane protein		
COG4804	4	Uncharacterized conserved protein		
COG4805	37	Uncharacterized protein conserved in bacteria		
COG4806	7	L-rhamnose isomerase		
COG4813	1	Trehalose utilization protein		
COG4819	11	Ethanolamine utilization protein, possible chaperonin protecting lyase from inhibition		
COG4821	5	Uncharacterized protein containing SIS (Sugar ISomerase) phosphosugar binding domain		
COG4825	7	Uncharacterized membrane-anchored protein conserved in bacteria		
COG4826	11	Serine protease inhibitor		
COG4829	4	Muconolactone delta-isomerase		
COG4830	1	Ribosomal protein S26		
COG4832	3	Uncharacterized conserved protein		
COG4833	1	Predicted glycosyl hydrolase		
COG4834	1	Uncharacterized protein conserved in bacteria		
COG4842	3	Uncharacterized protein conserved in bacteria		
COG4843	1	Uncharacterized protein conserved in bacteria		
COG4845	3	Chloramphenicol O-acetyltransferase		
COG4850	3	Uncharacterized conserved protein		
COG4856	1	Uncharacterized protein conserved in bacteria		
COG4861	2	Uncharacterized protein conserved in bacteria		
COG4864	1	Uncharacterized protein conserved in bacteria		
COG4865	4	Glutamate mutase epsilon subunit		
COG4867	19	Uncharacterized protein with a von Willebrand factor type A (vWA) domain		
COG4868	2	Uncharacterized protein conserved in bacteria		
COG4869	1	Propanediol utilization protein		
COG4870	10	Cysteine protease		
COG4874	1	Uncharacterized protein conserved in bacteria containing a pentein-type domain		
COG4877	2	Uncharacterized protein conserved in bacteria		
COG4881	4	Predicted membrane protein		
COG4883	1	Uncharacterized protein conserved in archaea		
COG4886	1	Leucine-rich repeat (LRR) protein		
COG4887	4	Uncharacterized metal-binding protein conserved in archaea		
COG4889	1	Predicted helicase		
COG4894	3	Uncharacterized conserved protein		
COG4898	1	Uncharacterized protein conserved in bacteria		
COG4901	1	Ribosomal protein S25		
COG4907	1	Predicted membrane protein		
COG4908	1	Uncharacterized protein containing a NRPS condensation (elongation) domain		
COG4909	4	Propanediol dehydratase, large subunit		
COG4911	10	Uncharacterized conserved protein		
COG4912	4	Predicted DNA alkylation repair enzyme		
COG4913	1	Uncharacterized protein conserved in bacteria		
COG4922	2	Uncharacterized protein conserved in bacteria		
COG4924	2	Uncharacterized protein conserved in bacteria		
COG4928	2	Predicted P-loop ATPase		
COG4929	1	Uncharacterized membrane-anchored protein		
COG4930	3	Predicted ATP-dependent Lon-type protease		
COG4934	19	Predicted protease		
COG4935	2	Regulatory P domain of the subtilisin-like proprotein convertases and other proteases		
COG4938	1	Uncharacterized conserved protein		
COG4941	52	Predicted RNA polymerase sigma factor containing a TPR repeat domain		
COG4942	6	Membrane-bound metallopeptidase		
COG4945	2	Membrane-anchored protein predicted to be involved in regulation of amylopullulanase		
COG4946	22	Uncharacterized protein related to the periplasmic component of the Tol biopolymer transport system		
COG4947	10	Uncharacterized protein conserved in bacteria		
COG4948	165	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily		

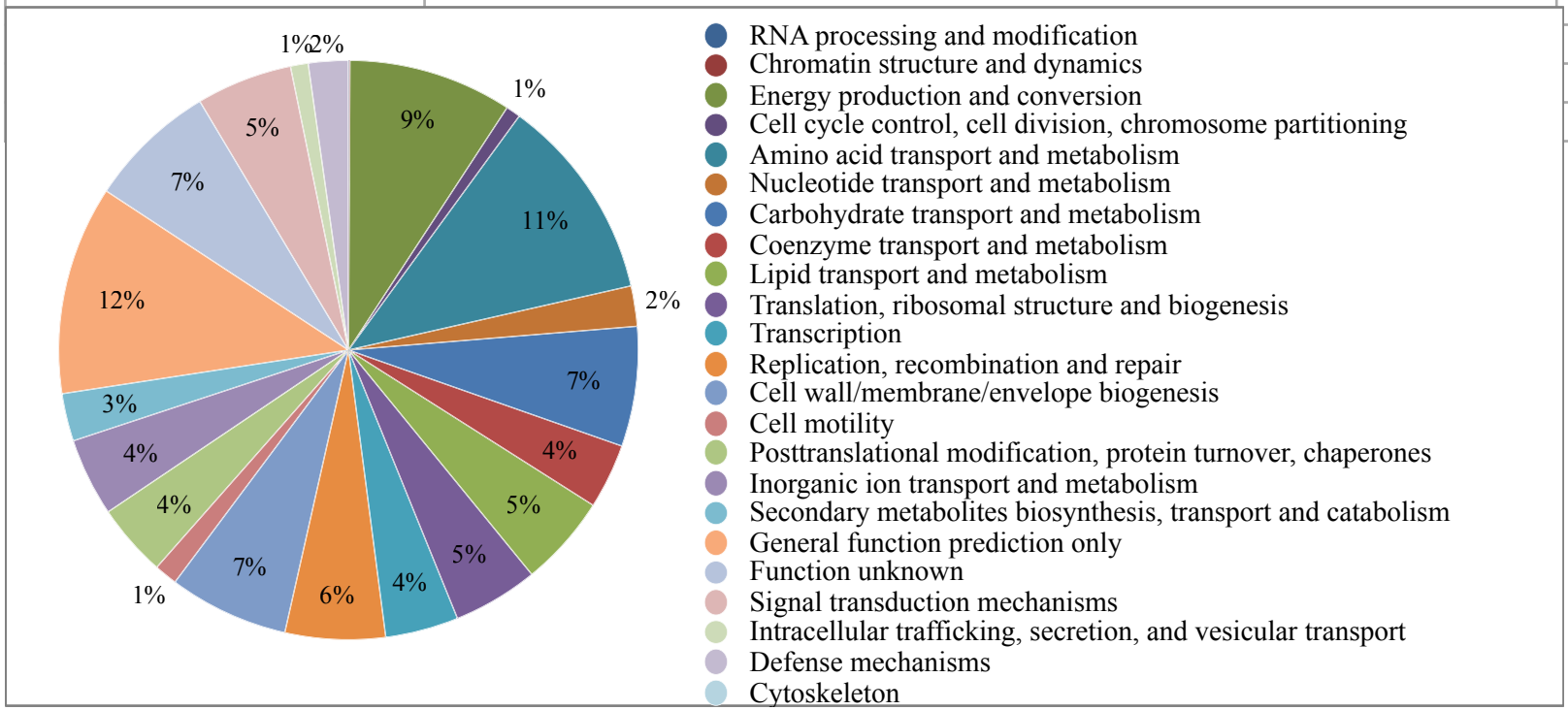
COG4951	1	Uncharacterized protein conserved in bacteria		
COG4952	3	Predicted sugar isomerase		
COG4953	18	Membrane carboxypeptidase/penicillin-binding protein PbpC		
COG4956	5	Integral membrane protein (PIN domain superfamily)		
COG4957	6	Predicted transcriptional regulator		
COG4959	1	Type IV secretory pathway, protease TraF		
COG4960	1	Flp pilus assembly protein, protease CpaA		
COG4961	1	Flp pilus assembly protein TadG		
COG4962	41	Flp pilus assembly protein, ATPase CpaF		
COG4963	6	Flp pilus assembly protein, ATPase CpaE		
COG4964	15	Flp pilus assembly protein, secretin CpaC		
COG4965	16	Flp pilus assembly protein TadB		
COG4966	4	Tfp pilus assembly protein PilW		
COG4967	2	Tfp pilus assembly protein PilV		
COG4968	1	Tfp pilus assembly protein PilE		
COG4969	6	Tfp pilus assembly protein, major pilin PilA		
COG4970	6	Tfp pilus assembly protein FimT		
COG4972	35	Tfp pilus assembly protein, ATPase PilM		
COG4973	20	Site-specific recombinase XerC		
COG4974	53	Site-specific recombinase XerD		
COG4976	5	Predicted methyltransferase (contains TPR repeat)		
COG4977	20	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain		
COG4978	2	Transcriptional regulator, effector-binding domain/component		
COG4984	1	Predicted membrane protein		
COG4985	1	ABC-type phosphate transport system, auxiliary component		
COG4986	6	ABC-type anion transport system, duplicated permease component		
COG4987	2	ABC-type transport system involved in cytochrome bd biosynthesis, fused ATPase and permease components		
COG4989	2	Predicted oxidoreductase		
COG4992	57	Ornithine/acetylornithine aminotransferase		
COG4993	98	Glucose dehydrogenase		
COG4994	1	Uncharacterized protein conserved in bacteria		
COG4995	17	Uncharacterized protein conserved in bacteria		
COG5000	35	Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation		
COG5001	15	Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain		
COG5002	10	Signal transduction histidine kinase		
COG5006	6	Predicted permease, DMT superfamily		
COG5007	4	Predicted transcriptional regulator, BolA superfamily		
COG5008	13	Tfp pilus assembly protein, ATPase PilU		
COG5009	65	Membrane carboxypeptidase/penicillin-binding protein		
COG5011	6	Uncharacterized protein conserved in bacteria		
COG5012	10	Predicted cobalamin binding protein		
COG5013	23	Nitrate reductase alpha subunit		
COG5016	13	Pyruvate/oxaloacetate carboxyltransferase		
COG5021	1	Ubiquitin-protein ligase		
COG5022	1	Myosin heavy chain		
COG5023	1	Tubulin		
COG5045	1	Ribosomal protein S10E		
COG5048	8	FOG: Zn-finger		
COG5108	1	Mitochondrial DNA-directed RNA polymerase		
COG5126	1	Ca2+-binding protein (EF-Hand superfamily)		
COG5159	1	26S proteasome regulatory complex component		
COG5163	1	Protein required for biogenesis of the 60S ribosomal subunit		
COG5171	2	Ran GTPase-activating protein (Ran-binding protein)		
COG5181	1	U2 snRNP spliceosome subunit		
COG5184	24	Alpha-tubulin suppressor and related RCC1 domain-containing proteins		
COG5192	1	GTP-binding protein required for 40S ribosome biogenesis		
COG5212	2	Low-affinity cAMP phosphodiesterase		
COG5239	1	mRNA deadenylase, exonuclease subunit and related nucleases		
COG5256	2	Translation elongation factor EF-1alpha (GTPase)		
COG5262	2	Histone H2A		
COG5263	1	FOG: Glucan-binding domain (YG repeat)		
COG5265	17	ABC-type transport system involved in Fe-S cluster assembly, permease and ATPase components		
COG5267	24	Uncharacterized protein conserved in bacteria		
COG5272	1	Ubiquitin		
COG5276	33	Uncharacterized conserved protein		
COG5277	2	Actin and related proteins		
COG5278	11	Predicted periplasmic ligand-binding sensor domain		
COG5280	1	Phage-related minor tail protein		
COG5282	14	Uncharacterized conserved protein		
COG5285	4	Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin		
COG5297	4	Cellobiohydrolase A (1,4-beta-cellobiosidase A)		
COG5298	3	Uncharacterized protein conserved in bacteria		
COG5304	1	Uncharacterized protein conserved in bacteria		
COG5305	16	Predicted membrane protein		
COG5309	4	Exo-beta-1,3-glucanase		
COG5310	4	Homospermidine synthase		
COG5316	20	Uncharacterized conserved protein		
COG5317	1	Uncharacterized protein conserved in bacteria		
COG5319	3	Uncharacterized protein conserved in bacteria		
COG5322	5	Predicted dehydrogenase		
COG5323	4	Uncharacterized conserved protein		
COG5324	1	Uncharacterized conserved protein		
COG5328	1	Uncharacterized protein conserved in bacteria		
COG5331	1	Uncharacterized protein conserved in bacteria		

COG5336	2	Uncharacterized protein conserved in bacteria		
COG5337	2	Spore coat assembly protein		
COG5340	3	Predicted transcriptional regulator		
COG5342	1	Invasion protein B, involved in pathogenesis		
COG5346	1	Predicted membrane protein		
COG5347	1	GTPase-activating protein that regulates ARFs (ADP-ribosylation factors), involved in ARF-mediated vesicular transport		
COG5350	1	Predicted protein tyrosine phosphatase		
COG5351	3	Uncharacterized protein conserved in bacteria		
COG5352	3	Uncharacterized protein conserved in bacteria		
COG5360	2	Uncharacterized protein conserved in bacteria		
COG5361	8	Uncharacterized conserved protein		
COG5362	3	Phage-related terminase		
COG5368	10	Uncharacterized protein conserved in bacteria		
COG5373	10	Predicted membrane protein		
COG5377	1	Phage-related protein, predicted endonuclease		
COG5383	1	Uncharacterized protein conserved in bacteria		
COG5385	1	Uncharacterized protein conserved in bacteria		
COG5389	1	Uncharacterized protein conserved in bacteria		
COG5394	9	Uncharacterized protein conserved in bacteria		
COG5395	4	Predicted membrane protein		
COG5403	2	Uncharacterized conserved protein		
COG5405	10	ATP-dependent protease HslVU (ClpYQ), peptidase subunit		
COG5410	1	Uncharacterized protein conserved in bacteria		
COG5412	1	Phage-related protein		
COG5421	7	Transposase		
COG5424	6	Pyrroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C		
COG5426	2	Uncharacterized membrane protein		
COG5427	6	Uncharacterized membrane protein		
COG5429	3	Uncharacterized secreted protein		
COG5430	9	Uncharacterized secreted protein		
COG5433	21	Transposase		
COG5434	7	Endopolygalacturonase		
COG5438	4	Predicted multitransmembrane protein		
COG5441	4	Uncharacterized conserved protein		
COG5442	1	Flagellar biosynthesis regulator FlaF		
COG5443	1	Flagellar biosynthesis regulator FlbT		
COG5448	1	Uncharacterized conserved protein		
COG5449	1	Uncharacterized conserved protein		
COG5450	1	Transcription regulator of the Arc/MetJ class		
COG5452	1	Uncharacterized conserved protein		
COG5459	1	Predicted rRNA methylase		
COG5462	1	Predicted secreted (periplasmic) protein		
COG5465	2	Uncharacterized conserved protein		
COG5466	1	Predicted small metal-binding protein		
COG5468	1	Predicted secreted (periplasmic) protein		
COG5470	12	Uncharacterized conserved protein		
COG5472	2	Predicted small integral membrane protein		
COG5473	5	Predicted integral membrane protein		
COG5476	20	Uncharacterized conserved protein		
COG5478	4	Predicted small integral membrane protein		
COG5479	14	Uncharacterized protein potentially involved in peptidoglycan biosynthesis		
COG5483	4	Uncharacterized conserved protein		
COG5485	16	Predicted ester cyclase		
COG5486	11	Predicted metal-binding integral membrane protein		
COG5488	6	Integral membrane protein		
COG5490	1	Uncharacterized conserved protein		
COG5492	6	Bacterial surface proteins containing Ig-like domains		
COG5495	8	Uncharacterized conserved protein		
COG5496	9	Predicted thioesterase		
COG5499	5	Predicted transcription regulator containing HTH domain		
COG5501	3	Predicted secreted protein		
COG5507	5	Uncharacterized conserved protein		
COG5511	6	Bacteriophage capsid protein		
COG5512	3	Zn-ribbon-containing, possibly RNA-binding protein and truncated derivatives		
COG5513	1	Predicted secreted protein		
COG5514	3	Uncharacterized conserved protein		
COG5516	4	Conserved protein containing a Zn-ribbon-like motif, possibly RNA-binding		
COG5517	9	Small subunit of phenylpropionate dioxygenase		
COG5518	1	Bacteriophage capsid portal protein		
COG5520	3	O-Glycosyl hydrolase		
COG5522	4	Predicted integral membrane protein		
COG5525	12	Bacteriophage tail assembly protein		
COG5526	2	Uncharacterized conserved protein		
COG5528	2	Predicted integral membrane protein		
COG5531	1	SWIB-domain-containing proteins implicated in chromatin remodeling		
COG5542	1	Predicted integral membrane protein		
COG5545	1	Predicted P-loop ATPase and inactivated derivatives		
COG5549	1	Predicted Zn-dependent protease		
COG5552	4	Uncharacterized conserved protein		
COG5553	11	Predicted metal-dependent enzyme of the double-stranded beta helix superfamily		
COG5557	44	Polysulphide reductase		
COG5563	12	Predicted integral membrane proteins containing uncharacterized repeats		
COG5564	2	Predicted TIM-barrel enzyme, possibly a dioxygenase		
COG5569	4	Uncharacterized conserved protein		

COG5572	1	Predicted integral membrane protein		
COG5573	3	Predicted nucleic-acid-binding protein, contains PIN domain		
COG5576	1	Homeodomain-containing transcription factor		
COG5579	3	Uncharacterized conserved protein		
COG5581	2	Predicted glycosyltransferase		
COG5583	1	Uncharacterized small protein		
COG5585	1	NAD+--asparagine ADP-ribosyltransferase		
COG5587	6	Uncharacterized conserved protein		
COG5588	13	Uncharacterized conserved protein		
COG5590	1	Uncharacterized conserved protein		
COG5591	3	Uncharacterized conserved protein		
COG5592	3	Uncharacterized conserved protein		
COG5598	22	Trimethylamine:corrinoid methyltransferase		
COG5605	2	Predicted small integral membrane protein		
COG5606	2	Uncharacterized conserved small protein		
COG5607	4	Uncharacterized conserved protein		
COG5609	2	Uncharacterized conserved protein		
COG5611	1	Predicted nucleic-acid-binding protein, contains PIN domain		
COG5615	1	Predicted integral membrane protein		
COG5616	71	Predicted integral membrane protein		
COG5619	1	Uncharacterized conserved protein		
COG5621	12	Predicted secreted hydrolase		
COG5632	1	N-acetylmuramoyl-L-alanine amidase		
COG5635	13	Predicted NTPase (NACHT family)		
COG5637	9	Predicted integral membrane protein		
COG5640	9	Secreted trypsin-like serine protease		
COG5642	2	Uncharacterized conserved protein		
COG5646	5	Uncharacterized conserved protein		
COG5649	6	Uncharacterized conserved protein		
COG5650	3	Predicted integral membrane protein		
COG5651	1	PPE-repeat proteins		
COG5652	5	Predicted integral membrane protein		
COG5653	2	Protein involved in cellulose biosynthesis (CelD)		
COG5654	4	Uncharacterized conserved protein		
COG5655	1	Plasmid rolling circle replication initiator protein and truncated derivatives		
COG5658	1	Predicted integral membrane protein		
COG5659	30	FOG: Transposase		
COG5660	3	Predicted integral membrane protein		
COG5662	12	Predicted transmembrane transcriptional regulator (anti-sigma factor)		

Functional categories	Sequence count	COG categories
A	RNA processing and modification	18
B	Chromatin structure and dynamics	50
C	Energy production and conversion	7775
D	Cell cycle control, cell division, chromosome partitioning	692
E	Amino acid transport and metabolism	9706
F	Nucleotide transport and metabolism	1913
G	Carbohydrate transport and metabolism	5688
H	Coenzyme transport and metabolism	3083
I	Lipid transport and metabolism	4336
J	Translation, ribosomal structure and biogenesis	4051
K	Transcription	3471
L	Replication, recombination and repair	4751
M	Cell wall/membrane/envelope biogenesis	5688
N	Cell motility	1097
O	Posttranslational modification, protein turnover, chaperones	3454
P	Inorganic ion transport and metabolism	3709
Q	Secondary metabolites biosynthesis, transport and catabolism	2264
R	General function prediction only	9923

S	Function unknown	6105
T	Signal transduction mechanisms	4559
U	Intracellular trafficking, secretion, and vesicular transport	841
V	Defense mechanisms	1888
Z	Cytoskeleton	4



K00001	181	alcohol dehydrogenase [EC:1.1.1.1]		
K00002	3	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]		
K00003	74	homoserine dehydrogenase [EC:1.1.1.3]		
K00004	3	(R,R)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4		
K00005	10	glycerol dehydrogenase [EC:1.1.1.6]		
K00008	37	L-iditol 2-dehydrogenase [EC:1.1.1.14]		
K00009	4	mannitol-1-phosphate 5-dehydrogenase [EC:1.1.1.17]		
K00010	96	myo-inositol 2-dehydrogenase [EC:1.1.1.18]		
K00011	4	aldehyde reductase [EC:1.1.1.21]		
K00012	45	UDPglucose 6-dehydrogenase [EC:1.1.1.22]		
K00013	43	histidinol dehydrogenase [EC:1.1.1.23]		
K00014	37	shikimate dehydrogenase [EC:1.1.1.25]		
K00015	39	glyoxylate reductase [EC:1.1.1.26]		
K00016	26	L-lactate dehydrogenase [EC:1.1.1.27]		
K00018	11	glycerate dehydrogenase [EC:1.1.1.29]		
K00019	33	3-hydroxybutyrate dehydrogenase [EC:1.1.1.30]		
K00020	92	3-hydroxyisobutyrate dehydrogenase [EC:1.1.1.31]		
K00021	14	3-hydroxy-3-methylglutaryl-CoA reductase [EC:1.1.1.34]		
K00023	24	acetoacetyl-CoA reductase [EC:1.1.1.36]		
K00024	35	malate dehydrogenase [EC:1.1.1.37]		
K00027	40	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]		
K00028	4	malate dehydrogenase (decarboxylating) [EC:1.1.1.39]		
K00029	39	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)		
K00030	19	isocitrate dehydrogenase (NAD+) [EC:1.1.1.41]		
K00031	37	isocitrate dehydrogenase [EC:1.1.1.42]		
K00032	1	phosphogluconate 2-dehydrogenase [EC:1.1.1.43]		
K00033	37	6-phosphogluconate dehydrogenase [EC:1.1.1.44]		
K00034	25	glucose 1-dehydrogenase [EC:1.1.1.47]		
K00035	1	D-galactose 1-dehydrogenase [EC:1.1.1.48]		
K00036	118	glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49]		
K00037	2	3-alpha-hydroxysteroid dehydrogenase [EC:1.1.1.50]		
K00038	6	3alpha(or 20beta)-hydroxysteroid dehydrogenase [EC:1.1.1.53]		
K00040	4	fructuronate reductase [EC:1.1.1.57]		
K00042	60	2-hydroxy-3-oxopropionate reductase [EC:1.1.1.60]		
K00043	6	4-hydroxybutyrate dehydrogenase [EC:1.1.1.61]		
K00044	10	estradiol 17beta-dehydrogenase [EC:1.1.1.62]		
K00045	4	mannitol 2-dehydrogenase [EC:1.1.1.67]		
K00046	33	gluconate 5-dehydrogenase [EC:1.1.1.69]		
K00048	20	lactaldehyde reductase [EC:1.1.1.77]		
K00050	46	hydroxypyruvate reductase [EC:1.1.1.81]		
K00051	10	malate dehydrogenase (NADP+) [EC:1.1.1.82]		
K00052	66	3-isopropylmalate dehydrogenase [EC:1.1.1.85]		
K00053	17	ketol-acid reductoisomerase [EC:1.1.1.86]		
K00054	7	hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]		
K00055	2	aryl-alcohol dehydrogenase [EC:1.1.1.90]		
K00057	38	glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94]		
K00058	145	D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]		
K00059	312	3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]		
K00060	50	threonine 3-dehydrogenase [EC:1.1.1.103]		
K00064	7	D-threo-aldose 1-dehydrogenase [EC:1.1.1.122]		

K00065	29	2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]		
K00066	25	GDP-mannose 6-dehydrogenase [EC:1.1.1.132]		
K00067	36	dTDP-4-dehydrorhamnose reductase [EC:1.1.1.133]		
K00068	7	sorbitol-6-phosphate 2-dehydrogenase [EC:1.1.1.140]		
K00071	3	11beta-hydroxysteroid dehydrogenase [EC:1.1.1.146]		
K00073	35	ureidoglycolate dehydrogenase [EC:1.1.1.154]		
K00074	63	3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]		
K00075	37	UDP-N-acetylmuramate dehydrogenase [EC:1.1.1.158]		
K00076	5	7-alpha-hydroxysteroid dehydrogenase [EC:1.1.1.159]		
K00077	44	2-dehydropantoate 2-reductase [EC:1.1.1.169]		
K00079	12	carbonyl reductase (NADPH) [EC:1.1.1.184]		
K00082	9	5-amino-6-(5-phosphoribosylamino)uracil reductase [EC:1.1.1.193]		
K00083	2	cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]		
K00086	5	1,3-propanediol dehydrogenase [EC:1.1.1.202]		
K00087	105	xanthine dehydrogenase molybdenum-binding subunit [EC:1.17.1.4]		
K00088	84	IMP dehydrogenase [EC:1.1.1.205]		
K00090	13	gluconate 2-dehydrogenase [EC:1.1.1.215]		
K00091	22	dihydroflavonol-4-reductase [EC:1.1.1.219]		
K00094	1	galactitol-1-phosphate 5-dehydrogenase [EC:1.1.1.251]		
K00096	3	glycerol-1-phosphate dehydrogenase [NAD(P)] [EC:1.1.1.261]		
K00097	42	4-hydroxythreonine-4-phosphate dehydrogenase [EC:1.1.1.262]		
K00098	4	L-idonate 5-dehydrogenase [EC:1.1.1.264]		
K00099	51	1-deoxy-D-xylulose-5-phosphate reductoisomerase [EC:1.1.1.267]		
K00100	439	Unclassified; E1.1.1.-		
K00101	50	L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]		
K00102	85	D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]		
K00103	10	L-gulonolactone oxidase [EC:1.1.3.8]		
K00104	91	glycolate oxidase [EC:1.1.3.15]		
K00105	3	alpha-glycerophosphate oxidase [EC:1.1.3.21]		
K00108	51	choline dehydrogenase [EC:1.1.99.1]		
K00109	14	2-hydroxyglutarate dehydrogenase [EC:1.1.99.2]		
K00111	53	glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]		
K00112	2	glycerol-3-phosphate dehydrogenase subunit B [EC:1.1.5.3]		
K00113	10	glycerol-3-phosphate dehydrogenase subunit C [EC:1.1.5.3]		
K00114	80	alcohol dehydrogenase (acceptor) [EC:1.1.99.8]		
K00116	24	malate dehydrogenase (quinone) [EC:1.1.5.4]		
K00117	55	quinoprotein glucose dehydrogenase [EC:1.1.5.2]		
K00118	12	glucose-fructose oxidoreductase [EC:1.1.99.28]		
K00119	103	Unclassified; E1.1.99.-		
K00120	82	Unclassified; E1.1.-.-		
K00121	49	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase		
K00122	100	formate dehydrogenase [EC:1.2.1.2]		
K00123	164	formate dehydrogenase, alpha subunit [EC:1.2.1.2]		
K00124	24	formate dehydrogenase, beta subunit [EC:1.2.1.2]		
K00127	21	formate dehydrogenase, gamma subunit [EC:1.2.1.2]		
K00128	152	aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]		
K00129	2	aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]		
K00130	60	betaine-aldehyde dehydrogenase [EC:1.2.1.8]		
K00131	21	glyceraldehyde-3-phosphate dehydrogenase (NADP) [EC:1.2.1.9]		
K00132	6	acetaldehyde dehydrogenase (acetylating) [EC:1.2.1.10]		

K00133	35	aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]		
K00134	29	glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]		
K00135	94	succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]		
K00137	5	aminobutyraldehyde dehydrogenase [EC:1.2.1.19]		
K00138	6	aldehyde dehydrogenase [EC:1.2.1.-]		
K00140	32	methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.27]		
K00141	6	benzaldehyde dehydrogenase (NAD) [EC:1.2.1.28]		
K00145	50	N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]		
K00146	17	phenylacetaldehyde dehydrogenase [EC:1.2.1.39]		
K00147	25	glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41]		
K00148	5	glutathione-independent formaldehyde dehydrogenase [EC:1.2.1.46]		
K00150	2	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]		
K00151	15	5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase		
K00152	5	salicylaldehyde dehydrogenase [EC:1.2.1.65]		
K00153	7	NAD/factor-dependent formaldehyde dehydrogenase [EC:1.2.1.66]		
K00154	3	coniferyl-aldehyde dehydrogenase [EC:1.2.1.68]		
K00155	81	Unclassified; E1.2.1.-		
K00156	27	pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]		
K00157	22	aldehyde oxidase [EC:1.2.3.1]		
K00158	6	pyruvate oxidase [EC:1.2.3.3]		
K00161	65	pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]		
K00162	66	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]		
K00163	45	pyruvate dehydrogenase E1 component [EC:1.2.4.1]		
K00164	41	2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]		
K00166	32	2-oxoisovalerate dehydrogenase E1 component, alpha subunit		
K00167	31	2-oxoisovalerate dehydrogenase E1 component, beta subunit		
K00169	37	pyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.1]		
K00170	17	pyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.1]		
K00171	15	pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]		
K00172	16	pyruvate ferredoxin oxidoreductase, gamma subunit [EC:1.2.7.1]		
K00174	70	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]		
K00175	41	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]		
K00176	10	2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7.3]		
K00177	12	2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]		
K00178	23	oxidoreductase containing iron-sulfur protein [EC:1.2.7.-]		
K00179	43	indolepyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.8]		
K00180	23	indolepyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.8]		
K00183	52	molybdopterin oxidoreductase, molybdopterin binding subunit		
K00184	53	molybdopterin oxidoreductase, iron-sulfur binding subunit		
K00185	44	molybdopterin oxidoreductase, membrane subunit [EC:1.2.7.-]		
K00186	10	2-oxoisovalerate ferredoxin oxidoreductase, alpha subunit		
K00187	7	2-oxoisovalerate ferredoxin oxidoreductase, beta subunit		
K00191	7	CO-methylating acetyl-CoA synthase [EC:2.3.1.169]		
K00194	1	carbon-monoxide dehydrogenase delta subunit [EC:1.2.99.2]		
K00197	5	carbon-monoxide dehydrogenase gamma subunit [EC:1.2.99.2]		
K00198	3	carbon-monoxide dehydrogenase catalytic subunit [EC:1.2.99.2]		
K00200	8	formylmethanofuran dehydrogenase subunit A [EC:1.2.99.5]		
K00201	1	formylmethanofuran dehydrogenase subunit B [EC:1.2.99.5]		
K00202	2	formylmethanofuran dehydrogenase subunit C [EC:1.2.99.5]		
K00206	1	Unclassified; E1.2.-.-		

K00207	10	dihydropyrimidine dehydrogenase (NADP+) [EC:1.3.1.2]		
K00208	71	enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9]		
K00209	3	enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific)		
K00210	23	prephenate dehydrogenase [EC:1.3.1.12]		
K00214	1	biliverdin reductase [EC:1.3.1.24]		
K00215	29	dihydrodipicolinate reductase [EC:1.3.1.26]		
K00216	2	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [EC:1.3.1.28]		
K00217	4	maleylacetate reductase [EC:1.3.1.32]		
K00218	9	protochlorophyllide reductase [EC:1.3.1.33]		
K00219	58	2,4-dienoyl-CoA reductase (NADPH2) [EC:1.3.1.34]		
K00220	4	cyclohexadienyl dehydrogenase [EC:1.3.1.43]		
K00224	11	Unclassified; E1.3.1.-		
K00226	72	dihydroorotate oxidase [EC:1.3.3.1]		
K00227	3	lathosterol oxidase [EC:1.14.21.6]		
K00228	17	coproporphyrinogen III oxidase [EC:1.3.3.3]		
K00230	8	protoporphyrinogen oxidase [EC:1.3.3.4]		
K00231	27	protoporphyrinogen oxidase [EC:1.3.3.4]		
K00232	1	acyl-CoA oxidase [EC:1.3.3.6]		
K00239	70	succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]		
K00240	31	succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]		
K00241	21	succinate dehydrogenase cytochrome b-556 subunit [EC:1.3.99.1]		
K00242	5	succinate dehydrogenase hydrophobic membrane anchor protein		
K00244	39	fumarate reductase flavoprotein subunit [EC:1.3.99.1]		
K00245	7	fumarate reductase iron-sulfur protein [EC:1.3.99.1]		
K00246	13	fumarate reductase subunit C [EC:1.3.99.1]		
K00247	5	fumarate reductase subunit D [EC:1.3.99.1]		
K00248	107	butyryl-CoA dehydrogenase [EC:1.3.99.2]		
K00249	223	acyl-CoA dehydrogenase [EC:1.3.99.3]		
K00252	32	glutaryl-CoA dehydrogenase [EC:1.3.99.7]		
K00253	67	isovaleryl-CoA dehydrogenase [EC:1.3.99.10]		
K00255	14	long-chain-acyl-CoA dehydrogenase [EC:1.3.99.13]		
K00256	109	isoquinoline 1-oxidoreductase [EC:1.3.99.16]		
K00257	333	Unclassified; E1.3.99.-		
K00258	29	Unclassified; E1.3.-.-		
K00259	29	alanine dehydrogenase [EC:1.4.1.1]		
K00260	63	glutamate dehydrogenase [EC:1.4.1.2]		
K00261	38	glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]		
K00262	26	glutamate dehydrogenase (NADP+) [EC:1.4.1.4]		
K00263	17	leucine dehydrogenase [EC:1.4.1.9]		
K00265	89	glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14]		
K00266	101	glutamate synthase (NADPH/NADH) small chain [EC:1.4.1.13 1.4.1.14]		
K00271	14	valine dehydrogenase [EC:1.4.1.-]		
K00273	15	D-amino-acid oxidase [EC:1.4.3.3]		
K00274	21	monoamine oxidase [EC:1.4.3.4]		
K00275	18	pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]		
K00276	60	primary-amine oxidase [EC:1.4.3.21]		
K00278	44	L-aspartate oxidase [EC:1.4.3.16]		
K00279	15	cytokinin dehydrogenase [EC:1.5.99.12]		
K00280	8	Unclassified; E1.4.3.-		
K00281	24	glycine dehydrogenase [EC:1.4.4.2]		

K00282	30	glycine dehydrogenase subunit 1 [EC:1.4.4.2]		
K00283	25	glycine dehydrogenase subunit 2 [EC:1.4.4.2]		
K00284	28	glutamate synthase (ferredoxin) [EC:1.4.7.1]		
K00285	34	D-amino-acid dehydrogenase [EC:1.4.99.1]		
K00286	27	pyrroline-5-carboxylate reductase [EC:1.5.1.2]		
K00287	56	dihydrofolate reductase [EC:1.5.1.3]		
K00290	30	saccharopine dehydrogenase (NAD+, L-lysine forming) [EC:1.5.1.7]		
K00292	2	saccharopine dehydrogenase (NAD+, L-glutamate forming) [EC:1.5.1.9]		
K00294	69	1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]		
K00297	67	methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]		
K00299	34	FMN reductase [EC:1.5.1.29]		
K00301	35	sarcosine oxidase [EC:1.5.3.1]		
K00302	11	sarcosine oxidase, subunit alpha [EC:1.5.3.1]		
K00303	37	sarcosine oxidase, subunit beta [EC:1.5.3.1]		
K00304	2	sarcosine oxidase, subunit delta [EC:1.5.3.1]		
K00305	1	sarcosine oxidase, subunit gamma [EC:1.5.3.1]		
K00309	57	Unclassified; E1.5.3.-		
K00311	35	electron-transferring-flavoprotein dehydrogenase [EC:1.5.5.1]		
K00313	5	electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]		
K00314	44	sarcosine dehydrogenase [EC:1.5.99.1]		
K00315	21	dimethylglycine dehydrogenase [EC:1.5.99.2]		
K00317	11	trimethylamine dehydrogenase [EC:1.5.8.2]		
K00318	21	proline dehydrogenase [EC:1.5.99.8]		
K00320	25	coenzyme F420-dependent N5,N10-methenyltetrahydromethanopterin		
K00321	1	Unclassified; E1.5.99.-		
K00322	12	NAD(P) transhydrogenase [EC:1.6.1.1]		
K00324	34	NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]		
K00325	18	NAD(P) transhydrogenase subunit beta [EC:1.6.1.2]		
K00326	1	cytochrome-b5 reductase [EC:1.6.2.2]		
K00327	1	NADPH-ferrihemoprotein reductase [EC:1.6.2.4]		
K00329	36	NADH dehydrogenase [EC:1.6.5.3]		
K00330	25	NADH dehydrogenase I subunit A [EC:1.6.5.3]		
K00331	27	NADH dehydrogenase I subunit B [EC:1.6.5.3]		
K00332	21	NADH dehydrogenase I subunit C [EC:1.6.5.3]		
K00333	64	NADH dehydrogenase I subunit D [EC:1.6.5.3]		
K00334	43	NADH dehydrogenase I subunit E [EC:1.6.5.3]		
K00335	80	NADH dehydrogenase I subunit F [EC:1.6.5.3]		
K00336	63	NADH dehydrogenase I subunit G [EC:1.6.5.3]		
K00337	55	NADH dehydrogenase I subunit H [EC:1.6.5.3]		
K00338	26	NADH dehydrogenase I subunit I [EC:1.6.5.3]		
K00339	20	NADH dehydrogenase I subunit J [EC:1.6.5.3]		
K00340	15	NADH dehydrogenase I subunit K [EC:1.6.5.3]		
K00341	57	NADH dehydrogenase I subunit L [EC:1.6.5.3]		
K00342	63	NADH dehydrogenase I subunit M [EC:1.6.5.3]		
K00343	62	NADH dehydrogenase I subunit N [EC:1.6.5.3]		
K00344	170	NADPH2:quinone reductase [EC:1.6.5.5]		
K00346	2	Na+-transporting NADH:ubiquinone oxidoreductase subunit A		
K00347	10	Na+-transporting NADH:ubiquinone oxidoreductase subunit B		
K00348	7	Na+-transporting NADH:ubiquinone oxidoreductase subunit C		
K00349	2	Na+-transporting NADH:ubiquinone oxidoreductase subunit D		

K00350	9	Na+-transporting NADH:ubiquinone oxidoreductase subunit E		
K00351	4	Na+-transporting NADH:ubiquinone oxidoreductase subunit F		
K00353	1	Unclassified; E1.6.6.-		
K00354	18	NADPH2 dehydrogenase [EC:1.6.99.1]		
K00355	4	NAD(P)H dehydrogenase (quinone) [EC:1.6.5.2]		
K00356	59	NADH dehydrogenase [EC:1.6.99.3]		
K00358	10	Unclassified; E1.6.99.-		
K00359	38	NADH oxidase [EC:1.6.-.-]		
K00360	39	nitrate reductase (NADH) [EC:1.7.1.1]		
K00362	26	nitrite reductase (NAD(P)H) large subunit [EC:1.7.1.4]		
K00363	13	nitrite reductase (NAD(P)H) small subunit [EC:1.7.1.4]		
K00364	4	GMP reductase [EC:1.7.1.7]		
K00365	9	urate oxidase [EC:1.7.3.3]		
K00366	23	ferredoxin-nitrite reductase [EC:1.7.7.1]		
K00367	5	ferredoxin-nitrate reductase [EC:1.7.7.2]		
K00368	53	nitrite reductase (NO-forming) [EC:1.7.2.1]		
K00369	45	nitrate reductase [EC:1.7.99.4]		
K00370	34	nitrate reductase 1, alpha subunit [EC:1.7.99.4]		
K00371	12	nitrate reductase 1, beta subunit [EC:1.7.99.4]		
K00372	36	nitrate reductase catalytic subunit [EC:1.7.99.4]		
K00373	4	nitrate reductase 1, delta subunit [EC:1.7.99.4]		
K00374	4	nitrate reductase 1, gamma subunit [EC:1.7.99.4]		
K00375	33	GntR family transcriptional regulator / MocR family aminotransferase		
K00376	14	nitrous-oxide reductase [EC:1.7.99.6]		
K00378	3	hydroxylamine reductase [EC:1.7.-.-]		
K00380	19	sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]		
K00381	24	sulfite reductase (NADPH) hemoprotein beta-component [EC:1.8.1.2]		
K00382	97	dihydrolipoamide dehydrogenase [EC:1.8.1.4]		
K00383	19	glutathione reductase (NADPH) [EC:1.8.1.7]		
K00384	111	thioredoxin reductase (NADPH) [EC:1.8.1.9]		
K00385	1	anaerobic sulfite reductase subunit C [EC:1.8.1.-]		
K00386	20	Unclassified; E1.8.2.-		
K00387	22	sulfite oxidase [EC:1.8.3.1]		
K00389	9	putative membrane protein		
K00390	17	phosphoadenosine phosphosulfate reductase [EC:1.8.4.8]		
K00391	5	Unclassified; E1.8.4.-		
K00392	14	sulfite reductase (ferredoxin) [EC:1.8.7.1]		
K00394	11	adenylylsulfate reductase, subunit A [EC:1.8.99.2]		
K00395	3	adenylylsulfate reductase, subunit B [EC:1.8.99.2]		
K00397	12	anaerobic dimethyl sulfoxide reductase [EC:1.8.99.-]		
K00404	16	cb-type cytochrome c oxidase subunit I [EC:1.9.3.1]		
K00405	17	cb-type cytochrome c oxidase subunit II [EC:1.9.3.1]		
K00406	34	cb-type cytochrome c oxidase subunit III [EC:1.9.3.1]		
K00407	6	cb-type cytochrome c oxidase subunit IV [EC:1.9.3.1]		
K00411	10	ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.2]		
K00412	35	ubiquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.2]		
K00413	8	ubiquinol-cytochrome c reductase cytochrome c1 subunit [EC:1.10.2.2]		
K00421	4	Unclassified; E1.10.2.-		
K00423	22	L-ascorbate oxidase [EC:1.10.3.3]		
K00425	39	cytochrome bd-I oxidase subunit I [EC:1.10.3.-]		

K00426	23	cytochrome bd-I oxidase subunit II [EC:1.10.3.-]		
K00427	2	L-lactate permease		
K00428	51	cytochrome c peroxidase [EC:1.11.1.5]		
K00429	1	catalase [EC:1.11.1.6]		
K00432	7	glutathione peroxidase [EC:1.11.1.9]		
K00433	36	chloride peroxidase [EC:1.11.1.10]		
K00435	19	peroxiredoxin [EC:1.11.1.-]		
K00436	91	hydrogen dehydrogenase [EC:1.12.1.2]		
K00437	8	cytochrome-c3 hydrogenase [EC:1.12.2.1]		
K00441	4	coenzyme F420 hydrogenase beta subunit [EC:1.12.98.1]		
K00442	3	coenzyme F420 hydrogenase delta subunit		
K00446	7	catechol 2,3-dioxygenase [EC:1.13.11.2]		
K00448	10	protocatechuate 3,4-dioxygenase, alpha subunit [EC:1.13.11.3]		
K00449	6	protocatechuate 3,4-dioxygenase, beta subunit [EC:1.13.11.3]		
K00450	24	gentisate 1,2-dioxygenase [EC:1.13.11.4]		
K00451	27	homogentisate 1,2-dioxygenase [EC:1.13.11.5]		
K00453	11	tryptophan 2,3-dioxygenase [EC:1.13.11.11]		
K00455	1	3,4-dihydroxyphenylacetate 2,3-dioxygenase [EC:1.13.11.15]		
K00457	19	4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]		
K00459	54	nitronate monooxygenase [EC:1.13.12.16]		
K00462	4	biphenyl-2,3-diol 1,2-dioxygenase [EC:1.13.11.39]		
K00464	2	lignostilbene-alpha,beta-dioxygenase [EC:1.13.11.43]		
K00465	24	Unclassified; E1.13.11.-		
K00466	5	tryptophan 2-monooxygenase [EC:1.13.12.3]		
K00467	12	lactate 2-monooxygenase [EC:1.13.12.4]		
K00470	8	Unclassified; E1.14.1.-		
K00476	1	aspartate beta-hydroxylase [EC:1.14.11.16]		
K00477	2	phytanoyl-CoA hydroxylase [EC:1.14.11.18]		
K00478	6	Unclassified; E1.14.11.-		
K00479	6	Rieske 2Fe-2S family protein		
K00480	28	salicylate hydroxylase [EC:1.14.13.1]		
K00481	6	p-hydroxybenzoate 3-monooxygenase [EC:1.14.13.2]		
K00483	31	4-hydroxyphenylacetate-3-hydroxylase large chain [EC:1.14.13.3]		
K00484	2	4-hydroxyphenylacetate-3-hydroxylase small chain [EC:1.14.13.3]		
K00485	11	dimethylaniline monooxygenase (N-oxide forming) [EC:1.14.13.8]		
K00491	2	nitric-oxide synthase, bacterial [EC:1.14.13.39]		
K00492	81	Unclassified; E1.14.13.-		
K00493	46	unspecific monooxygenase [EC:1.14.14.1]		
K00494	70	alkanal monooxygenase (FMN-linked) [EC:1.14.14.3]		
K00495	10	Unclassified; E1.14.14.-		
K00499	10	choline monooxygenase [EC:1.14.15.7]		
K00500	17	phenylalanine-4-hydroxylase [EC:1.14.16.1]		
K00504	76	peptidylglycine monooxygenase [EC:1.14.17.3]		
K00507	40	stearoyl-CoA desaturase (delta-9 desaturase) [EC:1.14.19.1]		
K00508	4	linoleoyl-CoA desaturase [EC:1.14.19.3]		
K00514	1	zeta-carotene desaturase [EC:1.14.99.30]		
K00517	179	Unclassified; E1.14.-.-		
K00520	60	mercuric reductase [EC:1.16.1.1]		
K00523	25	CDP-4-dehydro-6-deoxyglucose reductase [EC:1.17.1.1]		
K00525	87	ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]		

K00526	14	ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1]		
K00527	5	ribonucleoside-triphosphate reductase [EC:1.17.4.2]		
K00528	42	ferredoxin--NADP+ reductase [EC:1.18.1.2]		
K00529	61	ferredoxin--NAD+ reductase [EC:1.18.1.3]		
K00530	11	Unclassified; E1.18.1.-		
K00532	22	ferredoxin hydrogenase [EC:1.12.7.2]		
K00533	4	ferredoxin hydrogenase large subunit [EC:1.12.7.2]		
K00534	11	ferredoxin hydrogenase small subunit [EC:1.12.7.2]		
K00535	2	Unclassified; E1.18.-.-		
K00537	7	arsenate reductase [EC:1.20.4.1]		
K00538	5	formate acetyltransferase activating enzyme [EC:1.97.1.4]		
K00539	1	Unclassified; E1.97.1.-		
K00540	1132	Unclassified; E1.-.-.-		
K00544	5	betaine-homocysteine S-methyltransferase [EC:2.1.1.5]		
K00547	33	homocysteine S-methyltransferase [EC:2.1.1.10]		
K00548	117	5-methyltetrahydrofolate--homocysteine methyltransferase		
K00549	72	5-methyltetrahydropteroyltriglutamate--homocysteine		
K00551	21	phosphatidylethanolamine N-methyltransferase [EC:2.1.1.17]		
K00554	30	tRNA (guanine-N1-)-methyltransferase [EC:2.1.1.31]		
K00556	3	tRNA (guanosine-2'-O-)-methyltransferase [EC:2.1.1.34]		
K00557	12	tRNA (uracil-5-)-methyltransferase [EC:2.1.1.35]		
K00558	15	DNA (cytosine-5-)-methyltransferase [EC:2.1.1.37]		
K00559	1	sterol 24-C-methyltransferase [EC:2.1.1.41]		
K00560	9	thymidylate synthase [EC:2.1.1.45]		
K00561	14	rRNA (adenine-N6-)-methyltransferase [EC:2.1.1.48]		
K00563	4	rRNA (guanine-N1-)-methyltransferase [EC:2.1.1.51]		
K00564	1	ribosomal RNA small subunit methyltransferase C [EC:2.1.1.52]		
K00566	48	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase		
K00567	30	methylated-DNA-[protein]-cysteine S-methyltransferase [EC:2.1.1.63]		
K00568	65	3-demethylubiquinone-9 3-methyltransferase [EC:2.1.1.- 2.1.1.64]		
K00569	4	thiopurine S-methyltransferase [EC:2.1.1.67]		
K00570	5	phosphatidyl-N-methylethanolamine N-methyltransferase [EC:2.1.1.71]		
K00571	26	site-specific DNA-methyltransferase (adenine-specific) [EC:2.1.1.72]		
K00573	52	protein-L-isoaspartate(D-aspartate) O-methyltransferase		
K00574	63	cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79]		
K00575	79	chemotaxis protein methyltransferase CheR [EC:2.1.1.80]		
K00584	1	tetrahydromethanopterin S-methyltransferase subunit H [EC:2.1.1.86]		
K00587	7	protein-S-isoprenylcysteine O-methyltransferase [EC:2.1.1.100]		
K00588	15	caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]		
K00590	11	site-specific DNA-methyltransferase (cytosine-N4-specific)		
K00594	3	xylitol oxidase [EC:1.1.3.41]		
K00595	6	precorrin-6Y C5,15-methyltransferase / precorrin-8W decarboxylase		
K00596	3	2,2-dialkylglycine decarboxylase (pyruvate) [EC:4.1.1.64]		
K00598	16	trans-aconitate 2-methyltransferase [EC:2.1.1.144]		
K00599	435	Unclassified; E2.1.1.-		
K00600	49	glycine hydroxymethyltransferase [EC:2.1.2.1]		
K00602	28	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP		
K00603	20	glutamate formiminotransferase [EC:2.1.2.5]		
K00604	50	methionyl-tRNA formyltransferase [EC:2.1.2.9]		
K00605	69	aminomethyltransferase [EC:2.1.2.10]		

K00606	26	3-methyl-2-oxobutanoate hydroxymethyltransferase [EC:2.1.2.11]		
K00607	3	Unclassified; E2.1.2.-		
K00609	35	aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]		
K00610	12	aspartate carbamoyltransferase regulatory subunit		
K00611	50	ornithine carbamoyltransferase [EC:2.1.3.3]		
K00612	37	carbamoyltransferase [EC:2.1.3.-]		
K00613	1	glycine amidinotransferase [EC:2.1.4.1]		
K00614	13	Unclassified; E2.1.-.-		
K00615	102	transketolase [EC:2.2.1.1]		
K00616	40	transaldolase [EC:2.2.1.2]		
K00617	1	Unclassified; E2.2.1.-		
K00619	22	amino-acid N-acetyltransferase [EC:2.3.1.1]		
K00620	31	glutamate N-acetyltransferase / amino-acid N-acetyltransferase		
K00622	5	arylamine N-acetyltransferase [EC:2.3.1.5]		
K00625	21	phosphate acetyltransferase [EC:2.3.1.8]		
K00626	211	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]		
K00627	68	pyruvate dehydrogenase E2 component (dihydrolipoamide		
K00631	12	glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]		
K00632	93	acetyl-CoA acyltransferase [EC:2.3.1.16]		
K00633	18	galactoside O-acetyltransferase [EC:2.3.1.18]		
K00634	11	phosphate butyryltransferase [EC:2.3.1.19]		
K00638	6	chloramphenicol O-acetyltransferase [EC:2.3.1.28]		
K00639	42	glycine C-acetyltransferase [EC:2.3.1.29]		
K00640	27	serine O-acetyltransferase [EC:2.3.1.30]		
K00641	37	homoserine O-acetyltransferase [EC:2.3.1.31]		
K00643	12	5-aminolevulinate synthase [EC:2.3.1.37]		
K00645	48	[acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]		
K00647	39	3-oxoacyl-[acyl-carrier-protein] synthase I [EC:2.3.1.41]		
K00648	79	3-oxoacyl-[acyl-carrier-protein] synthase III [EC:2.3.1.180]		
K00651	3	homoserine O-succinyltransferase [EC:2.3.1.46]		
K00652	51	8-amino-7-oxononanoate synthase [EC:2.3.1.47]		
K00654	7	serine palmitoyltransferase [EC:2.3.1.50]		
K00655	121	1-acyl-sn-glycerol-3-phosphate acyltransferase [EC:2.3.1.51]		
K00656	38	formate C-acetyltransferase [EC:2.3.1.54]		
K00657	13	diamine N-acetyltransferase [EC:2.3.1.57]		
K00658	41	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide		
K00660	12	chalcone synthase [EC:2.3.1.74]		
K00661	8	maltose O-acetyltransferase [EC:2.3.1.79]		
K00662	3	aminoglycoside N3'-acetyltransferase [EC:2.3.1.81]		
K00663	9	aminoglycoside N6'-acetyltransferase [EC:2.3.1.82]		
K00666	187	fatty-acyl-CoA synthase [EC:6.2.1.-]		
K00672	6	formylmethanofuran--tetrahydromethanopterin N-formyltransferase		
K00673	3	arginine N-succinyltransferase [EC:2.3.1.109]		
K00674	18	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase		
K00675	16	N-hydroxyarylamine O-acetyltransferase [EC:2.3.1.118]		
K00676	20	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]		
K00677	32	UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]		
K00680	275	Unclassified; E2.3.1.-		
K00681	137	gamma-glutamyltranspeptidase [EC:2.3.2.2]		
K00683	3	glutaminyl-peptide cyclotransferase [EC:2.3.2.5]		

K00684	12	leucyl/phenylalanyl-tRNA--protein transferase [EC:2.3.2.6]		
K00685	7	arginine-tRNA-protein transferase [EC:2.3.2.8]		
K00688	90	starch phosphorylase [EC:2.4.1.1]		
K00690	3	sucrose phosphorylase [EC:2.4.1.7]		
K00691	17	maltose phosphorylase [EC:2.4.1.8]		
K00693	14	glycogen(starch) synthase [EC:2.4.1.11]		
K00694	12	cellulose synthase (UDP-forming) [EC:2.4.1.12]		
K00695	2	sucrose synthase [EC:2.4.1.13]		
K00696	1	sucrose-phosphate synthase [EC:2.4.1.14]		
K00697	44	alpha,alpha-trehalose-phosphate synthase (UDP-forming) [EC:2.4.1.15]		
K00700	62	1,4-alpha-glucan branching enzyme [EC:2.4.1.18]		
K00701	2	cyclomaltodextrin glucanotransferase [EC:2.4.1.19]		
K00702	10	cellobiose phosphorylase [EC:2.4.1.20]		
K00703	39	starch synthase [EC:2.4.1.21]		
K00705	74	4-alpha-glucanotransferase [EC:2.4.1.25]		
K00712	3	poly(glycerol-phosphate) alpha-glucosyltransferase [EC:2.4.1.52]		
K00720	5	ceramide glucosyltransferase [EC:2.4.1.80]		
K00721	123	dolichol-phosphate mannosyltransferase [EC:2.4.1.83]		
K00743	2	N-acetyllactosaminide 3-alpha-galactosyltransferase [EC:2.4.1.87]		
K00748	28	lipid-A-disaccharide synthase [EC:2.4.1.182]		
K00752	7	hyaluronan synthase [EC:2.4.1.212]		
K00754	464	Unclassified; E2.4.1.-		
K00756	8	pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]		
K00757	2	uridine phosphorylase [EC:2.4.2.3]		
K00758	21	thymidine phosphorylase [EC:2.4.2.4]		
K00759	26	adenine phosphoribosyltransferase [EC:2.4.2.7]		
K00760	33	hypoxanthine phosphoribosyltransferase [EC:2.4.2.8]		
K00761	13	uracil phosphoribosyltransferase [EC:2.4.2.9]		
K00762	22	orotate phosphoribosyltransferase [EC:2.4.2.10]		
K00763	180	nicotinate phosphoribosyltransferase [EC:2.4.2.11]		
K00764	58	amidophosphoribosyltransferase [EC:2.4.2.14]		
K00765	31	ATP phosphoribosyltransferase [EC:2.4.2.17]		
K00766	31	anthranilate phosphoribosyltransferase [EC:2.4.2.18]		
K00767	54	nicotinate-nucleotide pyrophosphorylase (carboxylating)		
K00768	8	nicotinate-nucleotide--dimethylbenzimidazole		
K00772	30	5'-methylthioadenosine phosphorylase [EC:2.4.2.28]		
K00773	26	queuine tRNA-ribosyltransferase [EC:2.4.2.29]		
K00777	15	Unclassified; E2.4.2.-		
K00782	10	hypothetical protein		
K00783	10	hypothetical protein		
K00784	75	ribonuclease Z [EC:3.1.26.11]		
K00785	2	beta-galactosamide-alpha-2,3-sialyltransferase [EC:2.4.99.-]		
K00786	201	Unclassified; E2.4.-.-		
K00788	35	thiamine-phosphate pyrophosphorylase [EC:2.5.1.3]		
K00789	31	S-adenosylmethionine synthetase [EC:2.5.1.6]		
K00790	50	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7]		
K00791	29	tRNA dimethylallyltransferase [EC:2.5.1.75]		
K00793	31	riboflavin synthase alpha chain [EC:2.5.1.9]		
K00794	15	riboflavin synthase beta chain [EC:2.5.1.-]		
K00795	8	farnesyl diphosphate synthase [EC:2.5.1.1 2.5.1.10]		

K00796	35	dihydropteroate synthase [EC:2.5.1.15]		
K00797	37	spermidine synthase [EC:2.5.1.16]		
K00798	27	cob(I)alamin adenosyltransferase [EC:2.5.1.17]		
K00799	108	glutathione S-transferase [EC:2.5.1.18]		
K00800	62	3-phosphoshikimate 1-carboxyvinyltransferase [EC:2.5.1.19]		
K00801	13	farnesyl-diphosphate farnesyltransferase [EC:2.5.1.21]		
K00802	3	spermine synthase [EC:2.5.1.22]		
K00803	23	alkyldihydroxyacetonephosphate synthase [EC:2.5.1.26]		
K00805	9	heptaprenyl diphosphate synthase [EC:2.5.1.30]		
K00806	20	undecaprenyl diphosphate synthase [EC:2.5.1.31]		
K00808	4	homospermidine synthase [EC:2.5.1.44]		
K00809	18	deoxyhypusine synthase [EC:2.5.1.46]		
K00810	24	Unclassified; E2.5.1.-		
K00811	2	aspartate aminotransferase [EC:2.6.1.1]		
K00812	46	aspartate aminotransferase [EC:2.6.1.1]		
K00813	7	aspartate aminotransferase [EC:2.6.1.1]		
K00814	3	alanine transaminase [EC:2.6.1.2]		
K00817	59	histidinol-phosphate aminotransferase [EC:2.6.1.9]		
K00818	49	acetylornithine aminotransferase [EC:2.6.1.11]		
K00819	14	ornithine--oxo-acid transaminase [EC:2.6.1.13]		
K00820	67	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)		
K00821	47	acetylornithine/N-succinyldiaminopimelate aminotransferase		
K00822	14	beta-alanine--pyruvate transaminase [EC:2.6.1.18]		
K00823	47	4-aminobutyrate aminotransferase [EC:2.6.1.19]		
K00824	14	D-alanine transaminase [EC:2.6.1.21]		
K00825	17	2-aminoadipate transaminase [EC:2.6.1.39]		
K00826	73	branched-chain amino acid aminotransferase [EC:2.6.1.42]		
K00828	29	serine--glyoxylate transaminase [EC:2.6.1.45]		
K00831	23	phosphoserine aminotransferase [EC:2.6.1.52]		
K00832	8	aromatic-amino-acid transaminase [EC:2.6.1.57]		
K00833	19	adenosylmethionine-8-amino-7-oxononanoate aminotransferase		
K00835	12	valine--pyruvate aminotransferase [EC:2.6.1.66]		
K00836	5	diaminobutyrate-2-oxoglutarate transaminase [EC:2.6.1.76]		
K00837	274	Unclassified; E2.6.1.-		
K00839	38	aminotransferase [EC:2.6.1.-]		
K00840	1	succinylornithine aminotransferase [EC:2.6.1.81]		
K00841	1	aminotransferase [EC:2.6.1.-]		
K00842	11	aminotransferase [EC:2.6.1.-]		
K00843	6	Unclassified; E2.6.-.-		
K00845	73	glucokinase [EC:2.7.1.2]		
K00846	2	ketohexokinase [EC:2.7.1.3]		
K00847	33	fructokinase [EC:2.7.1.4]		
K00848	14	rhamnulokinase [EC:2.7.1.5]		
K00849	14	galactokinase [EC:2.7.1.6]		
K00850	56	6-phosphofructokinase [EC:2.7.1.11]		
K00851	14	gluconokinase [EC:2.7.1.12]		
K00852	25	ribokinase [EC:2.7.1.15]		
K00853	8	L-ribulokinase [EC:2.7.1.16]		
K00854	34	xylulokinase [EC:2.7.1.17]		
K00855	13	phosphoribulokinase [EC:2.7.1.19]		

K00856	21	adenosine kinase [EC:2.7.1.20]		
K00857	8	thymidine kinase [EC:2.7.1.21]		
K00858	35	NAD+ kinase [EC:2.7.1.23]		
K00859	35	dephospho-CoA kinase [EC:2.7.1.24]		
K00860	18	adenylylsulfate kinase [EC:2.7.1.25]		
K00861	3	riboflavin kinase [EC:2.7.1.26]		
K00862	1	erythritol kinase [EC:2.7.1.27]		
K00863	8	dihydroxyacetone kinase [EC:2.7.1.29]		
K00864	41	glycerol kinase [EC:2.7.1.30]		
K00865	12	glycerate kinase [EC:2.7.1.31]		
K00866	1	choline kinase [EC:2.7.1.32]		
K00867	2	type I pantothenate kinase [EC:2.7.1.33]		
K00868	445	pyridoxine kinase [EC:2.7.1.35]		
K00869	1	mevalonate kinase [EC:2.7.1.36]		
K00870	68	protein kinase [EC:2.7.1.37]		
K00872	9	homoserine kinase [EC:2.7.1.39]		
K00873	44	pyruvate kinase [EC:2.7.1.40]		
K00874	20	2-dehydro-3-deoxygluconokinase [EC:2.7.1.45]		
K00875	2	D-ribulokinase [EC:2.7.1.47]		
K00876	12	uridine kinase [EC:2.7.1.48]		
K00877	3	hydroxymethylpyrimidine kinase [EC:2.7.1.49]		
K00878	3	hydroxyethylthiazole kinase [EC:2.7.1.50]		
K00879	4	L-fuculokinase [EC:2.7.1.51]		
K00880	1	L-xylulokinase [EC:2.7.1.53]		
K00882	14	1-phosphofructokinase [EC:2.7.1.56]		
K00883	1	2-dehydro-3-deoxygalactonokinase [EC:2.7.1.58]		
K00884	7	N-acetylglucosamine kinase [EC:2.7.1.59]		
K00885	1	N-acylmannosamine kinase [EC:2.7.1.60]		
K00886	9	polyphosphate glucokinase [EC:2.7.1.63]		
K00887	10	undecaprenol kinase [EC:2.7.1.66]		
K00891	31	shikimate kinase [EC:2.7.1.71]		
K00894	3	ethanolamine kinase [EC:2.7.1.82]		
K00895	22	pyrophosphate--fructose-6-phosphate 1-phosphotransferase		
K00897	10	aminoglycoside 3'-phosphotransferase [EC:2.7.1.95]		
K00901	6	diacylglycerol kinase [EC:2.7.1.107]		
K00903	70	protein-tyrosine kinase [EC:2.7.10.-]		
K00904	18	deoxyguanosine kinase [EC:2.7.1.113]		
K00906	11	isocitrate dehydrogenase kinase/phosphatase [EC:2.7.11.5 3.1.3.-]		
K00908	216	Ca2+/calmodulin-dependent protein kinase [EC:2.7.11.17]		
K00912	13	tetraacyldisaccharide 4'-kinase [EC:2.7.1.130]		
K00917	9	tagatose 6-phosphate kinase [EC:2.7.1.144]		
K00919	25	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [EC:2.7.1.148]		
K00924	351	Unclassified; E2.7.1.-		
K00925	31	acetate kinase [EC:2.7.2.1]		
K00926	18	carbamate kinase [EC:2.7.2.2]		
K00927	35	phosphoglycerate kinase [EC:2.7.2.3]		
K00928	33	aspartate kinase [EC:2.7.2.4]		
K00929	3	butyrate kinase [EC:2.7.2.7]		
K00930	23	acetylglutamate kinase [EC:2.7.2.8]		
K00931	54	glutamate 5-kinase [EC:2.7.2.11]		

K00932	1	propionate kinase [EC:2.7.2.15]		
K00933	1	creatine kinase [EC:2.7.3.2]		
K00934	4	arginine kinase [EC:2.7.3.3]		
K00935	4	Unclassified; E2.7.3.9		
K00936	1280	Unclassified; E2.7.3.-		
K00937	60	polyphosphate kinase [EC:2.7.4.1]		
K00938	5	phosphomevalonate kinase [EC:2.7.4.2]		
K00939	34	adenylate kinase [EC:2.7.4.3]		
K00940	20	nucleoside-diphosphate kinase [EC:2.7.4.6]		
K00941	29	phosphomethylpyrimidine kinase [EC:2.7.4.7]		
K00942	26	guanylate kinase [EC:2.7.4.8]		
K00943	33	dTMP kinase [EC:2.7.4.9]		
K00945	33	cytidylate kinase [EC:2.7.4.14]		
K00946	33	thiamine-monophosphate kinase [EC:2.7.4.16]		
K00947	27	Unclassified; E2.7.4.-		
K00948	177	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]		
K00950	17	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase		
K00951	90	GTP pyrophosphokinase [EC:2.7.6.5]		
K00954	23	pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]		
K00955	28	bifunctional enzyme CysN/CysC [EC:2.7.7.4 2.7.1.25]		
K00956	29	sulfate adenylyltransferase subunit 1 [EC:2.7.7.4]		
K00957	10	sulfate adenylyltransferase subunit 2 [EC:2.7.7.4]		
K00958	25	sulfate adenylyltransferase [EC:2.7.7.4]		
K00960	7	DNA-directed RNA polymerase [EC:2.7.7.6]		
K00961	7	DNA polymerase [EC:2.7.7.7]		
K00962	39	polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]		
K00963	23	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]		
K00964	23	galactose-1-phosphate uridylyltransferase [EC:2.7.7.10]		
K00965	24	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]		
K00966	49	mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]		
K00969	56	nicotinate-nucleotide adenylyltransferase [EC:2.7.7.18]		
K00970	57	poly(A) polymerase [EC:2.7.7.19]		
K00971	42	mannose-1-phosphate guanylyltransferase [EC:2.7.7.22]		
K00972	3	UDP-N-acetylglucosamine pyrophosphorylase [EC:2.7.7.23]		
K00973	45	glucose-1-phosphate thymidylyltransferase [EC:2.7.7.24]		
K00974	27	tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.25		
K00975	42	glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]		
K00978	15	glucose-1-phosphate cytidylyltransferase [EC:2.7.7.33]		
K00979	26	3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase)		
K00980	8	glycerol-3-phosphate cytidylyltransferase [EC:2.7.7.39]		
K00981	27	phosphatidate cytidylyltransferase [EC:2.7.7.41]		
K00982	55	glutamate-ammonia-ligase adenylyltransferase [EC:2.7.7.42]		
K00983	2	N-acylneuraminate cytidylyltransferase [EC:2.7.7.43]		
K00985	6	RNA-directed RNA polymerase [EC:2.7.7.48]		
K00986	61	RNA-directed DNA polymerase [EC:2.7.7.49]		
K00989	19	ribonuclease PH [EC:2.7.7.56]		
K00990	45	[protein-PII] uridylyltransferase [EC:2.7.7.59]		
K00991	20	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase		
K00992	28	Unclassified; E2.7.7.-		
K00995	115	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase		

K00996	3	undecaprenyl-phosphate galactose phosphotransferase [EC:2.7.8.6]		
K00997	15	holo-[acyl-carrier protein] synthase [EC:2.7.8.7]		
K00998	20	phosphatidylserine synthase [EC:2.7.8.8]		
K00999	4	CDP-diacylglycerol--inositol 3-phosphatidyltransferase [EC:2.7.8.11]		
K01000	52	phospho-N-acetylmuramoyl-pentapeptide-transferase [EC:2.7.8.13]		
K01002	9	phosphoglycerol transferase [EC:2.7.8.20]		
K01003	30	carboxyvinyl-carboxyphosphonate phosphorylmutase [EC:2.7.8.23]		
K01005	35	Unclassified; E2.7.8.-		
K01006	55	pyruvate,orthophosphate dikinase [EC:2.7.9.1]		
K01007	80	pyruvate, water dikinase [EC:2.7.9.2]		
K01008	29	selenide, water dikinase [EC:2.7.9.3]		
K01010	60	thiosulfate sulfurtransferase [EC:2.8.1.1]		
K01011	21	3-mercaptopyruvate sulfurtransferase [EC:2.8.1.2]		
K01012	22	biotin synthetase [EC:2.8.1.6]		
K01013	25	Unclassified; E2.8.1.-		
K01026	7	propionate CoA-transferase [EC:2.8.3.1]		
K01027	3	3-oxoacid CoA-transferase [EC:2.8.3.5]		
K01028	6	3-oxoacid CoA-transferase subunit A [EC:2.8.3.5]		
K01029	3	3-oxoacid CoA-transferase subunit B [EC:2.8.3.5]		
K01031	3	3-oxoadipate CoA-transferase, alpha subunit [EC:2.8.3.6]		
K01032	3	3-oxoadipate CoA-transferase, beta subunit [EC:2.8.3.6]		
K01035	2	acetate CoA-transferase beta subunit [EC:2.8.3.8]		
K01036	1	butyrate-acetoacetate CoA-transferase [EC:2.8.3.9]		
K01039	25	glutaconate CoA-transferase, subunit A [EC:2.8.3.12]		
K01040	18	glutaconate CoA-transferase, subunit B [EC:2.8.3.12]		
K01041	111	Unclassified; E2.8.3.-		
K01042	37	L-seryl-tRNA(Ser) seleniumtransferase [EC:2.9.1.1]		
K01043	161	Unclassified; E2.-.-.-		
K01044	56	carboxylesterase [EC:3.1.1.1]		
K01046	68	triacylglycerol lipase [EC:3.1.1.3]		
K01048	6	lysophospholipase [EC:3.1.1.5]		
K01051	2	pectinesterase [EC:3.1.1.11]		
K01053	63	gluconolactonase [EC:3.1.1.17]		
K01054	3	acylglycerol lipase [EC:3.1.1.23]		
K01055	56	3-oxoadipate enol-lactonase [EC:3.1.1.24]		
K01056	29	peptidyl-tRNA hydrolase, PTH1 family [EC:3.1.1.29]		
K01057	24	6-phosphogluconolactonase [EC:3.1.1.31]		
K01058	8	phospholipase A1 [EC:3.1.1.32]		
K01060	3	cephalosporin-C deacetylase [EC:3.1.1.41]		
K01061	68	carboxymethylenebutenolidase [EC:3.1.1.45]		
K01062	1	1-alkyl-2-acetylglycerophosphocholine esterase [EC:3.1.1.47]		
K01066	94	esterase / lipase [EC:3.1.1.-]		
K01067	12	acetyl-CoA hydrolase [EC:3.1.2.1]		
K01068	5	palmitoyl-CoA hydrolase [EC:3.1.2.2]		
K01069	110	hydroxyacylglutathione hydrolase [EC:3.1.2.6]		
K01070	5	S-formylglutathione hydrolase [EC:3.1.2.12]		
K01071	2	oleoyl-[acyl-carrier-protein] hydrolase [EC:3.1.2.14]		
K01073	7	acyl-CoA hydrolase [EC:3.1.2.20]		
K01075	12	4-hydroxybenzoyl-CoA thioesterase [EC:3.1.2.23]		
K01076	26	Unclassified; E3.1.2.-		

K01077	90	alkaline phosphatase [EC:3.1.3.1]		
K01078	17	acid phosphatase [EC:3.1.3.2]		
K01079	34	phosphoserine phosphatase [EC:3.1.3.3]		
K01081	32	5'-nucleotidase [EC:3.1.3.5]		
K01083	1	3-phytase [EC:3.1.3.8]		
K01087	73	trehalose-phosphatase [EC:3.1.3.12]		
K01090	68	protein phosphatase [EC:3.1.3.16]		
K01091	72	phosphoglycolate phosphatase [EC:3.1.3.18]		
K01092	58	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]		
K01093	4	4-phytase / acid phosphatase [EC:3.1.3.26 3.1.3.2]		
K01095	8	phosphatidylglycerophosphatase A [EC:3.1.3.27]		
K01096	4	phosphatidylglycerophosphatase B [EC:3.1.3.27]		
K01101	7	4-nitrophenyl phosphatase [EC:3.1.3.41]		
K01103	1	fructose-2,6-bisphosphatase [EC:3.1.3.46]		
K01104	39	protein-tyrosine phosphatase [EC:3.1.3.48]		
K01112	32	Unclassified; E3.1.3.-		
K01113	42	phosphodiesterase/alkaline phosphatase D [EC:3.1.4.1]		
K01114	33	phospholipase C [EC:3.1.4.3]		
K01115	8	phospholipase D [EC:3.1.4.4]		
K01118	3	FMN-dependent NADH-azoreductase [EC:1.7.-.-]		
K01119	13	2',3'-cyclic-nucleotide 2'-phosphodiesterase [EC:3.1.4.16]		
K01120	22	3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]		
K01121	1	2',3'-cyclic-nucleotide 3'-phosphodiesterase [EC:3.1.4.37]		
K01126	47	glycerophosphoryl diester phosphodiesterase [EC:3.1.4.46]		
K01128	8	Unclassified; E3.1.4.-		
K01129	24	dGTPase [EC:3.1.5.1]		
K01130	86	arylsulfatase [EC:3.1.6.1]		
K01131	7	steryl-sulfatase [EC:3.1.6.2]		
K01132	17	N-acetylgalactosamine-6-sulfatase [EC:3.1.6.4]		
K01133	31	choline-sulfatase [EC:3.1.6.6]		
K01134	23	arylsulfatase A [EC:3.1.6.8]		
K01135	17	arylsulfatase B [EC:3.1.6.12]		
K01136	8	iduronate 2-sulfatase [EC:3.1.6.13]		
K01137	10	N-acetylglucosamine-6-sulfatase [EC:3.1.6.14]		
K01138	72	Unclassified; E3.1.6.-		
K01139	45	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase		
K01142	29	exodeoxyribonuclease III [EC:3.1.11.2]		
K01144	43	exodeoxyribonuclease V [EC:3.1.11.5]		
K01146	7	Unclassified; E3.1.11.-		
K01147	24	exoribonuclease II [EC:3.1.13.1]		
K01151	37	deoxyribonuclease IV [EC:3.1.21.2]		
K01152	2	type I restriction enzyme [EC:3.1.21.3]		
K01153	63	type I restriction enzyme, R subunit [EC:3.1.21.3]		
K01154	15	type I restriction enzyme, S subunit [EC:3.1.21.3]		
K01155	2	type II restriction enzyme [EC:3.1.21.4]		
K01156	7	type III restriction enzyme [EC:3.1.21.5]		
K01157	37	Unclassified; E3.1.21.-		
K01159	34	crossover junction endodeoxyribonuclease RuvC [EC:3.1.22.4]		
K01162	2	ribonuclease III [EC:3.1.26.3]		
K01166	1	ribonuclease T2 [EC:3.1.27.1]		

K01167	9	ribonuclease T1 [EC:3.1.27.3]		
K01172	1	Unclassified; E3.1.27.-		
K01173	1	endonuclease [EC:3.1.30.-]		
K01174	9	micrococcal nuclease [EC:3.1.31.1]		
K01175	109	Unclassified; E3.1.-.-		
K01176	36	alpha-amylase [EC:3.2.1.1]		
K01178	57	glucoamylase [EC:3.2.1.3]		
K01179	39	endoglucanase [EC:3.2.1.4]		
K01181	11	endo-1,4-beta-xylanase [EC:3.2.1.8]		
K01182	13	oligo-1,6-glucosidase [EC:3.2.1.10]		
K01183	28	chitinase [EC:3.2.1.14]		
K01184	1	polygalacturonase [EC:3.2.1.15]		
K01185	14	lysozyme [EC:3.2.1.17]		
K01186	2	sialidase-1 [EC:3.2.1.18]		
K01187	42	alpha-glucosidase [EC:3.2.1.20]		
K01188	77	beta-glucosidase [EC:3.2.1.21]		
K01190	51	beta-galactosidase [EC:3.2.1.23]		
K01191	17	alpha-mannosidase [EC:3.2.1.24]		
K01192	9	beta-mannosidase [EC:3.2.1.25]		
K01193	2	beta-fructofuranosidase [EC:3.2.1.26]		
K01194	6	alpha,alpha-trehalase [EC:3.2.1.28]		
K01195	8	beta-glucuronidase [EC:3.2.1.31]		
K01197	1	hyaluronoglucosaminidase [EC:3.2.1.35]		
K01198	9	xylan 1,4-beta-xylosidase [EC:3.2.1.37]		
K01199	9	glucan endo-1,3-beta-D-glucosidase [EC:3.2.1.39]		
K01200	4	pullulanase [EC:3.2.1.41]		
K01201	13	glucosylceramidase [EC:3.2.1.45]		
K01206	21	alpha-L-fucosidase [EC:3.2.1.51]		
K01207	53	beta-N-acetylhexosaminidase [EC:3.2.1.52]		
K01208	1	cyclomaltodextrinase [EC:3.2.1.54]		
K01209	22	alpha-N-arabinofuranosidase [EC:3.2.1.55]		
K01210	10	glucan 1,3-beta-glucosidase [EC:3.2.1.58]		
K01212	11	levanase [EC:3.2.1.65]		
K01213	6	galacturan 1,4-alpha-galacturonidase [EC:3.2.1.67]		
K01215	2	glucan 1,6-alpha-glucosidase [EC:3.2.1.70]		
K01216	10	licheninase [EC:3.2.1.73]		
K01218	6	mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]		
K01220	15	6-phospho-beta-galactosidase [EC:3.2.1.85]		
K01222	6	6-phospho-beta-glucosidase [EC:3.2.1.86]		
K01223	1	6-phospho-beta-glucosidase [EC:3.2.1.86]		
K01224	2	arabinogalactan endo-1,4-beta-galactosidase [EC:3.2.1.89]		
K01225	25	cellulose 1,4-beta-cellobiosidase [EC:3.2.1.91]		
K01226	3	trehalose-6-phosphate hydrolase [EC:3.2.1.93]		
K01234	2	neopullulanase [EC:3.2.1.135]		
K01235	3	alpha-glucuronidase [EC:3.2.1.139]		
K01236	28	maltooligosyltrehalose trehalohydrolase [EC:3.2.1.141]		
K01238	177	Unclassified; E3.2.1.-		
K01239	17	purine nucleosidase [EC:3.2.2.1]		
K01241	4	AMP nucleosidase [EC:3.2.2.4]		
K01243	6	S-adenosylhomocysteine/5'-methylthioadenosine nucleosidase		

K01246	12	DNA-3-methyladenine glycosylase I [EC:3.2.2.20]		
K01247	18	DNA-3-methyladenine glycosylase II [EC:3.2.2.21]		
K01249	33	DNA glycosylase [EC:3.2.2.-]		
K01250	8	pyrimidine-specific ribonucleoside hydrolase [EC:3.2.-.-]		
K01251	29	adenosylhomocysteinase [EC:3.3.1.1]		
K01253	35	microsomal epoxide hydrolase [EC:3.3.2.9]		
K01255	52	leucyl aminopeptidase [EC:3.4.11.1]		
K01256	102	aminopeptidase N [EC:3.4.11.2]		
K01258	13	tripeptide aminopeptidase [EC:3.4.11.4]		
K01259	49	proline iminopeptidase [EC:3.4.11.5]		
K01262	80	X-Pro aminopeptidase [EC:3.4.11.9]		
K01263	9	cytosol alanyl aminopeptidase [EC:3.4.11.14]		
K01264	9	aminopeptidase Y [EC:3.4.11.15]		
K01265	30	methionyl aminopeptidase [EC:3.4.11.18]		
K01266	19	D-aminopeptidase [EC:3.4.11.19]		
K01267	2	aspartyl aminopeptidase [EC:3.4.11.21]		
K01268	1	aminopeptidase I [EC:3.4.11.22]		
K01269	174	aminopeptidase [EC:3.4.11.-]		
K01270	3	aminoacylhistidine dipeptidase [EC:3.4.13.3]		
K01271	52	X-Pro dipeptidase [EC:3.4.13.9]		
K01273	44	membrane dipeptidase [EC:3.4.13.19]		
K01274	10	D-alanyl-D-alanine dipeptidase [EC:3.4.13.-]		
K01277	4	dipeptidyl-peptidase III [EC:3.4.14.4]		
K01278	26	dipeptidyl-peptidase 4 [EC:3.4.14.5]		
K01281	8	X-Pro dipeptidyl-peptidase [EC:3.4.14.11]		
K01283	4	peptidyl-dipeptidase A [EC:3.4.15.1]		
K01284	35	peptidyl-dipeptidase Dcp [EC:3.4.15.5]		
K01286	36	D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4]		
K01289	13	carboxypeptidase [EC:3.4.16.-]		
K01295	41	glutamate carboxypeptidase [EC:3.4.17.11]		
K01297	11	muramoyltetrapeptide carboxypeptidase [EC:3.4.17.13]		
K01299	20	carboxypeptidase Taq [EC:3.4.17.19]		
K01301	10	glutamate carboxypeptidase II [EC:3.4.17.21]		
K01302	1	Unclassified; E3.4.17.-		
K01303	93	acylaminoacyl-peptidase [EC:3.4.19.1]		
K01304	3	pyroglutamyl-peptidase [EC:3.4.19.3]		
K01312	9	trypsin [EC:3.4.21.4]		
K01318	1	glutamyl endopeptidase [EC:3.4.21.19]		
K01322	103	prolyl oligopeptidase [EC:3.4.21.26]		
K01325	2	tissue kallikrein [EC:3.4.21.35]		
K01338	158	ATP-dependent Lon protease [EC:3.4.21.53]		
K01341	5	kexin [EC:3.4.21.61]		
K01342	54	subtilisin [EC:3.4.21.62]		
K01344	1	protein C (activated) [EC:3.4.21.69]		
K01347	2	IgA-specific serine endopeptidase [EC:3.4.21.72]		
K01354	61	oligopeptidase B [EC:3.4.21.83]		
K01356	28	repressor LexA [EC:3.4.21.88]		
K01358	30	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]		
K01361	6	lactocepin [EC:3.4.21.96]		
K01362	487	Unclassified; E3.4.21.-		

K01372	2	bleomycin hydrolase [EC:3.4.22.40]		
K01376	12	Unclassified; E3.4.22.-		
K01387	13	microbial collagenase [EC:3.4.24.3]		
K01389	2	neprilysin [EC:3.4.24.11]		
K01392	9	thimet oligopeptidase [EC:3.4.24.15]		
K01400	2	bacillolysin [EC:3.4.24.28]		
K01401	1	aureolysin [EC:3.4.24.29]		
K01406	35	serralysin [EC:3.4.24.40]		
K01407	1	protease III [EC:3.4.24.55]		
K01409	44	O-sialoglycoprotein endopeptidase [EC:3.4.24.57]		
K01412	104	mitochondrial processing peptidase [EC:3.4.24.64]		
K01414	25	oligopeptidase A [EC:3.4.24.70]		
K01415	46	endothelin-converting enzyme [EC:3.4.24.71]		
K01416	2	snapalysin [EC:3.4.24.77]		
K01417	359	Unclassified; E3.4.24.-		
K01419	10	ATP-dependent HslUV protease, peptidase subunit HslV [EC:3.4.25.-]		
K01420	81	CRP/FNR family transcriptional regulator, anaerobic regulatory		
K01421	2	putative membrane protein		
K01422	101	Unclassified; E3.4.99.-		
K01423	395	Unclassified; E3.4.-.-		
K01424	54	L-asparaginase [EC:3.5.1.1]		
K01425	10	glutaminase [EC:3.5.1.2]		
K01426	156	amidase [EC:3.5.1.4]		
K01428	11	urease alpha subunit [EC:3.5.1.5]		
K01429	3	urease beta subunit [EC:3.5.1.5]		
K01430	6	urease gamma subunit [EC:3.5.1.5]		
K01431	27	beta-ureidopropionase [EC:3.5.1.6]		
K01433	7	formyltetrahydrofolate deformylase [EC:3.5.1.10]		
K01434	69	penicillin amidase [EC:3.5.1.11]		
K01436	74	aminoacylase [EC:3.5.1.14]		
K01438	28	acetylornithine deacetylase [EC:3.5.1.16]		
K01439	82	succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]		
K01443	68	N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]		
K01444	9	N4-(beta-N-acetylglucosaminyl)-L-asparaginase [EC:3.5.1.26]		
K01446	2	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K01447	31	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K01448	611	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K01449	4	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K01451	45	hippurate hydrolase [EC:3.5.1.32]		
K01452	38	chitin deacetylase [EC:3.5.1.41]		
K01453	19	Unclassified; E3.5.1.46		
K01454	11	Unclassified; E3.5.1.48		
K01455	26	formamidase [EC:3.5.1.49]		
K01457	9	allophanate hydrolase [EC:3.5.1.54]		
K01458	6	N-formylglutamate deformylase [EC:3.5.1.68]		
K01459	6	Unclassified; E3.5.1.77		
K01461	67	Unclassified; E3.5.1.82		
K01462	44	Unclassified; E3.5.1.88		
K01463	176	Unclassified; E3.5.1.-		
K01464	42	dihydropyrimidinase [EC:3.5.2.2]		

K01465	147	dihydroorotase [EC:3.5.2.3]		
K01466	28	allantoinase [EC:3.5.2.5]		
K01467	153	beta-lactamase [EC:3.5.2.6]		
K01468	45	imidazolonepropionase [EC:3.5.2.7]		
K01469	35	5-oxoprolinase (ATP-hydrolysing) [EC:3.5.2.9]		
K01470	24	creatinine amidohydrolase [EC:3.5.2.10]		
K01471	12	Unclassified; E3.5.2.12		
K01473	68	N-methylhydantoinase A [EC:3.5.2.14]		
K01474	76	N-methylhydantoinase B [EC:3.5.2.14]		
K01476	13	arginase [EC:3.5.3.1]		
K01477	8	allantoicase [EC:3.5.3.4]		
K01478	10	arginine deiminase [EC:3.5.3.6]		
K01479	4	formiminoglutamase [EC:3.5.3.8]		
K01480	40	agmatinase [EC:3.5.3.11]		
K01482	9	dimethylargininase [EC:3.5.3.18]		
K01483	1	ureidoglycolate hydrolase [EC:3.5.3.19]		
K01484	1	succinylarginine dihydrolase [EC:3.5.3.23]		
K01485	25	cytosine deaminase [EC:3.5.4.1]		
K01486	15	adenine deaminase [EC:3.5.4.2]		
K01487	12	guanine deaminase [EC:3.5.4.3]		
K01488	35	adenosine deaminase [EC:3.5.4.4]		
K01489	21	cytidine deaminase [EC:3.5.4.5]		
K01491	34	methylenetetrahydrofolate dehydrogenase (NADP+) /		
K01492	2	phosphoribosylaminoimidazolecarboxamide formyltransferase		
K01493	13	dCMP deaminase [EC:3.5.4.12]		
K01494	20	dCTP deaminase [EC:3.5.4.13]		
K01495	28	GTP cyclohydrolase I [EC:3.5.4.16]		
K01496	6	phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]		
K01497	24	GTP cyclohydrolase II [EC:3.5.4.25]		
K01498	1	diaminohydroxyphosphoribosylaminopyrimidine deaminase [EC:3.5.4.26]		
K01499	3	methenyltetrahydromethanopterin cyclohydrolase [EC:3.5.4.27]		
K01500	18	Unclassified; E3.5.4.-		
K01501	28	nitrilase [EC:3.5.5.1]		
K01502	12	aliphatic nitrilase [EC:3.5.5.7]		
K01503	10	Unclassified; E3.5.5.-		
K01504	6	glucosamine-6-phosphate isomerase [EC:3.5.99.6]		
K01505	4	1-aminocyclopropane-1-carboxylate deaminase [EC:3.5.99.7]		
K01506	64	Unclassified; E3.5.-.-		
K01507	54	inorganic pyrophosphatase [EC:3.6.1.1]		
K01512	16	acylphosphatase [EC:3.6.1.7]		
K01514	57	exopolyphosphatase [EC:3.6.1.11]		
K01515	41	ADP-ribose pyrophosphatase [EC:3.6.1.13]		
K01516	30	nucleoside-triphosphatase [EC:3.6.1.15]		
K01518	13	bis(5'-nucleosidyl)-tetraphosphatase [EC:3.6.1.17]		
K01520	14	dUTP pyrophosphatase [EC:3.6.1.23]		
K01523	4	phosphoribosyl-ATP pyrophosphohydrolase [EC:3.6.1.31]		
K01524	18	guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase		
K01525	13	bis(5'-nucleosyl)-tetraphosphatase (symmetrical) [EC:3.6.1.41]		
K01529	223	Unclassified; E3.6.1.-		
K01531	33	Mg2+-importing ATPase [EC:3.6.3.2]		

K01533	135	Cu2+-exporting ATPase [EC:3.6.3.4]		
K01534	28	Cd2+/Zn2+-exporting ATPase [EC:3.6.3.3 3.6.3.5]		
K01535	2	H+-transporting ATPase [EC:3.6.3.6]		
K01537	113	Ca2+-transporting ATPase [EC:3.6.3.8]		
K01539	6	sodium/potassium-transporting ATPase subunit alpha [EC:3.6.3.9]		
K01546	18	K+-transporting ATPase ATPase A chain [EC:3.6.3.12]		
K01547	19	K+-transporting ATPase ATPase B chain [EC:3.6.3.12]		
K01548	14	K+-transporting ATPase ATPase C chain [EC:3.6.3.12]		
K01551	26	arsenite-transporting ATPase [EC:3.6.3.16]		
K01552	141	Unclassified; E3.6.3.-		
K01554	4	Unclassified; E3.6.-.-		
K01555	12	fumarylacetoacetase [EC:3.7.1.2]		
K01556	30	kynureninase [EC:3.7.1.3]		
K01557	5	acylpyruvate hydrolase [EC:3.7.1.5]		
K01559	14	Unclassified; E3.7.1.-		
K01560	34	2-haloacid dehalogenase [EC:3.8.1.2]		
K01561	20	haloacetate dehalogenase [EC:3.8.1.3]		
K01563	44	haloalkane dehalogenase [EC:3.8.1.5]		
K01564	47	Unclassified; E3.8.1.-		
K01567	169	Unclassified; E3.-.-.-		
K01568	1	pyruvate decarboxylase [EC:4.1.1.1]		
K01571	11	oxaloacetate decarboxylase, alpha subunit [EC:4.1.1.3]		
K01572	9	oxaloacetate decarboxylase, beta subunit [EC:4.1.1.3]		
K01576	25	benzoylformate decarboxylase [EC:4.1.1.7]		
K01577	9	oxalyl-CoA decarboxylase [EC:4.1.1.8]		
K01578	19	malonyl-CoA decarboxylase [EC:4.1.1.9]		
K01579	12	aspartate 1-decarboxylase [EC:4.1.1.11]		
K01580	8	glutamate decarboxylase [EC:4.1.1.15]		
K01581	17	ornithine decarboxylase [EC:4.1.1.17]		
K01582	22	lysine decarboxylase [EC:4.1.1.18]		
K01583	17	arginine decarboxylase [EC:4.1.1.19]		
K01584	17	arginine decarboxylase [EC:4.1.1.19]		
K01585	30	arginine decarboxylase [EC:4.1.1.19]		
K01586	61	diaminopimelate decarboxylase [EC:4.1.1.20]		
K01588	20	5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]		
K01589	16	5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]		
K01591	30	orotidine-5'-phosphate decarboxylase [EC:4.1.1.23]		
K01592	14	tyrosine decarboxylase [EC:4.1.1.25]		
K01593	61	aromatic-L-amino-acid decarboxylase [EC:4.1.1.28]		
K01594	14	sulfinoalanine decarboxylase [EC:4.1.1.29]		
K01595	40	phosphoenolpyruvate carboxylase [EC:4.1.1.31]		
K01596	30	phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]		
K01598	9	phosphopantothenoylcysteine decarboxylase [EC:4.1.1.36]		
K01599	38	uroporphyrinogen decarboxylase [EC:4.1.1.37]		
K01601	7	ribulose-bisphosphate carboxylase large chain [EC:4.1.1.39]		
K01602	3	ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]		
K01605	1	methylmalonyl-CoA decarboxylase beta chain [EC:4.1.1.41]		
K01606	11	methylmalonyl-CoA decarboxylase gamma chain [EC:4.1.1.41]		
K01607	55	4-carboxymuconolactone decarboxylase [EC:4.1.1.44]		
K01608	8	tartronate-semialdehyde synthase [EC:4.1.1.47]		

K01609	19	indole-3-glycerol phosphate synthase [EC:4.1.1.48]		
K01610	22	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]		
K01611	4	S-adenosylmethionine decarboxylase [EC:4.1.1.50]		
K01612	5	4-hydroxybenzoate decarboxylase [EC:4.1.1.61]		
K01613	14	phosphatidylserine decarboxylase [EC:4.1.1.65]		
K01615	12	glutaconyl-CoA decarboxylase [EC:4.1.1.70]		
K01616	9	2-oxoglutarate decarboxylase [EC:4.1.1.71]		
K01617	5	4-oxalocrotonate decarboxylase [EC:4.1.1.77]		
K01618	62	Unclassified; E4.1.1.-		
K01619	13	deoxyribose-phosphate aldolase [EC:4.1.2.4]		
K01620	32	threonine aldolase [EC:4.1.2.5]		
K01621	20	phosphoketolase [EC:4.1.2.9]		
K01623	28	fructose-bisphosphate aldolase, class I [EC:4.1.2.13]		
K01624	8	fructose-bisphosphate aldolase, class II [EC:4.1.2.13]		
K01625	11	2-dehydro-3-deoxyphosphogluconate aldolase /		
K01626	26	3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]		
K01627	29	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase)		
K01628	51	L-fuculose-phosphate aldolase [EC:4.1.2.17]		
K01629	6	rhamnulose-1-phosphate aldolase [EC:4.1.2.19]		
K01630	13	2-dehydro-3-deoxyglucarate aldolase [EC:4.1.2.20]		
K01631	11	2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]		
K01632	12	fructose-6-phosphate phosphoketolase [EC:4.1.2.22]		
K01633	13	dihydroneopterin aldolase [EC:4.1.2.25]		
K01634	7	sphinganine-1-phosphate aldolase [EC:4.1.2.27]		
K01635	10	tagatose 1,6-diphosphate aldolase [EC:4.1.2.40]		
K01636	37	Unclassified; E4.1.2.-		
K01637	13	isocitrate lyase [EC:4.1.3.1]		
K01638	23	malate synthase [EC:2.3.3.9]		
K01639	16	N-acetylneuraminate lyase [EC:4.1.3.3]		
K01640	23	hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]		
K01641	3	hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]		
K01643	11	citrate lyase subunit alpha / citrate CoA-transferase [EC:4.1.3.6		
K01644	42	citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.6 4.1.3.34]		
K01647	50	citrate synthase [EC:2.3.3.1]		
K01648	1	ATP citrate (pro-S)-lyase [EC:2.3.3.8]		
K01649	82	2-isopropylmalate synthase [EC:2.3.3.13]		
K01652	178	acetolactate synthase I/II/III large subunit [EC:2.2.1.6]		
K01653	22	acetolactate synthase I/III small subunit [EC:2.2.1.6]		
K01654	14	N-acetylneuraminate synthase [EC:2.5.1.56]		
K01655	8	homocitrate synthase [EC:2.3.3.14]		
K01657	59	anthranilate synthase component I [EC:4.1.3.27]		
K01658	28	anthranilate synthase component II [EC:4.1.3.27]		
K01659	6	2-methylcitrate synthase [EC:2.3.3.5]		
K01661	17	naphthoate synthase [EC:4.1.3.36]		
K01662	55	1-deoxy-D-xylulose-5-phosphate synthase [EC:2.2.1.7]		
K01664	14	para-aminobenzoate synthetase component II [EC:2.6.1.85]		
K01665	22	para-aminobenzoate synthetase component I [EC:2.6.1.85]		
K01666	4	4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]		
K01667	15	tryptophanase [EC:4.1.99.1]		
K01668	12	tyrosine phenol-lyase [EC:4.1.99.2]		

K01669	28	deoxyribodipyrimidine photo-lyase [EC:4.1.99.3]		
K01673	27	carbonic anhydrase [EC:4.2.1.1]		
K01676	23	fumarate hydratase, class I [EC:4.2.1.2]		
K01677	4	fumarate hydratase subunit alpha [EC:4.2.1.2]		
K01679	37	fumarate hydratase, class II [EC:4.2.1.2]		
K01681	81	aconitate hydratase 1 [EC:4.2.1.3]		
K01682	7	aconitate hydratase 2 [EC:4.2.1.3]		
K01684	33	galactonate dehydratase [EC:4.2.1.6]		
K01685	24	altronate hydrolase [EC:4.2.1.7]		
K01686	9	mannonate dehydratase [EC:4.2.1.8]		
K01687	73	dihydroxy-acid dehydratase [EC:4.2.1.9]		
K01689	42	enolase [EC:4.2.1.11]		
K01690	2	phosphogluconate dehydratase [EC:4.2.1.12]		
K01692	266	enoyl-CoA hydratase [EC:4.2.1.17]		
K01693	14	imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]		
K01695	29	tryptophan synthase alpha chain [EC:4.2.1.20]		
K01696	29	tryptophan synthase beta chain [EC:4.2.1.20]		
K01697	25	cystathionine beta-synthase [EC:4.2.1.22]		
K01698	18	porphobilinogen synthase [EC:4.2.1.24]		
K01699	4	propanediol dehydratase large subunit [EC:4.2.1.28]		
K01703	59	3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit		
K01704	24	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit		
K01705	1	homoaconitate hydratase [EC:4.2.1.36]		
K01706	7	glucarate dehydratase [EC:4.2.1.40]		
K01708	22	galactarate dehydratase [EC:4.2.1.42]		
K01709	15	CDP-glucose 4,6-dehydratase [EC:4.2.1.45]		
K01710	121	dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]		
K01711	34	GDPmannose 4,6-dehydratase [EC:4.2.1.47]		
K01712	17	urocanate hydratase [EC:4.2.1.49]		
K01713	19	prephenate dehydratase [EC:4.2.1.51]		
K01714	67	dihydrodipicolinate synthase [EC:4.2.1.52]		
K01715	61	3-hydroxybutyryl-CoA dehydratase [EC:4.2.1.55]		
K01716	1	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.60]		
K01718	4	pseudouridylate synthase [EC:4.2.1.70]		
K01719	22	uroporphyrinogen-III synthase [EC:4.2.1.75]		
K01720	63	2-methylcitrate dehydratase [EC:4.2.1.79]		
K01722	3	Unclassified; E4.2.1.89		
K01724	20	4a-hydroxytetrahydrobiopterin dehydratase [EC:4.2.1.96]		
K01725	1	cyanate lyase [EC:4.2.1.104]		
K01726	99	Unclassified; E4.2.1.-		
K01728	1	pectate lyase [EC:4.2.2.2]		
K01733	66	threonine synthase [EC:4.2.3.1]		
K01734	6	methylglyoxal synthase [EC:4.2.3.3]		
K01735	30	3-dehydroquinate synthase [EC:4.2.3.4]		
K01736	40	chorismate synthase [EC:4.2.3.5]		
K01737	25	6-pyruvoyl tetrahydrobiopterin synthase [EC:4.2.3.12]		
K01738	73	cysteine synthase A [EC:2.5.1.47]		
K01739	49	cystathionine gamma-synthase [EC:2.5.1.48]		
K01740	36	O-acetylhomoserine (thiol)-lyase [EC:2.5.1.49]		
K01741	3	DNA-(apurinic or apyrimidinic site) lyase [EC:4.2.99.18]		

K01743	3	Unclassified; E4.2.-.-		
K01744	18	aspartate ammonia-lyase [EC:4.3.1.1]		
K01745	32	histidine ammonia-lyase [EC:4.3.1.3]		
K01746	14	formiminotetrahydrofolate cyclodeaminase [EC:4.3.1.4]		
K01749	28	hydroxymethylbilane synthase [EC:2.5.1.61]		
K01750	39	ornithine cyclodeaminase [EC:4.3.1.12]		
K01751	4	diaminopropionate ammonia-lyase [EC:4.3.1.15]		
K01752	8	L-serine dehydratase [EC:4.3.1.17]		
K01754	80	threonine dehydratase [EC:4.3.1.19]		
K01755	59	argininosuccinate lyase [EC:4.3.2.1]		
K01756	53	adenylosuccinate lyase [EC:4.3.2.2]		
K01757	6	strictosidine synthase [EC:4.3.3.2]		
K01758	28	cystathionine gamma-lyase [EC:4.4.1.1]		
K01759	62	lactoylglutathione lyase [EC:4.4.1.5]		
K01760	59	cystathionine beta-lyase [EC:4.4.1.8]		
K01761	21	methionine-gamma-lyase [EC:4.4.1.11]		
K01768	403	adenylate cyclase [EC:4.6.1.1]		
K01769	7	guanylate cyclase, other [EC:4.6.1.2]		
K01770	23	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:4.6.1.12]		
K01772	32	ferrochelatase [EC:4.99.1.1]		
K01774	3	Unclassified; E4.-.-.-		
K01775	45	alanine racemase [EC:5.1.1.1]		
K01776	47	glutamate racemase [EC:5.1.1.3]		
K01777	12	proline racemase [EC:5.1.1.4]		
K01778	33	diaminopimelate epimerase [EC:5.1.1.7]		
K01779	30	aspartate racemase [EC:5.1.1.13]		
K01780	26	Unclassified; E5.1.1.-		
K01781	68	mandelate racemase [EC:5.1.2.2]		
K01782	36	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase /		
K01783	21	ribulose-phosphate 3-epimerase [EC:5.1.3.1]		
K01784	233	UDP-glucose 4-epimerase [EC:5.1.3.2]		
K01785	23	aldose 1-epimerase [EC:5.1.3.3]		
K01786	5	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]		
K01787	7	N-acylglucosamine 2-epimerase [EC:5.1.3.8]		
K01789	11	UDP-glucuronate 5'-epimerase [EC:5.1.3.12]		
K01790	33	dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13]		
K01791	43	UDP-N-acetylglucosamine 2-epimerase [EC:5.1.3.14]		
K01792	3	glucose-6-phosphate 1-epimerase [EC:5.1.3.15]		
K01795	128	Unclassified; E5.1.3.-		
K01796	35	alpha-methylacyl-CoA racemase [EC:5.1.99.4]		
K01797	89	Unclassified; E5.1.99.-		
K01798	3	Unclassified; E5.1.-.-		
K01799	14	maleate isomerase [EC:5.2.1.1]		
K01800	11	maleylacetoacetate isomerase [EC:5.2.1.2]		
K01801	8	maleylpyruvate isomerase [EC:5.2.1.4]		
K01802	87	peptidylprolyl isomerase [EC:5.2.1.8]		
K01803	29	triosephosphate isomerase (TIM) [EC:5.3.1.1]		
K01804	10	L-arabinose isomerase [EC:5.3.1.4]		
K01805	13	xylose isomerase [EC:5.3.1.5]		
K01807	12	ribose 5-phosphate isomerase A [EC:5.3.1.6]		

K01808	26	ribose 5-phosphate isomerase B [EC:5.3.1.6]		
K01809	44	mannose-6-phosphate isomerase [EC:5.3.1.8]		
K01810	53	glucose-6-phosphate isomerase [EC:5.3.1.9]		
K01811	10	putative family 31 glucosidase		
K01812	7	glucuronate isomerase [EC:5.3.1.12]		
K01813	9	L-rhamnose isomerase [EC:5.3.1.14]		
K01814	30	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide		
K01816	12	hydroxypyruvate isomerase [EC:5.3.1.22]		
K01817	27	phosphoribosylanthranilate isomerase [EC:5.3.1.24]		
K01818	6	L-fucose isomerase [EC:5.3.1.25]		
K01820	9	Unclassified; E5.3.1.-		
K01821	5	4-oxalocrotonate tautomerase [EC:5.3.2.-]		
K01822	1	steroid delta-isomerase [EC:5.3.3.1]		
K01823	12	isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]		
K01825	4	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase /		
K01826	20	5-carboxymethyl-2-hydroxymuconate isomerase [EC:5.3.3.10]		
K01828	20	Unclassified; E5.3.3.-		
K01829	20	protein disulfide-isomerase [EC:5.3.4.1]		
K01834	100	phosphoglycerate mutase [EC:5.4.2.1]		
K01835	41	phosphoglucomutase [EC:5.4.2.2]		
K01838	4	beta-phosphoglucomutase [EC:5.4.2.6]		
K01839	18	phosphopentomutase [EC:5.4.2.7]		
K01840	87	phosphomannomutase [EC:5.4.2.8]		
K01841	3	phosphoenolpyruvate phosphomutase [EC:5.4.2.9]		
K01842	5	Unclassified; E5.4.2.-		
K01843	25	lysine 2,3-aminomutase [EC:5.4.3.2]		
K01844	3	beta-lysine 5,6-aminomutase [EC:5.4.3.3]		
K01845	65	glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]		
K01846	4	methylaspartate mutase [EC:5.4.99.1]		
K01847	14	methylmalonyl-CoA mutase [EC:5.4.99.2]		
K01848	52	methylmalonyl-CoA mutase, N-terminal domain [EC:5.4.99.2]		
K01849	12	methylmalonyl-CoA mutase, C-terminal domain [EC:5.4.99.2]		
K01851	1	salicylate biosynthesis isochorismate synthase [EC:5.4.4.2]		
K01854	46	UDP-galactopyranose mutase [EC:5.4.99.9]		
K01856	36	muconate cycloisomerase [EC:5.5.1.1]		
K01857	15	3-carboxy-cis,cis-muconate cycloisomerase [EC:5.5.1.2]		
K01858	12	myo-inositol-1-phosphate synthase [EC:5.5.1.4]		
K01860	15	chloromuconate cycloisomerase [EC:5.5.1.7]		
K01865	17	Unclassified; E5.-.-.-		
K01866	51	tyrosyl-tRNA synthetase [EC:6.1.1.1]		
K01867	46	tryptophanyl-tRNA synthetase [EC:6.1.1.2]		
K01868	67	threonyl-tRNA synthetase [EC:6.1.1.3]		
K01869	73	leucyl-tRNA synthetase [EC:6.1.1.4]		
K01870	85	isoleucyl-tRNA synthetase [EC:6.1.1.5]		
K01872	71	alanyl-tRNA synthetase [EC:6.1.1.7]		
K01873	99	valyl-tRNA synthetase [EC:6.1.1.9]		
K01874	56	methionyl-tRNA synthetase [EC:6.1.1.10]		
K01875	59	seryl-tRNA synthetase [EC:6.1.1.11]		
K01876	57	aspartyl-tRNA synthetase [EC:6.1.1.12]		
K01878	12	glycyl-tRNA synthetase alpha chain [EC:6.1.1.14]		

K01879	36	glycyl-tRNA synthetase beta chain [EC:6.1.1.14]		
K01880	17	glycyl-tRNA synthetase [EC:6.1.1.14]		
K01881	50	prolyl-tRNA synthetase [EC:6.1.1.15]		
K01883	69	cysteinyl-tRNA synthetase [EC:6.1.1.16]		
K01885	74	glutamyl-tRNA synthetase [EC:6.1.1.17]		
K01886	28	glutaminyl-tRNA synthetase [EC:6.1.1.18]		
K01887	498	arginyl-tRNA synthetase [EC:6.1.1.19]		
K01889	40	phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]		
K01890	515	phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]		
K01892	46	histidyl-tRNA synthetase [EC:6.1.1.21]		
K01893	25	asparaginyl-tRNA synthetase [EC:6.1.1.22]		
K01894	20	glutamyl-Q tRNA(Asp) synthetase [EC:6.1.1.-]		
K01895	175	acetyl-CoA synthetase [EC:6.2.1.1]		
K01897	294	long-chain acyl-CoA synthetase [EC:6.2.1.3]		
K01902	19	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]		
K01903	30	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]		
K01904	37	4-coumarate--CoA ligase [EC:6.2.1.12]		
K01905	37	acetyl-CoA synthetase (ADP-forming) [EC:6.2.1.13]		
K01906	43	6-carboxyhexanoate--CoA ligase [EC:6.2.1.14]		
K01907	38	acetoacetyl-CoA synthetase [EC:6.2.1.16]		
K01908	12	propionyl-CoA synthetase [EC:6.2.1.17]		
K01911	22	O-succinylbenzoic acid--CoA ligase [EC:6.2.1.26]		
K01912	88	phenylacetate-CoA ligase [EC:6.2.1.30]		
K01913	125	Unclassified; E6.2.1.-		
K01914	7	aspartate--ammonia ligase [EC:6.3.1.1]		
K01915	141	glutamine synthetase [EC:6.3.1.2]		
K01916	33	NAD+ synthase [EC:6.3.1.5]		
K01917	15	glutathionylspermidine synthase [EC:6.3.1.8]		
K01918	21	pantoate--beta-alanine ligase [EC:6.3.2.1]		
K01919	16	glutamate--cysteine ligase [EC:6.3.2.2]		
K01920	20	glutathione synthase [EC:6.3.2.3]		
K01921	88	D-alanine-D-alanine ligase [EC:6.3.2.4]		
K01922	6	phosphopantothenate-cysteine ligase [EC:6.3.2.5]		
K01923	35	phosphoribosylaminoimidazole-succinocarboxamide synthase		
K01924	35	UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8]		
K01925	33	UDP-N-acetylmuramoylalanine--D-glutamate ligase [EC:6.3.2.9]		
K01926	7	AT-rich DNA-binding protein		
K01928	42	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase		
K01929	58	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-		
K01932	7	Unclassified; E6.3.2.-		
K01933	32	phosphoribosylformylglycinamidine cyclo-ligase [EC:6.3.3.1]		
K01934	15	5-formyltetrahydrofolate cyclo-ligase [EC:6.3.3.2]		
K01935	11	dethiobiotin synthetase [EC:6.3.3.3]		
K01937	42	CTP synthase [EC:6.3.4.2]		
K01938	23	formate--tetrahydrofolate ligase [EC:6.3.4.3]		
K01939	47	adenylosuccinate synthase [EC:6.3.4.4]		
K01940	34	argininosuccinate synthase [EC:6.3.4.5]		
K01941	8	urea carboxylase [EC:6.3.4.6]		
K01945	31	phosphoribosylamine--glycine ligase [EC:6.3.4.13]		
K01947	4	biotin-[acetyl-CoA-carboxylase] ligase / type III pantothenate		

K01950	63	NAD+ synthase (glutamine-hydrolysing) [EC:6.3.5.1]		
K01951	50	GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]		
K01952	89	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]		
K01953	160	asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]		
K01955	66	carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]		
K01956	39	carbamoyl-phosphate synthase small subunit [EC:6.3.5.5]		
K01957	10	glutamyl-tRNA (Gln) amidotransferase [EC:6.3.5.-]		
K01958	22	pyruvate carboxylase [EC:6.4.1.1]		
K01959	2	pyruvate carboxylase subunit A [EC:6.4.1.1]		
K01960	23	pyruvate carboxylase subunit B [EC:6.4.1.1]		
K01961	38	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2		
K01962	21	acetyl-CoA carboxylase carboxyl transferase subunit alpha		
K01963	31	acetyl-CoA carboxylase carboxyl transferase subunit beta		
K01965	36	propionyl-CoA carboxylase alpha chain [EC:6.4.1.3]		
K01966	69	propionyl-CoA carboxylase beta chain [EC:6.4.1.3]		
K01968	21	3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4]		
K01969	19	3-methylcrotonyl-CoA carboxylase beta subunit [EC:6.4.1.4]		
K01970	3	Unclassified; E6.4.-.-		
K01971	172	DNA ligase (ATP) [EC:6.5.1.1]		
K01972	63	DNA ligase (NAD+) [EC:6.5.1.2]		
K01974	6	RNA 3'-terminal phosphate cyclase [EC:6.5.1.4]		
K01975	8	2'-5' RNA ligase [EC:6.5.1.-]		
K01976	26	Unclassified; E6.-.-.-		
K01989	47	putative ABC transport system substrate-binding protein		
K01990	199	ABC-2 type transport system ATP-binding protein		
K01991	50	polysaccharide export outer membrane protein		
K01992	215	ABC-2 type transport system permease protein		
K01993	36	HlyD family secretion protein		
K01994	1	LuxR family transcriptional regulator, transcriptional regulator of		
K01995	126	branched-chain amino acid transport system ATP-binding protein		
K01996	125	branched-chain amino acid transport system ATP-binding protein		
K01997	153	branched-chain amino acid transport system permease protein		
K01998	326	branched-chain amino acid transport system permease protein		
K01999	254	branched-chain amino acid transport system substrate-binding protein		
K02000	5	glycine betaine/proline transport system ATP-binding protein		
K02001	2	glycine betaine/proline transport system permease protein		
K02002	2	glycine betaine/proline transport system substrate-binding protein		
K02003	126	Unclassified; ABC.CD.A		
K02004	274	Unclassified; ABC.CD.P		
K02005	128	HlyD family secretion protein		
K02006	28	cobalt/nickel transport system ATP-binding protein		
K02007	5	cobalt/nickel transport system permease protein		
K02008	17	cobalt/nickel transport system permease protein		
K02010	19	iron(III) transport system ATP-binding protein [EC:3.6.3.30]		
K02011	71	iron(III) transport system permease protein		
K02012	46	iron(III) transport system substrate-binding protein		
K02013	25	iron complex transport system ATP-binding protein [EC:3.6.3.34]		
K02014	205	iron complex outermembrane recepter protein		
K02015	23	iron complex transport system permease protein		
K02016	43	iron complex transport system substrate-binding protein		

K02017	11	molybdate transport system ATP-binding protein [EC:3.6.3.29]		
K02018	15	molybdate transport system permease protein		
K02019	7	molybdate transport system regulatory protein		
K02020	55	molybdate transport system substrate-binding protein		
K02021	41	putative ABC transport system ATP-binding protein		
K02022	18	Unclassified; ABC.MR.TX		
K02023	24	multiple sugar transport system ATP-binding protein		
K02024	1	maltoporin		
K02025	139	multiple sugar transport system permease protein		
K02026	137	multiple sugar transport system permease protein		
K02027	138	multiple sugar transport system substrate-binding protein		
K02028	18	polar amino acid transport system ATP-binding protein [EC:3.6.3.21]		
K02029	26	polar amino acid transport system permease protein		
K02030	96	polar amino acid transport system substrate-binding protein		
K02031	66	peptide/nickel transport system ATP-binding protein		
K02032	185	peptide/nickel transport system ATP-binding protein		
K02033	207	peptide/nickel transport system permease protein		
K02034	165	peptide/nickel transport system permease protein		
K02035	407	peptide/nickel transport system substrate-binding protein		
K02036	24	phosphate transport system ATP-binding protein [EC:3.6.3.27]		
K02037	43	phosphate transport system permease protein		
K02038	42	phosphate transport system permease protein		
K02039	31	phosphate transport system protein		
K02040	62	phosphate transport system substrate-binding protein		
K02041	11	phosphonate transport system ATP-binding protein		
K02042	4	phosphonate transport system permease protein		
K02044	24	phosphonate transport system substrate-binding protein		
K02045	11	sulfate transport system ATP-binding protein [EC:3.6.3.25]		
K02046	14	sulfate transport system permease protein		
K02047	9	sulfate transport system permease protein		
K02048	16	sulfate transport system substrate-binding protein		
K02049	46	sulfonate/nitrate/taurine transport system ATP-binding protein		
K02050	86	sulfonate/nitrate/taurine transport system permease protein		
K02051	109	sulfonate/nitrate/taurine transport system substrate-binding protein		
K02052	32	putative spermidine/putrescine transport system ATP-binding protein		
K02053	39	putative spermidine/putrescine transport system permease protein		
K02054	31	putative spermidine/putrescine transport system permease protein		
K02055	46	putative spermidine/putrescine transport system substrate-binding		
K02056	66	simple sugar transport system ATP-binding protein [EC:3.6.3.17]		
K02057	106	simple sugar transport system permease protein		
K02058	54	simple sugar transport system substrate-binding protein		
K02059	4	putative sulfate transport system ATP-binding protein		
K02060	7	putative sulfate transport system permease protein		
K02061	3	putative sulfate transport system substrate-binding protein		
K02063	7	thiamine transport system permease protein		
K02064	3	thiamine transport system substrate-binding protein		
K02065	37	putative ABC transport system ATP-binding protein		
K02066	51	putative ABC transport system permease protein		
K02067	57	putative ABC transport system substrate-binding protein		
K02068	1	putative ABC transport system ATP-binding protein		

K02069	5	putative ABC transport system permease protein		
K02071	4	D-methionine transport system ATP-binding protein		
K02073	2	D-methionine transport system substrate-binding protein		
K02074	9	zinc/manganese transport system ATP-binding protein		
K02075	17	zinc/manganese transport system permease protein		
K02076	2	Fur family transcriptional regulator, zinc uptake regulator		
K02077	30	zinc/manganese transport system substrate-binding protein		
K02078	15	acyl carrier protein		
K02079	2	N-acetylgalactosamine-6-phosphate deacetylase [EC:3.5.1.25]		
K02081	13	DeoR family transcriptional regulator, aga operon transcriptional		
K02082	2	tagatose-6-phosphate ketose/aldose isomerase [EC:5.-.-.-]		
K02083	5	allantoate deiminase [EC:3.5.3.9]		
K02099	3	AraC family transcriptional regulator, arabinose operon regulatory		
K02103	1	GntR family transcriptional regulator, arabinose operon		
K02106	4	short-chain fatty acids transporter		
K02108	50	F-type H+-transporting ATPase subunit a [EC:3.6.3.14]		
K02109	12	F-type H+-transporting ATPase subunit b [EC:3.6.3.14]		
K02110	10	F-type H+-transporting ATPase subunit c [EC:3.6.3.14]		
K02111	32	F-type H+-transporting ATPase subunit alpha [EC:3.6.3.14]		
K02112	21	F-type H+-transporting ATPase subunit beta [EC:3.6.3.14]		
K02113	26	F-type H+-transporting ATPase subunit delta [EC:3.6.3.14]		
K02114	7	F-type H+-transporting ATPase subunit epsilon [EC:3.6.3.14]		
K02115	35	F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]		
K02116	2	ATP synthase protein I		
K02117	20	V-type H+-transporting ATPase subunit A [EC:3.6.3.14]		
K02118	13	V-type H+-transporting ATPase subunit B [EC:3.6.3.14]		
K02120	3	V-type H+-transporting ATPase subunit D [EC:3.6.3.14]		
K02121	2	V-type H+-transporting ATPase subunit E [EC:3.6.3.14]		
K02123	15	V-type H+-transporting ATPase subunit I [EC:3.6.3.14]		
K02124	4	V-type H+-transporting ATPase subunit K [EC:3.6.3.14]		
K02160	11	acetyl-CoA carboxylase biotin carboxyl carrier protein		
K02164	4	nitric-oxide reductase NorE protein [EC:1.7.99.7]		
K02169	17	biotin synthesis protein BioC		
K02170	4	biotin biosynthesis protein BioH		
K02182	16	crotonobetaine/carnitine-CoA ligase [EC:6.2.1.-]		
K02188	4	cobalamin biosynthesis protein CbiD		
K02189	1	cobalamin biosynthesis protein CbiG		
K02193	29	heme exporter protein A [EC:3.6.3.41]		
K02194	15	heme exporter protein B		
K02195	42	heme exporter protein C		
K02197	10	cytochrome c-type biogenesis protein CcmE		
K02198	81	cytochrome c-type biogenesis protein CcmF		
K02199	52	cytochrome c biogenesis protein CcmG, thiol:disulfide interchange		
K02200	19	cytochrome c-type biogenesis protein CcmH		
K02203	6	phosphoserine / homoserine phosphotransferase [EC:3.1.3.3 2.7.1.39]		
K02204	5	homoserine kinase type II [EC:2.7.1.39]		
K02217	12	ferritin [EC:1.16.3.1]		
K02221	26	YggT family protein		
K02224	18	cobyrinic acid a,c-diamide synthase [EC:6.3.5.9 6.3.1.-]		
K02226	2	alpha-ribazole phosphatase [EC:3.1.3.73]		

K02227	11	adenosylcobinamide-phosphate synthase CobD [EC:6.3.1.10]		
K02229	1	precorrin-3B synthase [EC:1.14.13.83]		
K02230	13	cobaltochelatase CobN [EC:6.6.1.2]		
K02231	13	adenosylcobinamide kinase / adenosylcobinamide-phosphate		
K02232	9	adenosylcobyric acid synthase [EC:6.3.5.10]		
K02233	2	adenosylcobinamide-GDP ribazoletransferase [EC:2.7.8.26]		
K02234	13	cobalamin biosynthesis protein CobW		
K02236	9	leader peptidase (prepilin peptidase) / N-methyltransferase		
K02237	16	competence protein ComEA		
K02238	57	competence protein ComEC		
K02240	1	competence protein ComFA		
K02242	4	competence protein ComFC		
K02244	3	competence protein ComGB		
K02248	3	competence protein ComGF		
K02258	6	cytochrome c oxidase subunit XI assembly protein		
K02259	27	cytochrome c oxidase subunit XV assembly protein		
K02274	88	cytochrome c oxidase subunit I [EC:1.9.3.1]		
K02275	66	cytochrome c oxidase subunit II [EC:1.9.3.1]		
K02276	37	cytochrome c oxidase subunit III [EC:1.9.3.1]		
K02278	1	prepilin peptidase CpaA [EC:3.4.23.43]		
K02279	5	pilus assembly protein CpaB		
K02280	15	pilus assembly protein CpaC		
K02282	37	pilus assembly protein CpaE		
K02283	46	pilus assembly protein CpaF		
K02287	2	phycocyanin-associated, rod		
K02288	2	phycocyanobilin lyase alpha subunit [EC:4.-.-.-]		
K02291	30	phytoene synthase [EC:2.5.1.32]		
K02292	50	beta-carotene ketolase (CrtO type)		
K02293	3	phytoene dehydrogenase, phytoene desaturase [EC:1.14.99.-]		
K02297	3	cytochrome o ubiquinol oxidase subunit II [EC:1.10.3.-]		
K02298	6	cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]		
K02299	4	cytochrome o ubiquinol oxidase subunit III [EC:1.10.3.-]		
K02301	31	protoheme IX farnesyltransferase [EC:2.5.1.-]		
K02302	27	uroporphyrin-III C-methyltransferase / precorrin-2 dehydrogenase /		
K02303	22	uroporphyrin-III C-methyltransferase [EC:2.1.1.107]		
K02304	6	precorrin-2 dehydrogenase / sirohydrochlorin ferrochelatase		
K02305	3	nitric-oxide reductase, cytochrome c-containing subunit II		
K02312	5	2,3-dihydroxybenzoate-AMP ligase [EC:2.7.7.58]		
K02313	51	chromosomal replication initiator protein		
K02314	78	replicative DNA helicase [EC:3.6.1.-]		
K02315	8	DNA replication protein DnaC		
K02316	65	DNA primase [EC:2.7.7.-]		
K02319	11	DNA polymerase I [EC:2.7.7.7]		
K02330	6	DNA polymerase beta subunit [EC:2.7.7.7 4.2.99.-]		
K02334	43	DNA polymerase bacteriophage-type [EC:2.7.7.7]		
K02335	90	DNA polymerase I [EC:2.7.7.7]		
K02336	4	DNA polymerase II [EC:2.7.7.7]		
K02337	211	DNA polymerase III subunit alpha [EC:2.7.7.7]		
K02338	59	DNA polymerase III subunit beta [EC:2.7.7.7]		
K02339	6	DNA polymerase III subunit chi [EC:2.7.7.7]		

K02340	11	DNA polymerase III subunit delta [EC:2.7.7.7]		
K02341	35	DNA polymerase III subunit delta' [EC:2.7.7.7]		
K02342	60	DNA polymerase III subunit epsilon [EC:2.7.7.7]		
K02343	65	DNA polymerase III subunit gamma/tau [EC:2.7.7.7]		
K02345	1	DNA polymerase III subunit theta [EC:2.7.7.7]		
K02346	46	DNA polymerase IV [EC:2.7.7.7]		
K02347	45	DNA polymerase (family X)		
K02348	2	ElaA protein		
K02351	7	putative membrane protein		
K02352	1	drp35		
K02355	154	elongation factor EF-G [EC:3.6.5.3]		
K02356	32	elongation factor EF-P		
K02357	44	elongation factor EF-Ts		
K02358	138	elongation factor EF-Tu [EC:3.6.5.3]		
K02361	19	isochorismate synthase [EC:5.4.4.2]		
K02363	1	enterobactin 2,3-dihydroxybenzoate-AMP ligase /		
K02364	7	enterobactin synthetase component F [EC:2.7.7.-]		
K02371	8	enoyl-[acyl carrier protein] reductase II [EC:1.3.1.-]		
K02372	22	3R-hydroxymyristoyl ACP dehydrase [EC:4.2.1.-]		
K02377	24	GDP-L-fucose synthase [EC:1.1.1.271]		
K02379	19	FdhD protein		
K02380	5	FdhE protein		
K02381	6	FdrA protein		
K02382	3	flagellar protein FlbA		
K02384	3	flagellar protein FlbC		
K02386	1	flagella basal body P-ring formation protein FlgA		
K02387	12	flagellar basal-body rod protein FlgB		
K02388	133	flagellar basal-body rod protein FlgC		
K02389	14	flagellar basal-body rod modification protein FlgD		
K02390	14	flagellar hook protein FlgE		
K02391	4	flagellar basal-body rod protein FlgF		
K02392	15	flagellar basal-body rod protein FlgG		
K02393	4	flagellar L-ring protein precursor FlgH		
K02394	6	flagellar P-ring protein precursor FlgI		
K02395	11	flagellar protein FlgJ		
K02396	12	flagellar hook-associated protein 1 FlgK		
K02397	8	flagellar hook-associated protein 3 FlgL		
K02400	16	flagellar biosynthesis protein FlhA		
K02401	8	flagellar biosynthetic protein FlhB		
K02402	1	flagellar transcriptional activator FlhC		
K02404	6	flagellar biosynthesis protein FlhF		
K02405	21	RNA polymerase sigma factor for flagellar operon FliA		
K02406	10	flagellin		
K02407	17	flagellar hook-associated protein 2		
K02408	2	flagellar hook-basal body complex protein FliE		
K02409	14	flagellar M-ring protein FliF		
K02410	16	flagellar motor switch protein FliG		
K02411	3	flagellar assembly protein FliH		
K02412	12	flagellum-specific ATP synthase [EC:3.6.3.14]		
K02413	1	flagellar FliJ protein		

K02414	1	flagellar hook-length control protein FliK		
K02415	3	flagellar FliL protein		
K02416	15	flagellar motor switch protein FliM		
K02417	6	flagellar motor switch protein FliN/FliY		
K02418	2	flagellar protein FliO/FliZ		
K02419	7	flagellar biosynthetic protein FliP		
K02420	2	flagellar biosynthetic protein FliQ		
K02421	2	flagellar biosynthetic protein FliR		
K02422	3	flagellar protein FliS		
K02424	2	cystine transport system substrate-binding protein		
K02426	10	cysteine desulfuration protein SufE		
K02427	13	ribosomal RNA large subunit methyltransferase E [EC:2.1.1.-]		
K02428	30	nucleoside-triphosphate pyrophosphatase [EC:3.6.1.19]		
K02429	11	MFS transporter, FHS family, L-fucose permease		
K02431	1	L-fucose mutarotase [EC:5.1.3.-]		
K02433	141	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit A		
K02434	54	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit B		
K02435	18	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit C		
K02436	2	DeoR family transcriptional regulator, galactitol utilization operon		
K02437	29	glycine cleavage system H protein		
K02438	33	glycogen operon protein GlgX [EC:3.2.1.-]		
K02439	2	thiosulfate sulfurtransferase [EC:2.8.1.1]		
K02440	14	glycerol uptake facilitator protein		
K02441	1	GlpG protein		
K02444	5	DeoR family transcriptional regulator, glycerol-3-phosphate regulon		
K02445	1	MFS transporter, OPA family, glycerol-3-phosphate transporter		
K02446	28	fructose-1,6-bisphosphatase II [EC:3.1.3.11]		
K02448	3	nitric-oxide reductase NorD protein [EC:1.7.99.7]		
K02450	12	general secretion pathway protein A		
K02452	1	general secretion pathway protein C		
K02453	90	general secretion pathway protein D		
K02454	48	general secretion pathway protein E		
K02455	102	general secretion pathway protein F		
K02456	16	general secretion pathway protein G		
K02457	2	general secretion pathway protein H		
K02458	2	general secretion pathway protein I		
K02459	2	general secretion pathway protein J		
K02460	10	general secretion pathway protein K		
K02461	7	general secretion pathway protein L		
K02464	6	general secretion pathway protein O [EC:3.4.23.43 2.1.1.-]		
K02469	80	DNA gyrase subunit A [EC:5.99.1.3]		
K02470	50	DNA gyrase subunit B [EC:5.99.1.3]		
K02471	16	putative ATP-binding cassette transporter		
K02472	10	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.-]		
K02473	35	UDP-N-acetylglucosamine 4-epimerase [EC:5.1.3.7]		
K02474	11	UDP-N-acetyl-D-galactosamine dehydrogenase [EC:1.1.1.-]		
K02475	2	two-component system, CitB family, response regulator		
K02477	67	two-component system, LytT family, response regulator		
K02478	4	two-component system, LytT family, sensor kinase [EC:2.7.13.3]		
K02479	79	two-component system, NarL family, response regulator		

K02480	32	two-component system, NarL family, sensor kinase [EC:2.7.13.3]		
K02481	134	two-component system, NtrC family, response regulator		
K02482	143	two-component system, NtrC family, sensor kinase [EC:2.7.13.3]		
K02483	128	two-component system, OmpR family, response regulator		
K02484	139	two-component system, OmpR family, sensor kinase [EC:2.7.13.3]		
K02485	11	two-component system, unclassified family, response regulator		
K02486	15	two-component system, unclassified family, sensor kinase		
K02487	1	type IV pili sensor histidine kinase and response regulator		
K02488	217	two-component system, cell cycle response regulator		
K02489	49	two-component system, cell cycle sensor kinase and response		
K02490	30	two-component system, response regulator, stage 0 sporulation		
K02491	8	two-component system, sporulation sensor kinase A [EC:2.7.13.3]		
K02492	42	glutamyl-tRNA reductase [EC:1.2.1.70]		
K02493	32	methyltransferase [EC:2.1.1.-]		
K02494	3	outer membrane lipoprotein LolB		
K02495	53	oxygen-independent coproporphyrinogen III oxidase [EC:1.3.99.22]		
K02496	3	uroporphyrin-III C-methyltransferase [EC:2.1.1.107]		
K02497	2	HemX protein		
K02498	3	HemY protein		
K02499	13	tetrapyrrole methylase family protein / MazG family protein		
K02500	27	cyclase HisF [EC:4.1.3.-]		
K02501	31	glutamine amidotransferase [EC:2.4.2.-]		
K02502	22	ATP phosphoribosyltransferase regulatory subunit		
K02503	30	Hit-like protein involved in cell-cycle regulation		
K02504	1	protein transport protein HofB		
K02507	4	protein transport protein HofQ		
K02508	2	AraC family transcriptional regulator, 4-hydroxyphenylacetate		
K02509	7	2-oxo-hept-3-ene-1,7-dioate hydratase [EC:4.2.1.-]		
K02510	35	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [EC:4.1.2.-]		
K02511	1	MFS transporter, ACS family, 4-hydroxyphenylacetate permease		
K02517	28	lipid A biosynthesis lauroyl acyltransferase [EC:2.3.1.-]		
K02518	13	translation initiation factor IF-1		
K02519	44	translation initiation factor IF-2		
K02520	31	translation initiation factor IF-3		
K02523	22	octaprenyl diphosphate synthase [EC:2.5.1.-]		
K02525	1	LacI family transcriptional regulator, kdg operon repressor		
K02526	3	2-keto-3-deoxygluconate permease		
K02527	16	3-deoxy-D-manno-octulosonic-acid transferase [EC:2.-.-.-]		
K02528	35	dimethyladenosine transferase [EC:2.1.1.-]		
K02529	80	LacI family transcriptional regulator		
K02532	1	MFS transporter, OHS family, lactose permease		
K02533	19	tRNA/rRNA methyltransferase [EC:2.1.1.-]		
K02535	25	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase		
K02536	33	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase		
K02545	2	penicillin-binding protein 2 prime		
K02547	1	methicillin resistance protein		
K02548	10	1,4-dihydroxy-2-naphthoate octaprenyltransferase [EC:2.5.1.-]		
K02549	20	O-succinylbenzoate synthase [EC:4.2.1.113]		
K02550	1	glycolate permease		
K02551	32	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate		

K02552	12	menaquinone-specific isochorismate synthase [EC:5.4.4.2]		
K02553	1	regulator of ribonuclease activity A		
K02554	5	2-keto-4-pentenoate hydratase [EC:4.2.1.80]		
K02556	5	chemotaxis protein MotA		
K02557	23	chemotaxis protein MotB		
K02558	24	UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate		
K02562	2	mannitol operon repressor		
K02563	30	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)		
K02564	23	glucosamine-6-phosphate deaminase [EC:3.5.99.6]		
K02565	5	N-acetylglucosamine repressor		
K02566	16	NagD protein		
K02567	28	periplasmic nitrate reductase NapA [EC:1.7.99.4]		
K02568	8	cytochrome c-type protein NapB		
K02569	3	cytochrome c-type protein NapC		
K02571	1	periplasmic nitrate reductase NapE		
K02572	2	ferredoxin-type protein NapF		
K02573	7	ferredoxin-type protein NapG		
K02574	7	ferredoxin-type protein NapH		
K02575	27	MFS transporter, NNP family, nitrate/nitrite transporter		
K02584	38	Nif-specific regulatory protein		
K02585	2	nitrogen fixation protein NifB		
K02586	4	nitrogenase molybdenum-iron protein alpha chain [EC:1.18.6.1]		
K02587	1	nitrogenase molybdenum-cofactor synthesis protein NifE		
K02588	1	nitrogenase iron protein NifH [EC:1.18.6.1]		
K02591	3	nitrogenase molybdenum-iron protein beta chain [EC:1.18.6.1]		
K02592	1	nitrogenase molybdenum-iron protein NifN		
K02594	3	homocitrate synthase NifV		
K02597	5	nitrogen fixation protein NifZ		
K02598	1	nitrite transporter NirC		
K02600	28	N utilization substance protein A		
K02601	16	transcriptional antiterminator NusG		
K02609	16	phenylacetic acid degradation protein		
K02610	4	phenylacetic acid degradation protein		
K02611	10	phenylacetic acid degradation protein		
K02612	14	phenylacetic acid degradation protein		
K02613	11	phenylacetic acid degradation NADH oxidoreductase		
K02614	21	phenylacetic acid degradation protein		
K02615	3	acetyl-CoA acetyltransferase [EC:2.3.1.-]		
K02616	6	phenylacetic acid degradation operon negative regulatory protein		
K02617	6	phenylacetic acid degradation protein		
K02618	19	phenylacetic acid degradation protein		
K02619	44	4-amino-4-deoxychorismate lyase [EC:4.1.3.38]		
K02621	13	topoisomerase IV subunit A [EC:5.99.1.-]		
K02622	18	topoisomerase IV subunit B [EC:5.99.1.-]		
K02623	10	LysR family transcriptional regulator, pca operon transcriptional		
K02624	13	IclR family transcriptional regulator, pca regulon regulatory		
K02626	5	arginine decarboxylase [EC:4.1.1.19]		
K02635	19	cytochrome b6		
K02636	14	cytochrome b6-f complex iron-sulfur subunit [EC:1.10.99.1]		
K02637	1	cytochrome b6-f complex subunit 4		

K02638	2	plastocyanin		
K02641	2	ferredoxin--NADP+ reductase [EC:1.18.1.2]		
K02647	2	carbohydrate diacid regulator		
K02650	7	type IV pilus assembly protein PilA		
K02651	5	pilus assembly protein Flp/PilA		
K02652	69	type IV pilus assembly protein PilB		
K02653	77	type IV pilus assembly protein PilC		
K02654	24	leader peptidase (prepilin peptidase) / N-methyltransferase		
K02655	6	type IV pilus assembly protein PilE		
K02656	15	type IV pilus assembly protein PilF		
K02657	13	twitching motility two-component system response regulator PilG		
K02658	37	twitching motility two-component system response regulator PilH		
K02659	5	twitching motility protein PilI		
K02660	18	twitching motility protein PilJ		
K02661	2	type IV pilus assembly protein PilK		
K02662	35	type IV pilus assembly protein PilM		
K02663	6	type IV pilus assembly protein PilN		
K02664	9	type IV pilus assembly protein PilO		
K02665	4	type IV pilus assembly protein PilP		
K02666	66	type IV pilus assembly protein PilQ		
K02667	64	two-component system, NtrC family, response regulator PilR		
K02668	66	two-component system, NtrC family, sensor histidine kinase PilS		
K02669	68	twitching motility protein PilT		
K02670	13	twitching motility protein PilU		
K02671	2	type IV pilus assembly protein PilV		
K02672	4	type IV pilus assembly protein PilW		
K02673	7	type IV pilus assembly protein PilX		
K02674	38	type IV pilus assembly protein PilY1		
K02676	2	type IV pilus assembly protein PilZ		
K02686	4	primosomal replication protein N		
K02687	27	ribosomal protein L11 methyltransferase [EC:2.1.1.-]		
K02688	2	transcriptional regulator, propionate catabolism operon regulatory		
K02690	1	photosystem I core protein Ib		
K02745	1	PTS system, N-acetylgalactosamine-specific IIB component		
K02755	1	PTS system, beta-glucosides-specific IIA component [EC:2.7.1.69]		
K02759	4	PTS system, cellobiose-specific IIA component [EC:2.7.1.69]		
K02761	9	PTS system, cellobiose-specific IIC component		
K02765	3	PTS system, D-glucosamine-specific IIC component		
K02768	6	PTS system, fructose-specific IIA component [EC:2.7.1.69]		
K02769	1	PTS system, fructose-specific IIB component [EC:2.7.1.69]		
K02770	12	PTS system, fructose-specific IIC component		
K02774	5	PTS system, galactitol-specific IIB component [EC:2.7.1.69]		
K02775	2	PTS system, galactitol-specific IIC component		
K02777	109	PTS system, glucose-specific IIA component [EC:2.7.1.69]		
K02779	2	PTS system, glucose-specific IIC component		
K02784	4	phosphocarrier protein HPr		
K02793	6	PTS system, mannose-specific IIA component [EC:2.7.1.69]		
K02794	3	PTS system, mannose-specific IIB component [EC:2.7.1.69]		
K02795	3	PTS system, mannose-specific IIC component		
K02796	6	PTS system, mannose-specific IID component		

K02799	2	PTS system, mannitol-specific IIB component [EC:2.7.1.69]		
K02800	3	PTS system, mannitol-specific IIC component		
K02804	1	PTS system, N-acetylglucosamine-specific IIC component		
K02805	4	lipopolysaccharide biosynthesis protein		
K02806	15	PTS system, nitrogen regulatory IIA component [EC:2.7.1.69]		
K02821	9	PTS system, ascorbate-specific IIA component [EC:2.7.1.69]		
K02823	18	dihydroorotate dehydrogenase electron transfer subunit		
K02824	6	uracil permease		
K02825	13	pyrimidine operon attenuation protein / uracil		
K02826	1	quinol oxidase polypeptide II [EC:1.9.3.-]		
K02827	1	quinol oxidase polypeptide I [EC:1.9.3.-]		
K02828	1	quinol oxidase polypeptide III [EC:1.9.3.-]		
K02834	16	ribosome-binding factor A		
K02835	26	peptide chain release factor RF-1		
K02836	23	peptide chain release factor RF-2		
K02837	18	peptide chain release factor RF-3		
K02838	30	ribosome recycling factor		
K02839	2	peptide chain release factor RF-H		
K02841	22	heptosyltransferase I [EC:2.4.-.-]		
K02843	38	heptosyltransferase II [EC:2.4.-.-]		
K02844	36	UDP-glucose:(heptosyl)LPS alpha-1,3-glucosyltransferase [EC:2.4.1.-]		
K02846	9	N-methyl-L-tryptophan oxidase [EC:1.5.3.-]		
K02849	21	heptosyltransferase III [EC:2.4.-.-]		
K02852	8	UDP-N-acetyl-D-mannosaminuronic acid transferase [EC:2.4.1.-]		
K02854	1	AraC family transcriptional regulator, L-rhamnose operon		
K02855	3	AraC family transcriptional regulator, L-rhamnose operon regulatory		
K02856	3	L-rhamnose-H+ transport protein		
K02858	40	3,4-dihydroxy 2-butanone 4-phosphate synthase [EC:4.1.99.12]		
K02860	41	16S rRNA processing protein RimM		
K02862	6	putative membrane protein		
K02863	21	large subunit ribosomal protein L1		
K02864	19	large subunit ribosomal protein L10		
K02867	17	large subunit ribosomal protein L11		
K02871	16	large subunit ribosomal protein L13		
K02874	22	large subunit ribosomal protein L14		
K02876	12	large subunit ribosomal protein L15		
K02878	19	large subunit ribosomal protein L16		
K02879	21	large subunit ribosomal protein L17		
K02881	11	large subunit ribosomal protein L18		
K02884	16	large subunit ribosomal protein L19		
K02886	47	large subunit ribosomal protein L2		
K02887	6	large subunit ribosomal protein L20		
K02888	23	large subunit ribosomal protein L21		
K02890	18	large subunit ribosomal protein L22		
K02892	34	large subunit ribosomal protein L23		
K02895	14	large subunit ribosomal protein L24		
K02897	28	large subunit ribosomal protein L25		
K02899	20	large subunit ribosomal protein L27		
K02902	9	large subunit ribosomal protein L28		
K02904	6	large subunit ribosomal protein L29		

K02906	36	large subunit ribosomal protein L3		
K02907	9	large subunit ribosomal protein L30		
K02909	22	large subunit ribosomal protein L31		
K02911	73	large subunit ribosomal protein L32		
K02913	9	large subunit ribosomal protein L33		
K02914	15	large subunit ribosomal protein L34		
K02916	7	large subunit ribosomal protein L35		
K02919	2	large subunit ribosomal protein L36		
K02926	30	large subunit ribosomal protein L4		
K02931	15	large subunit ribosomal protein L5		
K02933	28	large subunit ribosomal protein L6		
K02935	6	large subunit ribosomal protein L7/L12		
K02939	23	large subunit ribosomal protein L9		
K02945	47	small subunit ribosomal protein S1		
K02946	441	small subunit ribosomal protein S10		
K02948	11	small subunit ribosomal protein S11		
K02950	7	small subunit ribosomal protein S12		
K02952	15	small subunit ribosomal protein S13		
K02954	7	small subunit ribosomal protein S14		
K02956	8	small subunit ribosomal protein S15		
K02959	23	small subunit ribosomal protein S16		
K02961	10	small subunit ribosomal protein S17		
K02963	15	small subunit ribosomal protein S18		
K02965	4	small subunit ribosomal protein S19		
K02967	68	small subunit ribosomal protein S2		
K02968	28	small subunit ribosomal protein S20		
K02970	4	small subunit ribosomal protein S21		
K02982	20	small subunit ribosomal protein S3		
K02986	30	small subunit ribosomal protein S4		
K02988	13	small subunit ribosomal protein S5		
K02990	23	small subunit ribosomal protein S6		
K02992	15	small subunit ribosomal protein S7		
K02994	23	small subunit ribosomal protein S8		
K02996	16	small subunit ribosomal protein S9		
K03040	34	DNA-directed RNA polymerase subunit alpha [EC:2.7.7.6]		
K03043	77	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]		
K03046	516	DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]		
K03060	10	DNA-directed RNA polymerase subunit omega [EC:2.7.7.6]		
K03070	74	preprotein translocase subunit SecA		
K03071	7	preprotein translocase subunit SecB		
K03072	476	preprotein translocase subunit SecD		
K03073	2	preprotein translocase subunit SecE		
K03074	41	preprotein translocase subunit SecF		
K03075	3	preprotein translocase subunit SecG		
K03076	36	preprotein translocase subunit SecY		
K03077	3	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]		
K03080	2	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]		
K03086	56	RNA polymerase primary sigma factor		
K03087	22	RNA polymerase nonessential primary-like sigma factor		
K03088	405	RNA polymerase sigma-70 factor, ECF subfamily		

K03089	23	RNA polymerase sigma-32 factor		
K03090	20	RNA polymerase sigma-B factor		
K03091	8	RNA polymerase sporulation-specific sigma factor		
K03092	47	RNA polymerase sigma-54 factor		
K03093	27	RNA polymerase sigma factor		
K03098	2	outer membrane lipoprotein Blc		
K03100	92	signal peptidase I [EC:3.4.21.89]		
K03101	20	signal peptidase II [EC:3.4.23.36]		
K03106	47	signal recognition particle subunit SRP54		
K03110	23	fused signal recognition particle receptor		
K03111	34	single-strand DNA-binding protein		
K03113	2	translation initiation factor SUI1		
K03116	10	sec-independent protein translocase protein TatA		
K03117	4	sec-independent protein translocase protein TatB		
K03118	57	sec-independent protein translocase protein TatC		
K03119	43	taurine dioxygenase [EC:1.14.11.17]		
K03146	1	thiamine biosynthetic enzyme		
K03147	11	thiamine biosynthesis protein ThiC		
K03148	16	adenylyltransferase ThiF [EC:2.7.7.-]		
K03149	27	thiamine biosynthesis ThiG		
K03150	1	thiamine biosynthesis ThiH		
K03151	4	thiamine biosynthesis protein ThiI		
K03152	3	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis		
K03153	10	glycine oxidase [EC:1.4.3.19]		
K03154	5	thiamine biosynthesis ThiS		
K03166	6	DNA topoisomerase VI subunit A [EC:5.99.1.3]		
K03167	4	DNA topoisomerase VI subunit B [EC:5.99.1.3]		
K03168	100	DNA topoisomerase I [EC:5.99.1.2]		
K03169	32	DNA topoisomerase III [EC:5.99.1.2]		
K03177	42	tRNA pseudouridine synthase B [EC:5.4.99.12]		
K03179	26	4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]		
K03182	88	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiD [EC:4.1.1.-]		
K03183	77	ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.-]		
K03184	1	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase		
K03185	16	2-octaprenyl-6-methoxyphenol hydroxylase [EC:1.14.13.-]		
K03186	20	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiX [EC:4.1.1.-]		
K03187	2	urease accessory protein		
K03188	1	urease accessory protein		
K03189	3	urease accessory protein		
K03190	2	urease accessory protein		
K03192	1	urease accessory protein		
K03196	1	type IV secretion system protein VirB11		
K03197	2	type IV secretion system protein VirB2		
K03198	1	type IV secretion system protein VirB3		
K03199	8	type IV secretion system protein VirB4		
K03200	1	type IV secretion system protein VirB5		
K03201	2	type IV secretion system protein VirB6		
K03205	7	type IV secretion system protein VirD4		
K03208	1	colanic acid biosynthesis glycosyl transferase WcaI		
K03210	16	preprotein translocase subunit YajC		

K03215	31	RNA methyltransferase, TrmA family [EC:2.1.1.-]		
K03216	14	RNA methyltransferase, TrmH family, group 2 [EC:2.1.1.-]		
K03217	71	preprotein translocase subunit YidC		
K03218	28	RNA methyltransferase, TrmH family [EC:2.1.1.-]		
K03219	1	type III secretion protein SctC		
K03221	1	type III secretion protein SctF		
K03222	3	type III secretion protein SctJ		
K03223	1	type III secretion protein SctL		
K03224	1	ATP synthase in type III secretion protein SctN [EC:3.6.3.14]		
K03225	2	type III secretion protein SctQ		
K03227	2	type III secretion protein SctS		
K03228	2	type III secretion protein SctT		
K03229	1	type III secretion protein SctU		
K03230	2	type III secretion protein SctV		
K03265	1	peptide chain release factor eRF subunit 1		
K03269	5	UDP-2,3-diacylglucosamine hydrolase [EC:3.6.1.-]		
K03270	14	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P		
K03271	12	phosphoheptose isomerase [EC:5.-.-.-]		
K03272	33	D-beta-D-heptose 7-phosphate kinase / D-beta-D-heptose 1-phosphate		
K03273	14	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.-]		
K03274	9	ADP-L-glycero-D-manno-heptose 6-epimerase [EC:5.1.3.20]		
K03280	1	UDP-N-acetylglucosamine:(glucosyl)LPS		
K03281	27	chloride channel protein, CIC family		
K03282	26	large conductance mechanosensitive channel		
K03284	57	metal ion transporter, MIT family		
K03285	10	general bacterial porin, GBP family		
K03286	45	OmpA-OmpF porin, OOP family		
K03287	84	outer membrane factor, OMF family		
K03288	4	MFS transporter, MHS family, citrate/tricarballylate:H+ symporter		
K03289	2	MFS transporter, NHS family, nucleoside permease		
K03290	3	MFS transporter, SHS family, sialic acid transporter		
K03292	11	glycoside/pentoside/hexuronide:cation symporter, GPH family		
K03293	16	amino acid transporter, AAT family		
K03294	140	basic amino acid/polyamine antiporter, APA family		
K03295	35	cation efflux system protein, CDF family		
K03296	415	hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family		
K03297	2	small multidrug resistance protein, SMR family		
K03298	13	drug/metabolite transporter, DME family		
K03299	35	gluconate:H+ symporter, GntP family		
K03302	3	anaerobic C4-dicarboxylate transporter, Dcu family		
K03303	17	lactate transporter, LctP family		
K03304	4	tellurite resistance/dicarboxylate transporter, TDT family		
K03305	27	proton-dependent oligopeptide transporter, POT family		
K03306	31	inorganic phosphate transporter, PiT family		
K03307	78	solute:Na+ symporter, SSS family		
K03308	31	neurotransmitter:Na+ symporter, NSS family		
K03309	14	dicarboxylate/amino acid:cation (Na+ or H+) symporter, DAACS family		
K03312	1	glutamate:Na+ symporter, ESS family		
K03313	15	Na+:H+ antiporter, NhaA family		
K03315	2	Na+:H+ antiporter, NhaC family		

K03316	31	monovalent cation:H+ antiporter, CPA1 family		
K03317	19	concentrative nucleoside transporter, CNT family		
K03319	2	divalent anion:Na+ symporter, DASS family		
K03320	62	ammonium transporter, Amt family		
K03321	52	sulfate permease, SulP family		
K03322	54	manganese transport protein		
K03324	10	phosphate:Na+ symporter, PNaS family		
K03325	22	arsenite transporter, ACR3 family		
K03326	1	C4-dicarboxylate transporter, DcuC family		
K03327	27	multidrug resistance protein, MATE family		
K03328	25	polysaccharide transporter, PST family		
K03331	1	L-xylulose reductase [EC:1.1.1.10]		
K03332	2	fructan beta-fructosidase [EC:3.2.1.80]		
K03333	41	cholesterol oxidase [EC:1.1.3.6]		
K03335	20	inosose dehydratase [EC:4.2.1.44]		
K03336	12	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase [EC:3.7.1.-]		
K03337	2	5-deoxy-glucuronate isomerase [EC:5.3.1.-]		
K03338	5	5-dehydro-2-deoxygluconokinase [EC:2.7.1.92]		
K03339	1	6-phospho-5-dehydro-2-deoxy-D-gluconate aldolase [EC:4.1.2.29]		
K03342	7	para-aminobenzoate synthetase / 4-amino-4-deoxychorismate lyase		
K03343	8	putrescine oxidase [EC:1.4.3.10]		
K03366	4	(R,R)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4		
K03367	32	D-alanine-poly(phosphoribitol) ligase [EC:6.1.1.13]		
K03379	37	cyclohexanone monooxygenase [EC:1.14.13.22]		
K03380	35	phenol 2-monooxygenase [EC:1.14.13.7]		
K03381	13	catechol 1,2-dioxygenase [EC:1.13.11.1]		
K03382	5	hydroxyatrazine ethylaminohydrolase [EC:3.5.99.3]		
K03384	10	Unclassified; E1.14.12.-		
K03385	9	formate-dependent nitrite reductase, periplasmic cytochrome c552		
K03386	31	peroxiredoxin (alkyl hydroperoxide reductase subunit C)		
K03387	2	alkyl hydroperoxide reductase subunit F [EC:1.6.4.-]		
K03388	65	heterodisulfide reductase subunit A [EC:1.8.98.1]		
K03389	22	heterodisulfide reductase subunit B [EC:1.8.98.1]		
K03390	14	heterodisulfide reductase subunit C [EC:1.8.98.1]		
K03391	42	pentachlorophenol monooxygenase [EC:1.14.13.50]		
K03392	61	aminocarboxymuconate-semialdehyde decarboxylase [EC:4.1.1.45]		
K03394	1	precorrin-2 C20-methyltransferase / cobalt-factor-2		
K03396	1	S-(hydroxymethyl)glutathione synthase [EC:4.4.1.22]		
K03399	2	precorrin-6Y C5,15-methyltransferase [EC:2.1.1.132]		
K03402	7	transcriptional regulator of arginine metabolism		
K03403	4	magnesium chelatase subunit H [EC:6.6.1.1]		
K03404	10	magnesium chelatase subunit D [EC:6.6.1.1]		
K03405	29	magnesium chelatase subunit I [EC:6.6.1.1]		
K03406	186	methyl-accepting chemotaxis protein		
K03407	82	two-component system, chemotaxis family, sensor kinase CheA		
K03408	21	purine-binding chemotaxis protein CheW		
K03410	4	chemotaxis protein CheC		
K03411	16	chemotaxis protein CheD [EC:3.5.1.44]		
K03412	64	two-component system, chemotaxis family, response regulator CheB		
K03413	117	two-component system, chemotaxis family, response regulator CheY		

K03414	3	chemotaxis protein CheZ		
K03416	11	methylmalonyl-CoA carboxyltransferase [EC:2.1.3.1]		
K03417	36	methylisocitrate lyase [EC:4.1.3.30]		
K03423	57	Unclassified; E1.8.-.-		
K03424	47	TatD DNase family protein [EC:3.1.21.-]		
K03426	21	NAD+ diphosphatase [EC:3.6.1.22]		
K03427	48	type I restriction enzyme M protein [EC:2.1.1.72]		
K03429	22	1,2-diacylglycerol 3-glucosyltransferase [EC:2.4.1.157]		
K03430	5	2-aminoethylphosphonate-pyruvate transaminase [EC:2.6.1.37]		
K03431	33	phosphoglucosamine mutase [EC:5.4.2.10]		
K03432	2	proteasome alpha subunit [EC:3.4.25.1]		
K03433	9	proteasome beta subunit [EC:3.4.25.1]		
K03434	14	N-acetylglucosaminylphosphatidylinositol deacetylase [EC:3.5.1.89]		
K03435	5	LacI family transcriptional regulator, fructose operon		
K03436	5	DeoR family transcriptional regulator, fructose operon		
K03437	25	RNA methyltransferase, TrmH family		
K03438	31	S-adenosyl-methyltransferase [EC:2.1.1.-]		
K03439	7	tRNA (guanine-N7-)-methyltransferase [EC:2.1.1.33]		
K03442	38	small conductance mechanosensitive channel		
K03445	2	MFS transporter, DHA1 family, purine ribonucleoside efflux pump		
K03446	127	MFS transporter, DHA2 family, multidrug resistance protein B		
K03449	8	MFS transporter, CP family, cyanate transporter		
K03453	3	bile acid:Na+ symporter, BASS family		
K03455	84	monovalent cation:H+ antiporter-2, CPA2 family		
K03457	23	nucleobase:cation symporter-1, NCS1 family		
K03458	12	nucleobase:cation symporter-2, NCS2 family		
K03463	5	Unclassified; E5.5.1.-		
K03464	2	muconolactone D-isomerase [EC:5.3.3.4]		
K03465	12	thymidylate synthase (FAD) [EC:2.1.1.148]		
K03466	493	DNA segregation ATPase FtsK/SpoIIIE, S-DNA-T family		
K03469	41	ribonuclease HI [EC:3.1.26.4]		
K03470	44	ribonuclease HII [EC:3.1.26.4]		
K03471	3	ribonuclease HIII [EC:3.1.26.4]		
K03473	1	erythronate-4-phosphate dehydrogenase [EC:1.1.1.290]		
K03474	23	pyridoxine 5-phosphate synthase [EC:2.6.99.2]		
K03475	1	PTS system, ascorbate-specific IIC component		
K03476	18	L-ascorbate 6-phosphate lactonase [EC:3.1.1.-]		
K03478	5	hypothetical protein		
K03484	4	LacI family transcriptional regulator, sucrose operon repressor		
K03495	39	glucose inhibited division protein A		
K03496	82	chromosome partitioning protein		
K03497	69	chromosome partitioning protein, ParB family		
K03498	19	trk system potassium uptake protein TrkH		
K03499	59	trk system potassium uptake protein TrkA		
K03500	54	ribosomal RNA small subunit methyltransferase B [EC:2.1.1.-]		
K03501	26	glucose inhibited division protein B [EC:2.1.-.-]		
K03502	3	DNA polymerase V		
K03517	23	quinolinate synthase [EC:2.5.1.72]		
K03518	27	carbon-monoxide dehydrogenase small subunit [EC:1.2.99.2]		
K03519	52	carbon-monoxide dehydrogenase medium subunit [EC:1.2.99.2]		

K03520	196	carbon-monoxide dehydrogenase large subunit [EC:1.2.99.2]		
K03521	32	electron transfer flavoprotein beta subunit		
K03522	30	electron transfer flavoprotein alpha subunit		
K03523	5	putative biotin biosynthesis protein BioY		
K03524	31	BirA family transcriptional regulator, biotin operon repressor /		
K03525	31	type III pantothenate kinase [EC:2.7.1.33]		
K03526	24	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase [EC:1.17.7.1]		
K03527	34	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [EC:1.17.1.2]		
K03529	61	chromosome segregation protein		
K03530	59	DNA-binding protein HU-beta		
K03531	44	cell division protein FtsZ		
K03532	3	trimethylamine-N-oxide reductase (cytochrome c) 1, cytochrome c-type		
K03534	1	L-rhamnose mutarotase [EC:5.1.3.-]		
K03535	12	MFS transporter, ACS family, glucarate transporter		
K03536	21	ribonuclease P protein component [EC:3.1.26.5]		
K03540	15	ribonuclease P subunit RPR2 [EC:3.1.26.5]		
K03543	22	multidrug resistance protein A		
K03544	21	ATP-dependent Clp protease ATP-binding subunit ClpX		
K03545	53	trigger factor		
K03546	16	exonuclease SbcC		
K03547	5	exonuclease SbcD		
K03548	14	putative permease		
K03549	37	KUP system potassium uptake protein		
K03550	21	holliday junction DNA helicase RuvA		
K03551	35	holliday junction DNA helicase RuvB		
K03553	41	recombination protein RecA		
K03555	79	DNA mismatch repair protein MutS		
K03556	63	LuxR family transcriptional regulator, maltose regulon positive		
K03557	4	Fis family transcriptional regulator, factor for inversion		
K03558	4	membrane protein required for colicin V production		
K03559	16	biopolymer transport protein ExbD		
K03560	7	biopolymer transport protein TolR		
K03561	29	biopolymer transport protein ExbB		
K03562	14	biopolymer transport protein TolQ		
K03563	5	carbon storage regulator		
K03564	47	peroxiredoxin Q/BCP [EC:1.11.1.15]		
K03565	29	regulatory protein		
K03566	22	LysR family transcriptional regulator, glycine cleavage system		
K03567	1	glycine cleavage system transcriptional repressor		
K03568	39	TldD protein		
K03569	45	rod shape-determining protein MreB and related proteins		
K03570	25	rod shape-determining protein MreC		
K03571	3	rod shape-determining protein MreD		
K03572	44	DNA mismatch repair protein MutL		
K03574	44	7,8-dihydro-8-oxoguanine triphosphatase [EC:3.6.1.-]		
K03575	41	A/G-specific adenine glycosylase [EC:3.2.2.-]		
K03576	19	LysR family transcriptional regulator, regulator for metE and metH		
K03577	16	TetR/AcrR family transcriptional regulator, acrAB operon repressor		
K03578	38	ATP-dependent helicase HrpA [EC:3.6.1.-]		
K03579	15	ATP-dependent helicase HrpB [EC:3.6.1.-]		

K03580	7	ATP-dependent helicase HepA [EC:3.6.1.-]		
K03581	29	exodeoxyribonuclease V alpha subunit [EC:3.1.11.5]		
K03582	8	exodeoxyribonuclease V beta subunit [EC:3.1.11.5]		
K03583	15	exodeoxyribonuclease V gamma subunit [EC:3.1.11.5]		
K03584	34	DNA repair protein RecO (recombination protein O)		
K03585	50	membrane fusion protein		
K03586	1	cell division protein FtsL		
K03587	74	cell division protein FtsI (penicillin-binding protein 3)		
K03588	46	cell division protein FtsW		
K03589	17	cell division protein FtsQ		
K03590	36	cell division protein FtsA		
K03592	45	PmbA protein		
K03593	48	ATP-binding protein involved in chromosome partitioning		
K03594	20	bacterioferritin		
K03595	464	GTP-binding protein Era		
K03596	50	GTP-binding protein LepA		
K03597	1	sigma-E factor negative regulatory protein RseA		
K03598	9	sigma-E factor negative regulatory protein RseB		
K03599	4	stringent starvation protein A		
K03600	4	stringent starvation protein B		
K03601	45	exodeoxyribonuclease VII large subunit [EC:3.1.11.6]		
K03602	5	exodeoxyribonuclease VII small subunit [EC:3.1.11.6]		
K03604	5	LacI family transcriptional regulator, purine nucleotide synthesis		
K03605	10	hydrogenase 1 maturation protease [EC:3.4.24.-]		
K03606	8	putative colanic acid biosysnthesis UDP-glucose lipid carrier		
K03608	2	cell division topological specificity factor		
K03609	12	septum site-determining protein MinD		
K03610	2	septum site-determining protein MinC		
K03611	2	disulfide bond formation protein DsbB		
K03612	2	electron transport complex protein RnfG		
K03613	26	electron transport complex protein RnfE		
K03614	3	electron transport complex protein RnfD		
K03615	13	electron transport complex protein RnfC		
K03616	8	electron transport complex protein RnfB		
K03617	4	electron transport complex protein RnfA		
K03618	1	hydrogenase-1 operon protein HyaF		
K03620	12	Ni/Fe-hydrogenase 1 B-type cytochrome subunit		
K03621	30	glycerol-3-phosphate acyltransferase PlsX [EC:2.3.1.15]		
K03624	24	transcription elongation factor GreA		
K03625	21	N utilization substance protein B		
K03628	36	transcription termination factor Rho		
K03629	18	DNA replication and repair protein RecF		
K03630	39	DNA repair protein RadC		
K03631	48	DNA repair protein RecN (Recombination protein N)		
K03634	10	outer membrane lipoprotein carrier protein		
K03635	22	molybdenum cofactor biosynthesis protein E		
K03636	10	molybdenum cofactor biosynthesis protein D		
K03637	16	molybdenum cofactor biosynthesis protein C		
K03638	9	molybdenum cofactor biosynthesis protein B		
K03639	47	molybdenum cofactor biosynthesis protein A		

K03640	41	peptidoglycan-associated lipoprotein		
K03641	109	TolB protein		
K03642	13	rare lipoprotein A		
K03643	6	LPS-assembly lipoprotein		
K03644	32	lipoic acid synthetase [EC:2.8.1.8]		
K03648	29	uracil-DNA glycosylase [EC:3.2.2.-]		
K03649	18	TDG/mug DNA glycosylase family protein [EC:3.2.2.-]		
K03650	36	tRNA modification GTPase		
K03651	6	Icc protein		
K03652	17	DNA-3-methyladenine glycosylase [EC:3.2.2.21]		
K03654	47	ATP-dependent DNA helicase RecQ [EC:3.6.1.-]		
K03655	58	ATP-dependent DNA helicase RecG [EC:3.6.1.-]		
K03656	16	ATP-dependent DNA helicase Rep [EC:3.6.1.-]		
K03657	133	DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.1.-]		
K03664	27	SsrA-binding protein		
K03665	26	GTP-binding protein HflX		
K03666	10	host factor-I protein		
K03667	21	ATP-dependent HslUV protease ATP-binding subunit HslU		
K03668	3	heat shock protein HslJ		
K03669	4	membrane glycosyltransferase [EC:2.4.1.-]		
K03670	4	periplasmic glucans biosynthesis protein		
K03671	33	thioredoxin 1		
K03672	8	thioredoxin 2 [EC:1.8.1.8]		
K03673	13	thiol:disulfide interchange protein DsbA		
K03676	7	glutaredoxin 3		
K03677	11	CysQ protein		
K03684	17	ribonuclease D [EC:3.1.13.5]		
K03685	34	ribonuclease III [EC:3.1.26.3]		
K03686	68	molecular chaperone DnaJ		
K03687	21	molecular chaperone GrpE		
K03688	57	ubiquinone biosynthesis protein		
K03690	5	hypothetical protein		
K03693	1	penicillin-binding protein		
K03694	10	ATP-dependent Clp protease ATP-binding subunit ClpA		
K03695	75	ATP-dependent Clp protease ATP-binding subunit ClpB		
K03696	39	ATP-dependent Clp protease ATP-binding subunit ClpC		
K03697	1	ATP-dependent Clp protease ATP-binding subunit ClpE		
K03698	6	CMP-binding protein		
K03699	57	putative hemolysin		
K03701	117	excinuclease ABC subunit A		
K03702	42	excinuclease ABC subunit B		
K03703	61	excinuclease ABC subunit C		
K03704	67	cold shock protein (beta-ribbon, CspA family)		
K03705	36	heat-inducible transcriptional repressor		
K03707	6	transcriptional activator TenA [EC:3.5.99.2]		
K03709	23	DtxR family transcriptional regulator, Mn-dependent transcriptional		
K03710	43	GntR family transcriptional regulator		
K03711	30	Fur family transcriptional regulator, ferric uptake regulator		
K03712	51	MarR family transcriptional regulator		
K03713	4	MerR family transcriptional regulator, glutamine synthetase		

K03715	6	1,2-diacylglycerol 3-beta-galactosyltransferase [EC:2.4.1.46]		
K03717	10	LysR family transcriptional regulator, transcriptional activator of		
K03718	11	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC		
K03719	24	Lrp/AsnC family transcriptional regulator, leucine-responsive		
K03721	11	transcriptional regulator of aroF, aroG, tyrA and aromatic amino		
K03722	55	ATP-dependent DNA helicase DinG [EC:3.6.1.-]		
K03723	74	transcription-repair coupling factor (superfamily II helicase)		
K03724	91	ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.1.-]		
K03726	1	helicase [EC:3.6.1.-]		
K03727	17	ATP-dependent RNA helicase HelY [EC:3.6.1.-]		
K03731	2	trehalose 6-phosphate phosphorylase [EC:2.4.1.216]		
K03732	1	ATP-dependent RNA helicase RhlB [EC:3.6.4.13]		
K03733	65	integrase/recombinase XerC		
K03734	31	thiamine biosynthesis lipoprotein		
K03735	4	ethanolamine ammonia-lyase large subunit [EC:4.3.1.7]		
K03736	1	ethanolamine ammonia-lyase small subunit [EC:4.3.1.7]		
K03737	30	putative pyruvate-flavodoxin oxidoreductase [EC:1.2.7.-]		
K03738	68	aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]		
K03740	1	D-alanine transfer protein		
K03741	27	arsenate reductase [EC:1.20.4.1]		
K03742	58	competence/damage-inducible protein CinA		
K03743	19	Unclassified; K03743		
K03744	31	LemA protein		
K03746	2	DNA-binding protein H-NS		
K03747	1	Smg protein		
K03748	3	SanA protein		
K03749	2	DedD protein		
K03750	62	molybdopterin biosynthesis protein MoeA		
K03751	39	molybdopterin biosynthesis protein MoeB		
K03752	10	molybdopterin-guanine dinucleotide biosynthesis protein A		
K03753	6	molybdopterin-guanine dinucleotide biosynthesis protein B		
K03756	3	putrescine:ornithine antiporter		
K03758	2	arginine:ornithine antiporter		
K03759	5	arginine:agmatine antiporter		
K03760	1	phosphoethanolamine transferase		
K03761	2	MFS transporter, MHS family, alpha-ketoglutarate permease		
K03762	32	MFS transporter, MHS family, proline/betaine transporter		
K03763	10	DNA polymerase III subunit alpha, Gram-positive type [EC:2.7.7.7]		
K03765	5	transcriptional activator of cad operon		
K03767	15	peptidyl-prolyl cis-trans isomerase A (cyclophilin A) [EC:5.2.1.8]		
K03768	25	peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]		
K03769	56	peptidyl-prolyl cis-trans isomerase C [EC:5.2.1.8]		
K03770	44	peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]		
K03771	59	peptidyl-prolyl cis-trans isomerase SurA [EC:5.2.1.8]		
K03772	10	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]		
K03773	4	FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8]		
K03774	1	FKBP-type peptidyl-prolyl cis-trans isomerase SlpA [EC:5.2.1.8]		
K03775	9	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [EC:5.2.1.8]		
K03776	16	aerotaxis receptor		
K03777	7	D-lactate dehydrogenase [EC:1.1.1.28]		

K03778	7	D-lactate dehydrogenase [EC:1.1.1.28]		
K03779	2	L(+)-tartrate dehydratase alpha subunit [EC:4.2.1.32]		
K03780	3	L(+)-tartrate dehydratase beta subunit [EC:4.2.1.32]		
K03781	12	catalase [EC:1.11.1.6]		
K03782	24	catalase/peroxidase [EC:1.11.1.6 1.11.1.7]		
K03783	27	purine-nucleoside phosphorylase [EC:2.4.2.1]		
K03784	5	purine-nucleoside phosphorylase [EC:2.4.2.1]		
K03785	2	3-dehydroquinate dehydratase I [EC:4.2.1.10]		
K03786	17	3-dehydroquinate dehydratase II [EC:4.2.1.10]		
K03787	26	5'-nucleotidase [EC:3.1.3.5]		
K03789	28	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]		
K03790	10	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]		
K03791	7	putative chitinase		
K03793	3	pteridine reductase [EC:1.5.1.33]		
K03795	10	sirohydrochlorin cobaltochelatase [EC:4.99.1.3]		
K03797	79	carboxyl-terminal processing protease [EC:3.4.21.102]		
K03798	73	cell division protease FtsH [EC:3.4.24.-]		
K03799	40	heat shock protein HtpX [EC:3.4.24.-]		
K03800	12	lipoate-protein ligase A [EC:2.7.7.63]		
K03801	27	lipoyl(octanoyl) transferase [EC:2.3.1.181]		
K03802	15	cyanophycin synthetase [EC:6.-.-.-]		
K03806	4	AmpD protein		
K03808	5	paraquat-inducible protein A		
K03809	6	Trp repressor binding protein		
K03810	12	virulence factor		
K03811	3	nicotinamide mononucleotide transporter		
K03814	19	monofunctional biosynthetic peptidoglycan transglycosylase		
K03815	1	xanthosine phosphorylase [EC:2.4.2.-]		
K03818	8	putative colanic acid biosynthesis acetyltransferase WcaF		
K03819	1	putative colanic acid biosynthesis acetyltransferase WcaB		
K03820	42	apolipoprotein N-acyltransferase [EC:2.3.1.-]		
K03821	52	polyhydroxyalkanoate synthase [EC:2.3.1.-]		
K03822	3	putative long chain acyl-CoA synthase [EC:6.2.1.-]		
K03823	23	phosphinothricin acetyltransferase [EC:2.3.1.183]		
K03824	4	putative acetyltransferase [EC:2.3.1.-]		
K03825	4	putative acetyltransferase [EC:2.3.1.-]		
K03826	2	putative acetyltransferase [EC:2.3.1.-]		
K03827	2	putative acetyltransferase [EC:2.3.1.-]		
K03828	9	putative acetyltransferase [EC:2.3.1.-]		
K03829	8	putative acetyltransferase [EC:2.3.1.-]		
K03831	8	molybdopterin biosynthesis protein Mog		
K03832	28	periplasmic protein TonB		
K03833	28	selenocysteine-specific elongation factor		
K03837	1	serine transporter		
K03839	5	flavodoxin I		
K03841	11	fructose-1,6-bisphosphatase I [EC:3.1.3.11]		
K03851	2	taurine-pyruvate aminotransferase [EC:2.6.1.77]		
K03852	6	sulfoacetaldehyde acetyltransferase [EC:2.3.3.15]		
K03856	30	3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]		
K03862	13	vanillate monooxygenase [EC:1.14.13.82]		

K03863	2	vanillate monooxygenase [EC:1.14.13.82]		
K03885	77	NADH dehydrogenase [EC:1.6.99.3]		
K03886	3	menaquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.-]		
K03887	9	menaquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.-]		
K03888	2	menaquinol-cytochrome c reductase cytochrome b/c subunit		
K03889	6	ubiquinol-cytochrome c reductase cytochrome c subunit		
K03890	3	ubiquinol-cytochrome c reductase iron-sulfur subunit		
K03891	15	ubiquinol-cytochrome c reductase cytochrome b subunit		
K03892	63	ArsR family transcriptional regulator		
K03893	12	arsenical pump membrane protein		
K03897	1	lysine N6-hydroxylase [EC:1.14.13.59]		
K03918	4	L-lysine 6-transaminase [EC:2.6.1.36]		
K03924	61	MoxR-like ATPase [EC:3.6.3.-]		
K03925	28	MraZ protein		
K03926	9	periplasmic divalent cation tolerance protein		
K03927	17	carboxylesterase type B [EC:3.1.1.1]		
K03928	9	carboxylesterase [EC:3.1.1.1]		
K03930	1	putative tributyrin esterase [EC:3.1.1.-]		
K03931	6	putative isomerase		
K03932	12	polyhydroxybutyrate depolymerase		
K03933	3	chitin-binding protein		
K03943	6	NADH dehydrogenase (ubiquinone) flavoprotein 2 [EC:1.6.5.3 1.6.99.3]		
K03969	18	phage shock protein A		
K03972	3	phage shock protein E		
K03973	8	phage shock protein C		
K03974	2	psp operon transcriptional activator		
K03975	32	membrane-associated protein		
K03977	56	GTP-binding protein		
K03978	19	GTP-binding protein		
K03979	43	GTP-binding protein		
K03980	50	virulence factor		
K03981	8	thiol:disulfide interchange protein DsbC [EC:5.3.4.1]		
K04014	24	formate-dependent nitrite reductase, Fe-S protein		
K04015	1	formate-dependent nitrate reductase complex, transmembrane protein		
K04016	4	formate-dependent nitrite reductase, possible assembly protein		
K04019	11	ethanolamine utilization protein EutA		
K04020	4	phosphotransacetylase		
K04021	1	aldehyde dehydrogenase		
K04027	5	ethanolamine utilization protein EutM		
K04028	4	ethanolamine utilization protein EutN		
K04033	1	AraC family transcriptional regulator, ethanolamine operon		
K04034	54	anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase		
K04035	62	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase		
K04041	6	fructose-1,6-bisphosphatase III [EC:3.1.3.11]		
K04042	55	bifunctional protein GlmU [EC:2.7.7.23 2.3.1.157]		
K04043	64	molecular chaperone DnaK		
K04044	18	molecular chaperone HscA		
K04045	1	molecular chaperone HscC		
K04046	1	hypothetical chaperone protein		
K04047	11	starvation-inducible DNA-binding protein		

K04061	2	flagellar biosynthesis protein		
K04063	19	osmotically inducible protein OsmC		
K04065	12	hyperosmotically inducible periplasmic protein		
K04066	67	primosomal protein N' (replication factor Y) (superfamily II		
K04067	9	primosomal replication protein N"		
K04069	36	pyruvate formate lyase activating enzyme [EC:1.97.1.4]		
K04070	12	putative pyruvate formate lyase activating enzyme [EC:1.97.1.4]		
K04072	15	acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10		
K04073	3	acetaldehyde dehydrogenase [EC:1.2.1.10]		
K04074	6	cell division initiation protein		
K04075	46	tRNA(Ile)-lysidine synthase [EC:6.3.4.-]		
K04076	10	Lon-like ATP-dependent protease [EC:3.4.21.-]		
K04077	43	chaperonin GroEL		
K04078	11	chaperonin GroES		
K04079	17	molecular chaperone HtpG		
K04080	2	molecular chaperone IbpA		
K04082	9	molecular chaperone HscB		
K04083	6	molecular chaperone Hsp33		
K04084	26	thiol:disulfide interchange protein DsbD [EC:1.8.1.8]		
K04085	8	tRNA 2-thiouridine synthesizing protein A [EC:2.8.1.-]		
K04087	11	membrane protease subunit HflC [EC:3.4.-.-]		
K04088	14	membrane protease subunit HflK [EC:3.4.-.-]		
K04090	44	indolepyruvate ferredoxin oxidoreductase [EC:1.2.7.8]		
K04091	50	alkanesulfonate monooxygenase [EC:1.14.14.5]		
K04094	26	glucose inhibited division protein Gid		
K04095	1	cell filamentation protein		
K04096	36	DNA processing protein		
K04097	7	glutathione S-transferase [EC:2.5.1.18]		
K04098	2	hydroxyquinol 1,2-dioxygenase [EC:1.13.11.37]		
K04103	3	indolepyruvate decarboxylase [EC:4.1.1.74]		
K04107	6	4-hydroxybenzoyl-CoA reductase subunit 1 [EC:1.3.99.20]		
K04108	42	4-hydroxybenzoyl-CoA reductase subunit 2 [EC:1.3.99.20]		
K04110	22	benzoate-CoA ligase [EC:6.2.1.25]		
K04112	1	benzoyl-CoA reductase subunit [EC:1.3.99.15]		
K04113	10	benzoyl-CoA reductase subunit [EC:1.3.99.15]		
K04114	29	benzoyl-CoA reductase subunit [EC:1.3.99.15]		
K04115	16	benzoyl-CoA reductase subunit [EC:1.3.99.15]		
K04117	32	cyclohexanecarboxyl-CoA dehydrogenase [EC:1.3.99.-]		
K04118	4	pimeloyl-CoA dehydrogenase [EC:1.3.1.62]		
K04126	1	isopenicillin-N synthase [EC:1.21.3.1]		
K04127	15	isopenicillin-N epimerase [EC:5.1.1.17]		
K04128	1	hydroxymethyl cephem carbamoyltransferase [EC:2.1.3.-]		
K04333	1	LuxR family transcriptional regulator, csgAB operon transcriptional		
K04340	1	scyllo-inosamine-4-phosphate amidinotransferase 1 [EC:2.1.4.2]		
K04477	11	putative hydrolase		
K04485	37	DNA repair protein RadA/Sms		
K04486	6	histidinol-phosphatase (PHP family) [EC:3.1.3.15]		
K04487	57	cysteine desulfurase [EC:2.8.1.7]		
K04488	14	nitrogen fixation protein NifU and related proteins		
K04496	9	C-terminal binding protein		

K04509	20	formate dehydrogenase (cytochrome) [EC:1.2.2.1]		
K04516	4	chorismate mutase [EC:5.4.99.5]		
K04517	16	prephenate dehydrogenase [EC:1.3.1.12]		
K04518	51	prephenate dehydratase [EC:4.2.1.51]		
K04561	21	nitric-oxide reductase, cytochrome b-containing subunit I		
K04562	441	flagellar biosynthesis protein FlhG		
K04564	27	superoxide dismutase, Fe-Mn family [EC:1.15.1.1]		
K04565	6	Cu/Zn superoxide dismutase [EC:1.15.1.1]		
K04566	6	lysyl-tRNA synthetase, class I [EC:6.1.1.6]		
K04567	51	lysyl-tRNA synthetase, class II [EC:6.1.1.6]		
K04568	7	lysyl-tRNA synthetase, class II [EC:6.1.1.6]		
K04651	3	hydrogenase nickel incorporation protein HypA		
K04652	9	hydrogenase nickel incorporation protein HypB		
K04653	11	hydrogenase expression/formation protein HypC		
K04654	11	hydrogenase expression/formation protein HypD		
K04655	20	hydrogenase expression/formation protein HypE		
K04656	44	hydrogenase maturation protein HypF		
K04691	13	serine protease DegS [EC:3.4.21.-]		
K04719	4	5,6-dimethylbenzimidazole biosynthesis protein BluB		
K04744	27	LPS-assembly protein		
K04748	8	nitric-oxide reductase NorQ protein [EC:1.7.99.7]		
K04749	22	anti-sigma B factor antagonist		
K04750	25	PhnB protein		
K04751	13	nitrogen regulatory protein P-II 1		
K04752	4	nitrogen regulatory protein P-II 2		
K04753	14	suppressor of ftsI		
K04754	6	lipoprotein		
K04755	9	ferredoxin, 2Fe-2S		
K04756	11	alkyl hydroperoxide reductase subunit D		
K04757	15	anti-sigma B factor [EC:2.7.11.1]		
K04758	2	ferrous iron transport protein A		
K04759	35	ferrous iron transport protein B		
K04760	10	transcription elongation factor GreB		
K04761	32	LysR family transcriptional regulator, hydrogen peroxide-inducible		
K04762	7	ribosome-associated heat shock protein Hsp15		
K04763	93	integrase/recombinase XerD		
K04764	11	integration host factor subunit alpha		
K04766	1	acetoin utilization protein AcuA [EC:2.3.1.-]		
K04767	18	acetoin utilization protein AcuB		
K04768	10	acetoin utilization protein AcuC		
K04769	1	AbrB family transcriptional regulator, stage V sporulation protein T		
K04770	25	Lon-like ATP-dependent protease [EC:3.4.21.-]		
K04771	6	serine protease Do [EC:3.4.21.107]		
K04772	20	serine protease DegQ [EC:3.4.21.-]		
K04773	37	protease IV [EC:3.4.21.-]		
K04774	3	serine protease SohB [EC:3.4.21.-]		
K04780	19	nonribosomal peptide synthetase DhbF		
K04782	8	isochorismate pyruvate-lyase [EC:4.1.3.-]		
K04783	2	yersiniabactin salicyl-AMP ligase [EC:6.3.2.-]		
K04786	3	yersiniabactin nonribosomal peptide/polyketide synthase		

K04787	6	mycobactin salicyl-AMP ligase [EC:6.3.2.-]		
K04794	1	peptidyl-tRNA hydrolase, PTH2 family [EC:3.1.1.29]		
K05020	1	glycine betaine transporter		
K05275	26	pyridoxine 4-dehydrogenase [EC:1.1.1.65]		
K05281	4	2'-hydroxyisoflavone reductase [EC:1.3.1.45]		
K05296	3	3(or 17)beta-hydroxysteroid dehydrogenase [EC:1.1.1.51]		
K05297	6	rubredoxin-NAD+ reductase [EC:1.18.1.1]		
K05299	10	formate dehydrogenase (NADP+) [EC:1.2.1.43]		
K05301	55	sulfite dehydrogenase [EC:1.8.2.1]		
K05306	2	phosphonoacetaldehyde hydrolase [EC:3.11.1.1]		
K05311	1	central glycolytic genes regulator		
K05337	22	ferredoxin		
K05338	12	holin-like protein		
K05339	1	holin-like protein LrgB		
K05340	2	glucose uptake protein		
K05341	5	amylosucrase [EC:2.4.1.4]		
K05343	42	maltose alpha-D-glucosyltransferase [EC:5.4.99.16]		
K05344	1	glucose-1-phosphate phosphodismutase [EC:2.7.1.41]		
K05345	21	putative cyclase [EC:4.6.1.-]		
K05348	2	2-hydroxycinnamic acid beta-D-glucosylisomelase [EC:5.2.1.-]		
K05349	79	beta-glucosidase [EC:3.2.1.21]		
K05350	31	beta-glucosidase [EC:3.2.1.21]		
K05351	2	D-xylulose reductase [EC:1.1.1.9]		
K05358	3	quinate dehydrogenase (pyrroloquinoline-quinone) [EC:1.1.99.25]		
K05359	1	carboxycyclohexadienyl dehydratase [EC:4.2.1.91]		
K05362	1	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase		
K05363	1	serine/alanine adding enzyme [EC:2.3.2.10]		
K05364	58	peptidoglycan glycosyltransferase [EC:2.4.1.129]		
K05365	12	penicillin-binding protein 1B [EC:2.4.1.129 3.4.-.-]		
K05366	129	penicillin-binding protein 1A [EC:2.4.1.- 3.4.-.-]		
K05367	18	penicillin-binding protein 1C [EC:2.4.1.-]		
K05368	1	aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3		
K05375	2	MbtH protein		
K05384	22	bilin biosynthesis protein		
K05386	8	bilin biosynthesis protein		
K05394	29	atrazine chlorohydrolase [EC:3.8.1.8]		
K05395	5	cystine reductase [EC:1.8.1.6]		
K05396	10	D-cysteine desulfhydrase [EC:4.4.1.15]		
K05499	15	LacI family transcriptional regulator, repressor for deo operon,		
K05501	11	TetR/AcrR family transcriptional regulator		
K05515	85	penicillin-binding protein 2		
K05516	22	curved DNA-binding protein		
K05517	1	nucleoside-specific channel-forming protein		
K05520	21	protease I [EC:3.2.-.-]		
K05521	16	ADP-ribosylglycohydrolase [EC:3.2.-.-]		
K05522	12	endonuclease VIII [EC:3.2.2.- 4.2.99.18]		
K05524	6	ferredoxin		
K05525	30	linalool 8-monooxygenase [EC:1.14.99.28]		
K05527	6	BolA protein		
K05539	2	tRNA-dihydrouridine synthase A [EC:1.-.-.-]		

K05540	28	tRNA-dihydrouridine synthase B [EC:1.-.-.-]		
K05541	1	tRNA-dihydrouridine synthase C [EC:1.-.-.-]		
K05549	11	benzoate 1,2-dioxygenase alpha subunit [EC:1.14.12.10]		
K05550	4	benzoate 1,2-dioxygenase beta subunit [EC:1.14.12.10]		
K05551	24	3-oxoacyl-ACP synthase I [EC:2.3.1.-]		
K05552	22	3-oxoacyl-ACP synthase II [EC:2.3.1.-]		
K05555	12	cyclase [EC:4.-.-.-]		
K05556	3	hydroxylacyl-CoA dehydrogenase [EC:1.1.1.-]		
K05557	16	MFS transporter, DHA2 family, integral membrane protein		
K05559	4	multicomponent K+:H+ antiporter subunit A		
K05561	2	multicomponent K+:H+ antiporter subunit D		
K05563	1	multicomponent K+:H+ antiporter subunit F		
K05564	1	multicomponent K+:H+ antiporter subunit G		
K05565	4	multicomponent Na+:H+ antiporter subunit A		
K05567	3	multicomponent Na+:H+ antiporter subunit C		
K05568	14	multicomponent Na+:H+ antiporter subunit D		
K05571	1	multicomponent Na+:H+ antiporter subunit G		
K05572	6	NADH dehydrogenase I subunit 1 [EC:1.6.5.3]		
K05573	9	NADH dehydrogenase I subunit 2 [EC:1.6.5.3]		
K05574	6	NADH dehydrogenase I subunit 3 [EC:1.6.5.3]		
K05575	8	NADH dehydrogenase I subunit 4 [EC:1.6.5.3]		
K05576	3	NADH dehydrogenase I subunit 4L [EC:1.6.5.3]		
K05577	7	NADH dehydrogenase I subunit 5 [EC:1.6.5.3]		
K05578	2	NADH dehydrogenase I subunit 6 [EC:1.6.5.3]		
K05579	2	NADH dehydrogenase I subunit 7 [EC:1.6.5.3]		
K05580	4	NADH dehydrogenase I subunit I [EC:1.6.5.3]		
K05586	3	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]		
K05587	6	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]		
K05588	3	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]		
K05589	1	cell division protein FtsB		
K05590	1	ATP-dependent RNA helicase SrmB [EC:2.7.7.-]		
K05591	4	ATP-independent RNA helicase DbpA [EC:3.6.4.13]		
K05592	36	ATP-dependent RNA helicase DeaD [EC:3.6.4.13]		
K05595	33	multiple antibiotic resistance protein		
K05597	1	glutamin-(asparagin-)ase [EC:3.5.1.38]		
K05599	2	anthranilate 1,2-dioxygenase (deaminating, decarboxylating) large		
K05600	2	anthranilate 1,2-dioxygenase (deaminating, decarboxylating) small		
K05601	2	hydroxylamine reductase [EC:1.7.99.1]		
K05603	10	formimidoylglutamate deiminase [EC:3.5.3.13]		
K05606	12	methylmalonyl-CoA epimerase [EC:5.1.99.1]		
K05685	60	macrolide transport system ATP-binding/permease protein [EC:3.6.3.-]		
K05692	2	actin beta/gamma 1		
K05708	9	large terminal subunit of phenylpropionate dioxygenase		
K05709	3	small terminal subunit of phenylpropionate dioxygenase		
K05710	16	ferredoxin subunit of phenylpropionate dioxygenase		
K05712	33	3-(3-hydroxy-phenyl)propionate hydroxylase [EC:1.14.13.-]		
K05714	5	2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase [EC:3.7.1.-]		
K05715	6	2-phosphoglycerate kinase [EC:2.7.2.-]		
K05772	8	putative tungstate transport system substrate-binding protein		
K05773	8	putative tungstate transport system permease protein		

K05776	4	molybdate transport system ATP-binding protein		
K05777	5	putative thiamine transport system substrate-binding protein		
K05780	2	putative phosphonate transport system ATP-binding protein		
K05781	1	putative phosphonate transport system ATP-binding protein		
K05782	6	benzoate membrane transport protein		
K05783	1	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase		
K05784	3	benzoate 1,2-dioxygenase electron transfer component		
K05785	1	transcriptional antiterminator RfaH		
K05786	10	chloramphenicol-sensitive protein RarD		
K05787	1	DNA-binding protein HU-alpha		
K05788	20	integration host factor subunit beta		
K05794	28	tellurite resistance protein TerC		
K05795	6	tellurium resistance protein TerD		
K05796	1	electron transport protein HydN		
K05797	3	4-cresol dehydrogenase (hydroxylating) [EC:1.17.99.1]		
K05798	12	LysR family transcriptional regulator, transcriptional activator for		
K05799	23	GntR family transcriptional regulator, transcriptional repressor for		
K05800	2	Lrp/AsnC family transcriptional regulator		
K05802	8	potassium efflux system protein KefA		
K05803	4	lipoprotein NlpI		
K05807	19	putative lipoprotein		
K05808	17	putative sigma-54 modulation protein		
K05810	27	conserved hypothetical protein		
K05812	1	conserved hypothetical protein		
K05813	23	sn-glycerol 3-phosphate transport system substrate-binding protein		
K05814	17	sn-glycerol 3-phosphate transport system permease protein		
K05815	10	sn-glycerol 3-phosphate transport system permease protein		
K05816	7	sn-glycerol 3-phosphate transport system ATP-binding protein		
K05817	27	LysR family transcriptional regulator, hca operon transcriptional		
K05820	4	MFS transporter, PPP family, 3-phenylpropionic acid transporter		
K05823	1	N-acetyldiaminopimelate deacetylase [EC:3.5.1.47]		
K05825	2	2-aminoadipate transaminase [EC:2.6.1.-]		
K05827	5	lysine biosynthesis protein LysX		
K05829	4	N-acetyl-gamma-aminoadipyl-phosphate reductase [EC:1.2.1.-]		
K05830	3	acetylornithine/acetyl-lysine aminotransferase [EC:2.6.1.11 2.6.1.-]		
K05831	2	acetyl-lysine deacetylase [EC:3.5.1.-]		
K05832	1	putative ABC transport system permease protein		
K05834	11	homoserine/homoserine lactone efflux protein		
K05835	1	threonine efflux protein		
K05836	9	GntR family transcriptional regulator, histidine utilization		
K05837	55	rod shape determining protein RodA		
K05838	12	putative thioredoxin		
K05841	12	sterol 3beta-glucosyltransferase [EC:2.4.1.173]		
K05844	10	ribosomal protein S6 modification protein		
K05845	22	osmoprotectant transport system substrate-binding protein		
K05846	27	osmoprotectant transport system permease protein		
K05847	6	osmoprotectant transport system ATP-binding protein		
K05873	1	adenylate cyclase, class 2 [EC:4.6.1.1]		
K05874	21	methyl-accepting chemotaxis protein I, serine sensor receptor		
K05875	8	methyl-accepting chemotaxis protein II, aspartate sensor receptor		

K05876	2	methyl-accepting chemotaxis protein III, ribose and galactose sensor		
K05878	8	dihydroxyacetone kinase, N-terminal domain [EC:2.7.1.-]		
K05879	5	dihydroxyacetone kinase, C-terminal domain [EC:2.7.1.-]		
K05881	1	PTS hybrid protein		
K05882	45	aryl-alcohol dehydrogenase (NADP+) [EC:1.1.1.91]		
K05883	2	Unclassified; E1.1.1.210		
K05885	35	2,5-diketo-D-gluconate reductase [EC:1.1.1.274]		
K05886	5	serine 3-dehydrogenase [EC:1.1.1.276]		
K05888	11	Unclassified; E1.1.2.-		
K05889	3	polyvinyl-alcohol dehydrogenase (acceptor) [EC:1.1.99.23]		
K05893	3	Unclassified; E1.3.1.35		
K05895	2	precorrin-6X reductase [EC:1.3.1.54]		
K05896	19	segregation and condensation protein A		
K05897	1	Unclassified; E1.3.3.-		
K05898	2	3-oxosteroid 1-dehydrogenase [EC:1.3.99.4]		
K05899	2	glycine oxidase [EC:1.4.3.19]		
K05903	108	NADH dehydrogenase (quinone) [EC:1.6.99.5]		
K05905	17	protein-disulfide reductase [EC:1.8.1.8]		
K05909	5	Unclassified; E1.10.3.2		
K05910	1	NADH peroxidase [EC:1.11.1.1]		
K05911	5	quinone-reactive Ni/Fe-hydrogenase [EC:1.12.5.1]		
K05912	20	Unclassified; E1.12.-.-		
K05914	35	Unclassified; E1.13.12.7		
K05915	9	Unclassified; E1.13.-.-		
K05916	3	nitric oxide dioxygenase [EC:1.14.12.17]		
K05917	1	cytochrome P450, family 51 (sterol 14-demethylase) [EC:1.14.13.70]		
K05918	8	Unclassified; E1.14.19.-		
K05921	16	5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase /		
K05922	19	quinone-reactive Ni/Fe-hydrogenase large subunit [EC:1.12.5.1]		
K05927	7	quinone-reactive Ni/Fe-hydrogenase small subunit [EC:1.12.5.1]		
K05928	8	tocopherol O-methyltransferase [EC:2.1.1.95]		
K05929	6	phosphoethanolamine N-methyltransferase [EC:2.1.1.103]		
K05934	6	precorrin-3B C17-methyltransferase [EC:2.1.1.131]		
K05936	4	precorrin-4 C11-methyltransferase [EC:2.1.1.133]		
K05939	12	acyl-[acyl-carrier-protein]-phospholipid O-acyltransferase /		
K05942	1	Unclassified; E2.3.-.-		
K05944	6	Unclassified; E2.4.1.56		
K05945	1	Unclassified; E2.4.1.58		
K05946	16	N-acetylglucosaminyldiphosphoundecaprenol [EC:2.4.1.187]		
K05949	5	Unclassified; E2.4.1.227		
K05957	4	L-glutamine:scyllo-inosose aminotransferase [EC:2.6.1.50]		
K05961	1	Unclassified; E2.7.1.145		
K05962	30	protein-histidine pros-kinase [EC:2.7.13.1]		
K05968	7	Unclassified; E3.1.1.6		
K05969	8	peptidyl-tRNA hydrolase [EC:3.1.1.29]		
K05971	43	Unclassified; E3.1.1.61		
K05972	1	Unclassified; E3.1.1.72		
K05973	12	poly(3-hydroxybutyrate) depolymerase [EC:3.1.1.75]		
K05979	11	2-phosphosulfolactate phosphatase [EC:3.1.3.71]		
K05982	8	deoxyribonuclease V [EC:3.1.21.7]		

K05984	4	excinuclease Cho [EC:3.1.25.-]		
K05985	445	ribonuclease M5 [EC:3.1.26.8]		
K05993	29	isochorismatase [EC:3.3.2.1]		
K05994	2	bacterial leucyl aminopeptidase [EC:3.4.11.10]		
K05995	7	dipeptidase E [EC:3.4.13.21]		
K05996	15	carboxypeptidase T [EC:3.4.17.18]		
K05997	3	Fe-S cluster assembly protein SufA		
K05998	2	pseudomonalisin [EC:3.4.21.100]		
K05999	5	xanthomonalisin [EC:3.4.21.101]		
K06001	31	tryptophan synthase beta chain [EC:4.2.1.20]		
K06010	5	Unclassified; E3.4.23.43		
K06013	29	STE24 endopeptidase [EC:3.4.24.84]		
K06015	85	Unclassified; E3.5.1.81		
K06016	27	N-carbamoyl-L-amino-acid hydrolase [EC:3.5.1.87]		
K06019	4	pyrophosphatase PpaX [EC:3.6.1.1]		
K06020	53	sulfate-transporting ATPase [EC:3.6.3.25]		
K06021	11	phosphate-transporting ATPase [EC:3.6.3.27]		
K06022	6	molybdate-transporting ATPase [EC:3.6.3.29]		
K06023	16	HPr kinase/phosphorylase [EC:2.7.11.- 2.7.4.-]		
K06024	17	segregation and condensation protein B		
K06026	35	Unclassified; E3.6.4.4		
K06027	29	vesicle-fusing ATPase [EC:3.6.4.6]		
K06031	6	Unclassified; E3.8.1.1		
K06033	3	Unclassified; E4.1.1.76		
K06034	5	sulfopyruvate decarboxylase subunit alpha [EC:4.1.1.79]		
K06037	1	Unclassified; E4.2.3.-		
K06039	4	uncharacterized protein involved in oxidation of intracellular		
K06041	24	arabinose-5-phosphate isomerase [EC:5.3.1.13]		
K06042	8	precorrin-8X methylmutase [EC:5.4.1.2]		
K06044	33	(1->4)-alpha-D-glucan 1-alpha-D-glucosylmutase [EC:5.4.99.15]		
K06045	23	squalene-hopene cyclase [EC:5.4.99.17]		
K06048	23	carboxylate-amine ligase [EC:6.3.-.-]		
K06049	10	magnesium chelatase accessory protein		
K06075	7	MarR family transcriptional regulator, transcriptional regulator for		
K06076	23	long-chain fatty acid transport protein		
K06077	1	outer membrane lipoprotein SlyB		
K06113	1	arabinan endo-1,5-alpha-L-arabinosidase [EC:3.2.1.99]		
K06118	5	UDP-sulfoquinovose synthase [EC:3.13.1.1]		
K06120	2	glycerol dehydratase large subunit [EC:4.2.1.30]		
K06121	1	glycerol dehydratase medium subunit [EC:4.2.1.30]		
K06131	35	cardiolipin synthase [EC:2.7.8.-]		
K06132	18	putative cardiolipin synthase [EC:2.7.8.-]		
K06134	3	ubiquinone biosynthesis monooxygenase Coq7 [EC:1.14.13.-]		
K06136	9	pyrroloquinoline quinone biosynthesis protein B		
K06137	5	pyrroloquinoline-quinone synthase [EC:1.3.3.11]		
K06138	1	pyrroloquinoline quinone biosynthesis protein D		
K06139	53	pyrroloquinoline quinone biosynthesis protein E		
K06140	4	regulator of nucleoside diphosphate kinase		
K06142	8	outer membrane protein		
K06143	10	inner membrane protein		

K06147	326	ATP-binding cassette, subfamily B, bacterial		
K06148	122	ATP-binding cassette, subfamily C, bacterial		
K06149	46	universal stress protein A		
K06151	40	gluconate 2-dehydrogenase alpha chain [EC:1.1.99.3]		
K06153	39	undecaprenyl-diphosphatase [EC:3.6.1.27]		
K06155	4	Gnt-I system high-affinity gluconate transporter		
K06158	42	ATP-binding cassette, sub-family F, member 3		
K06162	1	PhnM protein		
K06163	1	PhnJ protein		
K06164	3	PhnI protein		
K06167	14	PhnP protein		
K06168	67	bifunctional enzyme involved in thiolation and methylation of tRNA		
K06173	30	tRNA pseudouridine synthase A [EC:5.4.99.12]		
K06175	3	tRNA pseudouridine synthase C [EC:5.4.99.12]		
K06176	3	tRNA pseudouridine synthase D [EC:5.4.99.12]		
K06177	17	ribosomal large subunit pseudouridine synthase A [EC:5.4.99.12]		
K06178	41	ribosomal large subunit pseudouridine synthase B [EC:5.4.99.12]		
K06179	25	ribosomal large subunit pseudouridine synthase C [EC:5.4.99.12]		
K06180	45	ribosomal large subunit pseudouridine synthase D [EC:5.4.99.12]		
K06181	5	ribosomal large subunit pseudouridine synthase E [EC:5.4.99.12]		
K06182	2	ribosomal large subunit pseudouridine synthase F [EC:5.4.99.12]		
K06183	14	ribosomal small subunit pseudouridine synthase A [EC:5.4.99.12]		
K06186	4	small protein A		
K06187	21	recombination protein RecR		
K06188	15	aquaporin Z		
K06189	18	magnesium and cobalt transporter		
K06190	8	intracellular septation protein		
K06192	8	paraquat-inducible protein B		
K06193	1	phosphonoacetate hydrolase [EC:3.11.1.2]		
K06194	17	lipoprotein NlpD		
K06195	4	ApaG protein		
K06196	31	cytochrome c-type biogenesis protein		
K06197	3	cation transport regulator		
K06199	16	CrcB protein		
K06200	25	carbon starvation protein		
K06201	11	copper homeostasis protein		
K06202	1	CyaY protein		
K06204	29	DnaK suppressor protein		
K06205	2	MioC protein		
K06206	3	sugar fermentation stimulation protein A		
K06207	33	GTP-binding protein		
K06208	12	chorismate mutase [EC:5.4.99.5]		
K06211	1	HipB family transcriptional regulator, involved in the regulation of		
K06212	14	formate transporter		
K06213	42	magnesium transporter		
K06215	8	pyridoxine biosynthesis protein [EC:4.-.-.-]		
K06217	31	phosphate starvation-inducible protein PhoH and related proteins		
K06218	4	RelE protein		
K06219	4	S-adenosylmethionine-dependent methyltransferase		
K06221	8	2,5-diketo-D-gluconate reductase A [EC:1.1.1.274]		

K06222	1	2,5-diketo-D-gluconate reductase B [EC:1.1.1.274]		
K06223	4	DNA adenine methylase [EC:2.1.1.72]		
K06281	38	hydrogenase large subunit [EC:1.12.99.6]		
K06282	22	hydrogenase small subunit [EC:1.12.99.6]		
K06284	5	transcriptional pleiotropic regulator of transition state genes		
K06287	26	septum formation protein		
K06294	1	spore germination protein D		
K06306	15	spore germination protein		
K06308	1	spore germination protein		
K06320	3	spore maturation protein CgeB		
K06324	41	spore coat protein A		
K06329	1	spore coat protein F		
K06330	1	spore coat protein H		
K06345	3	spore cortex protein		
K06346	9	spoIIIJ-associated protein		
K06348	5	sporulation inhibitor KapD		
K06350	5	antagonist of KipI		
K06351	3	inhibitor of KinA		
K06370	4	morphogenetic protein associated with SpoVID		
K06373	4	spore maturation protein A		
K06374	5	spore maturation protein B		
K06378	14	stage II sporulation protein AA (anti-sigma F factor antagonist)		
K06379	6	stage II sporulation protein AB (anti-sigma F factor) [EC:2.7.11.1]		
K06381	23	stage II sporulation protein D		
K06384	1	stage II sporulation protein M		
K06390	4	stage III sporulation protein AA		
K06391	1	stage III sporulation protein AB		
K06399	2	stage IV sporulation protein B [EC:3.4.21.116]		
K06400	21	site-specific DNA recombinase		
K06402	3	stage IV sporulation protein FB [EC:3.4.24.-]		
K06405	1	stage V sporulation protein AC		
K06407	1	stage V sporulation protein AE		
K06408	4	stage V sporulation protein AF		
K06412	4	stage V sporulation protein G		
K06413	5	stage V sporulation protein K		
K06415	10	stage V sporulation protein R		
K06419	1	small acid-soluble spore protein B (major beta-type SASP)		
K06422	11	small acid-soluble spore protein E (minor gamma-type SASP)		
K06423	1	small acid-soluble spore protein F (minor alpha/beta-type SASP)		
K06428	1	small acid-soluble spore protein K (minor)		
K06434	6	small acid-soluble spore protein (thioredoxin-like protein)		
K06442	20	putative hemolysin		
K06445	16	acyl-CoA dehydrogenase [EC:1.3.99.-]		
K06446	6	acyl-CoA dehydrogenase [EC:1.3.99.-]		
K06447	2	succinylglutamic semialdehyde dehydrogenase [EC:1.2.1.71]		
K06518	4	holin-like protein		
K06595	4	heam-based aerotactic trancducer		
K06596	35	chemosensory pili system protein ChpA (sensor histidine		
K06600	1	chemosensory pili system protein ChpE		
K06601	1	flagellar protein FlbT		

K06602	1	flagellar protein FlaF		
K06603	1	flagellar protein FlaG		
K06605	1	myo-inositol catabolism protein IolH		
K06606	2	inosose isomerase [EC:5.3.99.-]		
K06607	2	myo-inositol catabolism protein IolS [EC:1.1.1.-]		
K06608	3	DeoR family transcriptional regulator, myo-inositol catabolism		
K06609	1	MFS transporter, SP family, major inositol transporter		
K06714	8	arginine utilization regulatory protein		
K06718	2	L-2,4-diaminobutyric acid acetyltransferase [EC:2.3.1.178]		
K06726	1	D-ribose pyranase [EC:5.-.-.-]		
K06857	10	putative tungstate transport system ATP-binding protein		
K06858	8	vitamin B12 transport system substrate-binding protein		
K06859	1	glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]		
K06860	19	Unclassified; K06860		
K06861	16	lipopolysaccharide export system ATP-binding protein [EC:3.6.3.-]		
K06864	13	Unclassified; K06864		
K06867	34	Unclassified; K06867		
K06871	16	Unclassified; K06871		
K06872	14	Unclassified; K06872		
K06873	3	Unclassified; K06873		
K06876	2	Unclassified; K06876		
K06877	43	Unclassified; K06877		
K06878	6	Unclassified; K06878		
K06881	34	Unclassified; K06881		
K06882	5	Unclassified; K06882		
K06883	14	Unclassified; K06883		
K06884	1	Unclassified; K06884		
K06885	9	Unclassified; K06885		
K06886	13	hemoglobin		
K06887	1	Unclassified; K06887		
K06888	45	Unclassified; K06888		
K06889	70	Unclassified; K06889		
K06890	28	Unclassified; K06890		
K06891	7	ATP-dependent Clp protease adaptor protein ClpS		
K06892	7	Unclassified; K06892		
K06893	19	Unclassified; K06893		
K06894	31	Unclassified; K06894		
K06895	6	Unclassified; K06895		
K06896	21	Unclassified; K06896		
K06897	12	Unclassified; K06897		
K06898	15	Unclassified; K06898		
K06899	1	Unclassified; K06899		
K06900	6	Unclassified; K06900		
K06901	37	putative MFS transporter, AGZA family, xanthine/uracil permease		
K06902	19	MFS transporter, UMF1 family		
K06903	7	Unclassified; K06903		
K06904	7	Unclassified; K06904		
K06905	6	Unclassified; K06905		
K06907	22	Unclassified; K06907		
K06909	7	Unclassified; K06909		

K06910	25	Unclassified; K06910		
K06911	105	Unclassified; K06911		
K06912	17	alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase		
K06915	44	Unclassified; K06915		
K06916	7	Unclassified; K06916		
K06917	3	tRNA 2-selenouridine synthase [EC:2.9.1.-]		
K06919	3	Unclassified; K06919		
K06920	21	queuosine biosynthesis protein QueC		
K06921	5	Unclassified; K06921		
K06922	4	Unclassified; K06922		
K06923	9	Unclassified; K06923		
K06925	17	Unclassified; K06925		
K06927	3	Unclassified; K06927		
K06929	33	Unclassified; K06929		
K06931	1	Unclassified; K06931		
K06934	2	Unclassified; K06934		
K06936	2	Unclassified; K06936		
K06937	23	Unclassified; K06937		
K06938	1	Unclassified; K06938		
K06940	16	Unclassified; K06940		
K06941	40	ribosomal RNA large subunit methyltransferase N [EC:2.1.1.-]		
K06942	31	Unclassified; K06942		
K06944	9	Unclassified; K06944		
K06947	1	Unclassified; K06947		
K06948	2	Unclassified; K06948		
K06949	40	ribosome biogenesis GTPase [EC:3.6.1.-]		
K06950	36	Unclassified; K06950		
K06951	7	Unclassified; K06951		
K06952	1	Unclassified; K06952		
K06953	2	Unclassified; K06953		
K06954	16	Unclassified; K06954		
K06955	5	Unclassified; K06955		
K06956	7	Unclassified; K06956		
K06958	20	Unclassified; K06958		
K06959	17	Unclassified; K06959		
K06960	10	Unclassified; K06960		
K06962	2	Unclassified; K06962		
K06966	34	Unclassified; K06966		
K06967	6	Unclassified; K06967		
K06968	3	Unclassified; K06968		
K06969	37	putative SAM-dependent methyltransferase		
K06971	6	Unclassified; K06971		
K06972	1	Unclassified; K06972		
K06973	3	Unclassified; K06973		
K06974	7	Unclassified; K06974		
K06975	3	Unclassified; K06975		
K06976	4	Unclassified; K06976		
K06977	1	Unclassified; K06977		
K06978	97	Unclassified; K06978		
K06979	58	Unclassified; K06979		

K06980	27	Unclassified; K06980		
K06981	1	Unclassified; K06981		
K06983	1	Unclassified; K06983		
K06985	5	aspartyl protease family protein		
K06986	1	Unclassified; K06986		
K06987	5	Unclassified; K06987		
K06988	27	Unclassified; K06988		
K06989	7	aspartate dehydrogenase [EC:1.4.1.21]		
K06990	27	Unclassified; K06990		
K06991	3	Unclassified; K06991		
K06992	1	Unclassified; K06992		
K06994	80	putative drug exporter of the RND superfamily		
K06996	29	Unclassified; K06996		
K06997	22	Unclassified; K06997		
K06998	53	Unclassified; K06998		
K06999	29	Unclassified; K06999		
K07000	5	Unclassified; K07000		
K07001	116	Unclassified; K07001		
K07002	5	Unclassified; K07002		
K07003	53	Unclassified; K07003		
K07004	22	Unclassified; K07004		
K07005	13	Unclassified; K07005		
K07006	21	Unclassified; K07006		
K07007	10	Unclassified; K07007		
K07008	22	Unclassified; K07008		
K07009	8	Unclassified; K07009		
K07010	19	putative glutamine amidotransferase		
K07011	57	Unclassified; K07011		
K07012	6	Unclassified; K07012		
K07014	4	Unclassified; K07014		
K07015	1	Unclassified; K07015		
K07017	5	Unclassified; K07017		
K07018	12	Unclassified; K07018		
K07019	16	Unclassified; K07019		
K07020	7	Unclassified; K07020		
K07021	40	Unclassified; K07021		
K07024	51	Unclassified; K07024		
K07025	74	putative hydrolase of the HAD superfamily		
K07027	59	Unclassified; K07027		
K07028	17	Unclassified; K07028		
K07029	47	Unclassified; K07029		
K07030	32	Unclassified; K07030		
K07031	8	Unclassified; K07031		
K07032	15	Unclassified; K07032		
K07033	8	Unclassified; K07033		
K07034	6	Unclassified; K07034		
K07037	17	Unclassified; K07037		
K07038	7	Unclassified; K07038		
K07039	2	Unclassified; K07039		
K07040	23	Unclassified; K07040		

K07042	16	Unclassified; K07042		
K07043	16	Unclassified; K07043		
K07044	5	Unclassified; K07044		
K07045	131	Unclassified; K07045		
K07046	35	Unclassified; K07046		
K07047	88	Unclassified; K07047		
K07048	14	Unclassified; K07048		
K07050	14	Unclassified; K07050		
K07051	5	Unclassified; K07051		
K07052	60	Unclassified; K07052		
K07053	27	Unclassified; K07053		
K07054	12	Unclassified; K07054		
K07056	37	Unclassified; K07056		
K07057	1	Unclassified; K07057		
K07058	51	Unclassified; K07058		
K07062	8	Unclassified; K07062		
K07063	2	Unclassified; K07063		
K07064	11	Unclassified; K07064		
K07065	4	Unclassified; K07065		
K07067	12	Unclassified; K07067		
K07068	21	Unclassified; K07068		
K07071	23	Unclassified; K07071		
K07072	2	Unclassified; K07072		
K07074	1	Unclassified; K07074		
K07075	6	Unclassified; K07075		
K07076	2	Unclassified; K07076		
K07077	14	Unclassified; K07077		
K07078	30	Unclassified; K07078		
K07079	38	Unclassified; K07079		
K07080	41	Unclassified; K07080		
K07081	8	Unclassified; K07081		
K07082	28	Unclassified; K07082		
K07083	18	Unclassified; K07083		
K07085	16	Unclassified; K07085		
K07086	2	Unclassified; K07086		
K07088	17	Unclassified; K07088		
K07089	22	Unclassified; K07089		
K07090	87	Unclassified; K07090		
K07091	25	lipopolysaccharide export system permease protein		
K07093	7	Unclassified; K07093		
K07094	1	Unclassified; K07094		
K07095	21	Unclassified; K07095		
K07096	25	Unclassified; K07096		
K07098	27	Unclassified; K07098		
K07100	43	Unclassified; K07100		
K07101	5	Unclassified; K07101		
K07102	16	Unclassified; K07102		
K07104	17	Unclassified; K07104		
K07106	20	N-acetylmuramic acid 6-phosphate etherase [EC:4.2.-.-]		
K07107	51	Unclassified; K07107		

K07110	12	Unclassified; K07110		
K07112	18	Unclassified; K07112		
K07113	5	Unclassified; K07113		
K07114	83	Unclassified; K07114		
K07115	2	Unclassified; K07115		
K07116	73	Unclassified; K07116		
K07117	6	Unclassified; K07117		
K07118	4	Unclassified; K07118		
K07119	19	Unclassified; K07119		
K07120	8	Unclassified; K07120		
K07121	4	Unclassified; K07121		
K07122	1	Unclassified; K07122		
K07124	34	Unclassified; K07124		
K07125	1	Unclassified; K07125		
K07126	43	Unclassified; K07126		
K07127	6	5-hydroxyisourate hydrolase [EC:3.5.2.17]		
K07130	24	Unclassified; K07130		
K07131	6	Unclassified; K07131		
K07133	13	Unclassified; K07133		
K07137	10	Unclassified; K07137		
K07138	10	Unclassified; K07138		
K07139	2	Unclassified; K07139		
K07140	12	Unclassified; K07140		
K07141	16	Unclassified; K07141		
K07145	11	Unclassified; K07145		
K07146	1	Unclassified; K07146		
K07147	73	Unclassified; K07147		
K07148	4	Unclassified; K07148		
K07149	5	Unclassified; K07149		
K07150	2	Unclassified; K07150		
K07152	50	Unclassified; K07152		
K07153	1	Unclassified; K07153		
K07154	7	Unclassified; K07154		
K07155	4	quercetin 2,3-dioxygenase [EC:1.13.11.24]		
K07156	4	Unclassified; pcoC		
K07157	17	Unclassified; K07157		
K07160	7	Unclassified; K07160		
K07161	34	Unclassified; K07161		
K07164	13	Unclassified; K07164		
K07165	1	transmembrane sensor		
K07168	7	CBS domain-containing membrane protein		
K07169	39	FHA domain-containing protein		
K07170	8	GAF domain-containing protein		
K07171	5	Unclassified; K07171		
K07172	1	Unclassified; K07172		
K07173	15	S-ribosylhomocysteine lyase [EC:4.4.1.21]		
K07175	20	PhoH-like ATPase		
K07177	6	PDZ domain-containing protein		
K07178	2	RIO kinase 1 [EC:2.7.11.1]		
K07180	31	serine protein kinase		

K07181	7	putative signal transduction protein containing EAL and modified		
K07182	60	CBS domain-containing protein		
K07183	14	response regulator NasT		
K07185	12	tryptophan-rich sensory protein		
K07186	2	membrane protein		
K07192	11	flotillin		
K07213	6	Unclassified; K07213		
K07214	12	enterochelin esterase and related enzymes		
K07216	14	hemerythrin		
K07217	5	Mn-containing catalase		
K07218	10	nitrous oxidase accessory protein		
K07219	16	putative molybdopterin biosynthesis protein		
K07220	19	hypothetical protein		
K07221	1	outer membrane porin		
K07222	30	putative flavoprotein involved in K+ transport		
K07223	13	putative iron-dependent peroxidase		
K07224	2	putative lipoprotein		
K07226	3	hypothetical protein		
K07228	2	TrkA domain protein		
K07229	3	Unclassified; K07229		
K07232	6	cation transport protein ChaC		
K07233	1	copper resistance protein B		
K07234	7	uncharacterized protein involved in response to NO		
K07236	1	tRNA 2-thiouridine synthesizing protein C		
K07237	3	tRNA 2-thiouridine synthesizing protein B		
K07238	18	zinc transporter, ZIP family		
K07239	116	heavy-metal exporter, HME family		
K07240	47	chromate transporter		
K07241	10	high-affinity nickel-transport protein		
K07243	27	high-affinity iron transporter		
K07245	21	putative copper resistance protein D		
K07246	8	tartrate dehydrogenase/decarboxylase / D-malate dehydrogenase		
K07248	4	lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase		
K07250	30	4-aminobutyrate aminotransferase / (S)-3-amino-2-methylpropionate		
K07257	5	spore coat polysaccharide biosynthesis protein SpsF		
K07258	136	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6)		
K07259	26	D-alanyl-D-alanine carboxypeptidase /		
K07260	7	D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4]		
K07262	11	D-alanyl-D-alanine endopeptidase (penicillin-binding protein 7)		
K07263	230	zinc protease [EC:3.4.99.-]		
K07264	23	4-amino-4-deoxy-L-arabinose transferase [EC:2.-.-.-]		
K07265	3	capsular polysaccharide export protein		
K07266	2	capsular polysaccharide export protein		
K07267	1	porin		
K07273	5	lysozyme		
K07274	6	outer membrane protein		
K07276	2	hypothetical protein		
K07277	60	outer membrane protein		
K07278	43	outer membrane protein		
K07279	41	hypothetical protein		

K07281	1	Unclassified; K07281		
K07282	27	poly-gamma-glutamate synthesis protein (capsule biosynthesis		
K07283	1	putative salt-induced outer membrane protein		
K07284	9	sortase A		
K07285	2	outer membrane lipoprotein		
K07287	7	lipoprotein-34		
K07288	17	uncharacterized membrane protein		
K07289	17	AsmA protein		
K07290	5	hypothetical protein		
K07300	25	Ca2+:H+ antiporter		
K07301	19	Unclassified; yrbG		
K07302	14	isoquinoline 1-oxidoreductase, alpha subunit [EC:1.3.99.16]		
K07303	95	isoquinoline 1-oxidoreductase, beta subunit [EC:1.3.99.16]		
K07304	33	peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]		
K07305	15	peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12]		
K07306	10	anaerobic dimethyl sulfoxide reductase subunit A [EC:1.8.99.-]		
K07307	10	anaerobic dimethyl sulfoxide reductase subunit B (DMSO reductase		
K07308	1	anaerobic dimethyl sulfoxide reductase subunit C (DMSO reductase		
K07309	1	putative dimethyl sulfoxide reductase subunit YnfE [EC:1.8.99.-]		
K07310	1	putative dimethyl sulfoxide reductase subunit YnfF [EC:1.8.99.-]		
K07313	3	serine/threonine protein phosphatase 1 [EC:3.1.3.16]		
K07315	66	sigma-B regulation protein RsbU (phosphoserine phosphatase)		
K07316	4	adenine-specific DNA-methyltransferase [EC:2.1.1.72]		
K07318	2	adenine-specific DNA-methyltransferase [EC:2.1.1.72]		
K07319	22	putative adenine-specific DNA-methyltransferase [EC:2.1.1.72]		
K07320	7	putative adenine-specific DNA-methyltransferase [EC:2.1.1.72]		
K07321	9	CO dehydrogenase maturation factor		
K07322	13	regulator of cell morphogenesis and NO signaling		
K07323	15	putative toluene tolerance protein		
K07326	7	hemolysin activation/secretion protein		
K07334	3	proteic killer suppression protein		
K07335	28	basic membrane protein A and related proteins		
K07336	1	PKHD-type hydroxylase [EC:1.14.11.-]		
K07337	3	hypothetical protein		
K07339	2	hypothetical protein		
K07341	6	death on curing protein		
K07343	3	DNA transformation protein and related proteins		
K07345	1	major type 1 subunit fimbrin (pilin)		
K07346	3	fimbrial chaperone protein		
K07347	11	outer membrane usher protein		
K07357	1	type 1 fimbriae regulatory protein FimB		
K07386	54	putative endopeptidase [EC:3.4.24.-]		
K07387	22	putative metalloprotease [EC:3.4.24.-]		
K07390	4	monothiol glutaredoxin		
K07391	65	magnesium chelatase family protein		
K07392	4	AAA family ATPase		
K07393	11	putative glutathione S-transferase		
K07395	4	putative proteasome-type protease		
K07396	1	putative protein-disulfide isomerase		
K07397	21	putative redox protein		

K07399	14	cytochrome c biogenesis protein		
K07400	2	Fe/S biogenesis protein NfuA		
K07401	1	selenoprotein W-related protein		
K07402	49	xanthine dehydrogenase accessory factor		
K07403	31	membrane-bound serine protease (ClpP class)		
K07404	25	6-phosphogluconolactonase [EC:3.1.1.31]		
K07405	7	alpha-amylase [EC:3.2.1.1]		
K07406	10	alpha-galactosidase [EC:3.2.1.22]		
K07407	12	alpha-galactosidase [EC:3.2.1.22]		
K07442	6	tRNA (adenine-N1-)-methyltransferase [EC:2.1.1.36]		
K07443	9	methylated-DNA-protein-cysteine methyltransferase related protein		
K07444	21	putative N6-adenine-specific DNA methylase		
K07445	12	putative DNA methylase		
K07447	18	putative holliday junction resolvase [EC:3.1.-.-]		
K07448	1	restriction system protein		
K07450	3	putative resolvase		
K07452	2	5-methylcytosine-specific restriction enzyme B [EC:3.1.21.-]		
K07454	6	putative restriction endonuclease		
K07455	9	recombination protein RecT		
K07456	34	DNA mismatch repair protein MutS2		
K07457	3	endonuclease III related protein		
K07458	8	DNA mismatch endonuclease, patch repair protein [EC:3.1.-.-]		
K07459	2	putative ATP-dependent endonuclease of the OLD family		
K07460	17	putative endonuclease		
K07461	8	putative endonuclease		
K07462	59	single-stranded-DNA-specific exonuclease [EC:3.1.-.-]		
K07464	3	putative RecB family exonuclease		
K07465	7	putative RecB family exonuclease		
K07467	1	phage replication initiation protein		
K07469	22	aldehyde dehydrogenase (FAD-independent) [EC:1.2.99.7]		
K07477	1	translin		
K07478	38	putative ATPase		
K07479	2	putative DNA topoisomerase		
K07480	1	insertion element IS1 protein InsB		
K07481	18	transposase, IS5 family		
K07482	19	transposase, IS30 family		
K07483	33	transposase		
K07484	48	transposase		
K07485	29	transposase		
K07486	162	transposase		
K07487	46	transposase		
K07488	4	transposase		
K07491	40	putative transposase		
K07492	38	putative transposase		
K07493	63	putative transposase		
K07494	80	putative transposase		
K07495	29	putative transposase		
K07496	10	putative transposase		
K07497	187	putative transposase		
K07498	4	putative transposase		

K07499	14	putative transposase		
K07501	8	hypothetical protein		
K07502	7	hypothetical protein		
K07503	8	hypothetical protein		
K07504	1	hypothetical protein		
K07505	1	hypothetical protein		
K07506	18	AraC family transcriptional regulator		
K07507	22	putative Mg2+ transporter-C (MgtC) family protein		
K07508	6	acetyl-CoA acyltransferase 2 [EC:2.3.1.16]		
K07516	43	3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]		
K07519	9	phthalate 4,5-dioxygenase [EC:1.14.12.7]		
K07533	21	foldase protein PrsA [EC:5.2.1.8]		
K07534	4	cyclohex-1-ene-1-carboxyl-CoA hydratase [EC:4.2.1.-]		
K07535	35	2-hydroxycyclohexanecarboxyl-CoA dehydrogenase [EC:1.1.1.-]		
K07537	4	cyclohexa-1,5-dienecarbonyl-CoA hydratase [EC:4.2.1.100]		
K07538	3	6-hydroxycyclohex-1-ene-1-carboxyl-CoA dehydrogenase [EC:1.1.1.-]		
K07543	23	benzylsuccinate CoA-transferase BbsE subunit [EC:2.8.3.15]		
K07544	22	benzylsuccinate CoA-transferase BbsF subunit [EC:2.8.3.15]		
K07545	1	(R)-benzylsuccinyl-CoA dehydro genase [EC:1.3.99.21]		
K07546	8	E-phenylitaconyl-CoA hydratase [EC:4.2.1.-]		
K07547	16	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsC subunit		
K07548	10	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsD subunit		
K07550	12	benzoylsuccinyl-CoA thiolase BbsB subunit [EC:2.3.1.-]		
K07552	14	MFS transporter, DHA1 family, bicyclomycin/chloramphenicol		
K07559	1	putative RNA 2'-phosphotransferase [EC:2.7.1.-]		
K07560	41	D-tyrosyl-tRNA(Tyr) deacylase [EC:3.1.-.-]		
K07566	44	putative translation factor		
K07567	68	TdcF protein		
K07568	35	S-adenosylmethionine:tRNA ribosyltransferase-isomerase [EC:5.-.-.-]		
K07570	6	general stress protein 13		
K07574	3	putative RNA-binding protein containing KH domain		
K07576	52	metallo-beta-lactamase family protein		
K07577	8	putative mRNA 3-end processing factor		
K07586	1	hypothetical protein		
K07588	27	LAO/AO transport system kinase [EC:2.7.-.-]		
K07592	4	LysR family transcriptional regulator, tdc operon transcriptional		
K07636	65	two-component system, OmpR family, phosphate regulon sensor		
K07637	1	two-component system, OmpR family, sensor histidine kinase PhoQ		
K07638	12	two-component system, OmpR family, osmolarity sensor histidine		
K07639	2	two-component system, OmpR family, sensor histidine kinase RstB		
K07640	6	two-component system, OmpR family, sensor histidine kinase CpxA		
K07641	4	two-component system, OmpR family, sensor histidine kinase CreC		
K07642	11	two-component system, OmpR family, sensor histidine kinase BaeS		
K07643	3	two-component system, OmpR family, sensor histidine kinase BasS		
K07644	26	two-component system, OmpR family, heavy metal sensor histidine		
K07645	33	two-component system, OmpR family, sensor histidine kinase QseC		
K07646	67	two-component system, OmpR family, sensor histidine kinase KdpD		
K07647	4	two-component system, OmpR family, sensor histidine kinase TorS		
K07648	1	two-component system, OmpR family, aerobic respiration control		
K07649	29	two-component system, OmpR family, sensor histidine kinase TctE		

K07651	11	two-component system, OmpR family, sensor histidine kinase ResE		
K07652	42	two-component system, OmpR family, sensor histidine kinase VicK		
K07653	6	two-component system, OmpR family, sensor histidine kinase MprB		
K07654	5	two-component system, OmpR family, sensor histidine kinase MtrB		
K07656	1	two-component system, OmpR family, sensor histidine kinase TrcS		
K07657	68	two-component system, OmpR family, phosphate regulon response		
K07658	67	two-component system, OmpR family, alkaline phosphatase synthesis		
K07659	12	two-component system, OmpR family, phosphate regulon response		
K07660	1	two-component system, OmpR family, response regulator PhoP		
K07661	1	two-component system, OmpR family, response regulator RstA		
K07662	5	two-component system, OmpR family, response regulator CpxR		
K07663	1	two-component system, OmpR family, catabolic regulation response		
K07664	5	two-component system, OmpR family, response regulator BaeR		
K07665	23	two-component system, OmpR family, copper resistance phosphate		
K07666	3	two-component system, OmpR family, response regulator QseB		
K07667	53	two-component system, OmpR family, KDP operon response regulator		
K07668	44	two-component system, OmpR family, response regulator VicR		
K07669	30	two-component system, OmpR family, response regulator MprA		
K07670	18	two-component system, OmpR family, response regulator MtrA		
K07671	1	two-component system, OmpR family, response regulator PrrA		
K07672	1	two-component system, OmpR family, response regulator TrcR		
K07673	10	two-component system, NarL family, nitrate/nitrite sensor histidine		
K07674	4	two-component system, NarL family, nitrate/nitrite sensor histidine		
K07675	49	two-component system, NarL family, sensor histidine kinase UhpB		
K07677	11	two-component system, NarL family, capsular synthesis sensor		
K07678	26	two-component system, NarL family, sensor histidine kinase BarA		
K07679	4	two-component system, NarL family, sensor histidine kinase EvgS		
K07680	15	two-component system, NarL family, sensor histidine kinase ComP		
K07681	1	two-component system, NarL family, vancomycin resistance sensor		
K07682	15	two-component system, NarL family, sensor histidine kinase DevS		
K07683	4	two-component system, NarL family, sensor histidine kinase NreB		
K07684	73	two-component system, NarL family, nitrate/nitrite response		
K07685	6	two-component system, NarL family, nitrate/nitrite response		
K07686	7	two-component system, NarL family, uhpT operon response regulator		
K07687	9	two-component system, NarL family, captular synthesis response		
K07689	20	two-component system, NarL family, invasion response regulator UvrY		
K07690	5	two-component system, NarL family, response regulator EvgA		
K07691	24	two-component system, NarL family, competent response regulator ComA		
K07692	37	two-component system, NarL family, response regulator DegU		
K07693	3	two-component system, NarL family, response regulator DesR		
K07694	4	two-component system, NarL family, vancomycin resistance associated		
K07695	13	two-component system, NarL family, response regulator DevR		
K07696	4	two-component system, NarL family, response regulator NreC		
K07697	11	two-component system, sporulation sensor kinase B [EC:2.7.13.3]		
K07699	1	two-component system, response regulator, stage 0 sporulation		
K07700	2	two-component system, CitB family, cit operon sensor histidine		
K07703	1	two-component system, CitB family, response regulator DcuR		
K07704	7	two-component system, LytT family, sensor histidine kinase LytS		
K07705	5	two-component system, LytT family, response regulator LytT		
K07707	4	two-component system, AgrA family, response regulator AgrA		

K07708	54	two-component system, NtrC family, nitrogen regulation sensor		
K07709	54	two-component system, NtrC family, sensor histidine kinase HydH		
K07710	39	two-component system, NtrC family, sensor histidine kinase AtoS		
K07711	10	two-component system, NtrC family, sensor histidine kinase YfhK		
K07712	112	two-component system, NtrC family, nitrogen regulation response		
K07713	64	two-component system, NtrC family, response regulator HydG		
K07714	48	two-component system, NtrC family, response regulator AtoC		
K07715	78	two-component system, NtrC family, response regulator YfhA		
K07716	16	two-component system, cell cycle sensor histidine kinase PleC		
K07718	1	two-component system, sensor histidine kinase YesM [EC:2.7.13.3]		
K07720	7	two-component system, response regulator YesN		
K07726	5	putative transcriptional regulator		
K07727	1	putative transcriptional regulator		
K07729	7	putative transcriptional regulator		
K07734	8	transcriptional regulator		
K07735	24	putative transcriptional regulator		
K07736	12	CarD family transcriptional regulator		
K07737	5	putative transcriptional regulator		
K07738	6	transcriptional repressor NrdR		
K07739	4	elongator complex protein 3 [EC:2.3.1.48]		
K07740	1	regulator of sigma D		
K07741	1	anti-repressor protein		
K07742	7	hypothetical protein		
K07743	2	hypothetical protein		
K07745	1	hypothetical protein		
K07746	2	hypothetical protein		
K07748	2	sterol-4alpha-carboxylate 3-dehydrogenase (decarboxylating)		
K07749	163	formyl-CoA transferase [EC:2.8.3.16]		
K07758	5	pyridoxal phosphatase [EC:3.1.3.74]		
K07768	3	two-component system, OmpR family, sensor histidine kinase SenX3		
K07769	5	two-component system, OmpR family, sensor histidine kinase NblS		
K07771	1	two-component system, OmpR family, response regulator BasR		
K07773	1	two-component system, OmpR family, aerobic respiration control		
K07774	14	two-component system, OmpR family, response regulator TctD		
K07775	5	two-component system, OmpR family, response regulator ResD		
K07776	43	two-component system, OmpR family, response regulator RegX3		
K07777	14	two-component system, NarL family, sensor histidine kinase DegS		
K07778	10	two-component system, NarL family, sensor histidine kinase DesK		
K07782	1	LuxR family transcriptional regulator		
K07783	2	MFS transporter, OPA family, sugar phosphate sensor protein UhpC		
K07785	1	MFS transporter, NRE family, putaive nickel resistance protein		
K07787	112	Cu(I)/Ag(I) efflux system membrane protein CusA		
K07788	66	RND superfamily, multidrug transport protein MdtB		
K07789	37	RND superfamily, multidrug transport protein MdtC		
K07790	1	putative membrane protein PagO		
K07791	3	anaerobic C4-dicarboxylate transporter DcuA		
K07792	4	anaerobic C4-dicarboxylate transporter DcuB		
K07793	90	putative tricarboxylic transport membrane protein		
K07795	87	putative tricarboxylic transport membrane protein		
K07796	16	Cu(I)/Ag(I) efflux system outer membrane protein CusC		

K07798	51	Cu(I)/Ag(I) efflux system membrane protein CusB		
K07799	33	putative multidrug efflux transporter MdtA		
K07805	1	putative membrane protein PagD		
K07806	20	UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase		
K07811	3	trimethylamine-N-oxide reductase (cytochrome c) 1 [EC:1.7.2.3]		
K07812	12	trimethylamine-N-oxide reductase (cytochrome c) 2 [EC:1.7.2.3]		
K07814	158	putative two-component system response regulator		
K07821	1	trimethylamine-N-oxide reductase (cytochrome c) 2, cytochrome c-type		
K07823	4	3-oxoadipyl-CoA thiolase [EC:2.3.1.174]		
K07824	6	benzoate 4-monooxygenase [EC:1.14.13.12]		
K07978	4	GntR family transcriptional regulator		
K07979	9	GntR family transcriptional regulator		
K08068	1	N-acetylglucosamine-6-phosphate 2-epimerase and phosphatase		
K08070	95	2-alkenal reductase [EC:1.3.1.74]		
K08078	2	3a,7a,12a-trihydroxy-5b-cholest-24-enoyl-CoA hydratase		
K08082	4	two-component system, LytT family, sensor histidine kinase AlgZ		
K08083	11	two-component system, LytT family, response regulator AlgR		
K08084	6	type IV fimbrial biogenesis protein FimT		
K08085	2	type IV fimbrial biogenesis protein FimU		
K08093	1	3-hexulose-6-phosphate synthase [EC:4.1.2.43]		
K08097	6	phosphosulfolactate synthase [EC:4.4.1.19]		
K08100	49	bilirubin oxidase [EC:1.3.3.5]		
K08137	1	MFS transporter, SP family, galactose:H+ symporter		
K08138	2	MFS transporter, SP family, xylose:H+ symportor		
K08139	13	MFS transporter, SP family, sugar:H+ symporter		
K08151	22	MFS transporter, DHA1 family, tetracycline resistance protein		
K08152	3	MFS transporter, DHA1 family, multidrug resistance protein B		
K08153	11	MFS transporter, DHA1 family, multidrug resistance protein		
K08154	1	MFS transporter, DHA1 family, 2-module integral membrane pump EmrD		
K08156	5	MFS transporter, DHA1 family, arabinose polymer transporter		
K08159	2	MFS transporter, DHA1 family,		
K08161	7	MFS transporter, DHA1 family, multidrug resistance protein		
K08162	18	MFS transporter, DHA1 family, multidrug resistance protein		
K08166	40	MFS transporter, DHA2 family, methylenomycin A resistance protein		
K08167	18	MFS transporter, DHA2 family, methyl viologen resistance protein		
K08169	16	MFS transporter, DHA2 family, multidrug resistance protein		
K08172	10	MFS transporter, MHS family, shikimate and dehydroshikimate		
K08173	7	MFS transporter, MHS family, metabolite:H+ symporter		
K08177	46	MFS transporter, OFA family, oxalate/formate antiporter		
K08178	5	MFS transporter, SHS family, lactate transporter		
K08191	15	MFS transporter, ACS family, hexuronate transporter		
K08194	23	MFS transporter, ACS family, D-galactonate transporter		
K08195	3	MFS transporter, AAHS family, 4-hydroxybenzoate transporter		
K08196	5	MFS transporter, AAHS family, cis,cis-muconate transporter		
K08217	15	MFS transporter, DHA3 family, macrolide efflux protein		
K08218	18	MFS transporter, PAT family, beta-lactamase induction signal		
K08221	3	MFS transporter, ACDE family, multidrug resistance protein		
K08223	20	MFS transporter, FSR family, fosmidomycin resistance protein		
K08224	9	MFS transporter, YNFM family, putative membrane transport protein		
K08225	95	MFS transporter, ENTS family, enterobactin (siderophore) exporter		

K08226	1	MFS transporter, BCD family, chlorophyll transporter		
K08227	12	MFS transporter, LPLT family, lysophospholipid transporter		
K08234	21	glyoxylase I family protein		
K08252	50	receptor protein-tyrosine kinase [EC:2.7.10.1]		
K08253	118	non-specific protein-tyrosine kinase [EC:2.7.10.2]		
K08256	27	phosphatidylinositol alpha-mannosyltransferase [EC:2.4.1.57]		
K08259	50	lysostaphin [EC:3.4.24.75]		
K08261	13	D-sorbitol dehydrogenase (acceptor) [EC:1.1.99.21]		
K08278	4	thr operon leader peptide		
K08279	14	carnitine operon protein CaiE		
K08281	14	nicotinamidase/pyrazinamidase [EC:3.5.1.19 3.5.1.-]		
K08282	355	non-specific serine/threonine protein kinase [EC:2.7.11.1]		
K08289	4	phosphoribosylglycinamide formyltransferase 2 [EC:2.1.2.2]		
K08295	5	2-aminobenzoate-CoA ligase [EC:6.2.1.32]		
K08296	12	phosphohistidine phosphatase [EC:3.1.3.-]		
K08297	2	crotonobetainyl-CoA dehydrogenase [EC:1.3.99.-]		
K08299	6	carnitinyl-CoA dehydratase [EC:4.2.1.-]		
K08300	19	ribonuclease E [EC:3.1.26.12]		
K08301	25	ribonuclease G [EC:3.1.26.-]		
K08302	1	tagatose 1,6-diphosphate aldolase [EC:4.1.2.40]		
K08303	23	putative protease [EC:3.4.-.-]		
K08304	13	membrane-bound lytic murein transglycosylase A [EC:3.2.1.-]		
K08305	5	membrane-bound lytic murein transglycosylase B [EC:3.2.1.-]		
K08307	30	membrane-bound lytic murein transglycosylase D [EC:3.2.1.-]		
K08309	44	soluble lytic murein transglycosylase [EC:3.2.1.-]		
K08310	5	dATP pyrophosphohydrolase [EC:3.6.1.-]		
K08311	4	putative (di)nucleoside polyphosphate hydrolase [EC:3.6.1.-]		
K08316	6	ribosomal RNA small subunit methyltransferase D [EC:2.1.1.52]		
K08318	2	putative dehydrogenase [EC:1.1.-.-]		
K08319	2	putative dehydrogenase [EC:1.1.-.-]		
K08320	3	CTP pyrophosphohydrolase [EC:3.6.1.-]		
K08321	3	putative autoinducer-2 (AI-2) aldolase [EC:4.1.2.-]		
K08322	8	starvation sensing protein RspB [EC:1.1.1.-]		
K08323	9	starvation sensing protein RspA		
K08324	3	aldehyde dehydrogenase family protein [EC:1.2.1.-]		
K08326	1	aminopeptidase [EC:3.4.11.-]		
K08344	1	suppressor for copper-sensitivity B		
K08345	2	nitrate reductase 2, alpha subunit [EC:1.7.99.4]		
K08346	6	nitrate reductase 2, beta subunit [EC:1.7.99.4]		
K08348	39	formate dehydrogenase-N, alpha subunit [EC:1.2.1.2]		
K08351	5	biotin sulfoxide reductase [EC:1.-.-.-]		
K08352	38	thiosulfate reductase [EC:1.-.-.-]		
K08353	5	thiosulfate reductase electron transport protein		
K08354	3	thiosulfate reductase cytochrome b subunit		
K08356	11	arsenite oxidase large subunit [EC:1.20.98.1]		
K08357	9	tetrathionate reductase subunit A		
K08358	27	tetrathionate reductase subunit B		
K08359	4	tetrathionate reductase subunit C		
K08364	10	periplasmic mercuric ion binding protein		
K08365	3	MerR family transcriptional regulator, mercuric resistance operon		

K08368	1	MFS transporter, putative metabolite transport protein		
K08369	27	MFS transporter, putative metabolite:H+ symporter		
K08372	45	putative serine protease PepD [EC:3.4.21.-]		
K08384	8	stage V sporulation protein D (sporulation-specific		
K08477	2	outer membrane protease E [EC:3.4.21.-]		
K08478	1	phosphoglycerate transport regulatory protein PgtC		
K08479	3	two-component system, OmpR family, clock-associated histidine kinase		
K08481	4	circadian clock protein KaiB		
K08482	37	circadian clock protein KaiC		
K08483	32	phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]		
K08484	7	phosphotransferase system, enzyme I, PtsP [EC:2.7.3.9]		
K08485	1	phosphocarrier protein NPr		
K08567	9	hydrogenase 2 maturation protease [EC:3.4.24.-]		
K08590	4	carbon-nitrogen hydrolase family protein		
K08591	25	glycerol-3-phosphate acyltransferase PlsY [EC:2.3.1.15]		
K08600	2	sortase B		
K08602	47	oligoendopeptidase F [EC:3.4.24.-]		
K08603	6	thermolysin [EC:3.4.24.27]		
K08605	1	coccolysin [EC:3.4.24.30]		
K08641	17	D-alanyl-D-alanine dipeptidase [EC:3.4.13.-]		
K08651	23	thermitase [EC:3.4.21.66]		
K08676	43	tricorn protease [EC:3.4.21.-]		
K08677	19	kumamolisin		
K08678	5	UDP-glucuronate decarboxylase [EC:4.1.1.35]		
K08679	5	UDP-glucuronate 4-epimerase [EC:5.1.3.6]		
K08680	8	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase		
K08681	4	glutamine amidotransferase [EC:2.6.-.-]		
K08682	2	acyl carrier protein phosphodiesterase [EC:3.1.4.14]		
K08684	2	methane monooxygenase [EC:1.14.13.25]		
K08686	15	2-chlorobenzoate 1,2-dioxygenase [EC:1.14.12.13]		
K08687	4	N-carbamoylsarcosine amidase [EC:3.5.1.59]		
K08688	9	creatinase [EC:3.5.3.3]		
K08693	4	3'-nucleotidase [EC:3.1.3.6]		
K08697	2	carbon dioxide concentrating mechanism protein CcmL		
K08698	1	carbon dioxide concentrating mechanism protein CcmM		
K08710	5	N-isopropylammelide isopropylaminohydrolase [EC:3.5.99.4]		
K08714	2	voltage-gated sodium channel		
K08720	3	outer membrane protein OmpU		
K08721	3	multidrug resistance outer membrane protein OprJ		
K08723	4	5'-nucleotidase [EC:3.1.3.5]		
K08724	5	penicillin-binding protein 2B		
K08738	12	cytochrome c		
K08777	1	neutral peptidase B [EC:3.4.24.-]		
K08884	560	serine/threonine protein kinase, bacterial [EC:2.7.11.1]		
K08900	1	mitochondrial chaperone BCS1		
K08942	8	photosystem P840 reaction center cytochrome c551		
K08963	23	methylthioribose-1-phosphate isomerase [EC:5.3.1.23]		
K08964	2	methylthioribulose-1-phosphate dehydratase [EC:4.2.1.109]		
K08965	1	2,3-diketo-5-methylthiopentyl-1-phosphate enolase [EC:3.1.3.77]		
K08966	3	2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase		

K08967	4	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase [EC:1.13.11.53		
K08969	1	aminotransferase [EC:2.6.1.-]		
K08970	5	nickel/cobalt exporter		
K08972	5	putative membrane protein		
K08973	5	putative membrane protein		
K08974	3	putative membrane protein		
K08977	3	putative membrane protein		
K08978	11	putative membrane protein		
K08981	2	putative membrane protein		
K08983	1	putative membrane protein		
K08984	7	putative membrane protein		
K08986	2	putative membrane protein		
K08987	2	putative membrane protein		
K08988	7	putative membrane protein		
K08989	3	putative membrane protein		
K08990	1	putative membrane protein		
K08992	1	putative membrane protein		
K08995	6	putative membrane protein		
K08997	11	hypothetical protein		
K08998	13	hypothetical protein		
K08999	19	hypothetical protein		
K09001	23	anhydro-N-acetylmuramic acid kinase [EC:2.7.1.-]		
K09003	8	hypothetical protein		
K09004	3	hypothetical protein		
K09005	16	hypothetical protein		
K09007	8	hypothetical protein		
K09008	4	hypothetical protein		
K09009	2	hypothetical protein		
K09011	7	D-citramalate synthase [EC:2.3.1.182]		
K09012	6	DeoR family transcriptional regulator, suf operon transcriptional		
K09013	19	Fe-S cluster assembly ATP-binding protein		
K09014	39	Fe-S cluster assembly protein SufB		
K09015	22	Fe-S cluster assembly protein SufD		
K09016	3	putative pyrimidine permease RutG		
K09017	38	TetR/AcrR family transcriptional regulator		
K09018	1	putative monooxygenase RutA [EC:1.14.-.-]		
K09019	4	putative NADH dehydrogenase/NAD(P)H nitroreductase RutE [EC:1.-.-.-]		
K09020	6	putative isochorismatase family protein RutB [EC:3.-.-.-]		
K09022	1	UPF0076 protein YjgF		
K09023	5	protein RutD		
K09024	2	putative flavin reductase RutF [EC:1.5.1.-]		
K09065	3	N-acetylornithine carbamoyltransferase [EC:2.1.3.9]		
K09116	3	hypothetical protein		
K09117	10	hypothetical protein		
K09118	29	hypothetical protein		
K09120	2	hypothetical protein		
K09121	25	hypothetical protein		
K09122	9	hypothetical protein		
K09123	12	hypothetical protein		
K09125	6	hypothetical protein		

K09128	3	hypothetical protein		
K09129	5	hypothetical protein		
K09131	12	hypothetical protein		
K09132	1	hypothetical protein		
K09134	98	hypothetical protein		
K09136	1	hypothetical protein		
K09137	13	hypothetical protein		
K09141	10	hypothetical protein		
K09143	3	hypothetical protein		
K09144	1	hypothetical protein		
K09146	2	hypothetical protein		
K09151	9	hypothetical protein		
K09153	4	hypothetical protein		
K09155	3	hypothetical protein		
K09157	3	hypothetical protein		
K09158	2	hypothetical protein		
K09159	2	hypothetical protein		
K09160	3	hypothetical protein		
K09162	15	hypothetical protein		
K09163	2	hypothetical protein		
K09164	7	hypothetical protein		
K09165	6	hypothetical protein		
K09166	8	hypothetical protein		
K09167	1	hypothetical protein		
K09181	129	hypothetical protein		
K09190	1	hypothetical protein		
K09251	10	putrescine aminotransferase [EC:2.6.1.82]		
K09252	3	feruloyl esterase [EC:3.1.1.73]		
K09384	1	hypothetical protein		
K09386	19	hypothetical protein		
K09456	23	putative acyl-CoA dehydrogenase		
K09457	12	7-cyano-7-deazaguanine reductase [EC:1.7.1.13]		
K09458	82	3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]		
K09459	5	phosphonopyruvate decarboxylase [EC:4.1.1.82]		
K09461	29	anthraniloyl-CoA monooxygenase [EC:1.14.13.40]		
K09471	25	gamma-glutamylputrescine oxidase [EC:1.4.3.-]		
K09472	7	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase [EC:1.2.1.-]		
K09474	2	acid phosphatase (class A) [EC:3.1.3.2]		
K09477	5	citrate:succinate antiporter		
K09516	1	all-trans-retinol 13,14-reductase [EC:1.3.99.23]		
K09607	31	immune inhibitor A [EC:3.4.24.-]		
K09680	3	type II pantothenate kinase [EC:2.7.1.33]		
K09681	11	LysR family transcriptional regulator, transcription activator of		
K09684	10	purine catabolism regulatory protein		
K09686	142	antibiotic transport system permease protein		
K09687	115	antibiotic transport system ATP-binding protein		
K09688	3	capsular polysaccharide transport system permease protein		
K09689	1	capsular polysaccharide transport system ATP-binding protein		
K09690	46	lipopolysaccharide transport system permease protein		
K09691	27	lipopolysaccharide transport system ATP-binding protein		

K09693	8	teichoic acid transport system ATP-binding protein [EC:3.6.3.40]		
K09694	20	lipooligosaccharide transport system permease protein		
K09695	6	lipooligosaccharide transport system ATP-binding protein		
K09697	5	sodium transport system ATP-binding protein		
K09698	20	nondiscriminating glutamyl-tRNA synthetase [EC:6.1.1.24]		
K09699	12	2-oxoisovalerate dehydrogenase E2 component (dihydrolipoyl		
K09700	2	hypothetical protein		
K09701	10	hypothetical protein		
K09702	2	hypothetical protein		
K09703	2	hypothetical protein		
K09704	1	hypothetical protein		
K09707	3	hypothetical protein		
K09709	9	hypothetical protein		
K09710	20	hypothetical protein		
K09711	3	hypothetical protein		
K09726	3	hypothetical protein		
K09729	2	hypothetical protein		
K09740	1	hypothetical protein		
K09747	16	hypothetical protein		
K09748	32	hypothetical protein		
K09749	6	hypothetical protein		
K09758	10	aspartate 4-decarboxylase [EC:4.1.1.12]		
K09759	2	nondiscriminating aspartyl-tRNA synthetase [EC:6.1.1.23]		
K09760	28	DNA recombination protein RmuC		
K09761	46	ribosomal RNA small subunit methyltransferase E [EC:2.1.1.-]		
K09762	5	hypothetical protein		
K09763	4	hypothetical protein		
K09764	6	hypothetical protein		
K09765	1	hypothetical protein		
K09766	3	hypothetical protein		
K09767	15	hypothetical protein		
K09768	8	hypothetical protein		
K09769	27	hypothetical protein		
K09770	9	hypothetical protein		
K09772	3	cell division inhibitor SepF		
K09773	10	hypothetical protein		
K09774	441	lipopolysaccharide export system protein LptA		
K09775	19	hypothetical protein		
K09776	1	hypothetical protein		
K09777	2	hypothetical protein		
K09778	5	hypothetical protein		
K09779	5	hypothetical protein		
K09780	2	hypothetical protein		
K09781	3	hypothetical protein		
K09786	18	hypothetical protein		
K09787	1	hypothetical protein		
K09788	41	hypothetical protein		
K09790	2	hypothetical protein		
K09791	3	hypothetical protein		
K09792	7	hypothetical protein		

K09793	1	hypothetical protein		
K09795	3	hypothetical protein		
K09796	6	hypothetical protein		
K09798	3	hypothetical protein		
K09799	2	hypothetical protein		
K09800	10	hypothetical protein		
K09801	2	hypothetical protein		
K09802	1	hypothetical protein		
K09803	7	hypothetical protein		
K09806	1	hypothetical protein		
K09807	9	hypothetical protein		
K09808	44	lipoprotein-releasing system permease protein		
K09809	13	CDP-glycerol glycerophosphotransferase [EC:2.7.8.12]		
K09810	59	lipoprotein-releasing system ATP-binding protein [EC:3.6.3.-]		
K09811	32	cell division transport system permease protein		
K09812	13	cell division transport system ATP-binding protein		
K09815	10	zinc transport system substrate-binding protein		
K09816	9	zinc transport system permease protein		
K09817	8	zinc transport system ATP-binding protein [EC:3.6.3.-]		
K09818	5	manganese/iron transport system substrate-binding protein		
K09819	8	manganese/iron transport system permease protein		
K09820	12	manganese/iron transport system ATP-binding protein		
K09822	6	hypothetical protein		
K09825	6	Fur family transcriptional regulator, peroxide stress response		
K09826	4	Fur family transcriptional regulator, iron response regulator		
K09833	1	homogenitisate phytyltransferase		
K09835	2	carotenoid isomerase [EC:5.-.-.-]		
K09845	3	methoxyneurosporene dehydrogenase [EC:1.14.99.-]		
K09846	18	hydroxyneurosporene methyltransferase [EC:2.1.1.-]		
K09858	1	SEC-C motif domain protein		
K09859	1	hypothetical protein		
K09862	6	hypothetical protein		
K09879	1	isorenieratene synthase		
K09882	3	cobaltochelatase CobS [EC:6.6.1.2]		
K09883	6	cobaltochelatase CobT [EC:6.6.1.2]		
K09888	10	cell division protein ZapA		
K09889	3	hypothetical protein		
K09891	1	hypothetical protein		
K09895	4	hypothetical protein		
K09903	23	uridylate kinase [EC:2.7.4.22]		
K09906	1	hypothetical protein		
K09909	2	hypothetical protein		
K09913	1	hypothetical protein		
K09914	4	putative lipoprotein		
K09915	12	hypothetical protein		
K09916	5	hypothetical protein		
K09917	1	hypothetical protein		
K09918	2	hypothetical protein		
K09919	9	hypothetical protein		
K09921	6	hypothetical protein		

K09922	3	hypothetical protein		
K09923	1	hypothetical protein		
K09924	5	hypothetical protein		
K09926	2	hypothetical protein		
K09927	30	hypothetical protein		
K09928	3	hypothetical protein		
K09930	9	hypothetical protein		
K09931	19	hypothetical protein		
K09933	8	hypothetical protein		
K09934	3	hypothetical protein		
K09935	1	hypothetical protein		
K09936	3	hypothetical protein		
K09937	2	hypothetical protein		
K09939	1	hypothetical protein		
K09941	1	hypothetical protein		
K09942	1	hypothetical protein		
K09949	15	hypothetical protein		
K09950	1	hypothetical protein		
K09951	1	CRISPR-associated protein Cas2		
K09952	6	hypothetical protein		
K09953	2	lipid A 3-O-deacylase		
K09955	22	hypothetical protein		
K09958	8	hypothetical protein		
K09959	1	hypothetical protein		
K09962	1	hypothetical protein		
K09966	6	hypothetical protein		
K09967	7	hypothetical protein		
K09969	7	general L-amino acid transport system substrate-binding protein		
K09970	2	general L-amino acid transport system permease protein		
K09971	7	general L-amino acid transport system permease protein		
K09972	2	general L-amino acid transport system ATP-binding protein		
K09973	11	hypothetical protein		
K09974	1	hypothetical protein		
K09978	1	hypothetical protein		
K09979	1	hypothetical protein		
K09981	4	hypothetical protein		
K09983	6	hypothetical protein		
K09984	4	hypothetical protein		
K09986	2	hypothetical protein		
K09988	2	hypothetical protein		
K09989	5	hypothetical protein		
K09990	7	hypothetical protein		
K09992	5	hypothetical protein		
K09994	1	PhnO protein [EC:2.3.1.-]		
K09996	9	arginine transport system substrate-binding protein		
K09999	2	arginine transport system permease protein		
K10001	14	glutamate/aspartate transport system substrate-binding protein		
K10002	5	glutamate/aspartate transport system permease protein		
K10003	8	glutamate/aspartate transport system permease protein		
K10004	3	glutamate/aspartate transport system ATP-binding protein		

K10005	1	glutamate transport system substrate-binding protein		
K10006	2	glutamate transport system permease protein		
K10007	2	glutamate transport system permease protein		
K10009	4	cystine transport system permease protein		
K10010	1	cystine transport system ATP-binding protein [EC:3.6.3.-]		
K10011	7	UDP-GlcUA decarboxylase/UDP-L-Ara4N formyltransferase		
K10012	8	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase		
K10014	1	histidine transport system substrate-binding protein		
K10017	1	histidine transport system ATP-binding protein [EC:3.6.3.21]		
K10026	15	queuosine biosynthesis protein QueE		
K10027	11	phytoene dehydrogenase [EC:1.14.99.-]		
K10036	2	glutamine transport system substrate-binding protein		
K10037	3	glutamine transport system permease protein		
K10039	6	putative glutamine transport system substrate-binding protein		
K10040	3	putative glutamine transport system permease protein		
K10041	2	putative glutamine transport system ATP-binding protein [EC:3.6.3.-]		
K10108	11	maltose/maltodextrin transport system substrate-binding protein		
K10109	5	maltose/maltodextrin transport system permease protein		
K10110	13	maltose/maltodextrin transport system permease protein		
K10111	2	maltose/maltodextrin transport system ATP-binding protein		
K10112	10	maltose/maltodextrin transport system ATP-binding protein		
K10117	1	multiple sugar transport system substrate-binding protein		
K10118	3	multiple sugar transport system permease protein		
K10119	3	multiple sugar transport system permease protein		
K10120	2	putative sugar transport system substrate-binding protein		
K10121	12	putative sugar transport system permease protein		
K10122	6	putative sugar transport system permease protein		
K10125	16	two-component system, NtrC family, C4-dicarboxylate transport sensor		
K10126	65	two-component system, NtrC family, C4-dicarboxylate transport		
K10188	9	lactose/L-arabinose transport system substrate-binding protein		
K10189	8	lactose/L-arabinose transport system permease protein		
K10190	19	lactose/L-arabinose transport system permease protein		
K10191	1	lactose/L-arabinose transport system ATP-binding protein		
K10193	2	oligogalacturonide transport system permease protein		
K10200	3	N-acetylglucosamine transport system substrate-binding protein		
K10201	3	N-acetylglucosamine transport system permease protein		
K10206	25	LL-diaminopimelate aminotransferase [EC:2.6.1.83]		
K10209	1	dehydrosqualene desaturase [EC:1.14.99.-]		
K10210	3	4,4'-diaponeurosporene oxidase [EC:1.-.-.-]		
K10215	11	monooxygenase [EC:1.14.13.-]		
K10217	4	aminomuconate-semialdehyde dehydrogenase [EC:1.2.1.32]		
K10218	5	4-hydroxy-4-methyl-2-oxoglutarate aldolase [EC:4.1.3.17]		
K10219	34	4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase		
K10220	52	4-oxalmesaconate hydratase [EC:4.2.1.83]		
K10221	17	2-pyrone-4,6-dicarboxylate lactonase [EC:3.1.1.57]		
K10227	10	sorbitol/mannitol transport system substrate-binding protein		
K10228	1	sorbitol/mannitol transport system permease protein		
K10229	2	sorbitol/mannitol transport system permease protein		
K10230	1	sorbitol/mannitol transport system ATP-binding protein		
K10231	10	kojibiose phosphorylase [EC:2.4.1.230]		

K10232	15	alpha-glucoside transport system substrate-binding protein		
K10233	5	alpha-glucoside transport system permease protein		
K10234	8	alpha-glucoside transport system permease protein		
K10236	6	trehalose/maltose transport system substrate-binding protein		
K10237	4	trehalose/maltose transport system permease protein		
K10238	3	trehalose/maltose transport system permease protein		
K10239	1	trehalose/maltose transport system ATP-binding protein		
K10240	2	cellobiose transport system substrate-binding protein		
K10241	1	cellobiose transport system permease protein		
K10242	1	cellobiose transport system permease protein		
K10243	2	cellobiose transport system ATP-binding protein		
K10253	2	DOPA 4,5-dioxygenase [EC:1.14.99.-]		
K10254	1	myosin-crossreactive antigen		
K10255	15	omega-6 fatty acid desaturase (delta-12 desaturase) [EC:1.14.19.-]		
K10353	5	deoxyadenosine kinase [EC:2.7.1.76]		
K10439	21	ribose transport system substrate-binding protein		
K10440	29	ribose transport system permease protein		
K10441	27	ribose transport system ATP-binding protein [EC:3.6.3.17]		
K10533	3	limonene-1,2-epoxide hydrolase [EC:3.3.2.8]		
K10536	12	agmatine deiminase [EC:3.5.3.12]		
K10538	1	L-arabinose transport system permease protein		
K10541	3	methyl-galactoside transport system permease protein		
K10542	1	methyl-galactoside transport system ATP-binding protein		
K10543	5	D-xylose transport system substrate-binding protein		
K10544	14	D-xylose transport system permease protein		
K10545	1	D-xylose transport system ATP-binding protein [EC:3.6.3.17]		
K10547	1	putative multiple sugar transport system permease protein		
K10549	2	D-allose transport system substrate-binding protein		
K10552	6	fructose transport system substrate-binding protein		
K10553	2	fructose transport system permease protein		
K10554	2	fructose transport system ATP-binding protein		
K10555	9	AI-2 transport system substrate-binding protein		
K10556	4	AI-2 transport system permease protein		
K10557	2	AI-2 transport system permease protein		
K10559	7	rhamnose transport system substrate-binding protein		
K10560	3	rhamnose transport system permease protein		
K10561	1	rhamnose transport system permease protein		
K10563	62	formamidopyrimidine-DNA glycosylase [EC:3.2.2.23 4.2.99.18]		
K10616	19	p-cymene monooxygenase [EC:1.14.13.-]		
K10617	7	p-cumic alcohol dehydrogenase		
K10618	7	p-cumic aldehyde dehydrogenase		
K10619	17	p-cumate dioxygenase [EC:1.14.12.-]		
K10620	1	2,3-dihydroxy-2,3-dihydro-p-cumate dehydrogenase [EC:1.3.1.58]		
K10621	5	2,3-dihydroxy-p-cumate-3,4-dioxygenase [EC:1.13.11.-]		
K10622	2	HCOMODA decarboxylase [EC:4.1.1.-]		
K10674	2	ectoine hydroxylase [EC:1.14.11.-]		
K10676	13	2,4-dichlorophenol 6-monooxygenase [EC:1.14.13.20]		
K10678	1	nitroreductase [EC:1.-.-.-]		
K10679	1	nitroreductase / dihydropteridine reductase [EC:1.-.-.- 1.5.1.34]		
K10680	11	N-ethylmaleimide reductase [EC:1.-.-.-]		

K10697	6	two-component system, OmpR family, response regulator RpaA		
K10700	13	ethylbenzene hydroxylase [EC:1.17.99.2]		
K10701	20	acetophenone carboxylase [EC:6.4.1.-]		
K10708	1	fructoselysine 6-phosphate deglycase [EC:3.5.-.-]		
K10711	1	GntR family transcriptional regulator, frlABCD operon		
K10713	1	formaldehyde-activating enzyme [EC:4.3.-.-]		
K10715	7	two-component system, sensor histidine kinase RpfC [EC:2.7.13.3]		
K10716	1	voltage-gated potassium channel		
K10747	4	DNA ligase 1 [EC:6.5.1.1]		
K10754	4	replication factor C subunit 1		
K10763	2	DnaA-homolog protein		
K10764	12	O-succinylhomoserine sulfhydrylase [EC:2.5.1.-]		
K10773	24	endonuclease III [EC:4.2.99.18]		
K10774	6	tyrosine ammonia-lyase [EC:4.3.1.23]		
K10775	1	phenylalanine ammonia-lyase [EC:4.3.1.24]		
K10778	19	AraC family transcriptional regulator, regulatory protein of		
K10780	3	enoyl-[acyl carrier protein] reductase III [EC:1.3.1.-]		
K10799	18	tankyrase [EC:2.4.2.30]		
K10804	10	acyl-CoA thioesterase I [EC:3.1.2.- 3.1.1.5]		
K10805	10	acyl-CoA thioesterase II [EC:3.1.2.-]		
K10806	4	acyl-CoA thioesterase YciA [EC:3.1.2.-]		
K10807	1	ribonucleoside-diphosphate reductase subunit M1 [EC:1.17.4.1]		
K10810	1	transcriptional regulator TenI		
K10815	1	hydrogen cyanide synthase HcnB [EC:1.4.99.5]		
K10816	2	hydrogen cyanide synthase HcnC [EC:1.4.99.5]		
K10817	32	erythronolide synthase [EC:2.3.1.94]		
K10819	143	histidine kinase		
K10820	13	monosaccharide-transporting ATPase [EC:3.6.3.17]		
K10822	21	nonpolar-amino-acid-transporting ATPase [EC:3.6.3.22]		
K10826	34	Fe3+-transporting ATPase [EC:3.6.3.30]		
K10828	1	quaternary-amine-transporting ATPase [EC:3.6.3.32]		
K10829	1	iron-chelate-transporting ATPase [EC:3.6.3.34]		
K10834	7	heme-transporting ATPase [EC:3.6.3.41]		
K10843	12	DNA excision repair protein ERCC-3 [EC:3.6.1.-]		
K10844	3	DNA excision repair protein ERCC-2 [EC:3.6.1.-]		
K10855	1	acetone carboxylase, beta subunit [EC:6.4.1.6]		
K10857	1	exodeoxyribonuclease X [EC:3.1.11.-]		
K10907	72	aminotransferase [EC:2.6.1.-]		
K10908	1	DNA-directed RNA polymerase, mitochondrial [EC:2.7.7.6]		
K10912	2	two-component system, repressor protein LuxO		
K10914	3	CRP/FNR family transcriptional regulator, cyclic AMP receptor		
K10915	1	CAI-1 autoinducer synthase [EC:2.3.-.-]		
K10917	8	PadR family transcriptional regulator, regulatory protein AphA		
K10918	14	LysR family transcriptional regulator, transcriptional activator		
K10941	18	sigma-54 specific transcriptional regulator, flagellar regulatory		
K10942	29	two-component system, sensor histidine kinase FlrB [EC:2.7.13.3]		
K10943	57	two component system, response regulator FlrC		
K10947	19	PadR family transcriptional regulator, regulatory protein PadR		
K10972	1	LysR family transcriptional regulator, transcriptional activator of		
K10979	36	DNA end-binding protein Ku		

K11003	4	hemolysin D		
K11004	5	ATP-binding cassette, subfamily B, bacterial HlyB/CyaB		
K11005	15	hemolysin A		
K11016	4	hemolysin		
K11017	8	hemolysin activation/secretion protein??		
K11029	4	anthrax edema toxin adenylate cyclase [EC:4.6.1.1]		
K11031	2	thiol-activated cytolysin		
K11041	2	exfoliative toxin A/B		
K11049	16	CylG protein		
K11053	3	CylF protein		
K11060	5	probable enterotoxin B		
K11062	1	probable enterotoxin D		
K11065	10	thiol peroxidase, atypical 2-Cys peroxiredoxin [EC:1.11.1.15]		
K11066	3	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K11068	27	hemolysin III		
K11069	17	spermidine/putrescine transport system substrate-binding protein		
K11070	19	spermidine/putrescine transport system permease protein		
K11071	27	spermidine/putrescine transport system permease protein		
K11072	19	spermidine/putrescine transport system ATP-binding protein		
K11073	4	putrescine transport system substrate-binding protein		
K11074	10	putrescine transport system permease protein		
K11075	10	putrescine transport system permease protein		
K11076	10	putrescine transport system ATP-binding protein		
K11079	3	mannopine transport system permease protein		
K11082	1	2-aminoethylphosphonate transport system permease protein		
K11085	118	ATP-binding cassette, subfamily B, bacterial MsbA [EC:3.6.3.-]		
K11102	12	proton glutamate symport protein		
K11103	9	aerobic C4-dicarboxylate transport protein		
K11105	21	cell volume regulation protein A		
K11106	6	L-tartrate/succinate antiporter		
K11144	8	primosomal protein DnaI		
K11145	2	ribonuclease III family protein		
K11159	3	carotenoid cleavage dioxygenase		
K11173	9	hydroxyacid-oxoacid transhydrogenase [EC:1.1.99.24]		
K11174	8	carbon-monoxide dehydrogenase (ferredoxin) [EC:1.2.7.4]		
K11175	32	phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]		
K11177	61	xanthine dehydrogenase YagR molybdenum-binding subunit [EC:1.17.1.4]		
K11178	19	xanthine dehydrogenase YagS FAD-binding subunit [EC:1.17.1.4]		
K11179	14	tRNA 2-thiouridine synthesizing protein E [EC:2.8.1.-]		
K11180	3	sulfite reductase, dissimilatory-type alpha subunit [EC:1.8.99.3]		
K11181	3	sulfite reductase, dissimilatory-type beta subunit [EC:1.8.99.3]		
K11183	16	phosphocarrier protein FPr		
K11189	29	phosphocarrier protein		
K11192	1	PTS system, N-acetylmuramic acid-specific IIC component		
K11201	2	PTS system, fructose-specific IIA-like component [EC:2.7.1.69]		
K11209	5	GST-like protein		
K11212	20	LPPG:FO 2-phospho-L-lactate transferase [EC:2.7.8.-]		
K11216	1	autoinducer 2 (AI-2) kinase [EC:2.7.1.-]		
K11249	1	cysteine/O-acetylserine efflux protein		
K11250	1	leucine efflux protein		

K11258	2	acetolactate synthase II small subunit [EC:2.2.1.6]		
K11261	6	formylmethanofuran dehydrogenase subunit E [EC:1.2.99.5]		
K11263	26	acetyl-/propionyl-CoA carboxylase, biotin carboxylase, biotin		
K11264	2	methylmalonyl-CoA decarboxylase [EC:4.1.1.41]		
K11311	2	anthranilate dioxygenase reductase		
K11312	6	cupin 2 domain-containing protein		
K11325	6	L-cysteine/cystine lyase		
K11326	7	cation efflux system protein involved in nickel and cobalt tolerance		
K11329	27	two-component system, OmpR family, response regulator RpaB		
K11333	1	chlorophyllide reductase iron protein subunit X [EC:1.18.6.1]		
K11337	3	3-hydroxyethyl bacteriochlorophyllide a dehydrogenase [EC:1.-.-.-]		
K11354	3	two-component system, chemotaxis family, sensor kinase Cph1		
K11355	3	two-component system, chemotaxis family, response regulator Rcp1		
K11356	2	two-component system, sensor histidine kinase and response regulator		
K11357	7	two-component system, cell cycle sensor histidine kinase DivJ		
K11358	4	aspartate aminotransferase [EC:2.6.1.1]		
K11381	62	2-oxoisovalerate dehydrogenase E1 component [EC:1.2.4.4]		
K11383	3	two-component system, NtrC family, sensor histidine kinase KinB		
K11384	7	two-component system, NtrC family, response regulator AlgB		
K11418	13	histone deacetylase 11 [EC:3.5.1.98]		
K11443	7	two-component system, cell cycle response regulator DivK		
K11444	8	two-component system, chemotaxis family, response regulator WspR		
K11472	15	glycolate oxidase FAD binding subunit		
K11473	36	glycolate oxidase iron-sulfur subunit		
K11475	15	GntR family transcriptional regulator, vanillate catabolism		
K11476	4	GntR family transcriptional regulator, gluconate operon		
K11477	13	glc operon protein GlcG		
K11523	4	two-component system, chemotaxis family, response regulator PixH		
K11525	1	methyl-accepting chemotaxis protein PixJ		
K11526	1	two-component system, chemotaxis family, sensor histidine kinase and		
K11527	58	two-component system, unclassified family, sensor histidine kinase		
K11528	4	UDP-N-acetylglucosamine pyrophosphorylase [EC:2.7.7.23]		
K11531	1	lsr operon transcriptional repressor		
K11532	1	fructose-1,6-bisphosphatase II / sedoheptulose-1,7-bisphosphatase		
K11533	1	fatty acid synthase, bacteria type [EC:2.3.1.-]		
K11537	6	MFS transporter, NHS family, xanthosine permease		
K11603	1	manganese transport system ATP-binding protein		
K11604	1	manganese/iron transport system substrate-binding protein		
K11606	3	manganese/iron transport system permease protein		
K11608	1	beta-ketoacyl ACP synthase [EC:2.3.1.-]		
K11609	1	beta-ketoacyl ACP synthase [EC:2.3.1.-]		
K11610	1	beta-ketoacyl ACP reductase [EC:1.1.1.100]		
K11611	8	enoyl ACP reductase [EC:1.3.1.9]		
K11615	3	two-component system, CitB family, response regulator MalR		
K11616	1	malate:Na+ symporter		
K11617	3	two-component system, NarL family, sensor histidine kinase LiaS		
K11618	39	two-component system, NarL family, response regulator LiaR		
K11619	11	lia operon protein LiaI		
K11621	1	lia operon protein LiaG		
K11624	2	two-component system, NarL family, response regulator YdfI		

K11625	9	membrane protein YdfJ		
K11634	1	two-component system, OmpR family, response regulator YxdJ		
K11646	1	dehydroquinate synthase II [EC:1.4.1.-]		
K11688	92	C4-dicarboxylate-binding protein DctP		
K11689	12	C4-dicarboxylate transporter, DctQ subunit		
K11690	144	C4-dicarboxylate transporter, DctM subunit		
K11693	2	peptidoglycan pentaglycine glycine transferase (the first glycine)		
K11710	3	manganese/zinc/iron transport system ATP- binding protein		
K11711	16	two-component system, LuxR family, sensor histidine kinase DctS		
K11712	12	two-component system, LuxR family, response regulator DctR		
K11717	72	cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]		
K11719	2	lipopolysaccharide export system protein LptC		
K11720	14	lipopolysaccharide export system permease protein		
K11731	6	citronellyl-CoA dehydrogenase [EC:1.3.99.-]		
K11740	2	bacteriophage N4 adsorption protein B		
K11741	6	quaternary ammonium compound-resistance protein SugE		
K11744	5	AI-2 transport protein TqsA		
K11745	10	glutathione-regulated potassium-efflux system ancillary protein KefC		
K11746	1	glutathione-regulated potassium-efflux system ancillary protein KefF		
K11747	9	glutathione-regulated potassium-efflux system protein KefB		
K11748	1	glutathione-regulated potassium-efflux system ancillary protein KefG		
K11749	54	regulator of sigma E protease [EC:3.4.24.-]		
K11750	11	esterase FrsA [EC:3.1.-.-]		
K11751	4	5'-nucleotidase / UDP-sugar diphosphatase [EC:3.1.3.5 3.6.1.45]		
K11752	32	diaminohydroxyphosphoribosylaminopyrimidine deaminase /		
K11753	31	riboflavin kinase / FMN adenylyltransferase [EC:2.7.1.26 2.7.7.2]		
K11754	47	dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12		
K11755	12	phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP		
K11777	1	HAD superfamily phosphatase		
K11779	20	FO synthase [EC:2.5.1.-]		
K11781	1	FO synthase subunit 2 [EC:2.5.1.-]		
K11782	5	chorismate futalosine-lyase [EC:4.1.99.-]		
K11784	17	de-hypoxanthine futalosine synthase [EC:1.21.-.-]		
K11785	2	1,4-dihydroxy-6-naphthoate synthase [EC:1.14.-.-]		
K11890	5	type VI secretion system protein ImpM		
K11891	8	type VI secretion system protein ImpL		
K11892	8	type VI secretion system protein ImpK		
K11893	9	type VI secretion system protein ImpJ		
K11894	3	type VI secretion system protein ImpI		
K11895	4	type VI secretion system protein ImpH		
K11896	7	type VI secretion system protein ImpG		
K11897	2	type VI secretion system protein ImpF		
K11898	1	type VI secretion system protein ImpE		
K11899	2	type VI secretion system protein ImpD		
K11900	10	type VI secretion system protein ImpC		
K11901	8	type VI secretion system protein ImpB		
K11902	6	type VI secretion system protein ImpA		
K11903	1	type VI secretion system secreted protein Hcp		
K11904	9	type VI secretion system secreted protein VgrG		
K11905	1	type VI secretion system protein		

K11906	7	type VI secretion system protein VasD		
K11907	13	type VI secretion system protein VasG		
K11910	2	type VI secretion system protein VasJ		
K11911	1	type VI secretion system protein VasL		
K11912	28	serine/threonine-protein kinase PpkA [EC:2.7.11.1]		
K11913	3	type VI secretion system protein		
K11914	2	sigma-54 dependent transcriptional regulator		
K11916	1	serine/threonine-protein kinase Stk1 [EC:2.7.11.-]		
K11917	3	sigma-54 specific transcriptional regulator		
K11921	10	LysR family transcriptional regulator		
K11922	1	GntR family transcriptional regulator, mannosyl-D-glycerate		
K11923	3	MerR family transcriptional regulator, copper efflux regulator		
K11924	4	DtxR family transcriptional regulator, manganese transport regulator		
K11925	1	SgrR family transcriptional regulator		
K11926	1	sigma factor-binding protein Crl		
K11927	27	ATP-dependent RNA helicase RhlE [EC:3.6.4.13]		
K11928	6	sodium/proline symporter		
K11930	1	periplasmic protein TorT		
K11931	5	biofilm PGA synthesis lipoprotein PgaB [EC:3.-.-.-]		
K11933	4	NADH oxidoreductase Hcr [EC:1.-.-.-]		
K11936	26	biofilm PGA synthesis N-glycosyltransferase PgaC [EC:2.4.-.-]		
K11938	1	HMP-PP phosphatase [EC:3.6.1.-]		
K11939	8	inner membrane transporter RhtA		
K11940	2	heat shock protein HspQ		
K11942	14	methylmalonyl-CoA mutase [EC:5.4.99.2]		
K11948	2	1-hydroxy-2-naphthoate dioxygenase [EC:1.13.11.38]		
K11949	1	4-(2-carboxyphenyl)-2-oxobut-3-enoate aldolase [EC:4.1.2.34]		
K11953	1	bicarbonate transport system ATP-binding protein [EC:3.6.3.-]		
K11954	2	neutral amino acid transport system substrate-binding protein		
K11955	1	neutral amino acid transport system permease protein		
K11956	1	neutral amino acid transport system permease protein		
K11957	2	neutral amino acid transport system ATP-binding protein		
K11958	2	neutral amino acid transport system ATP-binding protein		
K11959	4	urea transport system substrate-binding protein		
K11960	1	urea transport system permease protein		
K11961	2	urea transport system permease protein		
K11963	1	urea transport system ATP-binding protein		
K11987	1	prostaglandin-endoperoxide synthase 2 [EC:1.14.99.1]		
K11991	12	tRNA-specific adenosine deaminase [EC:3.5.4.-]		
K12059	1	conjugal transfer pilus assembly protein TrbC		
K12063	2	conjugal transfer ATP-binding protein TraC		
K12065	1	conjugal transfer pilus assembly protein TraB		
K12073	3	1,4-dihydroxy-2-naphthoyl-CoA thioesterase [EC:3.1.2.-]		
K12111	2	evolved beta-galactosidase subunit alpha [EC:3.2.1.23]		
K12137	9	hydrogenase-4 component B [EC:1.-.-.-]		
K12138	10	hydrogenase-4 component C [EC:1.-.-.-]		
K12139	6	hydrogenase-4 component D [EC:1.-.-.-]		
K12140	6	hydrogenase-4 component E [EC:1.-.-.-]		
K12141	14	hydrogenase-4 component F [EC:1.-.-.-]		
K12142	1	hydrogenase-4 component G [EC:1.-.-.-]		

K12143	4	hydrogenase-4 component H		
K12146	16	hydrogenase-4 transcriptional activator		
K12148	3	biofilm regulator BssS		
K12150	1	HIT-like protein HinT		
K12152	3	phosphatase NudJ [EC:3.6.1.-]		
K12203	34	defect in organelle trafficking protein DotB		
K12206	6	intracellular multiplication protein IcmB		
K12209	3	intracellular multiplication protein IcmE		
K12210	6	intracellular multiplication protein IcmF		
K12213	10	intracellular multiplication protein IcmK		
K12214	5	intracellular multiplication protein IcmL		
K12216	1	intracellular multiplication protein IcmN		
K12234	9	F420-0:gamma-glutamyl ligase [EC:6.3.2.-]		
K12238	5	pyochelin biosynthesis protein PchD		
K12240	1	pyochelin synthetase		
K12251	28	N-carbamoylputrescine amidase [EC:3.5.1.53]		
K12252	2	arginine:pyruvate transaminase [EC:2.6.1.84]		
K12253	4	5-guanidino-2-oxopentanoate decarboxylase [EC:4.1.1.75]		
K12254	3	4-guanidinobutyraldehyde dehydrogenase / NAD-dependent aldehyde		
K12255	4	guanidinobutyrase [EC:3.5.3.7]		
K12256	7	putrescine aminotransferase [EC:2.6.1.-]		
K12257	30	SecD/SecF fusion protein		
K12262	5	cytochrome b561		
K12264	2	anaerobic nitric oxide reductase flavorubredoxin		
K12265	1	nitric oxide reductase FlRd-NAD(+) reductase [EC:1.18.1.-]		
K12266	6	anaerobic nitric oxide reductase transcription regulator		
K12267	22	peptide methionine sulfoxide reductase msrA/msrB [EC:1.8.4.11		
K12276	10	MSHA biogenesis protein MshE		
K12278	8	MSHA biogenesis protein MshG		
K12282	9	MSHA biogenesis protein MshL		
K12283	7	MSHA biogenesis protein MshM		
K12287	4	MSHA biogenesis protein MshQ		
K12297	4	ribosomal RNA large subunit methyltransferase L [EC:2.1.1.52]		
K12299	1	MFS transporter, ACS family, probable galactarate transporter		
K12308	35	beta-galactosidase [EC:3.2.1.23]		
K12339	16	cysteine synthase B [EC:2.5.1.47]		
K12340	36	outer membrane channel protein TolC		
K12343	4	3-oxo-5-alpha-steroid 4-dehydrogenase 1 [EC:1.3.99.5]		
K12344	4	3-oxo-5-alpha-steroid 4-dehydrogenase 2 [EC:1.3.99.5]		
K12368	17	dipeptide transport system substrate-binding protein		
K12369	12	dipeptide transport system permease protein		
K12370	10	dipeptide transport system permease protein		
K12371	6	dipeptide transport system ATP-binding protein		
K12372	1	dipeptide transport system ATP-binding protein		
K12373	31	beta-hexosaminidase [EC:3.2.1.52]		
K12410	28	NAD-dependent deacetylase [EC:3.5.1.-]		
K12420	16	ketoacyl reductase [EC:1.3.1.-]		
K12421	1	fatty acid CoA ligase FadD9		
K12423	2	fatty acid CoA ligase FadD21		
K12424	2	fatty acid CoA ligase FadD22		

K12427	1	fatty acid CoA ligase FadD28		
K12428	1	fatty acid CoA ligase FadD32		
K12429	5	fatty acid CoA ligase FadD36		
K12430	3	polyketide synthase 1/15		
K12432	1	polyketide synthase 3/4		
K12436	22	polyketide synthase 12		
K12437	1	polyketide synthase 13		
K12441	1	phenolpthiocerol synthesis type-I polyketide synthase B		
K12442	1	phenolpthiocerol synthesis type-I polyketide synthase C		
K12444	3	phenolpthiocerol synthesis type-I polyketide synthase E		
K12445	2	trans enoyl reductase [EC:1.3.1.-]		
K12452	6	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase		
K12454	22	CDP-paratose 2-epimerase [EC:5.1.3.10]		
K12500	1	thioesterase III [EC:3.1.2.-]		
K12503	5	short-chain Z-isoprenyl diphosphate synthase [EC:2.5.1.68]		
K12506	29	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase /		
K12507	2	acyl-CoA synthetase [EC:6.2.1.-]		
K12508	42	feruloyl-CoA synthase [EC:6.2.1.34]		
K12510	17	tight adherence protein B		
K12511	16	tight adherence protein C		
K12524	14	bifunctional aspartokinase/homoserine dehydrogenase 1 [EC:2.7.2.4		
K12525	1	bifunctional aspartokinase/homoserine dehydrogenase 2 [EC:2.7.2.4		
K12526	1	bifunctional diaminopimelate decarboxylase/aspartate kinase		
K12527	2	putative selenate reductase [EC:1.97.1.9]		
K12528	2	putative selenate reductase molybdopterin-binding subunit		
K12536	4	ATP-binding cassette, subfamily C, bacterial HasD		
K12537	2	protease secretion protein HasE		
K12538	1	outer membrane protein HasF		
K12541	3	ATP-binding cassette, subfamily C, bacterial LapB		
K12542	1	membrane fusion protein LapC		
K12543	1	outer membrane protein LapE		
K12544	1	S-layer protein		
K12549	12	surface adhesion protein		
K12555	1	penicillin-binding protein 2A [EC:2.4.1.129 2.3.2.-]		
K12573	53	ribonuclease R [EC:3.1.-.-]		
K12574	39	ribonuclease J [EC:3.1.-.-]		
K12583	6	phosphatidylinositol alpha 1,6-mannosyltransferase [EC:2.4.1.-]		
K12645	13	epi-isozizaene 5-monooxygenase [EC:1.14.13.106]		
K12658	5	4-hydroxyproline epimerase [EC:5.1.1.8]		
K12660	5	2-dehydro-3-deoxy-L-rhamnonate aldolase [EC:4.1.2.-]		
K12661	1	L-rhamnonate dehydratase [EC:4.2.1.90]		
K12673	2	N2-(2-carboxyethyl)arginine synthase [EC:2.5.1.66]		
K12686	2	outer membrane lipase/esterase		
K12688	2	autotransporter serine protease [EC:3.4.21.-]		
K12941	17	aminobenzoyl-glutamate utilization protein B		
K12942	5	aminobenzoyl-glutamate transport protein		
K12943	2	lipoprotein YgeR		
K12949	13	cation-transporting P-type ATPase A/B [EC:3.6.3.-]		
K12950	1	cation-transporting P-type ATPase C [EC:3.6.3.-]		
K12952	7	cation-transporting ATPase E [EC:3.6.3.-]		

K12953	6	cation-transporting ATPase F [EC:3.6.3.-]		
K12956	10	cation-transporting ATPase V [EC:3.6.3.-]		
K12960	17	5-methylthioadenosine/S-adenosylhomocysteine deaminase		
K12961	2	DnaA initiator-associating protein		
K12972	5	gyoxylate/hydroxypyruvate reductase A [EC:1.1.1.79 1.1.1.81]		
K12979	2	beta-hydroxylase [EC:1.14.11.-]		
K12982	2	heptosyltransferase I [EC:2.4.-.-]		
K12984	12	(heptosyl)LPS beta-1,4-glucosyltransferase [EC:2.4.1.-]		
K12987	3	alpha-1,6-rhamnosyltransferase [EC:2.4.1.-]		
K12988	2	alpha-1,3-rhamnosyltransferase [EC:2.4.1.-]		
K12989	2	mannosyltransferase [EC:2.4.1.-]		
K12990	3	rhamnosyltransferase [EC:2.4.1.-]		
K12992	1	rhamnosyltransferase [EC:2.4.1.-]		
K12994	6	alpha-1,3-rhamnosyltransferase [EC:2.4.1.-]		
K12995	3	rhamnosyltransferase [EC:2.4.1.-]		
K12996	4	rhamnosyltransferase [EC:2.4.1.-]		
K12997	1	rhamnosyltransferase [EC:2.4.1.-]		
K13001	4	mannosyltransferase [EC:2.4.1.-]		
K13002	3	glycosyltransferase [EC:2.4.1.-]		
K13004	5	galacturonosyltransferase [EC:2.4.1.-]		
K13006	4	UDP-perosamine 4-acetyltransferase [EC:2.3.1.-]		
K13007	1	Fuc2NAc and GlcNAc transferase [EC:2.4.1.-]		
K13010	16	perosamine synthetase		
K13013	17	O-antigen biosynthesis protein WbqV		
K13014	2	undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]		
K13015	28	UDP-N-acetyl-D-glucosamine dehydrogenase [EC:1.1.1.-]		
K13016	1	UDP-D-GlcNAcA oxidase [EC:1.1.1.-]		
K13017	16	UDP-3-keto-D-GlcNAcA aminotransferase [EC:2.6.1.-]		
K13018	4	UDP-D-GlcNAc3NA acetyltransferase [EC:2.3.1.-]		
K13019	9	UDP-GlcNAc3NAcA epimerase [EC:5.1.3.23]		
K13020	21	UDP-D-GlcNAcA oxidase [EC:1.1.1.-]		
K13021	6	MFS transporter, ACS family, tartrate transporter		
K13038	42	phosphopantothenoylcysteine decarboxylase /		
K13039	5	sulfopyruvate decarboxylase subunit beta [EC:4.1.1.79]		
K13041	1	two-component system, LuxR family, response regulator TtrR		
K13042	2	dimethylglycine N-methyltransferase [EC:2.1.1.161]		
K13043	3	N-succinyl-L-ornithine transcarbamylase [EC:2.1.3.11]		
K13049	48	carboxypeptidase PM20D1 [EC:3.4.17.-]		
K13051	19	beta-aspartyl-peptidase (threonine type) [EC:3.4.19.5]		
K13052	1	cell division protein DivIC		
K13057	14	trehalose synthase [EC:2.4.1.245]		
K13058	1	mannosylfructose-phosphate synthase [EC:2.4.1.246]		
K13063	1	phenazine biosynthesis protein phzE [EC:2.6.1.86]		
K13069	3	diguanylate cyclase [EC:2.7.7.65]		
K13074	8	biflaviolin synthase [EC:1.14.21.7]		
K13075	16	N-acyl homoserine lactone hydrolase [EC:3.1.1.81]		
K13237	3	peroxisomal 2,4-dienoyl-CoA reductase [EC:1.3.1.34]		
K13243	2	c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]		
K13244	1	c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]		
K13245	7	c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]		

K13252	1	putrescine carbamoyltransferase [EC:2.1.3.6]		
K13256	3	protein PsiE		
K13274	5	cell wall-associated protease [EC:3.4.21.-]		
K13275	2	major intracellular serine protease [EC:3.4.21.-]		
K13276	3	bacillopeptidase F [EC:3.4.21.-]		
K13277	3	minor extracellular protease Epr [EC:3.4.21.-]		
K13280	2	signal peptidase, endoplasmic reticulum-type [EC:3.4.-.-]		
K13281	2	UV DNA damage endonuclease [EC:3.-.-.-]		
K13282	2	cyanophycinase [EC:3.4.15.6]		
K13283	57	ferrous-iron efflux pump FieF		
K13285	1	invasin B		
K13288	10	oligoribonuclease [EC:3.1.-.-]		
K13292	27	phosphatidylglycerol:prolipoprotein diacylglycerol transferase		
K13317	3	NDP-4-keto-2,6-dideoxyhexose 3-C-methyltransferase		
K13318	6	dTDP-4-keto-6-deoxy-L-hexose 4-reductase		
K13378	29	NADH dehydrogenase I subunit C/D [EC:1.6.5.3]		
K13380	1	NADH dehydrogenase I subunit B/C/D [EC:1.6.5.3]		
K13408	2	membrane fusion protein RaxA		
K13409	1	ATP-binding cassette, subfamily B, bacterial RaxB		
K13419	13	serine/threonine-protein kinase PknK [EC:2.7.11.1]		
K13421	1	uridine monophosphate synthetase [EC:2.4.2.10 4.1.1.23]		
K13479	1	xanthine dehydrogenase FAD-binding subunit [EC:1.17.1.4]		
K13481	2	xanthine dehydrogenase small subunit [EC:1.17.1.4]		
K13482	10	xanthine dehydrogenase large subunit [EC:1.17.1.4]		
K13483	14	xanthine dehydrogenase YagT iron-sulfur-binding subunit		
K13486	2	chemotaxis protein methyltransferase WspC		
K13490	5	two-component system, chemotaxis family, sensor histidine kinase and		
K13491	1	two-component system, chemotaxis family, response regulator WspF		
K13497	7	anthranilate synthase/phosphoribosyltransferase [EC:4.1.3.27		
K13498	7	indole-3-glycerol phosphate synthase / phosphoribosylanthranilate		
K13500	1	chondroitin synthase [EC:2.4.1.175 2.4.1.226]		
K13503	3	anthranilate synthase [EC:4.1.3.27]		
K13522	2	bifunctional NMN adenylyltransferase/nudix hydrolase [EC:2.7.7.1		
K13525	23	transitional endoplasmic reticulum ATPase		
K13527	10	proteasome-associated ATPase		
K13529	16	AraC family transcriptional regulator, regulatory protein of		
K13530	4	AraC family transcriptional regulator, regulatory protein of		
K13531	1	methylated-DNA-[protein]-cysteine S-methyltransferase [EC:2.1.1.63]		
K13532	2	two-component system, sporulation sensor kinase D [EC:2.7.13.3]		
K13533	7	two-component system, sporulation sensor kinase E [EC:2.7.13.3]		
K13540	2	precorrin-2 C20-methyltransferase / precorrin-3B		
K13541	3	cobalamin biosynthesis protein CbiG / precorrin-3B		
K13542	25	uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107		
K13543	6	uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107		
K13571	4	proteasome accessory factor A [EC:6.3.2.-]		
K13572	7	proteasome accessory factor B		
K13573	11	proteasome accessory factor C		
K13574	10	uncharacterized oxidoreductase [EC:1.1.1.-]		
K13581	4	modification methylase [EC:2.1.1.72]		
K13582	2	localization factor PodJL		

K13583	3	GcrA cell cycle regulator		
K13584	1	two-component system, cell cycle response regulator CtrA		
K13587	41	two-component system, cell cycle sensor histidine kinase and		
K13588	1	histidine phosphotransferase ChpT		
K13589	2	two-component system, cell cycle response regulator CpdR		
K13590	30	diguanylate cyclase		
K13592	1	regulator of CtrA degradation		
K13593	1	cyclic-di-GMP phosphodiesterase, flagellum assembly factor TipF		
K13598	35	two-component system, NtrC family, nitrogen regulation sensor		
K13599	57	two-component system, NtrC family, nitrogen regulation response		
K13601	26	bacteriochlorophyll C8 methyltransferase [EC:2.1.1.-]		
K13602	20	bacteriochlorophyll C12 methyltransferase [EC:2.1.1.-]		
K13604	7	bacteriochlorophyll C20 methyltransferase [EC:2.1.1.-]		
K13607	4	cinnamoyl-CoA:phenyllactate CoA-transferase [EC:2.8.3.17]		
K13611	6	polyketide synthase PksJ		
K13612	1	polyketide synthase PksL		
K13614	6	polyketide synthase PksN		
K13628	22	iron-sulfur cluster assembly protein		
K13633	20	AraC family transcriptional regulator, transcriptional activator		
K13634	7	LysR family transcriptional regulator, cys regulon transcriptional		
K13635	7	LysR family transcriptional regulator, cys regulon transcriptional		
K13637	1	GntR family transcriptional regulator, uxuAB operon transcriptional		
K13638	4	MerR family transcriptional regulator, Zn(II)-responsive regulator		
K13639	5	MerR family transcriptional regulator, redox-sensitive		
K13640	10	MerR family transcriptional regulator, heat shock protein HspR		
K13641	40	IclR family transcriptional regulator, acetate operon repressor		
K13642	7	CRP/FNR family transcriptional regulator, transcriptional activator		
K13643	24	Rrf2 family transcriptional regulator, iron-sulfur cluster assembly		
K13652	4	AraC family transcriptional regulator		
K13653	3	AraC family transcriptional regulator		
K13654	5	GntR family transcriptional regulator, colanic acid and biofilm gene		
K13660	1	beta-1,4-glucosyltransferase [EC:2.4.1.-]		
K13661	9	GumC protein		
K13668	21	phosphatidylinositol alpha-1,6-mannosyltransferase [EC:2.4.1.-]		
K13670	1	alpha-1,6-mannosyltransferase [EC:2.4.1.-]		
K13678	1	monoglucosyldiacylglycerol glycosyltransferase [EC:2.4.1.-]		
K13683	1	putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]		
K13684	1	putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]		
K13685	27	UDP-N-acetylglucosamine:undecaprenyl-P N-acetylglucosaminyl 1-P		
K13688	38	cyclic beta-1,2-glucan synthetase [EC:2.4.1.-]		
K13693	8	glucosyl-3-phosphoglycerate synthase [EC:2.4.1.-]		
K13694	3	lipoprotein Spr		
K13695	3	probable lipoprotein NlpC		
K13730	107	internalin A		
K13735	100	adhesin/invasin		
K13741	1	guanine nucleotide exchange factor SopE		
K13742	1	protein IpgB1		
K13745	5	L-2,4-diaminobutyrate decarboxylase [EC:4.1.1.86]		
K13746	1	carboxynorspermidine dehydrogenase		
K13747	2	carboxynorspermidine decarboxylase [EC:4.1.1.-]		

K13766	13	methylglutaconyl-CoA hydratase [EC:4.2.1.18]		
K13767	5	enoyl-CoA hydratase [EC:4.2.1.17]		
K13770	16	TetR/AcrR family transcriptional regulator, fatty acid metabolism		
K13771	2	Rrf2 family transcriptional regulator, nitric oxide-sensitive		
K13774	3	citronellol/citronellal dehydrogenase		
K13775	5	citronellol/citronellal dehydrogenase		
K13776	1	citronellyl-CoA synthetase [EC:6.2.1.-]		
K13777	1	geranyl-CoA carboxylase alpha subunit [EC:6.4.1.5]		
K13778	4	geranyl-CoA carboxylase beta subunit [EC:6.4.1.5]		
K13787	9	geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10		
K13788	5	phosphate acetyltransferase [EC:2.3.1.8]		
K13789	15	geranylgeranyl diphosphate synthase, type II [EC:2.5.1.1 2.5.1.10		
K13794	1	LysR family transcriptional regulator, regulatory protein for tcuABC		
K13795	4	citrate/tricarballylate utilization protein		
K13796	11	tricarballylate dehydrogenase		
K13797	2	DNA-directed RNA polymerase subunit beta-beta' [EC:2.7.7.6]		
K13799	8	pantoate ligase / cytidylate kinase [EC:6.3.2.1 2.7.4.14]		
K13810	14	transaldolase / glucose-6-phosphate isomerase [EC:2.2.1.2 5.3.1.9]		
K13811	3	3'-phosphoadenosine 5'-phosphosulfate synthase [EC:2.7.7.4 2.7.1.25]		
K13815	21	two-component system, response regulator RpfG		
K13816	7	DSF synthase		
K13819	3	NifU-like protein		
K13820	1	flagellar biosynthetic protein FliR/FlhB		
K13821	28	proline dehydrogenase / delta 1-pyrroline-5-carboxylate		
K13829	16	shikimate kinase / 3-dehydroquinate synthase [EC:2.7.1.71 4.2.3.4]		
K13832	9	3-dehydroquinate dehydratase / shikimate dehydrogenase [EC:4.2.1.10		
K13874	3	L-arabinonolactonase [EC:3.1.1.15]		
K13875	7	L-arabonate dehydrase [EC:4.2.1.25]		
K13876	5	2-keto-3-deoxy-L-arabinonate dehydratase [EC:4.2.1.43]		
K13888	53	macrolide-specific efflux protein MacA		
K13889	13	glutathione transport system substrate-binding protein		
K13890	6	glutathione transport system permease protein		
K13891	2	glutathione transport system permease protein		
K13892	4	glutathione transport system ATP-binding protein		
K13893	9	microcin C transport system substrate-binding protein		
K13894	2	microcin C transport system permease protein		
K13895	4	microcin C transport system permease protein		
K13896	3	microcin C transport system ATP-binding protein		
K13919	1	propanediol dehydratase medium subunit [EC:4.2.1.28]		
K13922	1	propionaldehyde dehydrogenase		
K13924	124	two-component system, chemotaxis family, CheB/CheR fusion protein		
K13926	4	ribosome-dependent ATPase		
K13940	13	dihydroneopterin aldolase /		
K13950	9	para-aminobenzoate synthetase [EC:2.6.1.85]		
K13953	52	alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]		
K13954	5	alcohol dehydrogenase [EC:1.1.1.1]		
K13955	7	zinc-binding alcohol dehydrogenase/oxidoreductase		
K13963	11	serpin B		
K13979	9	uncharacterized zinc-type alcohol dehydrogenase-like protein		
K13990	19	glutamate formiminotransferase / formiminotetrahydrofolate		

K13993	58	HSP20 family protein		
K13995	2	maleamate amidohydrolase [EC:3.5.1.107]		

KEGG ID	Sequences	KEGG pathway		
K00001	181	alcohol dehydrogenase [EC:1.1.1.1]		
K00002	3	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]		
K00003	74	homoserine dehydrogenase [EC:1.1.1.3]		
K00004	3	(R,R)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4		
K00005	10	glycerol dehydrogenase [EC:1.1.1.6]		
K00008	37	L-iditol 2-dehydrogenase [EC:1.1.1.14]		
K00009	4	mannitol-1-phosphate 5-dehydrogenase [EC:1.1.1.17]		
K00010	96	myo-inositol 2-dehydrogenase [EC:1.1.1.18]		
K00011	4	aldehyde reductase [EC:1.1.1.21]		
K00012	45	UDPglucose 6-dehydrogenase [EC:1.1.1.22]		
K00013	43	histidinol dehydrogenase [EC:1.1.1.23]		
K00014	37	shikimate dehydrogenase [EC:1.1.1.25]		
K00015	39	glyoxylate reductase [EC:1.1.1.26]		
K00016	26	L-lactate dehydrogenase [EC:1.1.1.27]		
K00018	11	glycerate dehydrogenase [EC:1.1.1.29]		
K00019	33	3-hydroxybutyrate dehydrogenase [EC:1.1.1.30]		
K00020	92	3-hydroxyisobutyrate dehydrogenase [EC:1.1.1.31]		
K00021	14	3-hydroxy-3-methylglutaryl-CoA reductase [EC:1.1.1.34]		
K00023	24	acetoacetyl-CoA reductase [EC:1.1.1.36]		
K00024	35	malate dehydrogenase [EC:1.1.1.37]		
K00027	40	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]		
K00028	4	malate dehydrogenase (decarboxylating) [EC:1.1.1.39]		
K00029	39	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)		
K00030	19	isocitrate dehydrogenase (NAD+) [EC:1.1.1.41]		
K00031	37	isocitrate dehydrogenase [EC:1.1.1.42]		
K00032	1	phosphogluconate 2-dehydrogenase [EC:1.1.1.43]		
K00033	37	6-phosphogluconate dehydrogenase [EC:1.1.1.44]		
K00034	25	glucose 1-dehydrogenase [EC:1.1.1.47]		
K00035	1	D-galactose 1-dehydrogenase [EC:1.1.1.48]		
K00036	118	glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49]		
K00037	2	3-alpha-hydroxysteroid dehydrogenase [EC:1.1.1.50]		
K00038	6	3alpha(or 20beta)-hydroxysteroid dehydrogenase [EC:1.1.1.53]		
K00040	4	fructuronate reductase [EC:1.1.1.57]		
K00042	60	2-hydroxy-3-oxopropionate reductase [EC:1.1.1.60]		
K00043	6	4-hydroxybutyrate dehydrogenase [EC:1.1.1.61]		
K00044	10	estradiol 17beta-dehydrogenase [EC:1.1.1.62]		
K00045	4	mannitol 2-dehydrogenase [EC:1.1.1.67]		
K00046	33	gluconate 5-dehydrogenase [EC:1.1.1.69]		
K00048	20	lactaldehyde reductase [EC:1.1.1.77]		
K00050	46	hydroxypyruvate reductase [EC:1.1.1.81]		
K00051	10	malate dehydrogenase (NADP+) [EC:1.1.1.82]		
K00052	66	3-isopropylmalate dehydrogenase [EC:1.1.1.85]		
K00053	17	ketol-acid reductoisomerase [EC:1.1.1.86]		
K00054	7	hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]		
K00055	2	aryl-alcohol dehydrogenase [EC:1.1.1.90]		
K00057	38	glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94]		
K00058	145	D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]		
K00059	312	3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]		
K00060	50	threonine 3-dehydrogenase [EC:1.1.1.103]		
K00064	7	D-threo-aldose 1-dehydrogenase [EC:1.1.1.122]		
K00065	29	2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]		
K00066	25	GDP-mannose 6-dehydrogenase [EC:1.1.1.132]		
K00067	36	dTDP-4-dehydrorhamnose reductase [EC:1.1.1.133]		
K00068	7	sorbitol-6-phosphate 2-dehydrogenase [EC:1.1.1.140]		
K00071	3	11beta-hydroxysteroid dehydrogenase [EC:1.1.1.146]		
K00073	35	ureidoglycolate dehydrogenase [EC:1.1.1.154]		
K00074	63	3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]		
K00075	37	UDP-N-acetylmuramate dehydrogenase [EC:1.1.1.158]		

K00076	5	7-alpha-hydroxysteroid dehydrogenase [EC:1.1.1.159]		
K00077	44	2-dehydropantoate 2-reductase [EC:1.1.1.169]		
K00079	12	carbonyl reductase (NADPH) [EC:1.1.1.184]		
K00082	9	5-amino-6-(5-phosphoribosylamino)uracil reductase [EC:1.1.1.193]		
K00083	2	cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]		
K00086	5	1,3-propanediol dehydrogenase [EC:1.1.1.202]		
K00087	105	xanthine dehydrogenase molybdenum-binding subunit [EC:1.17.1.4]		
K00088	84	IMP dehydrogenase [EC:1.1.1.205]		
K00090	13	gluconate 2-dehydrogenase [EC:1.1.1.215]		
K00091	22	dihydroflavonol-4-reductase [EC:1.1.1.219]		
K00094	1	galactitol-1-phosphate 5-dehydrogenase [EC:1.1.1.251]		
K00096	3	glycerol-1-phosphate dehydrogenase [NAD(P)] [EC:1.1.1.261]		
K00097	42	4-hydroxythreonine-4-phosphate dehydrogenase [EC:1.1.1.262]		
K00098	4	L-idonate 5-dehydrogenase [EC:1.1.1.264]		
K00099	51	1-deoxy-D-xylulose-5-phosphate reductoisomerase [EC:1.1.1.267]		
K00100	439	Unclassified; E1.1.1.-		
K00101	50	L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]		
K00102	85	D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]		
K00103	10	L-gulonolactone oxidase [EC:1.1.3.8]		
K00104	91	glycolate oxidase [EC:1.1.3.15]		
K00105	3	alpha-glycerophosphate oxidase [EC:1.1.3.21]		
K00108	51	choline dehydrogenase [EC:1.1.99.1]		
K00109	14	2-hydroxyglutarate dehydrogenase [EC:1.1.99.2]		
K00111	53	glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]		
K00112	2	glycerol-3-phosphate dehydrogenase subunit B [EC:1.1.5.3]		
K00113	10	glycerol-3-phosphate dehydrogenase subunit C [EC:1.1.5.3]		
K00114	80	alcohol dehydrogenase (acceptor) [EC:1.1.99.8]		
K00116	24	malate dehydrogenase (quinone) [EC:1.1.5.4]		
K00117	55	quinoprotein glucose dehydrogenase [EC:1.1.5.2]		
K00118	12	glucose-fructose oxidoreductase [EC:1.1.99.28]		
K00119	103	Unclassified; E1.1.99.-		
K00120	82	Unclassified; E1.1.-.-		
K00121	49	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase		
K00122	100	formate dehydrogenase [EC:1.2.1.2]		
K00123	164	formate dehydrogenase, alpha subunit [EC:1.2.1.2]		
K00124	24	formate dehydrogenase, beta subunit [EC:1.2.1.2]		
K00127	21	formate dehydrogenase, gamma subunit [EC:1.2.1.2]		
K00128	152	aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]		
K00129	2	aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]		
K00130	60	betaine-aldehyde dehydrogenase [EC:1.2.1.8]		
K00131	21	glyceraldehyde-3-phosphate dehydrogenase (NADP) [EC:1.2.1.9]		
K00132	6	acetaldehyde dehydrogenase (acetylating) [EC:1.2.1.10]		
K00133	35	aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]		
K00134	29	glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]		
K00135	94	succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]		
K00137	5	aminobutyraldehyde dehydrogenase [EC:1.2.1.19]		
K00138	6	aldehyde dehydrogenase [EC:1.2.1.-]		
K00140	32	methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.27]		
K00141	6	benzaldehyde dehydrogenase (NAD) [EC:1.2.1.28]		
K00145	50	N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]		
K00146	17	phenylacetaldehyde dehydrogenase [EC:1.2.1.39]		
K00147	25	glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41]		
K00148	5	glutathione-independent formaldehyde dehydrogenase [EC:1.2.1.46]		
K00150	2	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]		
K00151	15	5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase		
K00152	5	salicylaldehyde dehydrogenase [EC:1.2.1.65]		
K00153	7	NAD/factor-dependent formaldehyde dehydrogenase [EC:1.2.1.66]		
K00154	3	coniferyl-aldehyde dehydrogenase [EC:1.2.1.68]		
K00155	81	Unclassified; E1.2.1.-		

K00156	27	pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]		
K00157	22	aldehyde oxidase [EC:1.2.3.1]		
K00158	6	pyruvate oxidase [EC:1.2.3.3]		
K00161	65	pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]		
K00162	66	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]		
K00163	45	pyruvate dehydrogenase E1 component [EC:1.2.4.1]		
K00164	41	2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]		
K00166	32	2-oxoisovalerate dehydrogenase E1 component, alpha subunit		
K00167	31	2-oxoisovalerate dehydrogenase E1 component, beta subunit		
K00169	37	pyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.1]		
K00170	17	pyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.1]		
K00171	15	pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]		
K00172	16	pyruvate ferredoxin oxidoreductase, gamma subunit [EC:1.2.7.1]		
K00174	70	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]		
K00175	41	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]		
K00176	10	2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7.3]		
K00177	12	2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]		
K00178	23	oxidoreductase containing iron-sulfur protein [EC:1.2.7.-]		
K00179	43	indolepyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.8]		
K00180	23	indolepyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.8]		
K00183	52	molybdopterin oxidoreductase, molybdopterin binding subunit		
K00184	53	molybdopterin oxidoreductase, iron-sulfur binding subunit		
K00185	44	molybdopterin oxidoreductase, membrane subunit [EC:1.2.7.-]		
K00186	10	2-oxoisovalerate ferredoxin oxidoreductase, alpha subunit		
K00187	7	2-oxoisovalerate ferredoxin oxidoreductase, beta subunit		
K00191	7	CO-methylating acetyl-CoA synthase [EC:2.3.1.169]		
K00194	1	carbon-monoxide dehydrogenase delta subunit [EC:1.2.99.2]		
K00197	5	carbon-monoxide dehydrogenase gamma subunit [EC:1.2.99.2]		
K00198	3	carbon-monoxide dehydrogenase catalytic subunit [EC:1.2.99.2]		
K00200	8	formylmethanofuran dehydrogenase subunit A [EC:1.2.99.5]		
K00201	1	formylmethanofuran dehydrogenase subunit B [EC:1.2.99.5]		
K00202	2	formylmethanofuran dehydrogenase subunit C [EC:1.2.99.5]		
K00206	1	Unclassified; E1.2.-.-		
K00207	10	dihydropyrimidine dehydrogenase (NADP+) [EC:1.3.1.2]		
K00208	71	enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9]		
K00209	3	enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific)		
K00210	23	prephenate dehydrogenase [EC:1.3.1.12]		
K00214	1	biliverdin reductase [EC:1.3.1.24]		
K00215	29	dihydrodipicolinate reductase [EC:1.3.1.26]		
K00216	2	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [EC:1.3.1.28]		
K00217	4	maleylacetate reductase [EC:1.3.1.32]		
K00218	9	protochlorophyllide reductase [EC:1.3.1.33]		
K00219	58	2,4-dienoyl-CoA reductase (NADPH2) [EC:1.3.1.34]		
K00220	4	cyclohexadienyl dehydrogenase [EC:1.3.1.43]		
K00224	11	Unclassified; E1.3.1.-		
K00226	72	dihydroorotate oxidase [EC:1.3.3.1]		
K00227	3	lathosterol oxidase [EC:1.14.21.6]		
K00228	17	coproporphyrinogen III oxidase [EC:1.3.3.3]		
K00230	8	protoporphyrinogen oxidase [EC:1.3.3.4]		
K00231	27	protoporphyrinogen oxidase [EC:1.3.3.4]		
K00232	1	acyl-CoA oxidase [EC:1.3.3.6]		
K00239	70	succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]		
K00240	31	succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]		
K00241	21	succinate dehydrogenase cytochrome b-556 subunit [EC:1.3.99.1]		
K00242	5	succinate dehydrogenase hydrophobic membrane anchor protein		
K00244	39	fumarate reductase flavoprotein subunit [EC:1.3.99.1]		
K00245	7	fumarate reductase iron-sulfur protein [EC:1.3.99.1]		
K00246	13	fumarate reductase subunit C [EC:1.3.99.1]		
K00247	5	fumarate reductase subunit D [EC:1.3.99.1]		

K00248	107	butyryl-CoA dehydrogenase [EC:1.3.99.2]		
K00249	223	acyl-CoA dehydrogenase [EC:1.3.99.3]		
K00252	32	glutaryl-CoA dehydrogenase [EC:1.3.99.7]		
K00253	67	isovaleryl-CoA dehydrogenase [EC:1.3.99.10]		
K00255	14	long-chain-acyl-CoA dehydrogenase [EC:1.3.99.13]		
K00256	109	isoquinoline 1-oxidoreductase [EC:1.3.99.16]		
K00257	333	Unclassified; E1.3.99.-		
K00258	29	Unclassified; E1.3.-.-		
K00259	29	alanine dehydrogenase [EC:1.4.1.1]		
K00260	63	glutamate dehydrogenase [EC:1.4.1.2]		
K00261	38	glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]		
K00262	26	glutamate dehydrogenase (NADP+) [EC:1.4.1.4]		
K00263	17	leucine dehydrogenase [EC:1.4.1.9]		
K00265	89	glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14]		
K00266	101	glutamate synthase (NADPH/NADH) small chain [EC:1.4.1.13 1.4.1.14]		
K00271	14	valine dehydrogenase [EC:1.4.1.-]		
K00273	15	D-amino-acid oxidase [EC:1.4.3.3]		
K00274	21	monoamine oxidase [EC:1.4.3.4]		
K00275	18	pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]		
K00276	60	primary-amine oxidase [EC:1.4.3.21]		
K00278	44	L-aspartate oxidase [EC:1.4.3.16]		
K00279	15	cytokinin dehydrogenase [EC:1.5.99.12]		
K00280	8	Unclassified; E1.4.3.-		
K00281	24	glycine dehydrogenase [EC:1.4.4.2]		
K00282	30	glycine dehydrogenase subunit 1 [EC:1.4.4.2]		
K00283	25	glycine dehydrogenase subunit 2 [EC:1.4.4.2]		
K00284	28	glutamate synthase (ferredoxin) [EC:1.4.7.1]		
K00285	34	D-amino-acid dehydrogenase [EC:1.4.99.1]		
K00286	27	pyrroline-5-carboxylate reductase [EC:1.5.1.2]		
K00287	56	dihydrofolate reductase [EC:1.5.1.3]		
K00290	30	saccharopine dehydrogenase (NAD+, L-lysine forming) [EC:1.5.1.7]		
K00292	2	saccharopine dehydrogenase (NAD+, L-glutamate forming) [EC:1.5.1.9]		
K00294	69	1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]		
K00297	67	methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]		
K00299	34	FMN reductase [EC:1.5.1.29]		
K00301	35	sarcosine oxidase [EC:1.5.3.1]		
K00302	11	sarcosine oxidase, subunit alpha [EC:1.5.3.1]		
K00303	37	sarcosine oxidase, subunit beta [EC:1.5.3.1]		
K00304	2	sarcosine oxidase, subunit delta [EC:1.5.3.1]		
K00305	1	sarcosine oxidase, subunit gamma [EC:1.5.3.1]		
K00309	57	Unclassified; E1.5.3.-		
K00311	35	electron-transferring-flavoprotein dehydrogenase [EC:1.5.5.1]		
K00313	5	electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]		
K00314	44	sarcosine dehydrogenase [EC:1.5.99.1]		
K00315	21	dimethylglycine dehydrogenase [EC:1.5.99.2]		
K00317	11	trimethylamine dehydrogenase [EC:1.5.8.2]		
K00318	21	proline dehydrogenase [EC:1.5.99.8]		
K00320	25	coenzyme F420-dependent N5,N10-methenyltetrahydromethanopterin		
K00321	1	Unclassified; E1.5.99.-		
K00322	12	NAD(P) transhydrogenase [EC:1.6.1.1]		
K00324	34	NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]		
K00325	18	NAD(P) transhydrogenase subunit beta [EC:1.6.1.2]		
K00326	1	cytochrome-b5 reductase [EC:1.6.2.2]		
K00327	1	NADPH-ferrihemoprotein reductase [EC:1.6.2.4]		
K00329	36	NADH dehydrogenase [EC:1.6.5.3]		
K00330	25	NADH dehydrogenase I subunit A [EC:1.6.5.3]		
K00331	27	NADH dehydrogenase I subunit B [EC:1.6.5.3]		
K00332	21	NADH dehydrogenase I subunit C [EC:1.6.5.3]		
K00333	64	NADH dehydrogenase I subunit D [EC:1.6.5.3]		

K00334	43	NADH dehydrogenase I subunit E [EC:1.6.5.3]		
K00335	80	NADH dehydrogenase I subunit F [EC:1.6.5.3]		
K00336	63	NADH dehydrogenase I subunit G [EC:1.6.5.3]		
K00337	55	NADH dehydrogenase I subunit H [EC:1.6.5.3]		
K00338	26	NADH dehydrogenase I subunit I [EC:1.6.5.3]		
K00339	20	NADH dehydrogenase I subunit J [EC:1.6.5.3]		
K00340	15	NADH dehydrogenase I subunit K [EC:1.6.5.3]		
K00341	57	NADH dehydrogenase I subunit L [EC:1.6.5.3]		
K00342	63	NADH dehydrogenase I subunit M [EC:1.6.5.3]		
K00343	62	NADH dehydrogenase I subunit N [EC:1.6.5.3]		
K00344	170	NADPH2:quinone reductase [EC:1.6.5.5]		
K00346	2	Na+-transporting NADH:ubiquinone oxidoreductase subunit A		
K00347	10	Na+-transporting NADH:ubiquinone oxidoreductase subunit B		
K00348	7	Na+-transporting NADH:ubiquinone oxidoreductase subunit C		
K00349	2	Na+-transporting NADH:ubiquinone oxidoreductase subunit D		
K00350	9	Na+-transporting NADH:ubiquinone oxidoreductase subunit E		
K00351	4	Na+-transporting NADH:ubiquinone oxidoreductase subunit F		
K00353	1	Unclassified; E1.6.6.-		
K00354	18	NADPH2 dehydrogenase [EC:1.6.99.1]		
K00355	4	NAD(P)H dehydrogenase (quinone) [EC:1.6.5.2]		
K00356	59	NADH dehydrogenase [EC:1.6.99.3]		
K00358	10	Unclassified; E1.6.99.-		
K00359	38	NADH oxidase [EC:1.6.-.-]		
K00360	39	nitrate reductase (NADH) [EC:1.7.1.1]		
K00362	26	nitrite reductase (NAD(P)H) large subunit [EC:1.7.1.4]		
K00363	13	nitrite reductase (NAD(P)H) small subunit [EC:1.7.1.4]		
K00364	4	GMP reductase [EC:1.7.1.7]		
K00365	9	urate oxidase [EC:1.7.3.3]		
K00366	23	ferredoxin-nitrite reductase [EC:1.7.7.1]		
K00367	5	ferredoxin-nitrate reductase [EC:1.7.7.2]		
K00368	53	nitrite reductase (NO-forming) [EC:1.7.2.1]		
K00369	45	nitrate reductase [EC:1.7.99.4]		
K00370	34	nitrate reductase 1, alpha subunit [EC:1.7.99.4]		
K00371	12	nitrate reductase 1, beta subunit [EC:1.7.99.4]		
K00372	36	nitrate reductase catalytic subunit [EC:1.7.99.4]		
K00373	4	nitrate reductase 1, delta subunit [EC:1.7.99.4]		
K00374	4	nitrate reductase 1, gamma subunit [EC:1.7.99.4]		
K00375	33	GntR family transcriptional regulator / MocR family aminotransferase		
K00376	14	nitrous-oxide reductase [EC:1.7.99.6]		
K00378	3	hydroxylamine reductase [EC:1.7.-.-]		
K00380	19	sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]		
K00381	24	sulfite reductase (NADPH) hemoprotein beta-component [EC:1.8.1.2]		
K00382	97	dihydrolipoamide dehydrogenase [EC:1.8.1.4]		
K00383	19	glutathione reductase (NADPH) [EC:1.8.1.7]		
K00384	111	thioredoxin reductase (NADPH) [EC:1.8.1.9]		
K00385	1	anaerobic sulfite reductase subunit C [EC:1.8.1.-]		
K00386	20	Unclassified; E1.8.2.-		
K00387	22	sulfite oxidase [EC:1.8.3.1]		
K00389	9	putative membrane protein		
K00390	17	phosphoadenosine phosphosulfate reductase [EC:1.8.4.8]		
K00391	5	Unclassified; E1.8.4.-		
K00392	14	sulfite reductase (ferredoxin) [EC:1.8.7.1]		
K00394	11	adenylylsulfate reductase, subunit A [EC:1.8.99.2]		
K00395	3	adenylylsulfate reductase, subunit B [EC:1.8.99.2]		
K00397	12	anaerobic dimethyl sulfoxide reductase [EC:1.8.99.-]		
K00404	16	cb-type cytochrome c oxidase subunit I [EC:1.9.3.1]		
K00405	17	cb-type cytochrome c oxidase subunit II [EC:1.9.3.1]		
K00406	34	cb-type cytochrome c oxidase subunit III [EC:1.9.3.1]		
K00407	6	cb-type cytochrome c oxidase subunit IV [EC:1.9.3.1]		

K00411	10	ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.2]		
K00412	35	ubiquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.2]		
K00413	8	ubiquinol-cytochrome c reductase cytochrome c1 subunit [EC:1.10.2.2]		
K00421	4	Unclassified; E1.10.2.-		
K00423	22	L-ascorbate oxidase [EC:1.10.3.3]		
K00425	39	cytochrome bd-I oxidase subunit I [EC:1.10.3.-]		
K00426	23	cytochrome bd-I oxidase subunit II [EC:1.10.3.-]		
K00427	2	L-lactate permease		
K00428	51	cytochrome c peroxidase [EC:1.11.1.5]		
K00429	1	catalase [EC:1.11.1.6]		
K00432	7	glutathione peroxidase [EC:1.11.1.9]		
K00433	36	chloride peroxidase [EC:1.11.1.10]		
K00435	19	peroxiredoxin [EC:1.11.1.-]		
K00436	91	hydrogen dehydrogenase [EC:1.12.1.2]		
K00437	8	cytochrome-c3 hydrogenase [EC:1.12.2.1]		
K00441	4	coenzyme F420 hydrogenase beta subunit [EC:1.12.98.1]		
K00442	3	coenzyme F420 hydrogenase delta subunit		
K00446	7	catechol 2,3-dioxygenase [EC:1.13.11.2]		
K00448	10	protocatechuate 3,4-dioxygenase, alpha subunit [EC:1.13.11.3]		
K00449	6	protocatechuate 3,4-dioxygenase, beta subunit [EC:1.13.11.3]		
K00450	24	gentisate 1,2-dioxygenase [EC:1.13.11.4]		
K00451	27	homogentisate 1,2-dioxygenase [EC:1.13.11.5]		
K00453	11	tryptophan 2,3-dioxygenase [EC:1.13.11.11]		
K00455	1	3,4-dihydroxyphenylacetate 2,3-dioxygenase [EC:1.13.11.15]		
K00457	19	4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]		
K00459	54	nitronate monooxygenase [EC:1.13.12.16]		
K00462	4	biphenyl-2,3-diol 1,2-dioxygenase [EC:1.13.11.39]		
K00464	2	lignostilbene-alpha,beta-dioxygenase [EC:1.13.11.43]		
K00465	24	Unclassified; E1.13.11.-		
K00466	5	tryptophan 2-monooxygenase [EC:1.13.12.3]		
K00467	12	lactate 2-monooxygenase [EC:1.13.12.4]		
K00470	8	Unclassified; E1.14.1.-		
K00476	1	aspartate beta-hydroxylase [EC:1.14.11.16]		
K00477	2	phytanoyl-CoA hydroxylase [EC:1.14.11.18]		
K00478	6	Unclassified; E1.14.11.-		
K00479	6	Rieske 2Fe-2S family protein		
K00480	28	salicylate hydroxylase [EC:1.14.13.1]		
K00481	6	p-hydroxybenzoate 3-monooxygenase [EC:1.14.13.2]		
K00483	31	4-hydroxyphenylacetate-3-hydroxylase large chain [EC:1.14.13.3]		
K00484	2	4-hydroxyphenylacetate-3-hydroxylase small chain [EC:1.14.13.3]		
K00485	11	dimethylaniline monooxygenase (N-oxide forming) [EC:1.14.13.8]		
K00491	2	nitric-oxide synthase, bacterial [EC:1.14.13.39]		
K00492	81	Unclassified; E1.14.13.-		
K00493	46	unspecific monooxygenase [EC:1.14.14.1]		
K00494	70	alkanal monooxygenase (FMN-linked) [EC:1.14.14.3]		
K00495	10	Unclassified; E1.14.14.-		
K00499	10	choline monooxygenase [EC:1.14.15.7]		
K00500	17	phenylalanine-4-hydroxylase [EC:1.14.16.1]		
K00504	76	peptidylglycine monooxygenase [EC:1.14.17.3]		
K00507	40	stearoyl-CoA desaturase (delta-9 desaturase) [EC:1.14.19.1]		
K00508	4	linoleoyl-CoA desaturase [EC:1.14.19.3]		
K00514	1	zeta-carotene desaturase [EC:1.14.99.30]		
K00517	179	Unclassified; E1.14.-.-		
K00520	60	mercuric reductase [EC:1.16.1.1]		
K00523	25	CDP-4-dehydro-6-deoxyglucose reductase [EC:1.17.1.1]		
K00525	87	ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]		
K00526	14	ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1]		
K00527	5	ribonucleoside-triphosphate reductase [EC:1.17.4.2]		
K00528	42	ferredoxin--NADP+ reductase [EC:1.18.1.2]		

K00529	61	ferredoxin--NAD+ reductase [EC:1.18.1.3]		
K00530	11	Unclassified; E1.18.1.-		
K00532	22	ferredoxin hydrogenase [EC:1.12.7.2]		
K00533	4	ferredoxin hydrogenase large subunit [EC:1.12.7.2]		
K00534	11	ferredoxin hydrogenase small subunit [EC:1.12.7.2]		
K00535	2	Unclassified; E1.18.-.-		
K00537	7	arsenate reductase [EC:1.20.4.1]		
K00538	5	formate acetyltransferase activating enzyme [EC:1.97.1.4]		
K00539	1	Unclassified; E1.97.1.-		
K00540	1132	Unclassified; E1.-.-.-		
K00544	5	betaine-homocysteine S-methyltransferase [EC:2.1.1.5]		
K00547	33	homocysteine S-methyltransferase [EC:2.1.1.10]		
K00548	117	5-methyltetrahydrofolate--homocysteine methyltransferase		
K00549	72	5-methyltetrahydropteroyltriglutamate--homocysteine		
K00551	21	phosphatidylethanolamine N-methyltransferase [EC:2.1.1.17]		
K00554	30	tRNA (guanine-N1-)-methyltransferase [EC:2.1.1.31]		
K00556	3	tRNA (guanosine-2'-O-)-methyltransferase [EC:2.1.1.34]		
K00557	12	tRNA (uracil-5-)-methyltransferase [EC:2.1.1.35]		
K00558	15	DNA (cytosine-5-)-methyltransferase [EC:2.1.1.37]		
K00559	1	sterol 24-C-methyltransferase [EC:2.1.1.41]		
K00560	9	thymidylate synthase [EC:2.1.1.45]		
K00561	14	rRNA (adenine-N6-)-methyltransferase [EC:2.1.1.48]		
K00563	4	rRNA (guanine-N1-)-methyltransferase [EC:2.1.1.51]		
K00564	1	ribosomal RNA small subunit methyltransferase C [EC:2.1.1.52]		
K00566	48	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase		
K00567	30	methylated-DNA-[protein]-cysteine S-methyltransferase [EC:2.1.1.63]		
K00568	65	3-demethylubiquinone-9 3-methyltransferase [EC:2.1.1.- 2.1.1.64]		
K00569	4	thiopurine S-methyltransferase [EC:2.1.1.67]		
K00570	5	phosphatidyl-N-methylethanolamine N-methyltransferase [EC:2.1.1.71]		
K00571	26	site-specific DNA-methyltransferase (adenine-specific) [EC:2.1.1.72]		
K00573	52	protein-L-isoaspartate(D-aspartate) O-methyltransferase		
K00574	63	cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79]		
K00575	79	chemotaxis protein methyltransferase CheR [EC:2.1.1.80]		
K00584	1	tetrahydromethanopterin S-methyltransferase subunit H [EC:2.1.1.86]		
K00587	7	protein-S-isoprenylcysteine O-methyltransferase [EC:2.1.1.100]		
K00588	15	caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]		
K00590	11	site-specific DNA-methyltransferase (cytosine-N4-specific)		
K00594	3	xylitol oxidase [EC:1.1.3.41]		
K00595	6	precorrin-6Y C5,15-methyltransferase / precorrin-8W decarboxylase		
K00596	3	2,2-dialkylglycine decarboxylase (pyruvate) [EC:4.1.1.64]		
K00598	16	trans-aconitate 2-methyltransferase [EC:2.1.1.144]		
K00599	435	Unclassified; E2.1.1.-		
K00600	49	glycine hydroxymethyltransferase [EC:2.1.2.1]		
K00602	28	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP		
K00603	20	glutamate formiminotransferase [EC:2.1.2.5]		
K00604	50	methionyl-tRNA formyltransferase [EC:2.1.2.9]		
K00605	69	aminomethyltransferase [EC:2.1.2.10]		
K00606	26	3-methyl-2-oxobutanoate hydroxymethyltransferase [EC:2.1.2.11]		
K00607	3	Unclassified; E2.1.2.-		
K00609	35	aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]		
K00610	12	aspartate carbamoyltransferase regulatory subunit		
K00611	50	ornithine carbamoyltransferase [EC:2.1.3.3]		
K00612	37	carbamoyltransferase [EC:2.1.3.-]		
K00613	1	glycine amidinotransferase [EC:2.1.4.1]		
K00614	13	Unclassified; E2.1.-.-		
K00615	102	transketolase [EC:2.2.1.1]		
K00616	40	transaldolase [EC:2.2.1.2]		
K00617	1	Unclassified; E2.2.1.-		
K00619	22	amino-acid N-acetyltransferase [EC:2.3.1.1]		

K00620	31	glutamate N-acetyltransferase / amino-acid N-acetyltransferase		
K00622	5	arylamine N-acetyltransferase [EC:2.3.1.5]		
K00625	21	phosphate acetyltransferase [EC:2.3.1.8]		
K00626	211	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]		
K00627	68	pyruvate dehydrogenase E2 component (dihydrolipoamide		
K00631	12	glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]		
K00632	93	acetyl-CoA acyltransferase [EC:2.3.1.16]		
K00633	18	galactoside O-acetyltransferase [EC:2.3.1.18]		
K00634	11	phosphate butyryltransferase [EC:2.3.1.19]		
K00638	6	chloramphenicol O-acetyltransferase [EC:2.3.1.28]		
K00639	42	glycine C-acetyltransferase [EC:2.3.1.29]		
K00640	27	serine O-acetyltransferase [EC:2.3.1.30]		
K00641	37	homoserine O-acetyltransferase [EC:2.3.1.31]		
K00643	12	5-aminolevulinate synthase [EC:2.3.1.37]		
K00645	48	[acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]		
K00647	39	3-oxoacyl-[acyl-carrier-protein] synthase I [EC:2.3.1.41]		
K00648	79	3-oxoacyl-[acyl-carrier-protein] synthase III [EC:2.3.1.180]		
K00651	3	homoserine O-succinyltransferase [EC:2.3.1.46]		
K00652	51	8-amino-7-oxononanoate synthase [EC:2.3.1.47]		
K00654	7	serine palmitoyltransferase [EC:2.3.1.50]		
K00655	121	1-acyl-sn-glycerol-3-phosphate acyltransferase [EC:2.3.1.51]		
K00656	38	formate C-acetyltransferase [EC:2.3.1.54]		
K00657	13	diamine N-acetyltransferase [EC:2.3.1.57]		
K00658	41	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide		
K00660	12	chalcone synthase [EC:2.3.1.74]		
K00661	8	maltose O-acetyltransferase [EC:2.3.1.79]		
K00662	3	aminoglycoside N3'-acetyltransferase [EC:2.3.1.81]		
K00663	9	aminoglycoside N6'-acetyltransferase [EC:2.3.1.82]		
K00666	187	fatty-acyl-CoA synthase [EC:6.2.1.-]		
K00672	6	formylmethanofuran--tetrahydromethanopterin N-formyltransferase		
K00673	3	arginine N-succinyltransferase [EC:2.3.1.109]		
K00674	18	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase		
K00675	16	N-hydroxyarylamine O-acetyltransferase [EC:2.3.1.118]		
K00676	20	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]		
K00677	32	UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]		
K00680	275	Unclassified; E2.3.1.-		
K00681	137	gamma-glutamyltranspeptidase [EC:2.3.2.2]		
K00683	3	glutaminyl-peptide cyclotransferase [EC:2.3.2.5]		
K00684	12	leucyl/phenylalanyl-tRNA--protein transferase [EC:2.3.2.6]		
K00685	7	arginine-tRNA-protein transferase [EC:2.3.2.8]		
K00688	90	starch phosphorylase [EC:2.4.1.1]		
K00690	3	sucrose phosphorylase [EC:2.4.1.7]		
K00691	17	maltose phosphorylase [EC:2.4.1.8]		
K00693	14	glycogen(starch) synthase [EC:2.4.1.11]		
K00694	12	cellulose synthase (UDP-forming) [EC:2.4.1.12]		
K00695	2	sucrose synthase [EC:2.4.1.13]		
K00696	1	sucrose-phosphate synthase [EC:2.4.1.14]		
K00697	44	alpha,alpha-trehalose-phosphate synthase (UDP-forming) [EC:2.4.1.15]		
K00700	62	1,4-alpha-glucan branching enzyme [EC:2.4.1.18]		
K00701	2	cyclomaltodextrin glucanotransferase [EC:2.4.1.19]		
K00702	10	cellobiose phosphorylase [EC:2.4.1.20]		
K00703	39	starch synthase [EC:2.4.1.21]		
K00705	74	4-alpha-glucanotransferase [EC:2.4.1.25]		
K00712	3	poly(glycerol-phosphate) alpha-glucosyltransferase [EC:2.4.1.52]		
K00720	5	ceramide glucosyltransferase [EC:2.4.1.80]		
K00721	123	dolichol-phosphate mannosyltransferase [EC:2.4.1.83]		
K00743	2	N-acetyllactosaminide 3-alpha-galactosyltransferase [EC:2.4.1.87]		
K00748	28	lipid-A-disaccharide synthase [EC:2.4.1.182]		
K00752	7	hyaluronan synthase [EC:2.4.1.212]		

K00754	464	Unclassified; E2.4.1.-		
K00756	8	pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]		
K00757	2	uridine phosphorylase [EC:2.4.2.3]		
K00758	21	thymidine phosphorylase [EC:2.4.2.4]		
K00759	26	adenine phosphoribosyltransferase [EC:2.4.2.7]		
K00760	33	hypoxanthine phosphoribosyltransferase [EC:2.4.2.8]		
K00761	13	uracil phosphoribosyltransferase [EC:2.4.2.9]		
K00762	22	orotate phosphoribosyltransferase [EC:2.4.2.10]		
K00763	180	nicotinate phosphoribosyltransferase [EC:2.4.2.11]		
K00764	58	amidophosphoribosyltransferase [EC:2.4.2.14]		
K00765	31	ATP phosphoribosyltransferase [EC:2.4.2.17]		
K00766	31	anthranilate phosphoribosyltransferase [EC:2.4.2.18]		
K00767	54	nicotinate-nucleotide pyrophosphorylase (carboxylating)		
K00768	8	nicotinate-nucleotide--dimethylbenzimidazole		
K00772	30	5'-methylthioadenosine phosphorylase [EC:2.4.2.28]		
K00773	26	queuine tRNA-ribosyltransferase [EC:2.4.2.29]		
K00777	15	Unclassified; E2.4.2.-		
K00782	10	hypothetical protein		
K00783	10	hypothetical protein		
K00784	75	ribonuclease Z [EC:3.1.26.11]		
K00785	2	beta-galactosamide-alpha-2,3-sialyltransferase [EC:2.4.99.-]		
K00786	201	Unclassified; E2.4.-.-		
K00788	35	thiamine-phosphate pyrophosphorylase [EC:2.5.1.3]		
K00789	31	S-adenosylmethionine synthetase [EC:2.5.1.6]		
K00790	50	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7]		
K00791	29	tRNA dimethylallyltransferase [EC:2.5.1.75]		
K00793	31	riboflavin synthase alpha chain [EC:2.5.1.9]		
K00794	15	riboflavin synthase beta chain [EC:2.5.1.-]		
K00795	8	farnesyl diphosphate synthase [EC:2.5.1.1 2.5.1.10]		
K00796	35	dihydropteroate synthase [EC:2.5.1.15]		
K00797	37	spermidine synthase [EC:2.5.1.16]		
K00798	27	cob(I)alamin adenosyltransferase [EC:2.5.1.17]		
K00799	108	glutathione S-transferase [EC:2.5.1.18]		
K00800	62	3-phosphoshikimate 1-carboxyvinyltransferase [EC:2.5.1.19]		
K00801	13	farnesyl-diphosphate farnesyltransferase [EC:2.5.1.21]		
K00802	3	spermine synthase [EC:2.5.1.22]		
K00803	23	alkyldihydroxyacetonephosphate synthase [EC:2.5.1.26]		
K00805	9	heptaprenyl diphosphate synthase [EC:2.5.1.30]		
K00806	20	undecaprenyl diphosphate synthase [EC:2.5.1.31]		
K00808	4	homospermidine synthase [EC:2.5.1.44]		
K00809	18	deoxyhypusine synthase [EC:2.5.1.46]		
K00810	24	Unclassified; E2.5.1.-		
K00811	2	aspartate aminotransferase [EC:2.6.1.1]		
K00812	46	aspartate aminotransferase [EC:2.6.1.1]		
K00813	7	aspartate aminotransferase [EC:2.6.1.1]		
K00814	3	alanine transaminase [EC:2.6.1.2]		
K00817	59	histidinol-phosphate aminotransferase [EC:2.6.1.9]		
K00818	49	acetylornithine aminotransferase [EC:2.6.1.11]		
K00819	14	ornithine--oxo-acid transaminase [EC:2.6.1.13]		
K00820	67	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)		
K00821	47	acetylornithine/N-succinyldiaminopimelate aminotransferase		
K00822	14	beta-alanine--pyruvate transaminase [EC:2.6.1.18]		
K00823	47	4-aminobutyrate aminotransferase [EC:2.6.1.19]		
K00824	14	D-alanine transaminase [EC:2.6.1.21]		
K00825	17	2-aminoadipate transaminase [EC:2.6.1.39]		
K00826	73	branched-chain amino acid aminotransferase [EC:2.6.1.42]		
K00828	29	serine--glyoxylate transaminase [EC:2.6.1.45]		
K00831	23	phosphoserine aminotransferase [EC:2.6.1.52]		
K00832	8	aromatic-amino-acid transaminase [EC:2.6.1.57]		

K00833	19	adenosylmethionine-8-amino-7-oxononanoate aminotransferase		
K00835	12	valine--pyruvate aminotransferase [EC:2.6.1.66]		
K00836	5	diaminobutyrate-2-oxoglutarate transaminase [EC:2.6.1.76]		
K00837	274	Unclassified; E2.6.1.-		
K00839	38	aminotransferase [EC:2.6.1.-]		
K00840	1	succinylornithine aminotransferase [EC:2.6.1.81]		
K00841	1	aminotransferase [EC:2.6.1.-]		
K00842	11	aminotransferase [EC:2.6.1.-]		
K00843	6	Unclassified; E2.6.-.-		
K00845	73	glucokinase [EC:2.7.1.2]		
K00846	2	ketohexokinase [EC:2.7.1.3]		
K00847	33	fructokinase [EC:2.7.1.4]		
K00848	14	rhamnulokinase [EC:2.7.1.5]		
K00849	14	galactokinase [EC:2.7.1.6]		
K00850	56	6-phosphofructokinase [EC:2.7.1.11]		
K00851	14	gluconokinase [EC:2.7.1.12]		
K00852	25	ribokinase [EC:2.7.1.15]		
K00853	8	L-ribulokinase [EC:2.7.1.16]		
K00854	34	xylulokinase [EC:2.7.1.17]		
K00855	13	phosphoribulokinase [EC:2.7.1.19]		
K00856	21	adenosine kinase [EC:2.7.1.20]		
K00857	8	thymidine kinase [EC:2.7.1.21]		
K00858	35	NAD+ kinase [EC:2.7.1.23]		
K00859	35	dephospho-CoA kinase [EC:2.7.1.24]		
K00860	18	adenylylsulfate kinase [EC:2.7.1.25]		
K00861	3	riboflavin kinase [EC:2.7.1.26]		
K00862	1	erythritol kinase [EC:2.7.1.27]		
K00863	8	dihydroxyacetone kinase [EC:2.7.1.29]		
K00864	41	glycerol kinase [EC:2.7.1.30]		
K00865	12	glycerate kinase [EC:2.7.1.31]		
K00866	1	choline kinase [EC:2.7.1.32]		
K00867	2	type I pantothenate kinase [EC:2.7.1.33]		
K00868	445	pyridoxine kinase [EC:2.7.1.35]		
K00869	1	mevalonate kinase [EC:2.7.1.36]		
K00870	68	protein kinase [EC:2.7.1.37]		
K00872	9	homoserine kinase [EC:2.7.1.39]		
K00873	44	pyruvate kinase [EC:2.7.1.40]		
K00874	20	2-dehydro-3-deoxygluconokinase [EC:2.7.1.45]		
K00875	2	D-ribulokinase [EC:2.7.1.47]		
K00876	12	uridine kinase [EC:2.7.1.48]		
K00877	3	hydroxymethylpyrimidine kinase [EC:2.7.1.49]		
K00878	3	hydroxyethylthiazole kinase [EC:2.7.1.50]		
K00879	4	L-fuculokinase [EC:2.7.1.51]		
K00880	1	L-xylulokinase [EC:2.7.1.53]		
K00882	14	1-phosphofructokinase [EC:2.7.1.56]		
K00883	1	2-dehydro-3-deoxygalactonokinase [EC:2.7.1.58]		
K00884	7	N-acetylglucosamine kinase [EC:2.7.1.59]		
K00885	1	N-acylmannosamine kinase [EC:2.7.1.60]		
K00886	9	polyphosphate glucokinase [EC:2.7.1.63]		
K00887	10	undecaprenol kinase [EC:2.7.1.66]		
K00891	31	shikimate kinase [EC:2.7.1.71]		
K00894	3	ethanolamine kinase [EC:2.7.1.82]		
K00895	22	pyrophosphate--fructose-6-phosphate 1-phosphotransferase		
K00897	10	aminoglycoside 3'-phosphotransferase [EC:2.7.1.95]		
K00901	6	diacylglycerol kinase [EC:2.7.1.107]		
K00903	70	protein-tyrosine kinase [EC:2.7.10.-]		
K00904	18	deoxyguanosine kinase [EC:2.7.1.113]		
K00906	11	isocitrate dehydrogenase kinase/phosphatase [EC:2.7.11.5 3.1.3.-]		
K00908	216	Ca2+/calmodulin-dependent protein kinase [EC:2.7.11.17]		

K00912	13	tetraacyldisaccharide 4'-kinase [EC:2.7.1.130]		
K00917	9	tagatose 6-phosphate kinase [EC:2.7.1.144]		
K00919	25	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [EC:2.7.1.148]		
K00924	351	Unclassified; E2.7.1.-		
K00925	31	acetate kinase [EC:2.7.2.1]		
K00926	18	carbamate kinase [EC:2.7.2.2]		
K00927	35	phosphoglycerate kinase [EC:2.7.2.3]		
K00928	33	aspartate kinase [EC:2.7.2.4]		
K00929	3	butyrate kinase [EC:2.7.2.7]		
K00930	23	acetylglutamate kinase [EC:2.7.2.8]		
K00931	54	glutamate 5-kinase [EC:2.7.2.11]		
K00932	1	propionate kinase [EC:2.7.2.15]		
K00933	1	creatine kinase [EC:2.7.3.2]		
K00934	4	arginine kinase [EC:2.7.3.3]		
K00935	4	Unclassified; E2.7.3.9		
K00936	1280	Unclassified; E2.7.3.-		
K00937	60	polyphosphate kinase [EC:2.7.4.1]		
K00938	5	phosphomevalonate kinase [EC:2.7.4.2]		
K00939	34	adenylate kinase [EC:2.7.4.3]		
K00940	20	nucleoside-diphosphate kinase [EC:2.7.4.6]		
K00941	29	phosphomethylpyrimidine kinase [EC:2.7.4.7]		
K00942	26	guanylate kinase [EC:2.7.4.8]		
K00943	33	dTMP kinase [EC:2.7.4.9]		
K00945	33	cytidylate kinase [EC:2.7.4.14]		
K00946	33	thiamine-monophosphate kinase [EC:2.7.4.16]		
K00947	27	Unclassified; E2.7.4.-		
K00948	177	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]		
K00950	17	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase		
K00951	90	GTP pyrophosphokinase [EC:2.7.6.5]		
K00954	23	pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]		
K00955	28	bifunctional enzyme CysN/CysC [EC:2.7.7.4 2.7.1.25]		
K00956	29	sulfate adenylyltransferase subunit 1 [EC:2.7.7.4]		
K00957	10	sulfate adenylyltransferase subunit 2 [EC:2.7.7.4]		
K00958	25	sulfate adenylyltransferase [EC:2.7.7.4]		
K00960	7	DNA-directed RNA polymerase [EC:2.7.7.6]		
K00961	7	DNA polymerase [EC:2.7.7.7]		
K00962	39	polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]		
K00963	23	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]		
K00964	23	galactose-1-phosphate uridylyltransferase [EC:2.7.7.10]		
K00965	24	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]		
K00966	49	mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]		
K00969	56	nicotinate-nucleotide adenylyltransferase [EC:2.7.7.18]		
K00970	57	poly(A) polymerase [EC:2.7.7.19]		
K00971	42	mannose-1-phosphate guanylyltransferase [EC:2.7.7.22]		
K00972	3	UDP-N-acetylglucosamine pyrophosphorylase [EC:2.7.7.23]		
K00973	45	glucose-1-phosphate thymidylyltransferase [EC:2.7.7.24]		
K00974	27	tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.25		
K00975	42	glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]		
K00978	15	glucose-1-phosphate cytidylyltransferase [EC:2.7.7.33]		
K00979	26	3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase)		
K00980	8	glycerol-3-phosphate cytidylyltransferase [EC:2.7.7.39]		
K00981	27	phosphatidate cytidylyltransferase [EC:2.7.7.41]		
K00982	55	glutamate-ammonia-ligase adenylyltransferase [EC:2.7.7.42]		
K00983	2	N-acylneuraminate cytidylyltransferase [EC:2.7.7.43]		
K00985	6	RNA-directed RNA polymerase [EC:2.7.7.48]		
K00986	61	RNA-directed DNA polymerase [EC:2.7.7.49]		
K00989	19	ribonuclease PH [EC:2.7.7.56]		
K00990	45	[protein-PII] uridylyltransferase [EC:2.7.7.59]		
K00991	20	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase		

K00992	28	Unclassified; E2.7.7.-		
K00995	115	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase		
K00996	3	undecaprenyl-phosphate galactose phosphotransferase [EC:2.7.8.6]		
K00997	15	holo-[acyl-carrier protein] synthase [EC:2.7.8.7]		
K00998	20	phosphatidylserine synthase [EC:2.7.8.8]		
K00999	4	CDP-diacylglycerol--inositol 3-phosphatidyltransferase [EC:2.7.8.11]		
K01000	52	phospho-N-acetylmuramoyl-pentapeptide-transferase [EC:2.7.8.13]		
K01002	9	phosphoglycerol transferase [EC:2.7.8.20]		
K01003	30	carboxyvinyl-carboxyphosphonate phosphorylmutase [EC:2.7.8.23]		
K01005	35	Unclassified; E2.7.8.-		
K01006	55	pyruvate,orthophosphate dikinase [EC:2.7.9.1]		
K01007	80	pyruvate, water dikinase [EC:2.7.9.2]		
K01008	29	selenide, water dikinase [EC:2.7.9.3]		
K01010	60	thiosulfate sulfurtransferase [EC:2.8.1.1]		
K01011	21	3-mercaptopyruvate sulfurtransferase [EC:2.8.1.2]		
K01012	22	biotin synthetase [EC:2.8.1.6]		
K01013	25	Unclassified; E2.8.1.-		
K01026	7	propionate CoA-transferase [EC:2.8.3.1]		
K01027	3	3-oxoacid CoA-transferase [EC:2.8.3.5]		
K01028	6	3-oxoacid CoA-transferase subunit A [EC:2.8.3.5]		
K01029	3	3-oxoacid CoA-transferase subunit B [EC:2.8.3.5]		
K01031	3	3-oxoadipate CoA-transferase, alpha subunit [EC:2.8.3.6]		
K01032	3	3-oxoadipate CoA-transferase, beta subunit [EC:2.8.3.6]		
K01035	2	acetate CoA-transferase beta subunit [EC:2.8.3.8]		
K01036	1	butyrate-acetoacetate CoA-transferase [EC:2.8.3.9]		
K01039	25	glutaconate CoA-transferase, subunit A [EC:2.8.3.12]		
K01040	18	glutaconate CoA-transferase, subunit B [EC:2.8.3.12]		
K01041	111	Unclassified; E2.8.3.-		
K01042	37	L-seryl-tRNA(Ser) seleniumtransferase [EC:2.9.1.1]		
K01043	161	Unclassified; E2.-.-.-		
K01044	56	carboxylesterase [EC:3.1.1.1]		
K01046	68	triacylglycerol lipase [EC:3.1.1.3]		
K01048	6	lysophospholipase [EC:3.1.1.5]		
K01051	2	pectinesterase [EC:3.1.1.11]		
K01053	63	gluconolactonase [EC:3.1.1.17]		
K01054	3	acylglycerol lipase [EC:3.1.1.23]		
K01055	56	3-oxoadipate enol-lactonase [EC:3.1.1.24]		
K01056	29	peptidyl-tRNA hydrolase, PTH1 family [EC:3.1.1.29]		
K01057	24	6-phosphogluconolactonase [EC:3.1.1.31]		
K01058	8	phospholipase A1 [EC:3.1.1.32]		
K01060	3	cephalosporin-C deacetylase [EC:3.1.1.41]		
K01061	68	carboxymethylenebutenolidase [EC:3.1.1.45]		
K01062	1	1-alkyl-2-acetylglycerophosphocholine esterase [EC:3.1.1.47]		
K01066	94	esterase / lipase [EC:3.1.1.-]		
K01067	12	acetyl-CoA hydrolase [EC:3.1.2.1]		
K01068	5	palmitoyl-CoA hydrolase [EC:3.1.2.2]		
K01069	110	hydroxyacylglutathione hydrolase [EC:3.1.2.6]		
K01070	5	S-formylglutathione hydrolase [EC:3.1.2.12]		
K01071	2	oleoyl-[acyl-carrier-protein] hydrolase [EC:3.1.2.14]		
K01073	7	acyl-CoA hydrolase [EC:3.1.2.20]		
K01075	12	4-hydroxybenzoyl-CoA thioesterase [EC:3.1.2.23]		
K01076	26	Unclassified; E3.1.2.-		
K01077	90	alkaline phosphatase [EC:3.1.3.1]		
K01078	17	acid phosphatase [EC:3.1.3.2]		
K01079	34	phosphoserine phosphatase [EC:3.1.3.3]		
K01081	32	5'-nucleotidase [EC:3.1.3.5]		
K01083	1	3-phytase [EC:3.1.3.8]		
K01087	73	trehalose-phosphatase [EC:3.1.3.12]		
K01090	68	protein phosphatase [EC:3.1.3.16]		

K01091	72	phosphoglycolate phosphatase [EC:3.1.3.18]		
K01092	58	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]		
K01093	4	4-phytase / acid phosphatase [EC:3.1.3.26 3.1.3.2]		
K01095	8	phosphatidylglycerophosphatase A [EC:3.1.3.27]		
K01096	4	phosphatidylglycerophosphatase B [EC:3.1.3.27]		
K01101	7	4-nitrophenyl phosphatase [EC:3.1.3.41]		
K01103	1	fructose-2,6-bisphosphatase [EC:3.1.3.46]		
K01104	39	protein-tyrosine phosphatase [EC:3.1.3.48]		
K01112	32	Unclassified; E3.1.3.-		
K01113	42	phosphodiesterase/alkaline phosphatase D [EC:3.1.4.1]		
K01114	33	phospholipase C [EC:3.1.4.3]		
K01115	8	phospholipase D [EC:3.1.4.4]		
K01118	3	FMN-dependent NADH-azoreductase [EC:1.7.-.-]		
K01119	13	2',3'-cyclic-nucleotide 2'-phosphodiesterase [EC:3.1.4.16]		
K01120	22	3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]		
K01121	1	2',3'-cyclic-nucleotide 3'-phosphodiesterase [EC:3.1.4.37]		
K01126	47	glycerophosphoryl diester phosphodiesterase [EC:3.1.4.46]		
K01128	8	Unclassified; E3.1.4.-		
K01129	24	dGTPase [EC:3.1.5.1]		
K01130	86	arylsulfatase [EC:3.1.6.1]		
K01131	7	steryl-sulfatase [EC:3.1.6.2]		
K01132	17	N-acetylgalactosamine-6-sulfatase [EC:3.1.6.4]		
K01133	31	choline-sulfatase [EC:3.1.6.6]		
K01134	23	arylsulfatase A [EC:3.1.6.8]		
K01135	17	arylsulfatase B [EC:3.1.6.12]		
K01136	8	iduronate 2-sulfatase [EC:3.1.6.13]		
K01137	10	N-acetylglucosamine-6-sulfatase [EC:3.1.6.14]		
K01138	72	Unclassified; E3.1.6.-		
K01139	45	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase		
K01142	29	exodeoxyribonuclease III [EC:3.1.11.2]		
K01144	43	exodeoxyribonuclease V [EC:3.1.11.5]		
K01146	7	Unclassified; E3.1.11.-		
K01147	24	exoribonuclease II [EC:3.1.13.1]		
K01151	37	deoxyribonuclease IV [EC:3.1.21.2]		
K01152	2	type I restriction enzyme [EC:3.1.21.3]		
K01153	63	type I restriction enzyme, R subunit [EC:3.1.21.3]		
K01154	15	type I restriction enzyme, S subunit [EC:3.1.21.3]		
K01155	2	type II restriction enzyme [EC:3.1.21.4]		
K01156	7	type III restriction enzyme [EC:3.1.21.5]		
K01157	37	Unclassified; E3.1.21.-		
K01159	34	crossover junction endodeoxyribonuclease RuvC [EC:3.1.22.4]		
K01162	2	ribonuclease III [EC:3.1.26.3]		
K01166	1	ribonuclease T2 [EC:3.1.27.1]		
K01167	9	ribonuclease T1 [EC:3.1.27.3]		
K01172	1	Unclassified; E3.1.27.-		
K01173	1	endonuclease [EC:3.1.30.-]		
K01174	9	micrococcal nuclease [EC:3.1.31.1]		
K01175	109	Unclassified; E3.1.-.-		
K01176	36	alpha-amylase [EC:3.2.1.1]		
K01178	57	glucoamylase [EC:3.2.1.3]		
K01179	39	endoglucanase [EC:3.2.1.4]		
K01181	11	endo-1,4-beta-xylanase [EC:3.2.1.8]		
K01182	13	oligo-1,6-glucosidase [EC:3.2.1.10]		
K01183	28	chitinase [EC:3.2.1.14]		
K01184	1	polygalacturonase [EC:3.2.1.15]		
K01185	14	lysozyme [EC:3.2.1.17]		
K01186	2	sialidase-1 [EC:3.2.1.18]		
K01187	42	alpha-glucosidase [EC:3.2.1.20]		
K01188	77	beta-glucosidase [EC:3.2.1.21]		

K01190	51	beta-galactosidase [EC:3.2.1.23]		
K01191	17	alpha-mannosidase [EC:3.2.1.24]		
K01192	9	beta-mannosidase [EC:3.2.1.25]		
K01193	2	beta-fructofuranosidase [EC:3.2.1.26]		
K01194	6	alpha,alpha-trehalase [EC:3.2.1.28]		
K01195	8	beta-glucuronidase [EC:3.2.1.31]		
K01197	1	hyaluronoglucosaminidase [EC:3.2.1.35]		
K01198	9	xylan 1,4-beta-xylosidase [EC:3.2.1.37]		
K01199	9	glucan endo-1,3-beta-D-glucosidase [EC:3.2.1.39]		
K01200	4	pullulanase [EC:3.2.1.41]		
K01201	13	glucosylceramidase [EC:3.2.1.45]		
K01206	21	alpha-L-fucosidase [EC:3.2.1.51]		
K01207	53	beta-N-acetylhexosaminidase [EC:3.2.1.52]		
K01208	1	cyclomaltodextrinase [EC:3.2.1.54]		
K01209	22	alpha-N-arabinofuranosidase [EC:3.2.1.55]		
K01210	10	glucan 1,3-beta-glucosidase [EC:3.2.1.58]		
K01212	11	levanase [EC:3.2.1.65]		
K01213	6	galacturan 1,4-alpha-galacturonidase [EC:3.2.1.67]		
K01215	2	glucan 1,6-alpha-glucosidase [EC:3.2.1.70]		
K01216	10	licheninase [EC:3.2.1.73]		
K01218	6	mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]		
K01220	15	6-phospho-beta-galactosidase [EC:3.2.1.85]		
K01222	6	6-phospho-beta-glucosidase [EC:3.2.1.86]		
K01223	1	6-phospho-beta-glucosidase [EC:3.2.1.86]		
K01224	2	arabinogalactan endo-1,4-beta-galactosidase [EC:3.2.1.89]		
K01225	25	cellulose 1,4-beta-cellobiosidase [EC:3.2.1.91]		
K01226	3	trehalose-6-phosphate hydrolase [EC:3.2.1.93]		
K01234	2	neopullulanase [EC:3.2.1.135]		
K01235	3	alpha-glucuronidase [EC:3.2.1.139]		
K01236	28	maltooligosyltrehalose trehalohydrolase [EC:3.2.1.141]		
K01238	177	Unclassified; E3.2.1.-		
K01239	17	purine nucleosidase [EC:3.2.2.1]		
K01241	4	AMP nucleosidase [EC:3.2.2.4]		
K01243	6	S-adenosylhomocysteine/5'-methylthioadenosine nucleosidase		
K01246	12	DNA-3-methyladenine glycosylase I [EC:3.2.2.20]		
K01247	18	DNA-3-methyladenine glycosylase II [EC:3.2.2.21]		
K01249	33	DNA glycosylase [EC:3.2.2.-]		
K01250	8	pyrimidine-specific ribonucleoside hydrolase [EC:3.2.-.-]		
K01251	29	adenosylhomocysteinase [EC:3.3.1.1]		
K01253	35	microsomal epoxide hydrolase [EC:3.3.2.9]		
K01255	52	leucyl aminopeptidase [EC:3.4.11.1]		
K01256	102	aminopeptidase N [EC:3.4.11.2]		
K01258	13	tripeptide aminopeptidase [EC:3.4.11.4]		
K01259	49	proline iminopeptidase [EC:3.4.11.5]		
K01262	80	X-Pro aminopeptidase [EC:3.4.11.9]		
K01263	9	cytosol alanyl aminopeptidase [EC:3.4.11.14]		
K01264	9	aminopeptidase Y [EC:3.4.11.15]		
K01265	30	methionyl aminopeptidase [EC:3.4.11.18]		
K01266	19	D-aminopeptidase [EC:3.4.11.19]		
K01267	2	aspartyl aminopeptidase [EC:3.4.11.21]		
K01268	1	aminopeptidase I [EC:3.4.11.22]		
K01269	174	aminopeptidase [EC:3.4.11.-]		
K01270	3	aminoacylhistidine dipeptidase [EC:3.4.13.3]		
K01271	52	X-Pro dipeptidase [EC:3.4.13.9]		
K01273	44	membrane dipeptidase [EC:3.4.13.19]		
K01274	10	D-alanyl-D-alanine dipeptidase [EC:3.4.13.-]		
K01277	4	dipeptidyl-peptidase III [EC:3.4.14.4]		
K01278	26	dipeptidyl-peptidase 4 [EC:3.4.14.5]		
K01281	8	X-Pro dipeptidyl-peptidase [EC:3.4.14.11]		

K01283	4	peptidyl-dipeptidase A [EC:3.4.15.1]		
K01284	35	peptidyl-dipeptidase Dcp [EC:3.4.15.5]		
K01286	36	D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4]		
K01289	13	carboxypeptidase [EC:3.4.16.-]		
K01295	41	glutamate carboxypeptidase [EC:3.4.17.11]		
K01297	11	muramoyltetrapeptide carboxypeptidase [EC:3.4.17.13]		
K01299	20	carboxypeptidase Taq [EC:3.4.17.19]		
K01301	10	glutamate carboxypeptidase II [EC:3.4.17.21]		
K01302	1	Unclassified; E3.4.17.-		
K01303	93	acylaminoacyl-peptidase [EC:3.4.19.1]		
K01304	3	pyroglutamyl-peptidase [EC:3.4.19.3]		
K01312	9	trypsin [EC:3.4.21.4]		
K01318	1	glutamyl endopeptidase [EC:3.4.21.19]		
K01322	103	prolyl oligopeptidase [EC:3.4.21.26]		
K01325	2	tissue kallikrein [EC:3.4.21.35]		
K01338	158	ATP-dependent Lon protease [EC:3.4.21.53]		
K01341	5	kexin [EC:3.4.21.61]		
K01342	54	subtilisin [EC:3.4.21.62]		
K01344	1	protein C (activated) [EC:3.4.21.69]		
K01347	2	IgA-specific serine endopeptidase [EC:3.4.21.72]		
K01354	61	oligopeptidase B [EC:3.4.21.83]		
K01356	28	repressor LexA [EC:3.4.21.88]		
K01358	30	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]		
K01361	6	lactocepin [EC:3.4.21.96]		
K01362	487	Unclassified; E3.4.21.-		
K01372	2	bleomycin hydrolase [EC:3.4.22.40]		
K01376	12	Unclassified; E3.4.22.-		
K01387	13	microbial collagenase [EC:3.4.24.3]		
K01389	2	neprilysin [EC:3.4.24.11]		
K01392	9	thimet oligopeptidase [EC:3.4.24.15]		
K01400	2	bacillolysin [EC:3.4.24.28]		
K01401	1	aureolysin [EC:3.4.24.29]		
K01406	35	serralysin [EC:3.4.24.40]		
K01407	1	protease III [EC:3.4.24.55]		
K01409	44	O-sialoglycoprotein endopeptidase [EC:3.4.24.57]		
K01412	104	mitochondrial processing peptidase [EC:3.4.24.64]		
K01414	25	oligopeptidase A [EC:3.4.24.70]		
K01415	46	endothelin-converting enzyme [EC:3.4.24.71]		
K01416	2	snapalysin [EC:3.4.24.77]		
K01417	359	Unclassified; E3.4.24.-		
K01419	10	ATP-dependent HslUV protease, peptidase subunit HslV [EC:3.4.25.-]		
K01420	81	CRP/FNR family transcriptional regulator, anaerobic regulatory		
K01421	2	putative membrane protein		
K01422	101	Unclassified; E3.4.99.-		
K01423	395	Unclassified; E3.4.-.-		
K01424	54	L-asparaginase [EC:3.5.1.1]		
K01425	10	glutaminase [EC:3.5.1.2]		
K01426	156	amidase [EC:3.5.1.4]		
K01428	11	urease alpha subunit [EC:3.5.1.5]		
K01429	3	urease beta subunit [EC:3.5.1.5]		
K01430	6	urease gamma subunit [EC:3.5.1.5]		
K01431	27	beta-ureidopropionase [EC:3.5.1.6]		
K01433	7	formyltetrahydrofolate deformylase [EC:3.5.1.10]		
K01434	69	penicillin amidase [EC:3.5.1.11]		
K01436	74	aminoacylase [EC:3.5.1.14]		
K01438	28	acetylornithine deacetylase [EC:3.5.1.16]		
K01439	82	succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]		
K01443	68	N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]		
K01444	9	N4-(beta-N-acetylglucosaminyl)-L-asparaginase [EC:3.5.1.26]		

K01446	2	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K01447	31	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K01448	611	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K01449	4	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K01451	45	hippurate hydrolase [EC:3.5.1.32]		
K01452	38	chitin deacetylase [EC:3.5.1.41]		
K01453	19	Unclassified; E3.5.1.46		
K01454	11	Unclassified; E3.5.1.48		
K01455	26	formamidase [EC:3.5.1.49]		
K01457	9	allophanate hydrolase [EC:3.5.1.54]		
K01458	6	N-formylglutamate deformylase [EC:3.5.1.68]		
K01459	6	Unclassified; E3.5.1.77		
K01461	67	Unclassified; E3.5.1.82		
K01462	44	Unclassified; E3.5.1.88		
K01463	176	Unclassified; E3.5.1.-		
K01464	42	dihydropyrimidinase [EC:3.5.2.2]		
K01465	147	dihydroorotase [EC:3.5.2.3]		
K01466	28	allantoinase [EC:3.5.2.5]		
K01467	153	beta-lactamase [EC:3.5.2.6]		
K01468	45	imidazolonepropionase [EC:3.5.2.7]		
K01469	35	5-oxoprolinase (ATP-hydrolysing) [EC:3.5.2.9]		
K01470	24	creatinine amidohydrolase [EC:3.5.2.10]		
K01471	12	Unclassified; E3.5.2.12		
K01473	68	N-methylhydantoinase A [EC:3.5.2.14]		
K01474	76	N-methylhydantoinase B [EC:3.5.2.14]		
K01476	13	arginase [EC:3.5.3.1]		
K01477	8	allantoicase [EC:3.5.3.4]		
K01478	10	arginine deiminase [EC:3.5.3.6]		
K01479	4	formiminoglutamase [EC:3.5.3.8]		
K01480	40	agmatinase [EC:3.5.3.11]		
K01482	9	dimethylargininase [EC:3.5.3.18]		
K01483	1	ureidoglycolate hydrolase [EC:3.5.3.19]		
K01484	1	succinylarginine dihydrolase [EC:3.5.3.23]		
K01485	25	cytosine deaminase [EC:3.5.4.1]		
K01486	15	adenine deaminase [EC:3.5.4.2]		
K01487	12	guanine deaminase [EC:3.5.4.3]		
K01488	35	adenosine deaminase [EC:3.5.4.4]		
K01489	21	cytidine deaminase [EC:3.5.4.5]		
K01491	34	methylenetetrahydrofolate dehydrogenase (NADP+) /		
K01492	2	phosphoribosylaminoimidazolecarboxamide formyltransferase		
K01493	13	dCMP deaminase [EC:3.5.4.12]		
K01494	20	dCTP deaminase [EC:3.5.4.13]		
K01495	28	GTP cyclohydrolase I [EC:3.5.4.16]		
K01496	6	phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]		
K01497	24	GTP cyclohydrolase II [EC:3.5.4.25]		
K01498	1	diaminohydroxyphosphoribosylaminopyrimidine deaminase [EC:3.5.4.26]		
K01499	3	methenyltetrahydromethanopterin cyclohydrolase [EC:3.5.4.27]		
K01500	18	Unclassified; E3.5.4.-		
K01501	28	nitrilase [EC:3.5.5.1]		
K01502	12	aliphatic nitrilase [EC:3.5.5.7]		
K01503	10	Unclassified; E3.5.5.-		
K01504	6	glucosamine-6-phosphate isomerase [EC:3.5.99.6]		
K01505	4	1-aminocyclopropane-1-carboxylate deaminase [EC:3.5.99.7]		
K01506	64	Unclassified; E3.5.-.-		
K01507	54	inorganic pyrophosphatase [EC:3.6.1.1]		
K01512	16	acylphosphatase [EC:3.6.1.7]		
K01514	57	exopolyphosphatase [EC:3.6.1.11]		
K01515	41	ADP-ribose pyrophosphatase [EC:3.6.1.13]		
K01516	30	nucleoside-triphosphatase [EC:3.6.1.15]		

K01518	13	bis(5'-nucleosidyl)-tetraphosphatase [EC:3.6.1.17]		
K01520	14	dUTP pyrophosphatase [EC:3.6.1.23]		
K01523	4	phosphoribosyl-ATP pyrophosphohydrolase [EC:3.6.1.31]		
K01524	18	guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase		
K01525	13	bis(5'-nucleosyl)-tetraphosphatase (symmetrical) [EC:3.6.1.41]		
K01529	223	Unclassified; E3.6.1.-		
K01531	33	Mg2+-importing ATPase [EC:3.6.3.2]		
K01533	135	Cu2+-exporting ATPase [EC:3.6.3.4]		
K01534	28	Cd2+/Zn2+-exporting ATPase [EC:3.6.3.3 3.6.3.5]		
K01535	2	H+-transporting ATPase [EC:3.6.3.6]		
K01537	113	Ca2+-transporting ATPase [EC:3.6.3.8]		
K01539	6	sodium/potassium-transporting ATPase subunit alpha [EC:3.6.3.9]		
K01546	18	K+-transporting ATPase ATPase A chain [EC:3.6.3.12]		
K01547	19	K+-transporting ATPase ATPase B chain [EC:3.6.3.12]		
K01548	14	K+-transporting ATPase ATPase C chain [EC:3.6.3.12]		
K01551	26	arsenite-transporting ATPase [EC:3.6.3.16]		
K01552	141	Unclassified; E3.6.3.-		
K01554	4	Unclassified; E3.6.-.-		
K01555	12	fumarylacetoacetase [EC:3.7.1.2]		
K01556	30	kynureninase [EC:3.7.1.3]		
K01557	5	acylpyruvate hydrolase [EC:3.7.1.5]		
K01559	14	Unclassified; E3.7.1.-		
K01560	34	2-haloacid dehalogenase [EC:3.8.1.2]		
K01561	20	haloacetate dehalogenase [EC:3.8.1.3]		
K01563	44	haloalkane dehalogenase [EC:3.8.1.5]		
K01564	47	Unclassified; E3.8.1.-		
K01567	169	Unclassified; E3.-.-.-		
K01568	1	pyruvate decarboxylase [EC:4.1.1.1]		
K01571	11	oxaloacetate decarboxylase, alpha subunit [EC:4.1.1.3]		
K01572	9	oxaloacetate decarboxylase, beta subunit [EC:4.1.1.3]		
K01576	25	benzoylformate decarboxylase [EC:4.1.1.7]		
K01577	9	oxalyl-CoA decarboxylase [EC:4.1.1.8]		
K01578	19	malonyl-CoA decarboxylase [EC:4.1.1.9]		
K01579	12	aspartate 1-decarboxylase [EC:4.1.1.11]		
K01580	8	glutamate decarboxylase [EC:4.1.1.15]		
K01581	17	ornithine decarboxylase [EC:4.1.1.17]		
K01582	22	lysine decarboxylase [EC:4.1.1.18]		
K01583	17	arginine decarboxylase [EC:4.1.1.19]		
K01584	17	arginine decarboxylase [EC:4.1.1.19]		
K01585	30	arginine decarboxylase [EC:4.1.1.19]		
K01586	61	diaminopimelate decarboxylase [EC:4.1.1.20]		
K01588	20	5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]		
K01589	16	5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]		
K01591	30	orotidine-5'-phosphate decarboxylase [EC:4.1.1.23]		
K01592	14	tyrosine decarboxylase [EC:4.1.1.25]		
K01593	61	aromatic-L-amino-acid decarboxylase [EC:4.1.1.28]		
K01594	14	sulfinoalanine decarboxylase [EC:4.1.1.29]		
K01595	40	phosphoenolpyruvate carboxylase [EC:4.1.1.31]		
K01596	30	phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]		
K01598	9	phosphopantothenoylcysteine decarboxylase [EC:4.1.1.36]		
K01599	38	uroporphyrinogen decarboxylase [EC:4.1.1.37]		
K01601	7	ribulose-bisphosphate carboxylase large chain [EC:4.1.1.39]		
K01602	3	ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]		
K01605	1	methylmalonyl-CoA decarboxylase beta chain [EC:4.1.1.41]		
K01606	11	methylmalonyl-CoA decarboxylase gamma chain [EC:4.1.1.41]		
K01607	55	4-carboxymuconolactone decarboxylase [EC:4.1.1.44]		
K01608	8	tartronate-semialdehyde synthase [EC:4.1.1.47]		
K01609	19	indole-3-glycerol phosphate synthase [EC:4.1.1.48]		
K01610	22	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]		

K01611	4	S-adenosylmethionine decarboxylase [EC:4.1.1.50]		
K01612	5	4-hydroxybenzoate decarboxylase [EC:4.1.1.61]		
K01613	14	phosphatidylserine decarboxylase [EC:4.1.1.65]		
K01615	12	glutaconyl-CoA decarboxylase [EC:4.1.1.70]		
K01616	9	2-oxoglutarate decarboxylase [EC:4.1.1.71]		
K01617	5	4-oxalocrotonate decarboxylase [EC:4.1.1.77]		
K01618	62	Unclassified; E4.1.1.-		
K01619	13	deoxyribose-phosphate aldolase [EC:4.1.2.4]		
K01620	32	threonine aldolase [EC:4.1.2.5]		
K01621	20	phosphoketolase [EC:4.1.2.9]		
K01623	28	fructose-bisphosphate aldolase, class I [EC:4.1.2.13]		
K01624	8	fructose-bisphosphate aldolase, class II [EC:4.1.2.13]		
K01625	11	2-dehydro-3-deoxyphosphogluconate aldolase /		
K01626	26	3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]		
K01627	29	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase)		
K01628	51	L-fuculose-phosphate aldolase [EC:4.1.2.17]		
K01629	6	rhamnulose-1-phosphate aldolase [EC:4.1.2.19]		
K01630	13	2-dehydro-3-deoxyglucarate aldolase [EC:4.1.2.20]		
K01631	11	2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]		
K01632	12	fructose-6-phosphate phosphoketolase [EC:4.1.2.22]		
K01633	13	dihydroneopterin aldolase [EC:4.1.2.25]		
K01634	7	sphinganine-1-phosphate aldolase [EC:4.1.2.27]		
K01635	10	tagatose 1,6-diphosphate aldolase [EC:4.1.2.40]		
K01636	37	Unclassified; E4.1.2.-		
K01637	13	isocitrate lyase [EC:4.1.3.1]		
K01638	23	malate synthase [EC:2.3.3.9]		
K01639	16	N-acetylneuraminate lyase [EC:4.1.3.3]		
K01640	23	hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]		
K01641	3	hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]		
K01643	11	citrate lyase subunit alpha / citrate CoA-transferase [EC:4.1.3.6		
K01644	42	citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.6 4.1.3.34]		
K01647	50	citrate synthase [EC:2.3.3.1]		
K01648	1	ATP citrate (pro-S)-lyase [EC:2.3.3.8]		
K01649	82	2-isopropylmalate synthase [EC:2.3.3.13]		
K01652	178	acetolactate synthase I/II/III large subunit [EC:2.2.1.6]		
K01653	22	acetolactate synthase I/III small subunit [EC:2.2.1.6]		
K01654	14	N-acetylneuraminate synthase [EC:2.5.1.56]		
K01655	8	homocitrate synthase [EC:2.3.3.14]		
K01657	59	anthranilate synthase component I [EC:4.1.3.27]		
K01658	28	anthranilate synthase component II [EC:4.1.3.27]		
K01659	6	2-methylcitrate synthase [EC:2.3.3.5]		
K01661	17	naphthoate synthase [EC:4.1.3.36]		
K01662	55	1-deoxy-D-xylulose-5-phosphate synthase [EC:2.2.1.7]		
K01664	14	para-aminobenzoate synthetase component II [EC:2.6.1.85]		
K01665	22	para-aminobenzoate synthetase component I [EC:2.6.1.85]		
K01666	4	4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]		
K01667	15	tryptophanase [EC:4.1.99.1]		
K01668	12	tyrosine phenol-lyase [EC:4.1.99.2]		
K01669	28	deoxyribodipyrimidine photo-lyase [EC:4.1.99.3]		
K01673	27	carbonic anhydrase [EC:4.2.1.1]		
K01676	23	fumarate hydratase, class I [EC:4.2.1.2]		
K01677	4	fumarate hydratase subunit alpha [EC:4.2.1.2]		
K01679	37	fumarate hydratase, class II [EC:4.2.1.2]		
K01681	81	aconitate hydratase 1 [EC:4.2.1.3]		
K01682	7	aconitate hydratase 2 [EC:4.2.1.3]		
K01684	33	galactonate dehydratase [EC:4.2.1.6]		
K01685	24	altronate hydrolase [EC:4.2.1.7]		
K01686	9	mannonate dehydratase [EC:4.2.1.8]		
K01687	73	dihydroxy-acid dehydratase [EC:4.2.1.9]		

K01689	42	enolase [EC:4.2.1.11]		
K01690	2	phosphogluconate dehydratase [EC:4.2.1.12]		
K01692	266	enoyl-CoA hydratase [EC:4.2.1.17]		
K01693	14	imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]		
K01695	29	tryptophan synthase alpha chain [EC:4.2.1.20]		
K01696	29	tryptophan synthase beta chain [EC:4.2.1.20]		
K01697	25	cystathionine beta-synthase [EC:4.2.1.22]		
K01698	18	porphobilinogen synthase [EC:4.2.1.24]		
K01699	4	propanediol dehydratase large subunit [EC:4.2.1.28]		
K01703	59	3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit		
K01704	24	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit		
K01705	1	homoaconitate hydratase [EC:4.2.1.36]		
K01706	7	glucarate dehydratase [EC:4.2.1.40]		
K01708	22	galactarate dehydratase [EC:4.2.1.42]		
K01709	15	CDP-glucose 4,6-dehydratase [EC:4.2.1.45]		
K01710	121	dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]		
K01711	34	GDPmannose 4,6-dehydratase [EC:4.2.1.47]		
K01712	17	urocanate hydratase [EC:4.2.1.49]		
K01713	19	prephenate dehydratase [EC:4.2.1.51]		
K01714	67	dihydrodipicolinate synthase [EC:4.2.1.52]		
K01715	61	3-hydroxybutyryl-CoA dehydratase [EC:4.2.1.55]		
K01716	1	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.60]		
K01718	4	pseudouridylate synthase [EC:4.2.1.70]		
K01719	22	uroporphyrinogen-III synthase [EC:4.2.1.75]		
K01720	63	2-methylcitrate dehydratase [EC:4.2.1.79]		
K01722	3	Unclassified; E4.2.1.89		
K01724	20	4a-hydroxytetrahydrobiopterin dehydratase [EC:4.2.1.96]		
K01725	1	cyanate lyase [EC:4.2.1.104]		
K01726	99	Unclassified; E4.2.1.-		
K01728	1	pectate lyase [EC:4.2.2.2]		
K01733	66	threonine synthase [EC:4.2.3.1]		
K01734	6	methylglyoxal synthase [EC:4.2.3.3]		
K01735	30	3-dehydroquinate synthase [EC:4.2.3.4]		
K01736	40	chorismate synthase [EC:4.2.3.5]		
K01737	25	6-pyruvoyl tetrahydrobiopterin synthase [EC:4.2.3.12]		
K01738	73	cysteine synthase A [EC:2.5.1.47]		
K01739	49	cystathionine gamma-synthase [EC:2.5.1.48]		
K01740	36	O-acetylhomoserine (thiol)-lyase [EC:2.5.1.49]		
K01741	3	DNA-(apurinic or apyrimidinic site) lyase [EC:4.2.99.18]		
K01743	3	Unclassified; E4.2.-.-		
K01744	18	aspartate ammonia-lyase [EC:4.3.1.1]		
K01745	32	histidine ammonia-lyase [EC:4.3.1.3]		
K01746	14	formiminotetrahydrofolate cyclodeaminase [EC:4.3.1.4]		
K01749	28	hydroxymethylbilane synthase [EC:2.5.1.61]		
K01750	39	ornithine cyclodeaminase [EC:4.3.1.12]		
K01751	4	diaminopropionate ammonia-lyase [EC:4.3.1.15]		
K01752	8	L-serine dehydratase [EC:4.3.1.17]		
K01754	80	threonine dehydratase [EC:4.3.1.19]		
K01755	59	argininosuccinate lyase [EC:4.3.2.1]		
K01756	53	adenylosuccinate lyase [EC:4.3.2.2]		
K01757	6	strictosidine synthase [EC:4.3.3.2]		
K01758	28	cystathionine gamma-lyase [EC:4.4.1.1]		
K01759	62	lactoylglutathione lyase [EC:4.4.1.5]		
K01760	59	cystathionine beta-lyase [EC:4.4.1.8]		
K01761	21	methionine-gamma-lyase [EC:4.4.1.11]		
K01768	403	adenylate cyclase [EC:4.6.1.1]		
K01769	7	guanylate cyclase, other [EC:4.6.1.2]		
K01770	23	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:4.6.1.12]		
K01772	32	ferrochelatase [EC:4.99.1.1]		

K01774	3	Unclassified; E4.-.-.-		
K01775	45	alanine racemase [EC:5.1.1.1]		
K01776	47	glutamate racemase [EC:5.1.1.3]		
K01777	12	proline racemase [EC:5.1.1.4]		
K01778	33	diaminopimelate epimerase [EC:5.1.1.7]		
K01779	30	aspartate racemase [EC:5.1.1.13]		
K01780	26	Unclassified; E5.1.1.-		
K01781	68	mandelate racemase [EC:5.1.2.2]		
K01782	36	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase /		
K01783	21	ribulose-phosphate 3-epimerase [EC:5.1.3.1]		
K01784	233	UDP-glucose 4-epimerase [EC:5.1.3.2]		
K01785	23	aldose 1-epimerase [EC:5.1.3.3]		
K01786	5	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]		
K01787	7	N-acylglucosamine 2-epimerase [EC:5.1.3.8]		
K01789	11	UDP-glucuronate 5'-epimerase [EC:5.1.3.12]		
K01790	33	dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13]		
K01791	43	UDP-N-acetylglucosamine 2-epimerase [EC:5.1.3.14]		
K01792	3	glucose-6-phosphate 1-epimerase [EC:5.1.3.15]		
K01795	128	Unclassified; E5.1.3.-		
K01796	35	alpha-methylacyl-CoA racemase [EC:5.1.99.4]		
K01797	89	Unclassified; E5.1.99.-		
K01798	3	Unclassified; E5.1.-.-		
K01799	14	maleate isomerase [EC:5.2.1.1]		
K01800	11	maleylacetoacetate isomerase [EC:5.2.1.2]		
K01801	8	maleylpyruvate isomerase [EC:5.2.1.4]		
K01802	87	peptidylprolyl isomerase [EC:5.2.1.8]		
K01803	29	triosephosphate isomerase (TIM) [EC:5.3.1.1]		
K01804	10	L-arabinose isomerase [EC:5.3.1.4]		
K01805	13	xylose isomerase [EC:5.3.1.5]		
K01807	12	ribose 5-phosphate isomerase A [EC:5.3.1.6]		
K01808	26	ribose 5-phosphate isomerase B [EC:5.3.1.6]		
K01809	44	mannose-6-phosphate isomerase [EC:5.3.1.8]		
K01810	53	glucose-6-phosphate isomerase [EC:5.3.1.9]		
K01811	10	putative family 31 glucosidase		
K01812	7	glucuronate isomerase [EC:5.3.1.12]		
K01813	9	L-rhamnose isomerase [EC:5.3.1.14]		
K01814	30	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide		
K01816	12	hydroxypyruvate isomerase [EC:5.3.1.22]		
K01817	27	phosphoribosylanthranilate isomerase [EC:5.3.1.24]		
K01818	6	L-fucose isomerase [EC:5.3.1.25]		
K01820	9	Unclassified; E5.3.1.-		
K01821	5	4-oxalocrotonate tautomerase [EC:5.3.2.-]		
K01822	1	steroid delta-isomerase [EC:5.3.3.1]		
K01823	12	isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]		
K01825	4	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase /		
K01826	20	5-carboxymethyl-2-hydroxymuconate isomerase [EC:5.3.3.10]		
K01828	20	Unclassified; E5.3.3.-		
K01829	20	protein disulfide-isomerase [EC:5.3.4.1]		
K01834	100	phosphoglycerate mutase [EC:5.4.2.1]		
K01835	41	phosphoglucomutase [EC:5.4.2.2]		
K01838	4	beta-phosphoglucomutase [EC:5.4.2.6]		
K01839	18	phosphopentomutase [EC:5.4.2.7]		
K01840	87	phosphomannomutase [EC:5.4.2.8]		
K01841	3	phosphoenolpyruvate phosphomutase [EC:5.4.2.9]		
K01842	5	Unclassified; E5.4.2.-		
K01843	25	lysine 2,3-aminomutase [EC:5.4.3.2]		
K01844	3	beta-lysine 5,6-aminomutase [EC:5.4.3.3]		
K01845	65	glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]		
K01846	4	methylaspartate mutase [EC:5.4.99.1]		

K01847	14	methylmalonyl-CoA mutase [EC:5.4.99.2]		
K01848	52	methylmalonyl-CoA mutase, N-terminal domain [EC:5.4.99.2]		
K01849	12	methylmalonyl-CoA mutase, C-terminal domain [EC:5.4.99.2]		
K01851	1	salicylate biosynthesis isochorismate synthase [EC:5.4.4.2]		
K01854	46	UDP-galactopyranose mutase [EC:5.4.99.9]		
K01856	36	muconate cycloisomerase [EC:5.5.1.1]		
K01857	15	3-carboxy-cis,cis-muconate cycloisomerase [EC:5.5.1.2]		
K01858	12	myo-inositol-1-phosphate synthase [EC:5.5.1.4]		
K01860	15	chloromuconate cycloisomerase [EC:5.5.1.7]		
K01865	17	Unclassified; E5.-.-.-		
K01866	51	tyrosyl-tRNA synthetase [EC:6.1.1.1]		
K01867	46	tryptophanyl-tRNA synthetase [EC:6.1.1.2]		
K01868	67	threonyl-tRNA synthetase [EC:6.1.1.3]		
K01869	73	leucyl-tRNA synthetase [EC:6.1.1.4]		
K01870	85	isoleucyl-tRNA synthetase [EC:6.1.1.5]		
K01872	71	alanyl-tRNA synthetase [EC:6.1.1.7]		
K01873	99	valyl-tRNA synthetase [EC:6.1.1.9]		
K01874	56	methionyl-tRNA synthetase [EC:6.1.1.10]		
K01875	59	seryl-tRNA synthetase [EC:6.1.1.11]		
K01876	57	aspartyl-tRNA synthetase [EC:6.1.1.12]		
K01878	12	glycyl-tRNA synthetase alpha chain [EC:6.1.1.14]		
K01879	36	glycyl-tRNA synthetase beta chain [EC:6.1.1.14]		
K01880	17	glycyl-tRNA synthetase [EC:6.1.1.14]		
K01881	50	prolyl-tRNA synthetase [EC:6.1.1.15]		
K01883	69	cysteinyl-tRNA synthetase [EC:6.1.1.16]		
K01885	74	glutamyl-tRNA synthetase [EC:6.1.1.17]		
K01886	28	glutaminyl-tRNA synthetase [EC:6.1.1.18]		
K01887	498	arginyl-tRNA synthetase [EC:6.1.1.19]		
K01889	40	phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]		
K01890	515	phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]		
K01892	46	histidyl-tRNA synthetase [EC:6.1.1.21]		
K01893	25	asparaginyl-tRNA synthetase [EC:6.1.1.22]		
K01894	20	glutamyl-Q tRNA(Asp) synthetase [EC:6.1.1.-]		
K01895	175	acetyl-CoA synthetase [EC:6.2.1.1]		
K01897	294	long-chain acyl-CoA synthetase [EC:6.2.1.3]		
K01902	19	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]		
K01903	30	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]		
K01904	37	4-coumarate--CoA ligase [EC:6.2.1.12]		
K01905	37	acetyl-CoA synthetase (ADP-forming) [EC:6.2.1.13]		
K01906	43	6-carboxyhexanoate--CoA ligase [EC:6.2.1.14]		
K01907	38	acetoacetyl-CoA synthetase [EC:6.2.1.16]		
K01908	12	propionyl-CoA synthetase [EC:6.2.1.17]		
K01911	22	O-succinylbenzoic acid--CoA ligase [EC:6.2.1.26]		
K01912	88	phenylacetate-CoA ligase [EC:6.2.1.30]		
K01913	125	Unclassified; E6.2.1.-		
K01914	7	aspartate--ammonia ligase [EC:6.3.1.1]		
K01915	141	glutamine synthetase [EC:6.3.1.2]		
K01916	33	NAD+ synthase [EC:6.3.1.5]		
K01917	15	glutathionylspermidine synthase [EC:6.3.1.8]		
K01918	21	pantoate--beta-alanine ligase [EC:6.3.2.1]		
K01919	16	glutamate--cysteine ligase [EC:6.3.2.2]		
K01920	20	glutathione synthase [EC:6.3.2.3]		
K01921	88	D-alanine-D-alanine ligase [EC:6.3.2.4]		
K01922	6	phosphopantothenate-cysteine ligase [EC:6.3.2.5]		
K01923	35	phosphoribosylaminoimidazole-succinocarboxamide synthase		
K01924	35	UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8]		
K01925	33	UDP-N-acetylmuramoylalanine--D-glutamate ligase [EC:6.3.2.9]		
K01926	7	AT-rich DNA-binding protein		
K01928	42	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase		

K01929	58	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-		
K01932	7	Unclassified; E6.3.2.-		
K01933	32	phosphoribosylformylglycinamidine cyclo-ligase [EC:6.3.3.1]		
K01934	15	5-formyltetrahydrofolate cyclo-ligase [EC:6.3.3.2]		
K01935	11	dethiobiotin synthetase [EC:6.3.3.3]		
K01937	42	CTP synthase [EC:6.3.4.2]		
K01938	23	formate--tetrahydrofolate ligase [EC:6.3.4.3]		
K01939	47	adenylosuccinate synthase [EC:6.3.4.4]		
K01940	34	argininosuccinate synthase [EC:6.3.4.5]		
K01941	8	urea carboxylase [EC:6.3.4.6]		
K01945	31	phosphoribosylamine--glycine ligase [EC:6.3.4.13]		
K01947	4	biotin-[acetyl-CoA-carboxylase] ligase / type III pantothenate		
K01950	63	NAD+ synthase (glutamine-hydrolysing) [EC:6.3.5.1]		
K01951	50	GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]		
K01952	89	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]		
K01953	160	asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]		
K01955	66	carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]		
K01956	39	carbamoyl-phosphate synthase small subunit [EC:6.3.5.5]		
K01957	10	glutamyl-tRNA (Gln) amidotransferase [EC:6.3.5.-]		
K01958	22	pyruvate carboxylase [EC:6.4.1.1]		
K01959	2	pyruvate carboxylase subunit A [EC:6.4.1.1]		
K01960	23	pyruvate carboxylase subunit B [EC:6.4.1.1]		
K01961	38	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2		
K01962	21	acetyl-CoA carboxylase carboxyl transferase subunit alpha		
K01963	31	acetyl-CoA carboxylase carboxyl transferase subunit beta		
K01965	36	propionyl-CoA carboxylase alpha chain [EC:6.4.1.3]		
K01966	69	propionyl-CoA carboxylase beta chain [EC:6.4.1.3]		
K01968	21	3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4]		
K01969	19	3-methylcrotonyl-CoA carboxylase beta subunit [EC:6.4.1.4]		
K01970	3	Unclassified; E6.4.-.-		
K01971	172	DNA ligase (ATP) [EC:6.5.1.1]		
K01972	63	DNA ligase (NAD+) [EC:6.5.1.2]		
K01974	6	RNA 3'-terminal phosphate cyclase [EC:6.5.1.4]		
K01975	8	2'-5' RNA ligase [EC:6.5.1.-]		
K01976	26	Unclassified; E6.-.-.-		
K01989	47	putative ABC transport system substrate-binding protein		
K01990	199	ABC-2 type transport system ATP-binding protein		
K01991	50	polysaccharide export outer membrane protein		
K01992	215	ABC-2 type transport system permease protein		
K01993	36	HlyD family secretion protein		
K01994	1	LuxR family transcriptional regulator, transcriptional regulator of		
K01995	126	branched-chain amino acid transport system ATP-binding protein		
K01996	125	branched-chain amino acid transport system ATP-binding protein		
K01997	153	branched-chain amino acid transport system permease protein		
K01998	326	branched-chain amino acid transport system permease protein		
K01999	254	branched-chain amino acid transport system substrate-binding protein		
K02000	5	glycine betaine/proline transport system ATP-binding protein		
K02001	2	glycine betaine/proline transport system permease protein		
K02002	2	glycine betaine/proline transport system substrate-binding protein		
K02003	126	Unclassified; ABC.CD.A		
K02004	274	Unclassified; ABC.CD.P		
K02005	128	HlyD family secretion protein		
K02006	28	cobalt/nickel transport system ATP-binding protein		
K02007	5	cobalt/nickel transport system permease protein		
K02008	17	cobalt/nickel transport system permease protein		
K02010	19	iron(III) transport system ATP-binding protein [EC:3.6.3.30]		
K02011	71	iron(III) transport system permease protein		
K02012	46	iron(III) transport system substrate-binding protein		
K02013	25	iron complex transport system ATP-binding protein [EC:3.6.3.34]		

K02014	205	iron complex outermembrane recepter protein		
K02015	23	iron complex transport system permease protein		
K02016	43	iron complex transport system substrate-binding protein		
K02017	11	molybdate transport system ATP-binding protein [EC:3.6.3.29]		
K02018	15	molybdate transport system permease protein		
K02019	7	molybdate transport system regulatory protein		
K02020	55	molybdate transport system substrate-binding protein		
K02021	41	putative ABC transport system ATP-binding protein		
K02022	18	Unclassified; ABC.MR.TX		
K02023	24	multiple sugar transport system ATP-binding protein		
K02024	1	maltoporin		
K02025	139	multiple sugar transport system permease protein		
K02026	137	multiple sugar transport system permease protein		
K02027	138	multiple sugar transport system substrate-binding protein		
K02028	18	polar amino acid transport system ATP-binding protein [EC:3.6.3.21]		
K02029	26	polar amino acid transport system permease protein		
K02030	96	polar amino acid transport system substrate-binding protein		
K02031	66	peptide/nickel transport system ATP-binding protein		
K02032	185	peptide/nickel transport system ATP-binding protein		
K02033	207	peptide/nickel transport system permease protein		
K02034	165	peptide/nickel transport system permease protein		
K02035	407	peptide/nickel transport system substrate-binding protein		
K02036	24	phosphate transport system ATP-binding protein [EC:3.6.3.27]		
K02037	43	phosphate transport system permease protein		
K02038	42	phosphate transport system permease protein		
K02039	31	phosphate transport system protein		
K02040	62	phosphate transport system substrate-binding protein		
K02041	11	phosphonate transport system ATP-binding protein		
K02042	4	phosphonate transport system permease protein		
K02044	24	phosphonate transport system substrate-binding protein		
K02045	11	sulfate transport system ATP-binding protein [EC:3.6.3.25]		
K02046	14	sulfate transport system permease protein		
K02047	9	sulfate transport system permease protein		
K02048	16	sulfate transport system substrate-binding protein		
K02049	46	sulfonate/nitrate/taurine transport system ATP-binding protein		
K02050	86	sulfonate/nitrate/taurine transport system permease protein		
K02051	109	sulfonate/nitrate/taurine transport system substrate-binding protein		
K02052	32	putative spermidine/putrescine transport system ATP-binding protein		
K02053	39	putative spermidine/putrescine transport system permease protein		
K02054	31	putative spermidine/putrescine transport system permease protein		
K02055	46	putative spermidine/putrescine transport system substrate-binding		
K02056	66	simple sugar transport system ATP-binding protein [EC:3.6.3.17]		
K02057	106	simple sugar transport system permease protein		
K02058	54	simple sugar transport system substrate-binding protein		
K02059	4	putative sulfate transport system ATP-binding protein		
K02060	7	putative sulfate transport system permease protein		
K02061	3	putative sulfate transport system substrate-binding protein		
K02063	7	thiamine transport system permease protein		
K02064	3	thiamine transport system substrate-binding protein		
K02065	37	putative ABC transport system ATP-binding protein		
K02066	51	putative ABC transport system permease protein		
K02067	57	putative ABC transport system substrate-binding protein		
K02068	1	putative ABC transport system ATP-binding protein		
K02069	5	putative ABC transport system permease protein		
K02071	4	D-methionine transport system ATP-binding protein		
K02073	2	D-methionine transport system substrate-binding protein		
K02074	9	zinc/manganese transport system ATP-binding protein		
K02075	17	zinc/manganese transport system permease protein		
K02076	2	Fur family transcriptional regulator, zinc uptake regulator		

K02077	30	zinc/manganese transport system substrate-binding protein		
K02078	15	acyl carrier protein		
K02079	2	N-acetylgalactosamine-6-phosphate deacetylase [EC:3.5.1.25]		
K02081	13	DeoR family transcriptional regulator, aga operon transcriptional		
K02082	2	tagatose-6-phosphate ketose/aldose isomerase [EC:5.-.-.-]		
K02083	5	allantoate deiminase [EC:3.5.3.9]		
K02099	3	AraC family transcriptional regulator, arabinose operon regulatory		
K02103	1	GntR family transcriptional regulator, arabinose operon		
K02106	4	short-chain fatty acids transporter		
K02108	50	F-type H+-transporting ATPase subunit a [EC:3.6.3.14]		
K02109	12	F-type H+-transporting ATPase subunit b [EC:3.6.3.14]		
K02110	10	F-type H+-transporting ATPase subunit c [EC:3.6.3.14]		
K02111	32	F-type H+-transporting ATPase subunit alpha [EC:3.6.3.14]		
K02112	21	F-type H+-transporting ATPase subunit beta [EC:3.6.3.14]		
K02113	26	F-type H+-transporting ATPase subunit delta [EC:3.6.3.14]		
K02114	7	F-type H+-transporting ATPase subunit epsilon [EC:3.6.3.14]		
K02115	35	F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]		
K02116	2	ATP synthase protein I		
K02117	20	V-type H+-transporting ATPase subunit A [EC:3.6.3.14]		
K02118	13	V-type H+-transporting ATPase subunit B [EC:3.6.3.14]		
K02120	3	V-type H+-transporting ATPase subunit D [EC:3.6.3.14]		
K02121	2	V-type H+-transporting ATPase subunit E [EC:3.6.3.14]		
K02123	15	V-type H+-transporting ATPase subunit I [EC:3.6.3.14]		
K02124	4	V-type H+-transporting ATPase subunit K [EC:3.6.3.14]		
K02160	11	acetyl-CoA carboxylase biotin carboxyl carrier protein		
K02164	4	nitric-oxide reductase NorE protein [EC:1.7.99.7]		
K02169	17	biotin synthesis protein BioC		
K02170	4	biotin biosynthesis protein BioH		
K02182	16	crotonobetaine/carnitine-CoA ligase [EC:6.2.1.-]		
K02188	4	cobalamin biosynthesis protein CbiD		
K02189	1	cobalamin biosynthesis protein CbiG		
K02193	29	heme exporter protein A [EC:3.6.3.41]		
K02194	15	heme exporter protein B		
K02195	42	heme exporter protein C		
K02197	10	cytochrome c-type biogenesis protein CcmE		
K02198	81	cytochrome c-type biogenesis protein CcmF		
K02199	52	cytochrome c biogenesis protein CcmG, thiol:disulfide interchange		
K02200	19	cytochrome c-type biogenesis protein CcmH		
K02203	6	phosphoserine / homoserine phosphotransferase [EC:3.1.3.3 2.7.1.39]		
K02204	5	homoserine kinase type II [EC:2.7.1.39]		
K02217	12	ferritin [EC:1.16.3.1]		
K02221	26	YggT family protein		
K02224	18	cobyrinic acid a,c-diamide synthase [EC:6.3.5.9 6.3.1.-]		
K02226	2	alpha-ribazole phosphatase [EC:3.1.3.73]		
K02227	11	adenosylcobinamide-phosphate synthase CobD [EC:6.3.1.10]		
K02229	1	precorrin-3B synthase [EC:1.14.13.83]		
K02230	13	cobaltochelatase CobN [EC:6.6.1.2]		
K02231	13	adenosylcobinamide kinase / adenosylcobinamide-phosphate		
K02232	9	adenosylcobyric acid synthase [EC:6.3.5.10]		
K02233	2	adenosylcobinamide-GDP ribazoletransferase [EC:2.7.8.26]		
K02234	13	cobalamin biosynthesis protein CobW		
K02236	9	leader peptidase (prepilin peptidase) / N-methyltransferase		
K02237	16	competence protein ComEA		
K02238	57	competence protein ComEC		
K02240	1	competence protein ComFA		
K02242	4	competence protein ComFC		
K02244	3	competence protein ComGB		
K02248	3	competence protein ComGF		
K02258	6	cytochrome c oxidase subunit XI assembly protein		

K02259	27	cytochrome c oxidase subunit XV assembly protein		
K02274	88	cytochrome c oxidase subunit I [EC:1.9.3.1]		
K02275	66	cytochrome c oxidase subunit II [EC:1.9.3.1]		
K02276	37	cytochrome c oxidase subunit III [EC:1.9.3.1]		
K02278	1	prepilin peptidase CpaA [EC:3.4.23.43]		
K02279	5	pilus assembly protein CpaB		
K02280	15	pilus assembly protein CpaC		
K02282	37	pilus assembly protein CpaE		
K02283	46	pilus assembly protein CpaF		
K02287	2	phycocyanin-associated, rod		
K02288	2	phycocyanobilin lyase alpha subunit [EC:4.-.-.-]		
K02291	30	phytoene synthase [EC:2.5.1.32]		
K02292	50	beta-carotene ketolase (CrtO type)		
K02293	3	phytoene dehydrogenase, phytoene desaturase [EC:1.14.99.-]		
K02297	3	cytochrome o ubiquinol oxidase subunit II [EC:1.10.3.-]		
K02298	6	cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]		
K02299	4	cytochrome o ubiquinol oxidase subunit III [EC:1.10.3.-]		
K02301	31	protoheme IX farnesyltransferase [EC:2.5.1.-]		
K02302	27	uroporphyrin-III C-methyltransferase / precorrin-2 dehydrogenase /		
K02303	22	uroporphyrin-III C-methyltransferase [EC:2.1.1.107]		
K02304	6	precorrin-2 dehydrogenase / sirohydrochlorin ferrochelatase		
K02305	3	nitric-oxide reductase, cytochrome c-containing subunit II		
K02312	5	2,3-dihydroxybenzoate-AMP ligase [EC:2.7.7.58]		
K02313	51	chromosomal replication initiator protein		
K02314	78	replicative DNA helicase [EC:3.6.1.-]		
K02315	8	DNA replication protein DnaC		
K02316	65	DNA primase [EC:2.7.7.-]		
K02319	11	DNA polymerase I [EC:2.7.7.7]		
K02330	6	DNA polymerase beta subunit [EC:2.7.7.7 4.2.99.-]		
K02334	43	DNA polymerase bacteriophage-type [EC:2.7.7.7]		
K02335	90	DNA polymerase I [EC:2.7.7.7]		
K02336	4	DNA polymerase II [EC:2.7.7.7]		
K02337	211	DNA polymerase III subunit alpha [EC:2.7.7.7]		
K02338	59	DNA polymerase III subunit beta [EC:2.7.7.7]		
K02339	6	DNA polymerase III subunit chi [EC:2.7.7.7]		
K02340	11	DNA polymerase III subunit delta [EC:2.7.7.7]		
K02341	35	DNA polymerase III subunit delta' [EC:2.7.7.7]		
K02342	60	DNA polymerase III subunit epsilon [EC:2.7.7.7]		
K02343	65	DNA polymerase III subunit gamma/tau [EC:2.7.7.7]		
K02345	1	DNA polymerase III subunit theta [EC:2.7.7.7]		
K02346	46	DNA polymerase IV [EC:2.7.7.7]		
K02347	45	DNA polymerase (family X)		
K02348	2	ElaA protein		
K02351	7	putative membrane protein		
K02352	1	drp35		
K02355	154	elongation factor EF-G [EC:3.6.5.3]		
K02356	32	elongation factor EF-P		
K02357	44	elongation factor EF-Ts		
K02358	138	elongation factor EF-Tu [EC:3.6.5.3]		
K02361	19	isochorismate synthase [EC:5.4.4.2]		
K02363	1	enterobactin 2,3-dihydroxybenzoate-AMP ligase /		
K02364	7	enterobactin synthetase component F [EC:2.7.7.-]		
K02371	8	enoyl-[acyl carrier protein] reductase II [EC:1.3.1.-]		
K02372	22	3R-hydroxymyristoyl ACP dehydrase [EC:4.2.1.-]		
K02377	24	GDP-L-fucose synthase [EC:1.1.1.271]		
K02379	19	FdhD protein		
K02380	5	FdhE protein		
K02381	6	FdrA protein		
K02382	3	flagellar protein FlbA		

K02384	3	flagellar protein FlbC		
K02386	1	flagella basal body P-ring formation protein FlgA		
K02387	12	flagellar basal-body rod protein FlgB		
K02388	133	flagellar basal-body rod protein FlgC		
K02389	14	flagellar basal-body rod modification protein FlgD		
K02390	14	flagellar hook protein FlgE		
K02391	4	flagellar basal-body rod protein FlgF		
K02392	15	flagellar basal-body rod protein FlgG		
K02393	4	flagellar L-ring protein precursor FlgH		
K02394	6	flagellar P-ring protein precursor FlgI		
K02395	11	flagellar protein FlgJ		
K02396	12	flagellar hook-associated protein 1 FlgK		
K02397	8	flagellar hook-associated protein 3 FlgL		
K02400	16	flagellar biosynthesis protein FlhA		
K02401	8	flagellar biosynthetic protein FlhB		
K02402	1	flagellar transcriptional activator FlhC		
K02404	6	flagellar biosynthesis protein FlhF		
K02405	21	RNA polymerase sigma factor for flagellar operon FliA		
K02406	10	flagellin		
K02407	17	flagellar hook-associated protein 2		
K02408	2	flagellar hook-basal body complex protein FliE		
K02409	14	flagellar M-ring protein FliF		
K02410	16	flagellar motor switch protein FliG		
K02411	3	flagellar assembly protein FliH		
K02412	12	flagellum-specific ATP synthase [EC:3.6.3.14]		
K02413	1	flagellar FliJ protein		
K02414	1	flagellar hook-length control protein FliK		
K02415	3	flagellar FliL protein		
K02416	15	flagellar motor switch protein FliM		
K02417	6	flagellar motor switch protein FliN/FliY		
K02418	2	flagellar protein FliO/FliZ		
K02419	7	flagellar biosynthetic protein FliP		
K02420	2	flagellar biosynthetic protein FliQ		
K02421	2	flagellar biosynthetic protein FliR		
K02422	3	flagellar protein FliS		
K02424	2	cystine transport system substrate-binding protein		
K02426	10	cysteine desulfuration protein SufE		
K02427	13	ribosomal RNA large subunit methyltransferase E [EC:2.1.1.-]		
K02428	30	nucleoside-triphosphate pyrophosphatase [EC:3.6.1.19]		
K02429	11	MFS transporter, FHS family, L-fucose permease		
K02431	1	L-fucose mutarotase [EC:5.1.3.-]		
K02433	141	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit A		
K02434	54	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit B		
K02435	18	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit C		
K02436	2	DeoR family transcriptional regulator, galactitol utilization operon		
K02437	29	glycine cleavage system H protein		
K02438	33	glycogen operon protein GlgX [EC:3.2.1.-]		
K02439	2	thiosulfate sulfurtransferase [EC:2.8.1.1]		
K02440	14	glycerol uptake facilitator protein		
K02441	1	GlpG protein		
K02444	5	DeoR family transcriptional regulator, glycerol-3-phosphate regulon		
K02445	1	MFS transporter, OPA family, glycerol-3-phosphate transporter		
K02446	28	fructose-1,6-bisphosphatase II [EC:3.1.3.11]		
K02448	3	nitric-oxide reductase NorD protein [EC:1.7.99.7]		
K02450	12	general secretion pathway protein A		
K02452	1	general secretion pathway protein C		
K02453	90	general secretion pathway protein D		
K02454	48	general secretion pathway protein E		
K02455	102	general secretion pathway protein F		

K02456	16	general secretion pathway protein G		
K02457	2	general secretion pathway protein H		
K02458	2	general secretion pathway protein I		
K02459	2	general secretion pathway protein J		
K02460	10	general secretion pathway protein K		
K02461	7	general secretion pathway protein L		
K02464	6	general secretion pathway protein O [EC:3.4.23.43 2.1.1.-]		
K02469	80	DNA gyrase subunit A [EC:5.99.1.3]		
K02470	50	DNA gyrase subunit B [EC:5.99.1.3]		
K02471	16	putative ATP-binding cassette transporter		
K02472	10	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.-]		
K02473	35	UDP-N-acetylglucosamine 4-epimerase [EC:5.1.3.7]		
K02474	11	UDP-N-acetyl-D-galactosamine dehydrogenase [EC:1.1.1.-]		
K02475	2	two-component system, CitB family, response regulator		
K02477	67	two-component system, LytT family, response regulator		
K02478	4	two-component system, LytT family, sensor kinase [EC:2.7.13.3]		
K02479	79	two-component system, NarL family, response regulator		
K02480	32	two-component system, NarL family, sensor kinase [EC:2.7.13.3]		
K02481	134	two-component system, NtrC family, response regulator		
K02482	143	two-component system, NtrC family, sensor kinase [EC:2.7.13.3]		
K02483	128	two-component system, OmpR family, response regulator		
K02484	139	two-component system, OmpR family, sensor kinase [EC:2.7.13.3]		
K02485	11	two-component system, unclassified family, response regulator		
K02486	15	two-component system, unclassified family, sensor kinase		
K02487	1	type IV pili sensor histidine kinase and response regulator		
K02488	217	two-component system, cell cycle response regulator		
K02489	49	two-component system, cell cycle sensor kinase and response		
K02490	30	two-component system, response regulator, stage 0 sporulation		
K02491	8	two-component system, sporulation sensor kinase A [EC:2.7.13.3]		
K02492	42	glutamyl-tRNA reductase [EC:1.2.1.70]		
K02493	32	methyltransferase [EC:2.1.1.-]		
K02494	3	outer membrane lipoprotein LolB		
K02495	53	oxygen-independent coproporphyrinogen III oxidase [EC:1.3.99.22]		
K02496	3	uroporphyrin-III C-methyltransferase [EC:2.1.1.107]		
K02497	2	HemX protein		
K02498	3	HemY protein		
K02499	13	tetrapyrrole methylase family protein / MazG family protein		
K02500	27	cyclase HisF [EC:4.1.3.-]		
K02501	31	glutamine amidotransferase [EC:2.4.2.-]		
K02502	22	ATP phosphoribosyltransferase regulatory subunit		
K02503	30	Hit-like protein involved in cell-cycle regulation		
K02504	1	protein transport protein HofB		
K02507	4	protein transport protein HofQ		
K02508	2	AraC family transcriptional regulator, 4-hydroxyphenylacetate		
K02509	7	2-oxo-hept-3-ene-1,7-dioate hydratase [EC:4.2.1.-]		
K02510	35	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [EC:4.1.2.-]		
K02511	1	MFS transporter, ACS family, 4-hydroxyphenylacetate permease		
K02517	28	lipid A biosynthesis lauroyl acyltransferase [EC:2.3.1.-]		
K02518	13	translation initiation factor IF-1		
K02519	44	translation initiation factor IF-2		
K02520	31	translation initiation factor IF-3		
K02523	22	octaprenyl diphosphate synthase [EC:2.5.1.-]		
K02525	1	LacI family transcriptional regulator, kdg operon repressor		
K02526	3	2-keto-3-deoxygluconate permease		
K02527	16	3-deoxy-D-manno-octulosonic-acid transferase [EC:2.-.-.-]		
K02528	35	dimethyladenosine transferase [EC:2.1.1.-]		
K02529	80	LacI family transcriptional regulator		
K02532	1	MFS transporter, OHS family, lactose permease		
K02533	19	tRNA/rRNA methyltransferase [EC:2.1.1.-]		

K02535	25	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase		
K02536	33	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase		
K02545	2	penicillin-binding protein 2 prime		
K02547	1	methicillin resistance protein		
K02548	10	1,4-dihydroxy-2-naphthoate octaprenyltransferase [EC:2.5.1.-]		
K02549	20	O-succinylbenzoate synthase [EC:4.2.1.113]		
K02550	1	glycolate permease		
K02551	32	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate		
K02552	12	menaquinone-specific isochorismate synthase [EC:5.4.4.2]		
K02553	1	regulator of ribonuclease activity A		
K02554	5	2-keto-4-pentenoate hydratase [EC:4.2.1.80]		
K02556	5	chemotaxis protein MotA		
K02557	23	chemotaxis protein MotB		
K02558	24	UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate		
K02562	2	mannitol operon repressor		
K02563	30	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)		
K02564	23	glucosamine-6-phosphate deaminase [EC:3.5.99.6]		
K02565	5	N-acetylglucosamine repressor		
K02566	16	NagD protein		
K02567	28	periplasmic nitrate reductase NapA [EC:1.7.99.4]		
K02568	8	cytochrome c-type protein NapB		
K02569	3	cytochrome c-type protein NapC		
K02571	1	periplasmic nitrate reductase NapE		
K02572	2	ferredoxin-type protein NapF		
K02573	7	ferredoxin-type protein NapG		
K02574	7	ferredoxin-type protein NapH		
K02575	27	MFS transporter, NNP family, nitrate/nitrite transporter		
K02584	38	Nif-specific regulatory protein		
K02585	2	nitrogen fixation protein NifB		
K02586	4	nitrogenase molybdenum-iron protein alpha chain [EC:1.18.6.1]		
K02587	1	nitrogenase molybdenum-cofactor synthesis protein NifE		
K02588	1	nitrogenase iron protein NifH [EC:1.18.6.1]		
K02591	3	nitrogenase molybdenum-iron protein beta chain [EC:1.18.6.1]		
K02592	1	nitrogenase molybdenum-iron protein NifN		
K02594	3	homocitrate synthase NifV		
K02597	5	nitrogen fixation protein NifZ		
K02598	1	nitrite transporter NirC		
K02600	28	N utilization substance protein A		
K02601	16	transcriptional antiterminator NusG		
K02609	16	phenylacetic acid degradation protein		
K02610	4	phenylacetic acid degradation protein		
K02611	10	phenylacetic acid degradation protein		
K02612	14	phenylacetic acid degradation protein		
K02613	11	phenylacetic acid degradation NADH oxidoreductase		
K02614	21	phenylacetic acid degradation protein		
K02615	3	acetyl-CoA acetyltransferase [EC:2.3.1.-]		
K02616	6	phenylacetic acid degradation operon negative regulatory protein		
K02617	6	phenylacetic acid degradation protein		
K02618	19	phenylacetic acid degradation protein		
K02619	44	4-amino-4-deoxychorismate lyase [EC:4.1.3.38]		
K02621	13	topoisomerase IV subunit A [EC:5.99.1.-]		
K02622	18	topoisomerase IV subunit B [EC:5.99.1.-]		
K02623	10	LysR family transcriptional regulator, pca operon transcriptional		
K02624	13	IclR family transcriptional regulator, pca regulon regulatory		
K02626	5	arginine decarboxylase [EC:4.1.1.19]		
K02635	19	cytochrome b6		
K02636	14	cytochrome b6-f complex iron-sulfur subunit [EC:1.10.99.1]		
K02637	1	cytochrome b6-f complex subunit 4		
K02638	2	plastocyanin		

K02641	2	ferredoxin--NADP+ reductase [EC:1.18.1.2]		
K02647	2	carbohydrate diacid regulator		
K02650	7	type IV pilus assembly protein PilA		
K02651	5	pilus assembly protein Flp/PilA		
K02652	69	type IV pilus assembly protein PilB		
K02653	77	type IV pilus assembly protein PilC		
K02654	24	leader peptidase (prepilin peptidase) / N-methyltransferase		
K02655	6	type IV pilus assembly protein PilE		
K02656	15	type IV pilus assembly protein PilF		
K02657	13	twitching motility two-component system response regulator PilG		
K02658	37	twitching motility two-component system response regulator PilH		
K02659	5	twitching motility protein PilI		
K02660	18	twitching motility protein PilJ		
K02661	2	type IV pilus assembly protein PilK		
K02662	35	type IV pilus assembly protein PilM		
K02663	6	type IV pilus assembly protein PilN		
K02664	9	type IV pilus assembly protein PilO		
K02665	4	type IV pilus assembly protein PilP		
K02666	66	type IV pilus assembly protein PilQ		
K02667	64	two-component system, NtrC family, response regulator PilR		
K02668	66	two-component system, NtrC family, sensor histidine kinase PilS		
K02669	68	twitching motility protein PilT		
K02670	13	twitching motility protein PilU		
K02671	2	type IV pilus assembly protein PilV		
K02672	4	type IV pilus assembly protein PilW		
K02673	7	type IV pilus assembly protein PilX		
K02674	38	type IV pilus assembly protein PilY1		
K02676	2	type IV pilus assembly protein PilZ		
K02686	4	primosomal replication protein N		
K02687	27	ribosomal protein L11 methyltransferase [EC:2.1.1.-]		
K02688	2	transcriptional regulator, propionate catabolism operon regulatory		
K02690	1	photosystem I core protein Ib		
K02745	1	PTS system, N-acetylgalactosamine-specific IIB component		
K02755	1	PTS system, beta-glucosides-specific IIA component [EC:2.7.1.69]		
K02759	4	PTS system, cellobiose-specific IIA component [EC:2.7.1.69]		
K02761	9	PTS system, cellobiose-specific IIC component		
K02765	3	PTS system, D-glucosamine-specific IIC component		
K02768	6	PTS system, fructose-specific IIA component [EC:2.7.1.69]		
K02769	1	PTS system, fructose-specific IIB component [EC:2.7.1.69]		
K02770	12	PTS system, fructose-specific IIC component		
K02774	5	PTS system, galactitol-specific IIB component [EC:2.7.1.69]		
K02775	2	PTS system, galactitol-specific IIC component		
K02777	109	PTS system, glucose-specific IIA component [EC:2.7.1.69]		
K02779	2	PTS system, glucose-specific IIC component		
K02784	4	phosphocarrier protein HPr		
K02793	6	PTS system, mannose-specific IIA component [EC:2.7.1.69]		
K02794	3	PTS system, mannose-specific IIB component [EC:2.7.1.69]		
K02795	3	PTS system, mannose-specific IIC component		
K02796	6	PTS system, mannose-specific IID component		
K02799	2	PTS system, mannitol-specific IIB component [EC:2.7.1.69]		
K02800	3	PTS system, mannitol-specific IIC component		
K02804	1	PTS system, N-acetylglucosamine-specific IIC component		
K02805	4	lipopolysaccharide biosynthesis protein		
K02806	15	PTS system, nitrogen regulatory IIA component [EC:2.7.1.69]		
K02821	9	PTS system, ascorbate-specific IIA component [EC:2.7.1.69]		
K02823	18	dihydroorotate dehydrogenase electron transfer subunit		
K02824	6	uracil permease		
K02825	13	pyrimidine operon attenuation protein / uracil		
K02826	1	quinol oxidase polypeptide II [EC:1.9.3.-]		

K02827	1	quinol oxidase polypeptide I [EC:1.9.3.-]		
K02828	1	quinol oxidase polypeptide III [EC:1.9.3.-]		
K02834	16	ribosome-binding factor A		
K02835	26	peptide chain release factor RF-1		
K02836	23	peptide chain release factor RF-2		
K02837	18	peptide chain release factor RF-3		
K02838	30	ribosome recycling factor		
K02839	2	peptide chain release factor RF-H		
K02841	22	heptosyltransferase I [EC:2.4.-.-]		
K02843	38	heptosyltransferase II [EC:2.4.-.-]		
K02844	36	UDP-glucose:(heptosyl)LPS alpha-1,3-glucosyltransferase [EC:2.4.1.-]		
K02846	9	N-methyl-L-tryptophan oxidase [EC:1.5.3.-]		
K02849	21	heptosyltransferase III [EC:2.4.-.-]		
K02852	8	UDP-N-acetyl-D-mannosaminuronic acid transferase [EC:2.4.1.-]		
K02854	1	AraC family transcriptional regulator, L-rhamnose operon		
K02855	3	AraC family transcriptional regulator, L-rhamnose operon regulatory		
K02856	3	L-rhamnose-H+ transport protein		
K02858	40	3,4-dihydroxy 2-butanone 4-phosphate synthase [EC:4.1.99.12]		
K02860	41	16S rRNA processing protein RimM		
K02862	6	putative membrane protein		
K02863	21	large subunit ribosomal protein L1		
K02864	19	large subunit ribosomal protein L10		
K02867	17	large subunit ribosomal protein L11		
K02871	16	large subunit ribosomal protein L13		
K02874	22	large subunit ribosomal protein L14		
K02876	12	large subunit ribosomal protein L15		
K02878	19	large subunit ribosomal protein L16		
K02879	21	large subunit ribosomal protein L17		
K02881	11	large subunit ribosomal protein L18		
K02884	16	large subunit ribosomal protein L19		
K02886	47	large subunit ribosomal protein L2		
K02887	6	large subunit ribosomal protein L20		
K02888	23	large subunit ribosomal protein L21		
K02890	18	large subunit ribosomal protein L22		
K02892	34	large subunit ribosomal protein L23		
K02895	14	large subunit ribosomal protein L24		
K02897	28	large subunit ribosomal protein L25		
K02899	20	large subunit ribosomal protein L27		
K02902	9	large subunit ribosomal protein L28		
K02904	6	large subunit ribosomal protein L29		
K02906	36	large subunit ribosomal protein L3		
K02907	9	large subunit ribosomal protein L30		
K02909	22	large subunit ribosomal protein L31		
K02911	73	large subunit ribosomal protein L32		
K02913	9	large subunit ribosomal protein L33		
K02914	15	large subunit ribosomal protein L34		
K02916	7	large subunit ribosomal protein L35		
K02919	2	large subunit ribosomal protein L36		
K02926	30	large subunit ribosomal protein L4		
K02931	15	large subunit ribosomal protein L5		
K02933	28	large subunit ribosomal protein L6		
K02935	6	large subunit ribosomal protein L7/L12		
K02939	23	large subunit ribosomal protein L9		
K02945	47	small subunit ribosomal protein S1		
K02946	441	small subunit ribosomal protein S10		
K02948	11	small subunit ribosomal protein S11		
K02950	7	small subunit ribosomal protein S12		
K02952	15	small subunit ribosomal protein S13		
K02954	7	small subunit ribosomal protein S14		

K02956	8	small subunit ribosomal protein S15		
K02959	23	small subunit ribosomal protein S16		
K02961	10	small subunit ribosomal protein S17		
K02963	15	small subunit ribosomal protein S18		
K02965	4	small subunit ribosomal protein S19		
K02967	68	small subunit ribosomal protein S2		
K02968	28	small subunit ribosomal protein S20		
K02970	4	small subunit ribosomal protein S21		
K02982	20	small subunit ribosomal protein S3		
K02986	30	small subunit ribosomal protein S4		
K02988	13	small subunit ribosomal protein S5		
K02990	23	small subunit ribosomal protein S6		
K02992	15	small subunit ribosomal protein S7		
K02994	23	small subunit ribosomal protein S8		
K02996	16	small subunit ribosomal protein S9		
K03040	34	DNA-directed RNA polymerase subunit alpha [EC:2.7.7.6]		
K03043	77	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]		
K03046	516	DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]		
K03060	10	DNA-directed RNA polymerase subunit omega [EC:2.7.7.6]		
K03070	74	preprotein translocase subunit SecA		
K03071	7	preprotein translocase subunit SecB		
K03072	476	preprotein translocase subunit SecD		
K03073	2	preprotein translocase subunit SecE		
K03074	41	preprotein translocase subunit SecF		
K03075	3	preprotein translocase subunit SecG		
K03076	36	preprotein translocase subunit SecY		
K03077	3	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]		
K03080	2	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]		
K03086	56	RNA polymerase primary sigma factor		
K03087	22	RNA polymerase nonessential primary-like sigma factor		
K03088	405	RNA polymerase sigma-70 factor, ECF subfamily		
K03089	23	RNA polymerase sigma-32 factor		
K03090	20	RNA polymerase sigma-B factor		
K03091	8	RNA polymerase sporulation-specific sigma factor		
K03092	47	RNA polymerase sigma-54 factor		
K03093	27	RNA polymerase sigma factor		
K03098	2	outer membrane lipoprotein Blc		
K03100	92	signal peptidase I [EC:3.4.21.89]		
K03101	20	signal peptidase II [EC:3.4.23.36]		
K03106	47	signal recognition particle subunit SRP54		
K03110	23	fused signal recognition particle receptor		
K03111	34	single-strand DNA-binding protein		
K03113	2	translation initiation factor SUI1		
K03116	10	sec-independent protein translocase protein TatA		
K03117	4	sec-independent protein translocase protein TatB		
K03118	57	sec-independent protein translocase protein TatC		
K03119	43	taurine dioxygenase [EC:1.14.11.17]		
K03146	1	thiamine biosynthetic enzyme		
K03147	11	thiamine biosynthesis protein ThiC		
K03148	16	adenylyltransferase ThiF [EC:2.7.7.-]		
K03149	27	thiamine biosynthesis ThiG		
K03150	1	thiamine biosynthesis ThiH		
K03151	4	thiamine biosynthesis protein ThiI		
K03152	3	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis		
K03153	10	glycine oxidase [EC:1.4.3.19]		
K03154	5	thiamine biosynthesis ThiS		
K03166	6	DNA topoisomerase VI subunit A [EC:5.99.1.3]		
K03167	4	DNA topoisomerase VI subunit B [EC:5.99.1.3]		
K03168	100	DNA topoisomerase I [EC:5.99.1.2]		

K03169	32	DNA topoisomerase III [EC:5.99.1.2]		
K03177	42	tRNA pseudouridine synthase B [EC:5.4.99.12]		
K03179	26	4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]		
K03182	88	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiD [EC:4.1.1.-]		
K03183	77	ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.-]		
K03184	1	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase		
K03185	16	2-octaprenyl-6-methoxyphenol hydroxylase [EC:1.14.13.-]		
K03186	20	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiX [EC:4.1.1.-]		
K03187	2	urease accessory protein		
K03188	1	urease accessory protein		
K03189	3	urease accessory protein		
K03190	2	urease accessory protein		
K03192	1	urease accessory protein		
K03196	1	type IV secretion system protein VirB11		
K03197	2	type IV secretion system protein VirB2		
K03198	1	type IV secretion system protein VirB3		
K03199	8	type IV secretion system protein VirB4		
K03200	1	type IV secretion system protein VirB5		
K03201	2	type IV secretion system protein VirB6		
K03205	7	type IV secretion system protein VirD4		
K03208	1	colanic acid biosynthesis glycosyl transferase WcaI		
K03210	16	preprotein translocase subunit YajC		
K03215	31	RNA methyltransferase, TrmA family [EC:2.1.1.-]		
K03216	14	RNA methyltransferase, TrmH family, group 2 [EC:2.1.1.-]		
K03217	71	preprotein translocase subunit YidC		
K03218	28	RNA methyltransferase, TrmH family [EC:2.1.1.-]		
K03219	1	type III secretion protein SctC		
K03221	1	type III secretion protein SctF		
K03222	3	type III secretion protein SctJ		
K03223	1	type III secretion protein SctL		
K03224	1	ATP synthase in type III secretion protein SctN [EC:3.6.3.14]		
K03225	2	type III secretion protein SctQ		
K03227	2	type III secretion protein SctS		
K03228	2	type III secretion protein SctT		
K03229	1	type III secretion protein SctU		
K03230	2	type III secretion protein SctV		
K03265	1	peptide chain release factor eRF subunit 1		
K03269	5	UDP-2,3-diacylglucosamine hydrolase [EC:3.6.1.-]		
K03270	14	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P		
K03271	12	phosphoheptose isomerase [EC:5.-.-.-]		
K03272	33	D-beta-D-heptose 7-phosphate kinase / D-beta-D-heptose 1-phosphate		
K03273	14	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.-]		
K03274	9	ADP-L-glycero-D-manno-heptose 6-epimerase [EC:5.1.3.20]		
K03280	1	UDP-N-acetylglucosamine:(glucosyl)LPS		
K03281	27	chloride channel protein, CIC family		
K03282	26	large conductance mechanosensitive channel		
K03284	57	metal ion transporter, MIT family		
K03285	10	general bacterial porin, GBP family		
K03286	45	OmpA-OmpF porin, OOP family		
K03287	84	outer membrane factor, OMF family		
K03288	4	MFS transporter, MHS family, citrate/tricarballylate:H+ symporter		
K03289	2	MFS transporter, NHS family, nucleoside permease		
K03290	3	MFS transporter, SHS family, sialic acid transporter		
K03292	11	glycoside/pentoside/hexuronide:cation symporter, GPH family		
K03293	16	amino acid transporter, AAT family		
K03294	140	basic amino acid/polyamine antiporter, APA family		
K03295	35	cation efflux system protein, CDF family		
K03296	415	hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family		
K03297	2	small multidrug resistance protein, SMR family		

K03298	13	drug/metabolite transporter, DME family		
K03299	35	gluconate:H+ symporter, GntP family		
K03302	3	anaerobic C4-dicarboxylate transporter, Dcu family		
K03303	17	lactate transporter, LctP family		
K03304	4	tellurite resistance/dicarboxylate transporter, TDT family		
K03305	27	proton-dependent oligopeptide transporter, POT family		
K03306	31	inorganic phosphate transporter, PiT family		
K03307	78	solute:Na+ symporter, SSS family		
K03308	31	neurotransmitter:Na+ symporter, NSS family		
K03309	14	dicarboxylate/amino acid:cation (Na+ or H+) symporter, DAACS family		
K03312	1	glutamate:Na+ symporter, ESS family		
K03313	15	Na+:H+ antiporter, NhaA family		
K03315	2	Na+:H+ antiporter, NhaC family		
K03316	31	monovalent cation:H+ antiporter, CPA1 family		
K03317	19	concentrative nucleoside transporter, CNT family		
K03319	2	divalent anion:Na+ symporter, DASS family		
K03320	62	ammonium transporter, Amt family		
K03321	52	sulfate permease, SulP family		
K03322	54	manganese transport protein		
K03324	10	phosphate:Na+ symporter, PNaS family		
K03325	22	arsenite transporter, ACR3 family		
K03326	1	C4-dicarboxylate transporter, DcuC family		
K03327	27	multidrug resistance protein, MATE family		
K03328	25	polysaccharide transporter, PST family		
K03331	1	L-xylulose reductase [EC:1.1.1.10]		
K03332	2	fructan beta-fructosidase [EC:3.2.1.80]		
K03333	41	cholesterol oxidase [EC:1.1.3.6]		
K03335	20	inososе dehydratase [EC:4.2.1.44]		
K03336	12	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase [EC:3.7.1.-]		
K03337	2	5-deoxy-glucuronate isomerase [EC:5.3.1.-]		
K03338	5	5-dehydro-2-deoxygluconokinase [EC:2.7.1.92]		
K03339	1	6-phospho-5-dehydro-2-deoxy-D-gluconate aldolase [EC:4.1.2.29]		
K03342	7	para-aminobenzoate synthetase / 4-amino-4-deoxychorismate lyase		
K03343	8	putrescine oxidase [EC:1.4.3.10]		
K03366	4	(R,R)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4		
K03367	32	D-alanine-poly(phosphoribitol) ligase [EC:6.1.1.13]		
K03379	37	cyclohexanone monooxygenase [EC:1.14.13.22]		
K03380	35	phenol 2-monooxygenase [EC:1.14.13.7]		
K03381	13	catechol 1,2-dioxygenase [EC:1.13.11.1]		
K03382	5	hydroxyatrazine ethylaminohydrolase [EC:3.5.99.3]		
K03384	10	Unclassified; E1.14.12.-		
K03385	9	formate-dependent nitrite reductase, periplasmic cytochrome c552		
K03386	31	peroxiredoxin (alkyl hydroperoxide reductase subunit C)		
K03387	2	alkyl hydroperoxide reductase subunit F [EC:1.6.4.-]		
K03388	65	heterodisulfide reductase subunit A [EC:1.8.98.1]		
K03389	22	heterodisulfide reductase subunit B [EC:1.8.98.1]		
K03390	14	heterodisulfide reductase subunit C [EC:1.8.98.1]		
K03391	42	pentachlorophenol monooxygenase [EC:1.14.13.50]		
K03392	61	aminocarboxymuconate-semialdehyde decarboxylase [EC:4.1.1.45]		
K03394	1	precorrin-2 C20-methyltransferase / cobalt-factor-2		
K03396	1	S-(hydroxymethyl)glutathione synthase [EC:4.4.1.22]		
K03399	2	precorrin-6Y C5,15-methyltransferase [EC:2.1.1.132]		
K03402	7	transcriptional regulator of arginine metabolism		
K03403	4	magnesium chelatase subunit H [EC:6.6.1.1]		
K03404	10	magnesium chelatase subunit D [EC:6.6.1.1]		
K03405	29	magnesium chelatase subunit I [EC:6.6.1.1]		
K03406	186	methyl-accepting chemotaxis protein		
K03407	82	two-component system, chemotaxis family, sensor kinase CheA		
K03408	21	purine-binding chemotaxis protein CheW		

K03410	4	chemotaxis protein CheC		
K03411	16	chemotaxis protein CheD [EC:3.5.1.44]		
K03412	64	two-component system, chemotaxis family, response regulator CheB		
K03413	117	two-component system, chemotaxis family, response regulator CheY		
K03414	3	chemotaxis protein CheZ		
K03416	11	methylmalonyl-CoA carboxyltransferase [EC:2.1.3.1]		
K03417	36	methylisocitrate lyase [EC:4.1.3.30]		
K03423	57	Unclassified; E1.8.-.-		
K03424	47	TatD DNase family protein [EC:3.1.21.-]		
K03426	21	NAD+ diphosphatase [EC:3.6.1.22]		
K03427	48	type I restriction enzyme M protein [EC:2.1.1.72]		
K03429	22	1,2-diacylglycerol 3-glucosyltransferase [EC:2.4.1.157]		
K03430	5	2-aminoethylphosphonate-pyruvate transaminase [EC:2.6.1.37]		
K03431	33	phosphoglucosamine mutase [EC:5.4.2.10]		
K03432	2	proteasome alpha subunit [EC:3.4.25.1]		
K03433	9	proteasome beta subunit [EC:3.4.25.1]		
K03434	14	N-acetylglucosaminylphosphatidylinositol deacetylase [EC:3.5.1.89]		
K03435	5	LacI family transcriptional regulator, fructose operon		
K03436	5	DeoR family transcriptional regulator, fructose operon		
K03437	25	RNA methyltransferase, TrmH family		
K03438	31	S-adenosyl-methyltransferase [EC:2.1.1.-]		
K03439	7	tRNA (guanine-N7-)-methyltransferase [EC:2.1.1.33]		
K03442	38	small conductance mechanosensitive channel		
K03445	2	MFS transporter, DHA1 family, purine ribonucleoside efflux pump		
K03446	127	MFS transporter, DHA2 family, multidrug resistance protein B		
K03449	8	MFS transporter, CP family, cyanate transporter		
K03453	3	bile acid:Na+ symporter, BASS family		
K03455	84	monovalent cation:H+ antiporter-2, CPA2 family		
K03457	23	nucleobase:cation symporter-1, NCS1 family		
K03458	12	nucleobase:cation symporter-2, NCS2 family		
K03463	5	Unclassified; E5.5.1.-		
K03464	2	muconolactone D-isomerase [EC:5.3.3.4]		
K03465	12	thymidylate synthase (FAD) [EC:2.1.1.148]		
K03466	493	DNA segregation ATPase FtsK/SpoIIIE, S-DNA-T family		
K03469	41	ribonuclease HI [EC:3.1.26.4]		
K03470	44	ribonuclease HII [EC:3.1.26.4]		
K03471	3	ribonuclease HIII [EC:3.1.26.4]		
K03473	1	erythronate-4-phosphate dehydrogenase [EC:1.1.1.290]		
K03474	23	pyridoxine 5-phosphate synthase [EC:2.6.99.2]		
K03475	1	PTS system, ascorbate-specific IIC component		
K03476	18	L-ascorbate 6-phosphate lactonase [EC:3.1.1.-]		
K03478	5	hypothetical protein		
K03484	4	LacI family transcriptional regulator, sucrose operon repressor		
K03495	39	glucose inhibited division protein A		
K03496	82	chromosome partitioning protein		
K03497	69	chromosome partitioning protein, ParB family		
K03498	19	trk system potassium uptake protein TrkH		
K03499	59	trk system potassium uptake protein TrkA		
K03500	54	ribosomal RNA small subunit methyltransferase B [EC:2.1.1.-]		
K03501	26	glucose inhibited division protein B [EC:2.1.-.-]		
K03502	3	DNA polymerase V		
K03517	23	quinolinate synthase [EC:2.5.1.72]		
K03518	27	carbon-monoxide dehydrogenase small subunit [EC:1.2.99.2]		
K03519	52	carbon-monoxide dehydrogenase medium subunit [EC:1.2.99.2]		
K03520	196	carbon-monoxide dehydrogenase large subunit [EC:1.2.99.2]		
K03521	32	electron transfer flavoprotein beta subunit		
K03522	30	electron transfer flavoprotein alpha subunit		
K03523	5	putative biotin biosynthesis protein BioY		
K03524	31	BirA family transcriptional regulator, biotin operon repressor /		

K03525	31	type III pantothenate kinase [EC:2.7.1.33]		
K03526	24	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase [EC:1.17.7.1]		
K03527	34	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [EC:1.17.1.2]		
K03529	61	chromosome segregation protein		
K03530	59	DNA-binding protein HU-beta		
K03531	44	cell division protein FtsZ		
K03532	3	trimethylamine-N-oxide reductase (cytochrome c) 1, cytochrome c-type		
K03534	1	L-rhamnose mutarotase [EC:5.1.3.-]		
K03535	12	MFS transporter, ACS family, glucarate transporter		
K03536	21	ribonuclease P protein component [EC:3.1.26.5]		
K03540	15	ribonuclease P subunit RPR2 [EC:3.1.26.5]		
K03543	22	multidrug resistance protein A		
K03544	21	ATP-dependent Clp protease ATP-binding subunit ClpX		
K03545	53	trigger factor		
K03546	16	exonuclease SbcC		
K03547	5	exonuclease SbcD		
K03548	14	putative permease		
K03549	37	KUP system potassium uptake protein		
K03550	21	holliday junction DNA helicase RuvA		
K03551	35	holliday junction DNA helicase RuvB		
K03553	41	recombination protein RecA		
K03555	79	DNA mismatch repair protein MutS		
K03556	63	LuxR family transcriptional regulator, maltose regulon positive		
K03557	4	Fis family transcriptional regulator, factor for inversion		
K03558	4	membrane protein required for colicin V production		
K03559	16	biopolymer transport protein ExbD		
K03560	7	biopolymer transport protein TolR		
K03561	29	biopolymer transport protein ExbB		
K03562	14	biopolymer transport protein TolQ		
K03563	5	carbon storage regulator		
K03564	47	peroxiredoxin Q/BCP [EC:1.11.1.15]		
K03565	29	regulatory protein		
K03566	22	LysR family transcriptional regulator, glycine cleavage system		
K03567	1	glycine cleavage system transcriptional repressor		
K03568	39	TldD protein		
K03569	45	rod shape-determining protein MreB and related proteins		
K03570	25	rod shape-determining protein MreC		
K03571	3	rod shape-determining protein MreD		
K03572	44	DNA mismatch repair protein MutL		
K03574	44	7,8-dihydro-8-oxoguanine triphosphatase [EC:3.6.1.-]		
K03575	41	A/G-specific adenine glycosylase [EC:3.2.2.-]		
K03576	19	LysR family transcriptional regulator, regulator for metE and metH		
K03577	16	TetR/AcrR family transcriptional regulator, acrAB operon repressor		
K03578	38	ATP-dependent helicase HrpA [EC:3.6.1.-]		
K03579	15	ATP-dependent helicase HrpB [EC:3.6.1.-]		
K03580	7	ATP-dependent helicase HepA [EC:3.6.1.-]		
K03581	29	exodeoxyribonuclease V alpha subunit [EC:3.1.11.5]		
K03582	8	exodeoxyribonuclease V beta subunit [EC:3.1.11.5]		
K03583	15	exodeoxyribonuclease V gamma subunit [EC:3.1.11.5]		
K03584	34	DNA repair protein RecO (recombination protein O)		
K03585	50	membrane fusion protein		
K03586	1	cell division protein FtsL		
K03587	74	cell division protein FtsI (penicillin-binding protein 3)		
K03588	46	cell division protein FtsW		
K03589	17	cell division protein FtsQ		
K03590	36	cell division protein FtsA		
K03592	45	PmbA protein		
K03593	48	ATP-binding protein involved in chromosome partitioning		
K03594	20	bacterioferritin		

K03595	464	GTP-binding protein Era		
K03596	50	GTP-binding protein LepA		
K03597	1	sigma-E factor negative regulatory protein RseA		
K03598	9	sigma-E factor negative regulatory protein RseB		
K03599	4	stringent starvation protein A		
K03600	4	stringent starvation protein B		
K03601	45	exodeoxyribonuclease VII large subunit [EC:3.1.11.6]		
K03602	5	exodeoxyribonuclease VII small subunit [EC:3.1.11.6]		
K03604	5	LacI family transcriptional regulator, purine nucleotide synthesis		
K03605	10	hydrogenase 1 maturation protease [EC:3.4.24.-]		
K03606	8	putative colanic acid biosysnthesis UDP-glucose lipid carrier		
K03608	2	cell division topological specificity factor		
K03609	12	septum site-determining protein MinD		
K03610	2	septum site-determining protein MinC		
K03611	2	disulfide bond formation protein DsbB		
K03612	2	electron transport complex protein RnfG		
K03613	26	electron transport complex protein RnfE		
K03614	3	electron transport complex protein RnfD		
K03615	13	electron transport complex protein RnfC		
K03616	8	electron transport complex protein RnfB		
K03617	4	electron transport complex protein RnfA		
K03618	1	hydrogenase-1 operon protein HyaF		
K03620	12	Ni/Fe-hydrogenase 1 B-type cytochrome subunit		
K03621	30	glycerol-3-phosphate acyltransferase PlsX [EC:2.3.1.15]		
K03624	24	transcription elongation factor GreA		
K03625	21	N utilization substance protein B		
K03628	36	transcription termination factor Rho		
K03629	18	DNA replication and repair protein RecF		
K03630	39	DNA repair protein RadC		
K03631	48	DNA repair protein RecN (Recombination protein N)		
K03634	10	outer membrane lipoprotein carrier protein		
K03635	22	molybdenum cofactor biosynthesis protein E		
K03636	10	molybdenum cofactor biosynthesis protein D		
K03637	16	molybdenum cofactor biosynthesis protein C		
K03638	9	molybdenum cofactor biosynthesis protein B		
K03639	47	molybdenum cofactor biosynthesis protein A		
K03640	41	peptidoglycan-associated lipoprotein		
K03641	109	TolB protein		
K03642	13	rare lipoprotein A		
K03643	6	LPS-assembly lipoprotein		
K03644	32	lipoic acid synthetase [EC:2.8.1.8]		
K03648	29	uracil-DNA glycosylase [EC:3.2.2.-]		
K03649	18	TDG/mug DNA glycosylase family protein [EC:3.2.2.-]		
K03650	36	tRNA modification GTPase		
K03651	6	Icc protein		
K03652	17	DNA-3-methyladenine glycosylase [EC:3.2.2.21]		
K03654	47	ATP-dependent DNA helicase RecQ [EC:3.6.1.-]		
K03655	58	ATP-dependent DNA helicase RecG [EC:3.6.1.-]		
K03656	16	ATP-dependent DNA helicase Rep [EC:3.6.1.-]		
K03657	133	DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.1.-]		
K03664	27	SsrA-binding protein		
K03665	26	GTP-binding protein HflX		
K03666	10	host factor-I protein		
K03667	21	ATP-dependent HslUV protease ATP-binding subunit HslU		
K03668	3	heat shock protein HslJ		
K03669	4	membrane glycosyltransferase [EC:2.4.1.-]		
K03670	4	periplasmic glucans biosynthesis protein		
K03671	33	thioredoxin 1		
K03672	8	thioredoxin 2 [EC:1.8.1.8]		

K03673	13	thiol:disulfide interchange protein DsbA		
K03676	7	glutaredoxin 3		
K03677	11	CysQ protein		
K03684	17	ribonuclease D [EC:3.1.13.5]		
K03685	34	ribonuclease III [EC:3.1.26.3]		
K03686	68	molecular chaperone DnaJ		
K03687	21	molecular chaperone GrpE		
K03688	57	ubiquinone biosynthesis protein		
K03690	5	hypothetical protein		
K03693	1	penicillin-binding protein		
K03694	10	ATP-dependent Clp protease ATP-binding subunit ClpA		
K03695	75	ATP-dependent Clp protease ATP-binding subunit ClpB		
K03696	39	ATP-dependent Clp protease ATP-binding subunit ClpC		
K03697	1	ATP-dependent Clp protease ATP-binding subunit ClpE		
K03698	6	CMP-binding protein		
K03699	57	putative hemolysin		
K03701	117	excinuclease ABC subunit A		
K03702	42	excinuclease ABC subunit B		
K03703	61	excinuclease ABC subunit C		
K03704	67	cold shock protein (beta-ribbon, CspA family)		
K03705	36	heat-inducible transcriptional repressor		
K03707	6	transcriptional activator TenA [EC:3.5.99.2]		
K03709	23	DtxR family transcriptional regulator, Mn-dependent transcriptional		
K03710	43	GntR family transcriptional regulator		
K03711	30	Fur family transcriptional regulator, ferric uptake regulator		
K03712	51	MarR family transcriptional regulator		
K03713	4	MerR family transcriptional regulator, glutamine synthetase		
K03715	6	1,2-diacylglycerol 3-beta-galactosyltransferase [EC:2.4.1.46]		
K03717	10	LysR family transcriptional regulator, transcriptional activator of		
K03718	11	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC		
K03719	24	Lrp/AsnC family transcriptional regulator, leucine-responsive		
K03721	11	transcriptional regulator of aroF, aroG, tyrA and aromatic amino		
K03722	55	ATP-dependent DNA helicase DinG [EC:3.6.1.-]		
K03723	74	transcription-repair coupling factor (superfamily II helicase)		
K03724	91	ATP-dependent helicase Lhr and Lhr-like helicase [EC:3.6.1.-]		
K03726	1	helicase [EC:3.6.1.-]		
K03727	17	ATP-dependent RNA helicase HelY [EC:3.6.1.-]		
K03731	2	trehalose 6-phosphate phosphorylase [EC:2.4.1.216]		
K03732	1	ATP-dependent RNA helicase RhlB [EC:3.6.4.13]		
K03733	65	integrase/recombinase XerC		
K03734	31	thiamine biosynthesis lipoprotein		
K03735	4	ethanolamine ammonia-lyase large subunit [EC:4.3.1.7]		
K03736	1	ethanolamine ammonia-lyase small subunit [EC:4.3.1.7]		
K03737	30	putative pyruvate-flavodoxin oxidoreductase [EC:1.2.7.-]		
K03738	68	aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]		
K03740	1	D-alanine transfer protein		
K03741	27	arsenate reductase [EC:1.20.4.1]		
K03742	58	competence/damage-inducible protein CinA		
K03743	19	Unclassified; K03743		
K03744	31	LemA protein		
K03746	2	DNA-binding protein H-NS		
K03747	1	Smg protein		
K03748	3	SanA protein		
K03749	2	DedD protein		
K03750	62	molybdopterin biosynthesis protein MoeA		
K03751	39	molybdopterin biosynthesis protein MoeB		
K03752	10	molybdopterin-guanine dinucleotide biosynthesis protein A		
K03753	6	molybdopterin-guanine dinucleotide biosynthesis protein B		
K03756	3	putrescine:ornithine antiporter		

K03758	2	arginine:ornithine antiporter		
K03759	5	arginine:agmatine antiporter		
K03760	1	phosphoethanolamine transferase		
K03761	2	MFS transporter, MHS family, alpha-ketoglutarate permease		
K03762	32	MFS transporter, MHS family, proline/betaine transporter		
K03763	10	DNA polymerase III subunit alpha, Gram-positive type [EC:2.7.7.7]		
K03765	5	transcriptional activator of cad operon		
K03767	15	peptidyl-prolyl cis-trans isomerase A (cyclophilin A) [EC:5.2.1.8]		
K03768	25	peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]		
K03769	56	peptidyl-prolyl cis-trans isomerase C [EC:5.2.1.8]		
K03770	44	peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]		
K03771	59	peptidyl-prolyl cis-trans isomerase SurA [EC:5.2.1.8]		
K03772	10	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]		
K03773	4	FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8]		
K03774	1	FKBP-type peptidyl-prolyl cis-trans isomerase SlpA [EC:5.2.1.8]		
K03775	9	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [EC:5.2.1.8]		
K03776	16	aerotaxis receptor		
K03777	7	D-lactate dehydrogenase [EC:1.1.1.28]		
K03778	7	D-lactate dehydrogenase [EC:1.1.1.28]		
K03779	2	L(+)-tartrate dehydratase alpha subunit [EC:4.2.1.32]		
K03780	3	L(+)-tartrate dehydratase beta subunit [EC:4.2.1.32]		
K03781	12	catalase [EC:1.11.1.6]		
K03782	24	catalase/peroxidase [EC:1.11.1.6 1.11.1.7]		
K03783	27	purine-nucleoside phosphorylase [EC:2.4.2.1]		
K03784	5	purine-nucleoside phosphorylase [EC:2.4.2.1]		
K03785	2	3-dehydroquinate dehydratase I [EC:4.2.1.10]		
K03786	17	3-dehydroquinate dehydratase II [EC:4.2.1.10]		
K03787	26	5'-nucleotidase [EC:3.1.3.5]		
K03789	28	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]		
K03790	10	ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]		
K03791	7	putative chitinase		
K03793	3	pteridine reductase [EC:1.5.1.33]		
K03795	10	sirohydrochlorin cobaltochelatase [EC:4.99.1.3]		
K03797	79	carboxyl-terminal processing protease [EC:3.4.21.102]		
K03798	73	cell division protease FtsH [EC:3.4.24.-]		
K03799	40	heat shock protein HtpX [EC:3.4.24.-]		
K03800	12	lipoate-protein ligase A [EC:2.7.7.63]		
K03801	27	lipoyl(octanoyl) transferase [EC:2.3.1.181]		
K03802	15	cyanophycin synthetase [EC:6.-.-.-]		
K03806	4	AmpD protein		
K03808	5	paraquat-inducible protein A		
K03809	6	Trp repressor binding protein		
K03810	12	virulence factor		
K03811	3	nicotinamide mononucleotide transporter		
K03814	19	monofunctional biosynthetic peptidoglycan transglycosylase		
K03815	1	xanthosine phosphorylase [EC:2.4.2.-]		
K03818	8	putative colanic acid biosynthesis acetyltransferase WcaF		
K03819	1	putative colanic acid biosynthesis acetyltransferase WcaB		
K03820	42	apolipoprotein N-acyltransferase [EC:2.3.1.-]		
K03821	52	polyhydroxyalkanoate synthase [EC:2.3.1.-]		
K03822	3	putative long chain acyl-CoA synthase [EC:6.2.1.-]		
K03823	23	phosphinothricin acetyltransferase [EC:2.3.1.183]		
K03824	4	putative acetyltransferase [EC:2.3.1.-]		
K03825	4	putative acetyltransferase [EC:2.3.1.-]		
K03826	2	putative acetyltransferase [EC:2.3.1.-]		
K03827	2	putative acetyltransferase [EC:2.3.1.-]		
K03828	9	putative acetyltransferase [EC:2.3.1.-]		
K03829	8	putative acetyltransferase [EC:2.3.1.-]		
K03831	8	molybdopterin biosynthesis protein Mog		

K03832	28	periplasmic protein TonB		
K03833	28	selenocysteine-specific elongation factor		
K03837	1	serine transporter		
K03839	5	flavodoxin I		
K03841	11	fructose-1,6-bisphosphatase I [EC:3.1.3.11]		
K03851	2	taurine-pyruvate aminotransferase [EC:2.6.1.77]		
K03852	6	sulfoacetaldehyde acetyltransferase [EC:2.3.3.15]		
K03856	30	3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]		
K03862	13	vanillate monooxygenase [EC:1.14.13.82]		
K03863	2	vanillate monooxygenase [EC:1.14.13.82]		
K03885	77	NADH dehydrogenase [EC:1.6.99.3]		
K03886	3	menaquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.-]		
K03887	9	menaquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.-]		
K03888	2	menaquinol-cytochrome c reductase cytochrome b/c subunit		
K03889	6	ubiquinol-cytochrome c reductase cytochrome c subunit		
K03890	3	ubiquinol-cytochrome c reductase iron-sulfur subunit		
K03891	15	ubiquinol-cytochrome c reductase cytochrome b subunit		
K03892	63	ArsR family transcriptional regulator		
K03893	12	arsenical pump membrane protein		
K03897	1	lysine N6-hydroxylase [EC:1.14.13.59]		
K03918	4	L-lysine 6-transaminase [EC:2.6.1.36]		
K03924	61	MoxR-like ATPase [EC:3.6.3.-]		
K03925	28	MraZ protein		
K03926	9	periplasmic divalent cation tolerance protein		
K03927	17	carboxylesterase type B [EC:3.1.1.1]		
K03928	9	carboxylesterase [EC:3.1.1.1]		
K03930	1	putative tributyrin esterase [EC:3.1.1.-]		
K03931	6	putative isomerase		
K03932	12	polyhydroxybutyrate depolymerase		
K03933	3	chitin-binding protein		
K03943	6	NADH dehydrogenase (ubiquinone) flavoprotein 2 [EC:1.6.5.3 1.6.99.3]		
K03969	18	phage shock protein A		
K03972	3	phage shock protein E		
K03973	8	phage shock protein C		
K03974	2	psp operon transcriptional activator		
K03975	32	membrane-associated protein		
K03977	56	GTP-binding protein		
K03978	19	GTP-binding protein		
K03979	43	GTP-binding protein		
K03980	50	virulence factor		
K03981	8	thiol:disulfide interchange protein DsbC [EC:5.3.4.1]		
K04014	24	formate-dependent nitrite reductase, Fe-S protein		
K04015	1	formate-dependent nitrate reductase complex, transmembrane protein		
K04016	4	formate-dependent nitrite reductase, possible assembly protein		
K04019	11	ethanolamine utilization protein EutA		
K04020	4	phosphotransacetylase		
K04021	1	aldehyde dehydrogenase		
K04027	5	ethanolamine utilization protein EutM		
K04028	4	ethanolamine utilization protein EutN		
K04033	1	AraC family transcriptional regulator, ethanolamine operon		
K04034	54	anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase		
K04035	62	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase		
K04041	6	fructose-1,6-bisphosphatase III [EC:3.1.3.11]		
K04042	55	bifunctional protein GlmU [EC:2.7.7.23 2.3.1.157]		
K04043	64	molecular chaperone DnaK		
K04044	18	molecular chaperone HscA		
K04045	1	molecular chaperone HscC		
K04046	1	hypothetical chaperone protein		
K04047	11	starvation-inducible DNA-binding protein		

K04061	2	flagellar biosynthesis protein		
K04063	19	osmotically inducible protein OsmC		
K04065	12	hyperosmotically inducible periplasmic protein		
K04066	67	primosomal protein N' (replication factor Y) (superfamily II		
K04067	9	primosomal replication protein N''		
K04069	36	pyruvate formate lyase activating enzyme [EC:1.97.1.4]		
K04070	12	putative pyruvate formate lyase activating enzyme [EC:1.97.1.4]		
K04072	15	acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10		
K04073	3	acetaldehyde dehydrogenase [EC:1.2.1.10]		
K04074	6	cell division initiation protein		
K04075	46	tRNA(Ile)-lysidine synthase [EC:6.3.4.-]		
K04076	10	Lon-like ATP-dependent protease [EC:3.4.21.-]		
K04077	43	chaperonin GroEL		
K04078	11	chaperonin GroES		
K04079	17	molecular chaperone HtpG		
K04080	2	molecular chaperone IbpA		
K04082	9	molecular chaperone HscB		
K04083	6	molecular chaperone Hsp33		
K04084	26	thiol:disulfide interchange protein DsbD [EC:1.8.1.8]		
K04085	8	tRNA 2-thiouridine synthesizing protein A [EC:2.8.1.-]		
K04087	11	membrane protease subunit HflC [EC:3.4.-.-]		
K04088	14	membrane protease subunit HflK [EC:3.4.-.-]		
K04090	44	indolepyruvate ferredoxin oxidoreductase [EC:1.2.7.8]		
K04091	50	alkanesulfonate monooxygenase [EC:1.14.14.5]		
K04094	26	glucose inhibited division protein Gid		
K04095	1	cell filamentation protein		
K04096	36	DNA processing protein		
K04097	7	glutathione S-transferase [EC:2.5.1.18]		
K04098	2	hydroxyquinol 1,2-dioxygenase [EC:1.13.11.37]		
K04103	3	indolepyruvate decarboxylase [EC:4.1.1.74]		
K04107	6	4-hydroxybenzoyl-CoA reductase subunit 1 [EC:1.3.99.20]		
K04108	42	4-hydroxybenzoyl-CoA reductase subunit 2 [EC:1.3.99.20]		
K04110	22	benzoate-CoA ligase [EC:6.2.1.25]		
K04112	1	benzoyl-CoA reductase subunit [EC:1.3.99.15]		
K04113	10	benzoyl-CoA reductase subunit [EC:1.3.99.15]		
K04114	29	benzoyl-CoA reductase subunit [EC:1.3.99.15]		
K04115	16	benzoyl-CoA reductase subunit [EC:1.3.99.15]		
K04117	32	cyclohexanecarboxyl-CoA dehydrogenase [EC:1.3.99.-]		
K04118	4	pimeloyl-CoA dehydrogenase [EC:1.3.1.62]		
K04126	1	isopenicillin-N synthase [EC:1.21.3.1]		
K04127	15	isopenicillin-N epimerase [EC:5.1.1.17]		
K04128	1	hydroxymethyl cephem carbamoyltransferase [EC:2.1.3.-]		
K04333	1	LuxR family transcriptional regulator, csgAB operon transcriptional		
K04340	1	scyllo-inosamine-4-phosphate amidinotransferase 1 [EC:2.1.4.2]		
K04477	11	putative hydrolase		
K04485	37	DNA repair protein RadA/Sms		
K04486	6	histidinol-phosphatase (PHP family) [EC:3.1.3.15]		
K04487	57	cysteine desulfurase [EC:2.8.1.7]		
K04488	14	nitrogen fixation protein NifU and related proteins		
K04496	9	C-terminal binding protein		
K04509	20	formate dehydrogenase (cytochrome) [EC:1.2.2.1]		
K04516	4	chorismate mutase [EC:5.4.99.5]		
K04517	16	prephenate dehydrogenase [EC:1.3.1.12]		
K04518	51	prephenate dehydratase [EC:4.2.1.51]		
K04561	21	nitric-oxide reductase, cytochrome b-containing subunit I		
K04562	441	flagellar biosynthesis protein FlhG		
K04564	27	superoxide dismutase, Fe-Mn family [EC:1.15.1.1]		
K04565	6	Cu/Zn superoxide dismutase [EC:1.15.1.1]		
K04566	6	lysyl-tRNA synthetase, class I [EC:6.1.1.6]		

K04567	51	lysyl-tRNA synthetase, class II [EC:6.1.1.6]		
K04568	7	lysyl-tRNA synthetase, class II [EC:6.1.1.6]		
K04651	3	hydrogenase nickel incorporation protein HypA		
K04652	9	hydrogenase nickel incorporation protein HypB		
K04653	11	hydrogenase expression/formation protein HypC		
K04654	11	hydrogenase expression/formation protein HypD		
K04655	20	hydrogenase expression/formation protein HypE		
K04656	44	hydrogenase maturation protein HypF		
K04691	13	serine protease DegS [EC:3.4.21.-]		
K04719	4	5,6-dimethylbenzimidazole biosynthesis protein BluB		
K04744	27	LPS-assembly protein		
K04748	8	nitric-oxide reductase NorQ protein [EC:1.7.99.7]		
K04749	22	anti-sigma B factor antagonist		
K04750	25	PhnB protein		
K04751	13	nitrogen regulatory protein P-II 1		
K04752	4	nitrogen regulatory protein P-II 2		
K04753	14	suppressor of ftsI		
K04754	6	lipoprotein		
K04755	9	ferredoxin, 2Fe-2S		
K04756	11	alkyl hydroperoxide reductase subunit D		
K04757	15	anti-sigma B factor [EC:2.7.11.1]		
K04758	2	ferrous iron transport protein A		
K04759	35	ferrous iron transport protein B		
K04760	10	transcription elongation factor GreB		
K04761	32	LysR family transcriptional regulator, hydrogen peroxide-inducible		
K04762	7	ribosome-associated heat shock protein Hsp15		
K04763	93	integrase/recombinase XerD		
K04764	11	integration host factor subunit alpha		
K04766	1	acetoin utilization protein AcuA [EC:2.3.1.-]		
K04767	18	acetoin utilization protein AcuB		
K04768	10	acetoin utilization protein AcuC		
K04769	1	AbrB family transcriptional regulator, stage V sporulation protein T		
K04770	25	Lon-like ATP-dependent protease [EC:3.4.21.-]		
K04771	6	serine protease Do [EC:3.4.21.107]		
K04772	20	serine protease DegQ [EC:3.4.21.-]		
K04773	37	protease IV [EC:3.4.21.-]		
K04774	3	serine protease SohB [EC:3.4.21.-]		
K04780	19	nonribosomal peptide synthetase DhbF		
K04782	8	isochorismate pyruvate-lyase [EC:4.1.3.-]		
K04783	2	yersiniabactin salicyl-AMP ligase [EC:6.3.2.-]		
K04786	3	yersiniabactin nonribosomal peptide/polyketide synthase		
K04787	6	mycobactin salicyl-AMP ligase [EC:6.3.2.-]		
K04794	1	peptidyl-tRNA hydrolase, PTH2 family [EC:3.1.1.29]		
K05020	1	glycine betaine transporter		
K05275	26	pyridoxine 4-dehydrogenase [EC:1.1.1.65]		
K05281	4	2'-hydroxyisoflavone reductase [EC:1.3.1.45]		
K05296	3	3(or 17)beta-hydroxysteroid dehydrogenase [EC:1.1.1.51]		
K05297	6	rubredoxin-NAD+ reductase [EC:1.18.1.1]		
K05299	10	formate dehydrogenase (NADP+) [EC:1.2.1.43]		
K05301	55	sulfite dehydrogenase [EC:1.8.2.1]		
K05306	2	phosphonoacetaldehyde hydrolase [EC:3.11.1.1]		
K05311	1	central glycolytic genes regulator		
K05337	22	ferredoxin		
K05338	12	holin-like protein		
K05339	1	holin-like protein LrgB		
K05340	2	glucose uptake protein		
K05341	5	amylosucrase [EC:2.4.1.4]		
K05343	42	maltose alpha-D-glucosyltransferase [EC:5.4.99.16]		
K05344	1	glucose-1-phosphate phosphodismutase [EC:2.7.1.41]		

K05345	21	putative cyclase [EC:4.6.1.-]		
K05348	2	2-hydroxycinnamic acid beta-D-glucosylisomelase [EC:5.2.1.-]		
K05349	79	beta-glucosidase [EC:3.2.1.21]		
K05350	31	beta-glucosidase [EC:3.2.1.21]		
K05351	2	D-xylulose reductase [EC:1.1.1.9]		
K05358	3	quinate dehydrogenase (pyrroloquinoline-quinone) [EC:1.1.99.25]		
K05359	1	carboxycyclohexadienyl dehydratase [EC:4.2.1.91]		
K05362	1	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase		
K05363	1	serine/alanine adding enzyme [EC:2.3.2.10]		
K05364	58	peptidoglycan glycosyltransferase [EC:2.4.1.129]		
K05365	12	penicillin-binding protein 1B [EC:2.4.1.129 3.4.-.-]		
K05366	129	penicillin-binding protein 1A [EC:2.4.1.- 3.4.-.-]		
K05367	18	penicillin-binding protein 1C [EC:2.4.1.-]		
K05368	1	aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3		
K05375	2	MbtH protein		
K05384	22	bilin biosynthesis protein		
K05386	8	bilin biosynthesis protein		
K05394	29	atrazine chlorohydrolase [EC:3.8.1.8]		
K05395	5	cystine reductase [EC:1.8.1.6]		
K05396	10	D-cysteine desulfhydrase [EC:4.4.1.15]		
K05499	15	LacI family transcriptional regulator, repressor for deo operon,		
K05501	11	TetR/AcrR family transcriptional regulator		
K05515	85	penicillin-binding protein 2		
K05516	22	curved DNA-binding protein		
K05517	1	nucleoside-specific channel-forming protein		
K05520	21	protease I [EC:3.2.-.-]		
K05521	16	ADP-ribosylglycohydrolase [EC:3.2.-.-]		
K05522	12	endonuclease VIII [EC:3.2.2.- 4.2.99.18]		
K05524	6	ferredoxin		
K05525	30	linalool 8-monooxygenase [EC:1.14.99.28]		
K05527	6	BolA protein		
K05539	2	tRNA-dihydrouridine synthase A [EC:1.-.-.-]		
K05540	28	tRNA-dihydrouridine synthase B [EC:1.-.-.-]		
K05541	1	tRNA-dihydrouridine synthase C [EC:1.-.-.-]		
K05549	11	benzoate 1,2-dioxygenase alpha subunit [EC:1.14.12.10]		
K05550	4	benzoate 1,2-dioxygenase beta subunit [EC:1.14.12.10]		
K05551	24	3-oxoacyl-ACP synthase I [EC:2.3.1.-]		
K05552	22	3-oxoacyl-ACP synthase II [EC:2.3.1.-]		
K05555	12	cyclase [EC:4.-.-.-]		
K05556	3	hydroxylacyl-CoA dehydrogenase [EC:1.1.1.-]		
K05557	16	MFS transporter, DHA2 family, integral membrane protein		
K05559	4	multicomponent K+:H+ antiporter subunit A		
K05561	2	multicomponent K+:H+ antiporter subunit D		
K05563	1	multicomponent K+:H+ antiporter subunit F		
K05564	1	multicomponent K+:H+ antiporter subunit G		
K05565	4	multicomponent Na+:H+ antiporter subunit A		
K05567	3	multicomponent Na+:H+ antiporter subunit C		
K05568	14	multicomponent Na+:H+ antiporter subunit D		
K05571	1	multicomponent Na+:H+ antiporter subunit G		
K05572	6	NADH dehydrogenase I subunit 1 [EC:1.6.5.3]		
K05573	9	NADH dehydrogenase I subunit 2 [EC:1.6.5.3]		
K05574	6	NADH dehydrogenase I subunit 3 [EC:1.6.5.3]		
K05575	8	NADH dehydrogenase I subunit 4 [EC:1.6.5.3]		
K05576	3	NADH dehydrogenase I subunit 4L [EC:1.6.5.3]		
K05577	7	NADH dehydrogenase I subunit 5 [EC:1.6.5.3]		
K05578	2	NADH dehydrogenase I subunit 6 [EC:1.6.5.3]		
K05579	2	NADH dehydrogenase I subunit 7 [EC:1.6.5.3]		
K05580	4	NADH dehydrogenase I subunit I [EC:1.6.5.3]		
K05586	3	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]		

K05587	6	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]		
K05588	3	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]		
K05589	1	cell division protein FtsB		
K05590	1	ATP-dependent RNA helicase SrmB [EC:2.7.7.-]		
K05591	4	ATP-independent RNA helicase DbpA [EC:3.6.4.13]		
K05592	36	ATP-dependent RNA helicase DeaD [EC:3.6.4.13]		
K05595	33	multiple antibiotic resistance protein		
K05597	1	glutamin-(asparagin-)ase [EC:3.5.1.38]		
K05599	2	anthranilate 1,2-dioxygenase (deaminating, decarboxylating) large		
K05600	2	anthranilate 1,2-dioxygenase (deaminating, decarboxylating) small		
K05601	2	hydroxylamine reductase [EC:1.7.99.1]		
K05603	10	formimidoylglutamate deiminase [EC:3.5.3.13]		
K05606	12	methylmalonyl-CoA epimerase [EC:5.1.99.1]		
K05685	60	macrolide transport system ATP-binding/permease protein [EC:3.6.3.-]		
K05692	2	actin beta/gamma 1		
K05708	9	large terminal subunit of phenylpropionate dioxygenase		
K05709	3	small terminal subunit of phenylpropionate dioxygenase		
K05710	16	ferredoxin subunit of phenylpropionate dioxygenase		
K05712	33	3-(3-hydroxy-phenyl)propionate hydroxylase [EC:1.14.13.-]		
K05714	5	2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase [EC:3.7.1.-]		
K05715	6	2-phosphoglycerate kinase [EC:2.7.2.-]		
K05772	8	putative tungstate transport system substrate-binding protein		
K05773	8	putative tungstate transport system permease protein		
K05776	4	molybdate transport system ATP-binding protein		
K05777	5	putative thiamine transport system substrate-binding protein		
K05780	2	putative phosphonate transport system ATP-binding protein		
K05781	1	putative phosphonate transport system ATP-binding protein		
K05782	6	benzoate membrane transport protein		
K05783	1	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase		
K05784	3	benzoate 1,2-dioxygenase electron transfer component		
K05785	1	transcriptional antiterminator RfaH		
K05786	10	chloramphenicol-sensitive protein RarD		
K05787	1	DNA-binding protein HU-alpha		
K05788	20	integration host factor subunit beta		
K05794	28	tellurite resistance protein TerC		
K05795	6	tellurium resistance protein TerD		
K05796	1	electron transport protein HydN		
K05797	3	4-cresol dehydrogenase (hydroxylating) [EC:1.17.99.1]		
K05798	12	LysR family transcriptional regulator, transcriptional activator for		
K05799	23	GntR family transcriptional regulator, transcriptional repressor for		
K05800	2	Lrp/AsnC family transcriptional regulator		
K05802	8	potassium efflux system protein KefA		
K05803	4	lipoprotein NlpI		
K05807	19	putative lipoprotein		
K05808	17	putative sigma-54 modulation protein		
K05810	27	conserved hypothetical protein		
K05812	1	conserved hypothetical protein		
K05813	23	sn-glycerol 3-phosphate transport system substrate-binding protein		
K05814	17	sn-glycerol 3-phosphate transport system permease protein		
K05815	10	sn-glycerol 3-phosphate transport system permease protein		
K05816	7	sn-glycerol 3-phosphate transport system ATP-binding protein		
K05817	27	LysR family transcriptional regulator, hca operon transcriptional		
K05820	4	MFS transporter, PPP family, 3-phenylpropionic acid transporter		
K05823	1	N-acetyldiaminopimelate deacetylase [EC:3.5.1.47]		
K05825	2	2-aminoadipate transaminase [EC:2.6.1.-]		
K05827	5	lysine biosynthesis protein LysX		
K05829	4	N-acetyl-gamma-aminoadipyl-phosphate reductase [EC:1.2.1.-]		
K05830	3	acetylornithine/acetyl-lysine aminotransferase [EC:2.6.1.11 2.6.1.-]		
K05831	2	acetyl-lysine deacetylase [EC:3.5.1.-]		

K05832	1	putative ABC transport system permease protein		
K05834	11	homoserine/homoserine lactone efflux protein		
K05835	1	threonine efflux protein		
K05836	9	GntR family transcriptional regulator, histidine utilization		
K05837	55	rod shape determining protein RodA		
K05838	12	putative thioredoxin		
K05841	12	sterol 3beta-glucosyltransferase [EC:2.4.1.173]		
K05844	10	ribosomal protein S6 modification protein		
K05845	22	osmoprotectant transport system substrate-binding protein		
K05846	27	osmoprotectant transport system permease protein		
K05847	6	osmoprotectant transport system ATP-binding protein		
K05873	1	adenylate cyclase, class 2 [EC:4.6.1.1]		
K05874	21	methyl-accepting chemotaxis protein I, serine sensor receptor		
K05875	8	methyl-accepting chemotaxis protein II, aspartate sensor receptor		
K05876	2	methyl-accepting chemotaxis protein III, ribose and galactose sensor		
K05878	8	dihydroxyacetone kinase, N-terminal domain [EC:2.7.1.-]		
K05879	5	dihydroxyacetone kinase, C-terminal domain [EC:2.7.1.-]		
K05881	1	PTS hybrid protein		
K05882	45	aryl-alcohol dehydrogenase (NADP+) [EC:1.1.1.91]		
K05883	2	Unclassified; E1.1.1.210		
K05885	35	2,5-diketo-D-gluconate reductase [EC:1.1.1.274]		
K05886	5	serine 3-dehydrogenase [EC:1.1.1.276]		
K05888	11	Unclassified; E1.1.2.-		
K05889	3	polyvinyl-alcohol dehydrogenase (acceptor) [EC:1.1.99.23]		
K05893	3	Unclassified; E1.3.1.35		
K05895	2	precorrin-6X reductase [EC:1.3.1.54]		
K05896	19	segregation and condensation protein A		
K05897	1	Unclassified; E1.3.3.-		
K05898	2	3-oxosteroid 1-dehydrogenase [EC:1.3.99.4]		
K05899	2	glycine oxidase [EC:1.4.3.19]		
K05903	108	NADH dehydrogenase (quinone) [EC:1.6.99.5]		
K05905	17	protein-disulfide reductase [EC:1.8.1.8]		
K05909	5	Unclassified; E1.10.3.2		
K05910	1	NADH peroxidase [EC:1.11.1.1]		
K05911	5	quinone-reactive Ni/Fe-hydrogenase [EC:1.12.5.1]		
K05912	20	Unclassified; E1.12.-.-		
K05914	35	Unclassified; E1.13.12.7		
K05915	9	Unclassified; E1.13.-.-		
K05916	3	nitric oxide dioxygenase [EC:1.14.12.17]		
K05917	1	cytochrome P450, family 51 (sterol 14-demethylase) [EC:1.14.13.70]		
K05918	8	Unclassified; E1.14.19.-		
K05921	16	5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase /		
K05922	19	quinone-reactive Ni/Fe-hydrogenase large subunit [EC:1.12.5.1]		
K05927	7	quinone-reactive Ni/Fe-hydrogenase small subunit [EC:1.12.5.1]		
K05928	8	tocopherol O-methyltransferase [EC:2.1.1.95]		
K05929	6	phosphoethanolamine N-methyltransferase [EC:2.1.1.103]		
K05934	6	precorrin-3B C17-methyltransferase [EC:2.1.1.131]		
K05936	4	precorrin-4 C11-methyltransferase [EC:2.1.1.133]		
K05939	12	acyl-[acyl-carrier-protein]-phospholipid O-acyltransferase /		
K05942	1	Unclassified; E2.3.-.-		
K05944	6	Unclassified; E2.4.1.56		
K05945	1	Unclassified; E2.4.1.58		
K05946	16	N-acetylglucosaminyldiphosphoundecaprenol [EC:2.4.1.187]		
K05949	5	Unclassified; E2.4.1.227		
K05957	4	L-glutamine:scyllo-inosose aminotransferase [EC:2.6.1.50]		
K05961	1	Unclassified; E2.7.1.145		
K05962	30	protein-histidine pros-kinase [EC:2.7.13.1]		
K05968	7	Unclassified; E3.1.1.6		
K05969	8	peptidyl-tRNA hydrolase [EC:3.1.1.29]		

K05971	43	Unclassified; E3.1.1.61		
K05972	1	Unclassified; E3.1.1.72		
K05973	12	poly(3-hydroxybutyrate) depolymerase [EC:3.1.1.75]		
K05979	11	2-phosphosulfolactate phosphatase [EC:3.1.3.71]		
K05982	8	deoxyribonuclease V [EC:3.1.21.7]		
K05984	4	excinuclease Cho [EC:3.1.25.-]		
K05985	445	ribonuclease M5 [EC:3.1.26.8]		
K05993	29	isochorismatase [EC:3.3.2.1]		
K05994	2	bacterial leucyl aminopeptidase [EC:3.4.11.10]		
K05995	7	dipeptidase E [EC:3.4.13.21]		
K05996	15	carboxypeptidase T [EC:3.4.17.18]		
K05997	3	Fe-S cluster assembly protein SufA		
K05998	2	pseudomonalisin [EC:3.4.21.100]		
K05999	5	xanthomonalisin [EC:3.4.21.101]		
K06001	31	tryptophan synthase beta chain [EC:4.2.1.20]		
K06010	5	Unclassified; E3.4.23.43		
K06013	29	STE24 endopeptidase [EC:3.4.24.84]		
K06015	85	Unclassified; E3.5.1.81		
K06016	27	N-carbamoyl-L-amino-acid hydrolase [EC:3.5.1.87]		
K06019	4	pyrophosphatase PpaX [EC:3.6.1.1]		
K06020	53	sulfate-transporting ATPase [EC:3.6.3.25]		
K06021	11	phosphate-transporting ATPase [EC:3.6.3.27]		
K06022	6	molybdate-transporting ATPase [EC:3.6.3.29]		
K06023	16	HPr kinase/phosphorylase [EC:2.7.11.- 2.7.4.-]		
K06024	17	segregation and condensation protein B		
K06026	35	Unclassified; E3.6.4.4		
K06027	29	vesicle-fusing ATPase [EC:3.6.4.6]		
K06031	6	Unclassified; E3.8.1.1		
K06033	3	Unclassified; E4.1.1.76		
K06034	5	sulfopyruvate decarboxylase subunit alpha [EC:4.1.1.79]		
K06037	1	Unclassified; E4.2.3.-		
K06039	4	uncharacterized protein involved in oxidation of intracellular		
K06041	24	arabinose-5-phosphate isomerase [EC:5.3.1.13]		
K06042	8	precorrin-8X methylmutase [EC:5.4.1.2]		
K06044	33	(1->4)-alpha-D-glucan 1-alpha-D-glucosylmutase [EC:5.4.99.15]		
K06045	23	squalene-hopene cyclase [EC:5.4.99.17]		
K06048	23	carboxylate-amine ligase [EC:6.3.-.-]		
K06049	10	magnesium chelatase accessory protein		
K06075	7	MarR family transcriptional regulator, transcriptional regulator for		
K06076	23	long-chain fatty acid transport protein		
K06077	1	outer membrane lipoprotein SlyB		
K06113	1	arabinan endo-1,5-alpha-L-arabinosidase [EC:3.2.1.99]		
K06118	5	UDP-sulfoquinovose synthase [EC:3.13.1.1]		
K06120	2	glycerol dehydratase large subunit [EC:4.2.1.30]		
K06121	1	glycerol dehydratase medium subunit [EC:4.2.1.30]		
K06131	35	cardiolipin synthase [EC:2.7.8.-]		
K06132	18	putative cardiolipin synthase [EC:2.7.8.-]		
K06134	3	ubiquinone biosynthesis monooxygenase Coq7 [EC:1.14.13.-]		
K06136	9	pyrroloquinoline quinone biosynthesis protein B		
K06137	5	pyrroloquinoline-quinone synthase [EC:1.3.3.11]		
K06138	1	pyrroloquinoline quinone biosynthesis protein D		
K06139	53	pyrroloquinoline quinone biosynthesis protein E		
K06140	4	regulator of nucleoside diphosphate kinase		
K06142	8	outer membrane protein		
K06143	10	inner membrane protein		
K06147	326	ATP-binding cassette, subfamily B, bacterial		
K06148	122	ATP-binding cassette, subfamily C, bacterial		
K06149	46	universal stress protein A		
K06151	40	gluconate 2-dehydrogenase alpha chain [EC:1.1.99.3]		

K06153	39	undecaprenyl-diphosphatase [EC:3.6.1.27]		
K06155	4	Gnt-I system high-affinity gluconate transporter		
K06158	42	ATP-binding cassette, sub-family F, member 3		
K06162	1	PhnM protein		
K06163	1	PhnJ protein		
K06164	3	PhnI protein		
K06167	14	PhnP protein		
K06168	67	bifunctional enzyme involved in thiolation and methylation of tRNA		
K06173	30	tRNA pseudouridine synthase A [EC:5.4.99.12]		
K06175	3	tRNA pseudouridine synthase C [EC:5.4.99.12]		
K06176	3	tRNA pseudouridine synthase D [EC:5.4.99.12]		
K06177	17	ribosomal large subunit pseudouridine synthase A [EC:5.4.99.12]		
K06178	41	ribosomal large subunit pseudouridine synthase B [EC:5.4.99.12]		
K06179	25	ribosomal large subunit pseudouridine synthase C [EC:5.4.99.12]		
K06180	45	ribosomal large subunit pseudouridine synthase D [EC:5.4.99.12]		
K06181	5	ribosomal large subunit pseudouridine synthase E [EC:5.4.99.12]		
K06182	2	ribosomal large subunit pseudouridine synthase F [EC:5.4.99.12]		
K06183	14	ribosomal small subunit pseudouridine synthase A [EC:5.4.99.12]		
K06186	4	small protein A		
K06187	21	recombination protein RecR		
K06188	15	aquaporin Z		
K06189	18	magnesium and cobalt transporter		
K06190	8	intracellular septation protein		
K06192	8	paraquat-inducible protein B		
K06193	1	phosphonoacetate hydrolase [EC:3.11.1.2]		
K06194	17	lipoprotein NlpD		
K06195	4	ApaG protein		
K06196	31	cytochrome c-type biogenesis protein		
K06197	3	cation transport regulator		
K06199	16	CrcB protein		
K06200	25	carbon starvation protein		
K06201	11	copper homeostasis protein		
K06202	1	CyaY protein		
K06204	29	DnaK suppressor protein		
K06205	2	MioC protein		
K06206	3	sugar fermentation stimulation protein A		
K06207	33	GTP-binding protein		
K06208	12	chorismate mutase [EC:5.4.99.5]		
K06211	1	HipB family transcriptional regulator, involved in the regulation of		
K06212	14	formate transporter		
K06213	42	magnesium transporter		
K06215	8	pyridoxine biosynthesis protein [EC:4.-.-.-]		
K06217	31	phosphate starvation-inducible protein PhoH and related proteins		
K06218	4	RelE protein		
K06219	4	S-adenosylmethionine-dependent methyltransferase		
K06221	8	2,5-diketo-D-gluconate reductase A [EC:1.1.1.274]		
K06222	1	2,5-diketo-D-gluconate reductase B [EC:1.1.1.274]		
K06223	4	DNA adenine methylase [EC:2.1.1.72]		
K06281	38	hydrogenase large subunit [EC:1.12.99.6]		
K06282	22	hydrogenase small subunit [EC:1.12.99.6]		
K06284	5	transcriptional pleiotropic regulator of transition state genes		
K06287	26	septum formation protein		
K06294	1	spore germination protein D		
K06306	15	spore germination protein		
K06308	1	spore germination protein		
K06320	3	spore maturation protein CgeB		
K06324	41	spore coat protein A		
K06329	1	spore coat protein F		
K06330	1	spore coat protein H		

K06345	3	spore cortex protein		
K06346	9	spoIIIJ-associated protein		
K06348	5	sporulation inhibitor KapD		
K06350	5	antagonist of KipI		
K06351	3	inhibitor of KinA		
K06370	4	morphogenetic protein associated with SpoVID		
K06373	4	spore maturation protein A		
K06374	5	spore maturation protein B		
K06378	14	stage II sporulation protein AA (anti-sigma F factor antagonist)		
K06379	6	stage II sporulation protein AB (anti-sigma F factor) [EC:2.7.11.1]		
K06381	23	stage II sporulation protein D		
K06384	1	stage II sporulation protein M		
K06390	4	stage III sporulation protein AA		
K06391	1	stage III sporulation protein AB		
K06399	2	stage IV sporulation protein B [EC:3.4.21.116]		
K06400	21	site-specific DNA recombinase		
K06402	3	stage IV sporulation protein FB [EC:3.4.24.-]		
K06405	1	stage V sporulation protein AC		
K06407	1	stage V sporulation protein AE		
K06408	4	stage V sporulation protein AF		
K06412	4	stage V sporulation protein G		
K06413	5	stage V sporulation protein K		
K06415	10	stage V sporulation protein R		
K06419	1	small acid-soluble spore protein B (major beta-type SASP)		
K06422	11	small acid-soluble spore protein E (minor gamma-type SASP)		
K06423	1	small acid-soluble spore protein F (minor alpha/beta-type SASP)		
K06428	1	small acid-soluble spore protein K (minor)		
K06434	6	small acid-soluble spore protein (thioredoxin-like protein)		
K06442	20	putative hemolysin		
K06445	16	acyl-CoA dehydrogenase [EC:1.3.99.-]		
K06446	6	acyl-CoA dehydrogenase [EC:1.3.99.-]		
K06447	2	succinylglutamic semialdehyde dehydrogenase [EC:1.2.1.71]		
K06518	4	holin-like protein		
K06595	4	heam-based aerotactic trancducer		
K06596	35	chemosensory pili system protein ChpA (sensor histidine		
K06600	1	chemosensory pili system protein ChpE		
K06601	1	flagellar protein FlbT		
K06602	1	flagellar protein FlaF		
K06603	1	flagellar protein FlaG		
K06605	1	myo-inositol catabolism protein IolH		
K06606	2	inososе isomerase [EC:5.3.99.-]		
K06607	2	myo-inositol catabolism protein IolS [EC:1.1.1.-]		
K06608	3	DeoR family transcriptional regulator, myo-inositol catabolism		
K06609	1	MFS transporter, SP family, major inositol transporter		
K06714	8	arginine utilization regulatory protein		
K06718	2	L-2,4-diaminobutyric acid acetyltransferase [EC:2.3.1.178]		
K06726	1	D-ribose pyranase [EC:5.-.-.-]		
K06857	10	putative tungstate transport system ATP-binding protein		
K06858	8	vitamin B12 transport system substrate-binding protein		
K06859	1	glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]		
K06860	19	Unclassified; K06860		
K06861	16	lipopolysaccharide export system ATP-binding protein [EC:3.6.3.-]		
K06864	13	Unclassified; K06864		
K06867	34	Unclassified; K06867		
K06871	16	Unclassified; K06871		
K06872	14	Unclassified; K06872		
K06873	3	Unclassified; K06873		
K06876	2	Unclassified; K06876		
K06877	43	Unclassified; K06877		

K06878	6	Unclassified; K06878		
K06881	34	Unclassified; K06881		
K06882	5	Unclassified; K06882		
K06883	14	Unclassified; K06883		
K06884	1	Unclassified; K06884		
K06885	9	Unclassified; K06885		
K06886	13	hemoglobin		
K06887	1	Unclassified; K06887		
K06888	45	Unclassified; K06888		
K06889	70	Unclassified; K06889		
K06890	28	Unclassified; K06890		
K06891	7	ATP-dependent Clp protease adaptor protein ClpS		
K06892	7	Unclassified; K06892		
K06893	19	Unclassified; K06893		
K06894	31	Unclassified; K06894		
K06895	6	Unclassified; K06895		
K06896	21	Unclassified; K06896		
K06897	12	Unclassified; K06897		
K06898	15	Unclassified; K06898		
K06899	1	Unclassified; K06899		
K06900	6	Unclassified; K06900		
K06901	37	putative MFS transporter, AGZA family, xanthine/uracil permease		
K06902	19	MFS transporter, UMF1 family		
K06903	7	Unclassified; K06903		
K06904	7	Unclassified; K06904		
K06905	6	Unclassified; K06905		
K06907	22	Unclassified; K06907		
K06909	7	Unclassified; K06909		
K06910	25	Unclassified; K06910		
K06911	105	Unclassified; K06911		
K06912	17	alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase		
K06915	44	Unclassified; K06915		
K06916	7	Unclassified; K06916		
K06917	3	tRNA 2-selenouridine synthase [EC:2.9.1.-]		
K06919	3	Unclassified; K06919		
K06920	21	queuosine biosynthesis protein QueC		
K06921	5	Unclassified; K06921		
K06922	4	Unclassified; K06922		
K06923	9	Unclassified; K06923		
K06925	17	Unclassified; K06925		
K06927	3	Unclassified; K06927		
K06929	33	Unclassified; K06929		
K06931	1	Unclassified; K06931		
K06934	2	Unclassified; K06934		
K06936	2	Unclassified; K06936		
K06937	23	Unclassified; K06937		
K06938	1	Unclassified; K06938		
K06940	16	Unclassified; K06940		
K06941	40	ribosomal RNA large subunit methyltransferase N [EC:2.1.1.-]		
K06942	31	Unclassified; K06942		
K06944	9	Unclassified; K06944		
K06947	1	Unclassified; K06947		
K06948	2	Unclassified; K06948		
K06949	40	ribosome biogenesis GTPase [EC:3.6.1.-]		
K06950	36	Unclassified; K06950		
K06951	7	Unclassified; K06951		
K06952	1	Unclassified; K06952		
K06953	2	Unclassified; K06953		
K06954	16	Unclassified; K06954		

K06955	5	Unclassified; K06955		
K06956	7	Unclassified; K06956		
K06958	20	Unclassified; K06958		
K06959	17	Unclassified; K06959		
K06960	10	Unclassified; K06960		
K06962	2	Unclassified; K06962		
K06966	34	Unclassified; K06966		
K06967	6	Unclassified; K06967		
K06968	3	Unclassified; K06968		
K06969	37	putative SAM-dependent methyltransferase		
K06971	6	Unclassified; K06971		
K06972	1	Unclassified; K06972		
K06973	3	Unclassified; K06973		
K06974	7	Unclassified; K06974		
K06975	3	Unclassified; K06975		
K06976	4	Unclassified; K06976		
K06977	1	Unclassified; K06977		
K06978	97	Unclassified; K06978		
K06979	58	Unclassified; K06979		
K06980	27	Unclassified; K06980		
K06981	1	Unclassified; K06981		
K06983	1	Unclassified; K06983		
K06985	5	aspartyl protease family protein		
K06986	1	Unclassified; K06986		
K06987	5	Unclassified; K06987		
K06988	27	Unclassified; K06988		
K06989	7	aspartate dehydrogenase [EC:1.4.1.21]		
K06990	27	Unclassified; K06990		
K06991	3	Unclassified; K06991		
K06992	1	Unclassified; K06992		
K06994	80	putative drug exporter of the RND superfamily		
K06996	29	Unclassified; K06996		
K06997	22	Unclassified; K06997		
K06998	53	Unclassified; K06998		
K06999	29	Unclassified; K06999		
K07000	5	Unclassified; K07000		
K07001	116	Unclassified; K07001		
K07002	5	Unclassified; K07002		
K07003	53	Unclassified; K07003		
K07004	22	Unclassified; K07004		
K07005	13	Unclassified; K07005		
K07006	21	Unclassified; K07006		
K07007	10	Unclassified; K07007		
K07008	22	Unclassified; K07008		
K07009	8	Unclassified; K07009		
K07010	19	putative glutamine amidotransferase		
K07011	57	Unclassified; K07011		
K07012	6	Unclassified; K07012		
K07014	4	Unclassified; K07014		
K07015	1	Unclassified; K07015		
K07017	5	Unclassified; K07017		
K07018	12	Unclassified; K07018		
K07019	16	Unclassified; K07019		
K07020	7	Unclassified; K07020		
K07021	40	Unclassified; K07021		
K07024	51	Unclassified; K07024		
K07025	74	putative hydrolase of the HAD superfamily		
K07027	59	Unclassified; K07027		
K07028	17	Unclassified; K07028		

K07029	47	Unclassified; K07029		
K07030	32	Unclassified; K07030		
K07031	8	Unclassified; K07031		
K07032	15	Unclassified; K07032		
K07033	8	Unclassified; K07033		
K07034	6	Unclassified; K07034		
K07037	17	Unclassified; K07037		
K07038	7	Unclassified; K07038		
K07039	2	Unclassified; K07039		
K07040	23	Unclassified; K07040		
K07042	16	Unclassified; K07042		
K07043	16	Unclassified; K07043		
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K07045	131	Unclassified; K07045		
K07046	35	Unclassified; K07046		
K07047	88	Unclassified; K07047		
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K07053	27	Unclassified; K07053		
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K07056	37	Unclassified; K07056		
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K07088	17	Unclassified; K07088		
K07089	22	Unclassified; K07089		
K07090	87	Unclassified; K07090		
K07091	25	lipopolysaccharide export system permease protein		
K07093	7	Unclassified; K07093		
K07094	1	Unclassified; K07094		
K07095	21	Unclassified; K07095		
K07096	25	Unclassified; K07096		
K07098	27	Unclassified; K07098		
K07100	43	Unclassified; K07100		
K07101	5	Unclassified; K07101		
K07102	16	Unclassified; K07102		
K07104	17	Unclassified; K07104		
K07106	20	N-acetylmuramic acid 6-phosphate etherase [EC:4.2.-.-]		

K07107	51	Unclassified; K07107		
K07110	12	Unclassified; K07110		
K07112	18	Unclassified; K07112		
K07113	5	Unclassified; K07113		
K07114	83	Unclassified; K07114		
K07115	2	Unclassified; K07115		
K07116	73	Unclassified; K07116		
K07117	6	Unclassified; K07117		
K07118	4	Unclassified; K07118		
K07119	19	Unclassified; K07119		
K07120	8	Unclassified; K07120		
K07121	4	Unclassified; K07121		
K07122	1	Unclassified; K07122		
K07124	34	Unclassified; K07124		
K07125	1	Unclassified; K07125		
K07126	43	Unclassified; K07126		
K07127	6	5-hydroxyisourate hydrolase [EC:3.5.2.17]		
K07130	24	Unclassified; K07130		
K07131	6	Unclassified; K07131		
K07133	13	Unclassified; K07133		
K07137	10	Unclassified; K07137		
K07138	10	Unclassified; K07138		
K07139	2	Unclassified; K07139		
K07140	12	Unclassified; K07140		
K07141	16	Unclassified; K07141		
K07145	11	Unclassified; K07145		
K07146	1	Unclassified; K07146		
K07147	73	Unclassified; K07147		
K07148	4	Unclassified; K07148		
K07149	5	Unclassified; K07149		
K07150	2	Unclassified; K07150		
K07152	50	Unclassified; K07152		
K07153	1	Unclassified; K07153		
K07154	7	Unclassified; K07154		
K07155	4	quercetin 2,3-dioxygenase [EC:1.13.11.24]		
K07156	4	Unclassified; pcoC		
K07157	17	Unclassified; K07157		
K07160	7	Unclassified; K07160		
K07161	34	Unclassified; K07161		
K07164	13	Unclassified; K07164		
K07165	1	transmembrane sensor		
K07168	7	CBS domain-containing membrane protein		
K07169	39	FHA domain-containing protein		
K07170	8	GAF domain-containing protein		
K07171	5	Unclassified; K07171		
K07172	1	Unclassified; K07172		
K07173	15	S-ribosylhomocysteine lyase [EC:4.4.1.21]		
K07175	20	PhoH-like ATPase		
K07177	6	PDZ domain-containing protein		
K07178	2	RIO kinase 1 [EC:2.7.11.1]		
K07180	31	serine protein kinase		
K07181	7	putative signal transduction protein containing EAL and modified		
K07182	60	CBS domain-containing protein		
K07183	14	response regulator NasT		
K07185	12	tryptophan-rich sensory protein		
K07186	2	membrane protein		
K07192	11	flotillin		
K07213	6	Unclassified; K07213		
K07214	12	enterochelin esterase and related enzymes		

K07216	14	hemerythrin		
K07217	5	Mn-containing catalase		
K07218	10	nitrous oxidase accessory protein		
K07219	16	putative molybdopterin biosynthesis protein		
K07220	19	hypothetical protein		
K07221	1	outer membrane porin		
K07222	30	putative flavoprotein involved in K+ transport		
K07223	13	putative iron-dependent peroxidase		
K07224	2	putative lipoprotein		
K07226	3	hypothetical protein		
K07228	2	TrkA domain protein		
K07229	3	Unclassified; K07229		
K07232	6	cation transport protein ChaC		
K07233	1	copper resistance protein B		
K07234	7	uncharacterized protein involved in response to NO		
K07236	1	tRNA 2-thiouridine synthesizing protein C		
K07237	3	tRNA 2-thiouridine synthesizing protein B		
K07238	18	zinc transporter, ZIP family		
K07239	116	heavy-metal exporter, HME family		
K07240	47	chromate transporter		
K07241	10	high-affinity nickel-transport protein		
K07243	27	high-affinity iron transporter		
K07245	21	putative copper resistance protein D		
K07246	8	tartrate dehydrogenase/decarboxylase / D-malate dehydrogenase		
K07248	4	lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase		
K07250	30	4-aminobutyrate aminotransferase / (S)-3-amino-2-methylpropionate		
K07257	5	spore coat polysaccharide biosynthesis protein SpsF		
K07258	136	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6)		
K07259	26	D-alanyl-D-alanine carboxypeptidase /		
K07260	7	D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4]		
K07262	11	D-alanyl-D-alanine endopeptidase (penicillin-binding protein 7)		
K07263	230	zinc protease [EC:3.4.99.-]		
K07264	23	4-amino-4-deoxy-L-arabinose transferase [EC:2.-.-.-]		
K07265	3	capsular polysaccharide export protein		
K07266	2	capsular polysaccharide export protein		
K07267	1	porin		
K07273	5	lysozyme		
K07274	6	outer membrane protein		
K07276	2	hypothetical protein		
K07277	60	outer membrane protein		
K07278	43	outer membrane protein		
K07279	41	hypothetical protein		
K07281	1	Unclassified; K07281		
K07282	27	poly-gamma-glutamate synthesis protein (capsule biosynthesis		
K07283	1	putative salt-induced outer membrane protein		
K07284	9	sortase A		
K07285	2	outer membrane lipoprotein		
K07287	7	lipoprotein-34		
K07288	17	uncharacterized membrane protein		
K07289	17	AsmA protein		
K07290	5	hypothetical protein		
K07300	25	Ca2+:H+ antiporter		
K07301	19	Unclassified; yrbG		
K07302	14	isoquinoline 1-oxidoreductase, alpha subunit [EC:1.3.99.16]		
K07303	95	isoquinoline 1-oxidoreductase, beta subunit [EC:1.3.99.16]		
K07304	33	peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]		
K07305	15	peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12]		
K07306	10	anaerobic dimethyl sulfoxide reductase subunit A [EC:1.8.99.-]		
K07307	10	anaerobic dimethyl sulfoxide reductase subunit B (DMSO reductase		

K07308	1	anaerobic dimethyl sulfoxide reductase subunit C (DMSO reductase		
K07309	1	putative dimethyl sulfoxide reductase subunit YnfE [EC:1.8.99.-]		
K07310	1	putative dimethyl sulfoxide reductase subunit YnfF [EC:1.8.99.-]		
K07313	3	serine/threonine protein phosphatase 1 [EC:3.1.3.16]		
K07315	66	sigma-B regulation protein RsbU (phosphoserine phosphatase)		
K07316	4	adenine-specific DNA-methyltransferase [EC:2.1.1.72]		
K07318	2	adenine-specific DNA-methyltransferase [EC:2.1.1.72]		
K07319	22	putative adenine-specific DNA-methyltransferase [EC:2.1.1.72]		
K07320	7	putative adenine-specific DNA-methyltransferase [EC:2.1.1.72]		
K07321	9	CO dehydrogenase maturation factor		
K07322	13	regulator of cell morphogenesis and NO signaling		
K07323	15	putative toluene tolerance protein		
K07326	7	hemolysin activation/secretion protein		
K07334	3	proteic killer suppression protein		
K07335	28	basic membrane protein A and related proteins		
K07336	1	PKHD-type hydroxylase [EC:1.14.11.-]		
K07337	3	hypothetical protein		
K07339	2	hypothetical protein		
K07341	6	death on curing protein		
K07343	3	DNA transformation protein and related proteins		
K07345	1	major type 1 subunit fimbrin (pilin)		
K07346	3	fimbrial chaperone protein		
K07347	11	outer membrane usher protein		
K07357	1	type 1 fimbriae regulatory protein FimB		
K07386	54	putative endopeptidase [EC:3.4.24.-]		
K07387	22	putative metalloprotease [EC:3.4.24.-]		
K07390	4	monothiol glutaredoxin		
K07391	65	magnesium chelatase family protein		
K07392	4	AAA family ATPase		
K07393	11	putative glutathione S-transferase		
K07395	4	putative proteasome-type protease		
K07396	1	putative protein-disulfide isomerase		
K07397	21	putative redox protein		
K07399	14	cytochrome c biogenesis protein		
K07400	2	Fe/S biogenesis protein NfuA		
K07401	1	selenoprotein W-related protein		
K07402	49	xanthine dehydrogenase accessory factor		
K07403	31	membrane-bound serine protease (ClpP class)		
K07404	25	6-phosphogluconolactonase [EC:3.1.1.31]		
K07405	7	alpha-amylase [EC:3.2.1.1]		
K07406	10	alpha-galactosidase [EC:3.2.1.22]		
K07407	12	alpha-galactosidase [EC:3.2.1.22]		
K07442	6	tRNA (adenine-N1-)-methyltransferase [EC:2.1.1.36]		
K07443	9	methylated-DNA-protein-cysteine methyltransferase related protein		
K07444	21	putative N6-adenine-specific DNA methylase		
K07445	12	putative DNA methylase		
K07447	18	putative holliday junction resolvase [EC:3.1.-.-]		
K07448	1	restriction system protein		
K07450	3	putative resolvase		
K07452	2	5-methylcytosine-specific restriction enzyme B [EC:3.1.21.-]		
K07454	6	putative restriction endonuclease		
K07455	9	recombination protein RecT		
K07456	34	DNA mismatch repair protein MutS2		
K07457	3	endonuclease III related protein		
K07458	8	DNA mismatch endonuclease, patch repair protein [EC:3.1.-.-]		
K07459	2	putative ATP-dependent endonuclease of the OLD family		
K07460	17	putative endonuclease		
K07461	8	putative endonuclease		
K07462	59	single-stranded-DNA-specific exonuclease [EC:3.1.-.-]		

K07464	3	putative RecB family exonuclease		
K07465	7	putative RecB family exonuclease		
K07467	1	phage replication initiation protein		
K07469	22	aldehyde dehydrogenase (FAD-independent) [EC:1.2.99.7]		
K07477	1	translin		
K07478	38	putative ATPase		
K07479	2	putative DNA topoisomerase		
K07480	1	insertion element IS1 protein InsB		
K07481	18	transposase, IS5 family		
K07482	19	transposase, IS30 family		
K07483	33	transposase		
K07484	48	transposase		
K07485	29	transposase		
K07486	162	transposase		
K07487	46	transposase		
K07488	4	transposase		
K07491	40	putative transposase		
K07492	38	putative transposase		
K07493	63	putative transposase		
K07494	80	putative transposase		
K07495	29	putative transposase		
K07496	10	putative transposase		
K07497	187	putative transposase		
K07498	4	putative transposase		
K07499	14	putative transposase		
K07501	8	hypothetical protein		
K07502	7	hypothetical protein		
K07503	8	hypothetical protein		
K07504	1	hypothetical protein		
K07505	1	hypothetical protein		
K07506	18	AraC family transcriptional regulator		
K07507	22	putative Mg2+ transporter-C (MgtC) family protein		
K07508	6	acetyl-CoA acyltransferase 2 [EC:2.3.1.16]		
K07516	43	3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]		
K07519	9	phthalate 4,5-dioxygenase [EC:1.14.12.7]		
K07533	21	foldase protein PrsA [EC:5.2.1.8]		
K07534	4	cyclohex-1-ene-1-carboxyl-CoA hydratase [EC:4.2.1.-]		
K07535	35	2-hydroxycyclohexanecarboxyl-CoA dehydrogenase [EC:1.1.1.-]		
K07537	4	cyclohexa-1,5-dienecarbonyl-CoA hydratase [EC:4.2.1.100]		
K07538	3	6-hydroxycyclohex-1-ene-1-carboxyl-CoA dehydrogenase [EC:1.1.1.-]		
K07543	23	benzylsuccinate CoA-transferase BbsE subunit [EC:2.8.3.15]		
K07544	22	benzylsuccinate CoA-transferase BbsF subunit [EC:2.8.3.15]		
K07545	1	(R)-benzylsuccinyl-CoA dehydro genase [EC:1.3.99.21]		
K07546	8	E-phenylitaconyl-CoA hydratase [EC:4.2.1.-]		
K07547	16	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsC subunit		
K07548	10	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsD subunit		
K07550	12	benzoylsuccinyl-CoA thiolase BbsB subunit [EC:2.3.1.-]		
K07552	14	MFS transporter, DHA1 family, bicyclomycin/chloramphenicol		
K07559	1	putative RNA 2'-phosphotransferase [EC:2.7.1.-]		
K07560	41	D-tyrosyl-tRNA(Tyr) deacylase [EC:3.1.-.-]		
K07566	44	putative translation factor		
K07567	68	TdcF protein		
K07568	35	S-adenosylmethionine:tRNA ribosyltransferase-isomerase [EC:5.-.-.-]		
K07570	6	general stress protein 13		
K07574	3	putative RNA-binding protein containing KH domain		
K07576	52	metallo-beta-lactamase family protein		
K07577	8	putative mRNA 3-end processing factor		
K07586	1	hypothetical protein		
K07588	27	LAO/AO transport system kinase [EC:2.7.-.-]		

K07592	4	LysR family transcriptional regulator, tdc operon transcriptional		
K07636	65	two-component system, OmpR family, phosphate regulon sensor		
K07637	1	two-component system, OmpR family, sensor histidine kinase PhoQ		
K07638	12	two-component system, OmpR family, osmolarity sensor histidine		
K07639	2	two-component system, OmpR family, sensor histidine kinase RstB		
K07640	6	two-component system, OmpR family, sensor histidine kinase CpxA		
K07641	4	two-component system, OmpR family, sensor histidine kinase CreC		
K07642	11	two-component system, OmpR family, sensor histidine kinase BaeS		
K07643	3	two-component system, OmpR family, sensor histidine kinase BasS		
K07644	26	two-component system, OmpR family, heavy metal sensor histidine		
K07645	33	two-component system, OmpR family, sensor histidine kinase QseC		
K07646	67	two-component system, OmpR family, sensor histidine kinase KdpD		
K07647	4	two-component system, OmpR family, sensor histidine kinase TorS		
K07648	1	two-component system, OmpR family, aerobic respiration control		
K07649	29	two-component system, OmpR family, sensor histidine kinase TctE		
K07651	11	two-component system, OmpR family, sensor histidine kinase ResE		
K07652	42	two-component system, OmpR family, sensor histidine kinase VicK		
K07653	6	two-component system, OmpR family, sensor histidine kinase MprB		
K07654	5	two-component system, OmpR family, sensor histidine kinase MtrB		
K07656	1	two-component system, OmpR family, sensor histidine kinase TrcS		
K07657	68	two-component system, OmpR family, phosphate regulon response		
K07658	67	two-component system, OmpR family, alkaline phosphatase synthesis		
K07659	12	two-component system, OmpR family, phosphate regulon response		
K07660	1	two-component system, OmpR family, response regulator PhoP		
K07661	1	two-component system, OmpR family, response regulator RstA		
K07662	5	two-component system, OmpR family, response regulator CpxR		
K07663	1	two-component system, OmpR family, catabolic regulation response		
K07664	5	two-component system, OmpR family, response regulator BaeR		
K07665	23	two-component system, OmpR family, copper resistance phosphate		
K07666	3	two-component system, OmpR family, response regulator QseB		
K07667	53	two-component system, OmpR family, KDP operon response regulator		
K07668	44	two-component system, OmpR family, response regulator VicR		
K07669	30	two-component system, OmpR family, response regulator MprA		
K07670	18	two-component system, OmpR family, response regulator MtrA		
K07671	1	two-component system, OmpR family, response regulator PrrA		
K07672	1	two-component system, OmpR family, response regulator TrcR		
K07673	10	two-component system, NarL family, nitrate/nitrite sensor histidine		
K07674	4	two-component system, NarL family, nitrate/nitrite sensor histidine		
K07675	49	two-component system, NarL family, sensor histidine kinase UhpB		
K07677	11	two-component system, NarL family, capsular synthesis sensor		
K07678	26	two-component system, NarL family, sensor histidine kinase BarA		
K07679	4	two-component system, NarL family, sensor histidine kinase EvgS		
K07680	15	two-component system, NarL family, sensor histidine kinase ComP		
K07681	1	two-component system, NarL family, vancomycin resistance sensor		
K07682	15	two-component system, NarL family, sensor histidine kinase DevS		
K07683	4	two-component system, NarL family, sensor histidine kinase NreB		
K07684	73	two-component system, NarL family, nitrate/nitrite response		
K07685	6	two-component system, NarL family, nitrate/nitrite response		
K07686	7	two-component system, NarL family, uhpT operon response regulator		
K07687	9	two-component system, NarL family, captular synthesis response		
K07689	20	two-component system, NarL family, invasion response regulator UvrY		
K07690	5	two-component system, NarL family, response regulator EvgA		
K07691	24	two-component system, NarL family, competent response regulator ComA		
K07692	37	two-component system, NarL family, response regulator DegU		
K07693	3	two-component system, NarL family, response regulator DesR		
K07694	4	two-component system, NarL family, vancomycin resistance associated		
K07695	13	two-component system, NarL family, response regulator DevR		
K07696	4	two-component system, NarL family, response regulator NreC		
K07697	11	two-component system, sporulation sensor kinase B [EC:2.7.13.3]		

K07699	1	two-component system, response regulator, stage 0 sporulation		
K07700	2	two-component system, CitB family, cit operon sensor histidine		
K07703	1	two-component system, CitB family, response regulator DcuR		
K07704	7	two-component system, LytT family, sensor histidine kinase LytS		
K07705	5	two-component system, LytT family, response regulator LytT		
K07707	4	two-component system, AgrA family, response regulator AgrA		
K07708	54	two-component system, NtrC family, nitrogen regulation sensor		
K07709	54	two-component system, NtrC family, sensor histidine kinase HydH		
K07710	39	two-component system, NtrC family, sensor histidine kinase AtoS		
K07711	10	two-component system, NtrC family, sensor histidine kinase YfhK		
K07712	112	two-component system, NtrC family, nitrogen regulation response		
K07713	64	two-component system, NtrC family, response regulator HydG		
K07714	48	two-component system, NtrC family, response regulator AtoC		
K07715	78	two-component system, NtrC family, response regulator YfhA		
K07716	16	two-component system, cell cycle sensor histidine kinase PleC		
K07718	1	two-component system, sensor histidine kinase YesM [EC:2.7.13.3]		
K07720	7	two-component system, response regulator YesN		
K07726	5	putative transcriptional regulator		
K07727	1	putative transcriptional regulator		
K07729	7	putative transcriptional regulator		
K07734	8	transcriptional regulator		
K07735	24	putative transcriptional regulator		
K07736	12	CarD family transcriptional regulator		
K07737	5	putative transcriptional regulator		
K07738	6	transcriptional repressor NrdR		
K07739	4	elongator complex protein 3 [EC:2.3.1.48]		
K07740	1	regulator of sigma D		
K07741	1	anti-repressor protein		
K07742	7	hypothetical protein		
K07743	2	hypothetical protein		
K07745	1	hypothetical protein		
K07746	2	hypothetical protein		
K07748	2	sterol-4alpha-carboxylate 3-dehydrogenase (decarboxylating)		
K07749	163	formyl-CoA transferase [EC:2.8.3.16]		
K07758	5	pyridoxal phosphatase [EC:3.1.3.74]		
K07768	3	two-component system, OmpR family, sensor histidine kinase SenX3		
K07769	5	two-component system, OmpR family, sensor histidine kinase NblS		
K07771	1	two-component system, OmpR family, response regulator BasR		
K07773	1	two-component system, OmpR family, aerobic respiration control		
K07774	14	two-component system, OmpR family, response regulator TctD		
K07775	5	two-component system, OmpR family, response regulator ResD		
K07776	43	two-component system, OmpR family, response regulator RegX3		
K07777	14	two-component system, NarL family, sensor histidine kinase DegS		
K07778	10	two-component system, NarL family, sensor histidine kinase DesK		
K07782	1	LuxR family transcriptional regulator		
K07783	2	MFS transporter, OPA family, sugar phosphate sensor protein UhpC		
K07785	1	MFS transporter, NRE family, putaive nickel resistance protein		
K07787	112	Cu(I)/Ag(I) efflux system membrane protein CusA		
K07788	66	RND superfamily, multidrug transport protein MdtB		
K07789	37	RND superfamily, multidrug transport protein MdtC		
K07790	1	putative membrane protein PagO		
K07791	3	anaerobic C4-dicarboxylate transporter DcuA		
K07792	4	anaerobic C4-dicarboxylate transporter DcuB		
K07793	90	putative tricarboxylic transport membrane protein		
K07795	87	putative tricarboxylic transport membrane protein		
K07796	16	Cu(I)/Ag(I) efflux system outer membrane protein CusC		
K07798	51	Cu(I)/Ag(I) efflux system membrane protein CusB		
K07799	33	putative multidrug efflux transporter MdtA		
K07805	1	putative membrane protein PagD		

K07806	20	UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase		
K07811	3	trimethylamine-N-oxide reductase (cytochrome c) 1 [EC:1.7.2.3]		
K07812	12	trimethylamine-N-oxide reductase (cytochrome c) 2 [EC:1.7.2.3]		
K07814	158	putative two-component system response regulator		
K07821	1	trimethylamine-N-oxide reductase (cytochrome c) 2, cytochrome c-type		
K07823	4	3-oxoadipyl-CoA thiolase [EC:2.3.1.174]		
K07824	6	benzoate 4-monooxygenase [EC:1.14.13.12]		
K07978	4	GntR family transcriptional regulator		
K07979	9	GntR family transcriptional regulator		
K08068	1	N-acetylglucosamine-6-phosphate 2-epimerase and phosphatase		
K08070	95	2-alkenal reductase [EC:1.3.1.74]		
K08078	2	3a,7a,12a-trihydroxy-5b-cholest-24-enoyl-CoA hydratase		
K08082	4	two-component system, LytT family, sensor histidine kinase AlgZ		
K08083	11	two-component system, LytT family, response regulator AlgR		
K08084	6	type IV fimbrial biogenesis protein FimT		
K08085	2	type IV fimbrial biogenesis protein FimU		
K08093	1	3-hexulose-6-phosphate synthase [EC:4.1.2.43]		
K08097	6	phosphosulfolactate synthase [EC:4.4.1.19]		
K08100	49	bilirubin oxidase [EC:1.3.3.5]		
K08137	1	MFS transporter, SP family, galactose:H+ symporter		
K08138	2	MFS transporter, SP family, xylose:H+ symportor		
K08139	13	MFS transporter, SP family, sugar:H+ symporter		
K08151	22	MFS transporter, DHA1 family, tetracycline resistance protein		
K08152	3	MFS transporter, DHA1 family, multidrug resistance protein B		
K08153	11	MFS transporter, DHA1 family, multidrug resistance protein		
K08154	1	MFS transporter, DHA1 family, 2-module integral membrane pump EmrD		
K08156	5	MFS transporter, DHA1 family, arabinose polymer transporter		
K08159	2	MFS transporter, DHA1 family,		
K08161	7	MFS transporter, DHA1 family, multidrug resistance protein		
K08162	18	MFS transporter, DHA1 family, multidrug resistance protein		
K08166	40	MFS transporter, DHA2 family, methylenomycin A resistance protein		
K08167	18	MFS transporter, DHA2 family, methyl viologen resistance protein		
K08169	16	MFS transporter, DHA2 family, multidrug resistance protein		
K08172	10	MFS transporter, MHS family, shikimate and dehydroshikimate		
K08173	7	MFS transporter, MHS family, metabolite:H+ symporter		
K08177	46	MFS transporter, OFA family, oxalate/formate antiporter		
K08178	5	MFS transporter, SHS family, lactate transporter		
K08191	15	MFS transporter, ACS family, hexuronate transporter		
K08194	23	MFS transporter, ACS family, D-galactonate transporter		
K08195	3	MFS transporter, AAHS family, 4-hydroxybenzoate transporter		
K08196	5	MFS transporter, AAHS family, cis,cis-muconate transporter		
K08217	15	MFS transporter, DHA3 family, macrolide efflux protein		
K08218	18	MFS transporter, PAT family, beta-lactamase induction signal		
K08221	3	MFS transporter, ACDE family, multidrug resistance protein		
K08223	20	MFS transporter, FSR family, fosmidomycin resistance protein		
K08224	9	MFS transporter, YNFM family, putative membrane transport protein		
K08225	95	MFS transporter, ENTS family, enterobactin (siderophore) exporter		
K08226	1	MFS transporter, BCD family, chlorophyll transporter		
K08227	12	MFS transporter, LPLT family, lysophospholipid transporter		
K08234	21	glyoxylase I family protein		
K08252	50	receptor protein-tyrosine kinase [EC:2.7.10.1]		
K08253	118	non-specific protein-tyrosine kinase [EC:2.7.10.2]		
K08256	27	phosphatidylinositol alpha-mannosyltransferase [EC:2.4.1.57]		
K08259	50	lysostaphin [EC:3.4.24.75]		
K08261	13	D-sorbitol dehydrogenase (acceptor) [EC:1.1.99.21]		
K08278	4	thr operon leader peptide		
K08279	14	carnitine operon protein CaiE		
K08281	14	nicotinamidase/pyrazinamidase [EC:3.5.1.19 3.5.1.-]		
K08282	355	non-specific serine/threonine protein kinase [EC:2.7.11.1]		

K08289	4	phosphoribosylglycinamide formyltransferase 2 [EC:2.1.2.2]		
K08295	5	2-aminobenzoate-CoA ligase [EC:6.2.1.32]		
K08296	12	phosphohistidine phosphatase [EC:3.1.3.-]		
K08297	2	crotonobetainyl-CoA dehydrogenase [EC:1.3.99.-]		
K08299	6	carnitinyl-CoA dehydratase [EC:4.2.1.-]		
K08300	19	ribonuclease E [EC:3.1.26.12]		
K08301	25	ribonuclease G [EC:3.1.26.-]		
K08302	1	tagatose 1,6-diphosphate aldolase [EC:4.1.2.40]		
K08303	23	putative protease [EC:3.4.-.-]		
K08304	13	membrane-bound lytic murein transglycosylase A [EC:3.2.1.-]		
K08305	5	membrane-bound lytic murein transglycosylase B [EC:3.2.1.-]		
K08307	30	membrane-bound lytic murein transglycosylase D [EC:3.2.1.-]		
K08309	44	soluble lytic murein transglycosylase [EC:3.2.1.-]		
K08310	5	dATP pyrophosphohydrolase [EC:3.6.1.-]		
K08311	4	putative (di)nucleoside polyphosphate hydrolase [EC:3.6.1.-]		
K08316	6	ribosomal RNA small subunit methyltransferase D [EC:2.1.1.52]		
K08318	2	putative dehydrogenase [EC:1.1.-.-]		
K08319	2	putative dehydrogenase [EC:1.1.-.-]		
K08320	3	CTP pyrophosphohydrolase [EC:3.6.1.-]		
K08321	3	putative autoinducer-2 (AI-2) aldolase [EC:4.1.2.-]		
K08322	8	starvation sensing protein RspB [EC:1.1.1.-]		
K08323	9	starvation sensing protein RspA		
K08324	3	aldehyde dehydrogenase family protein [EC:1.2.1.-]		
K08326	1	aminopeptidase [EC:3.4.11.-]		
K08344	1	suppressor for copper-sensitivity B		
K08345	2	nitrate reductase 2, alpha subunit [EC:1.7.99.4]		
K08346	6	nitrate reductase 2, beta subunit [EC:1.7.99.4]		
K08348	39	formate dehydrogenase-N, alpha subunit [EC:1.2.1.2]		
K08351	5	biotin sulfoxide reductase [EC:1.-.-.-]		
K08352	38	thiosulfate reductase [EC:1.-.-.-]		
K08353	5	thiosulfate reductase electron transport protein		
K08354	3	thiosulfate reductase cytochrome b subunit		
K08356	11	arsenite oxidase large subunit [EC:1.20.98.1]		
K08357	9	tetrathionate reductase subunit A		
K08358	27	tetrathionate reductase subunit B		
K08359	4	tetrathionate reductase subunit C		
K08364	10	periplasmic mercuric ion binding protein		
K08365	3	MerR family transcriptional regulator, mercuric resistance operon		
K08368	1	MFS transporter, putative metabolite transport protein		
K08369	27	MFS transporter, putative metabolite:H+ symporter		
K08372	45	putative serine protease PepD [EC:3.4.21.-]		
K08384	8	stage V sporulation protein D (sporulation-specific		
K08477	2	outer membrane protease E [EC:3.4.21.-]		
K08478	1	phosphoglycerate transport regulatory protein PgtC		
K08479	3	two-component system, OmpR family, clock-associated histidine kinase		
K08481	4	circadian clock protein KaiB		
K08482	37	circadian clock protein KaiC		
K08483	32	phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]		
K08484	7	phosphotransferase system, enzyme I, PtsP [EC:2.7.3.9]		
K08485	1	phosphocarrier protein NPr		
K08567	9	hydrogenase 2 maturation protease [EC:3.4.24.-]		
K08590	4	carbon-nitrogen hydrolase family protein		
K08591	25	glycerol-3-phosphate acyltransferase PlsY [EC:2.3.1.15]		
K08600	2	sortase B		
K08602	47	oligoendopeptidase F [EC:3.4.24.-]		
K08603	6	thermolysin [EC:3.4.24.27]		
K08605	1	coccolysin [EC:3.4.24.30]		
K08641	17	D-alanyl-D-alanine dipeptidase [EC:3.4.13.-]		
K08651	23	thermitase [EC:3.4.21.66]		

K08676	43	tricorn protease [EC:3.4.21.-]		
K08677	19	kumamolisin		
K08678	5	UDP-glucuronate decarboxylase [EC:4.1.1.35]		
K08679	5	UDP-glucuronate 4-epimerase [EC:5.1.3.6]		
K08680	8	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase		
K08681	4	glutamine amidotransferase [EC:2.6.-.-]		
K08682	2	acyl carrier protein phosphodiesterase [EC:3.1.4.14]		
K08684	2	methane monooxygenase [EC:1.14.13.25]		
K08686	15	2-chlorobenzoate 1,2-dioxygenase [EC:1.14.12.13]		
K08687	4	N-carbamoylsarcosine amidase [EC:3.5.1.59]		
K08688	9	creatinase [EC:3.5.3.3]		
K08693	4	3'-nucleotidase [EC:3.1.3.6]		
K08697	2	carbon dioxide concentrating mechanism protein CcmL		
K08698	1	carbon dioxide concentrating mechanism protein CcmM		
K08710	5	N-isopropylammelide isopropylaminohydrolase [EC:3.5.99.4]		
K08714	2	voltage-gated sodium channel		
K08720	3	outer membrane protein OmpU		
K08721	3	multidrug resistance outer membrane protein OprJ		
K08723	4	5'-nucleotidase [EC:3.1.3.5]		
K08724	5	penicillin-binding protein 2B		
K08738	12	cytochrome c		
K08777	1	neutral peptidase B [EC:3.4.24.-]		
K08884	560	serine/threonine protein kinase, bacterial [EC:2.7.11.1]		
K08900	1	mitochondrial chaperone BCS1		
K08942	8	photosystem P840 reaction center cytochrome c551		
K08963	23	methylthioribose-1-phosphate isomerase [EC:5.3.1.23]		
K08964	2	methylthioribulose-1-phosphate dehydratase [EC:4.2.1.109]		
K08965	1	2,3-diketo-5-methylthiopentyl-1-phosphate enolase [EC:3.1.3.77]		
K08966	3	2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase		
K08967	4	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase [EC:1.13.11.53		
K08969	1	aminotransferase [EC:2.6.1.-]		
K08970	5	nickel/cobalt exporter		
K08972	5	putative membrane protein		
K08973	5	putative membrane protein		
K08974	3	putative membrane protein		
K08977	3	putative membrane protein		
K08978	11	putative membrane protein		
K08981	2	putative membrane protein		
K08983	1	putative membrane protein		
K08984	7	putative membrane protein		
K08986	2	putative membrane protein		
K08987	2	putative membrane protein		
K08988	7	putative membrane protein		
K08989	3	putative membrane protein		
K08990	1	putative membrane protein		
K08992	1	putative membrane protein		
K08995	6	putative membrane protein		
K08997	11	hypothetical protein		
K08998	13	hypothetical protein		
K08999	19	hypothetical protein		
K09001	23	anhydro-N-acetylmuramic acid kinase [EC:2.7.1.-]		
K09003	8	hypothetical protein		
K09004	3	hypothetical protein		
K09005	16	hypothetical protein		
K09007	8	hypothetical protein		
K09008	4	hypothetical protein		
K09009	2	hypothetical protein		
K09011	7	D-citramalate synthase [EC:2.3.1.182]		
K09012	6	DeoR family transcriptional regulator, suf operon transcriptional		

K09013	19	Fe-S cluster assembly ATP-binding protein		
K09014	39	Fe-S cluster assembly protein SufB		
K09015	22	Fe-S cluster assembly protein SufD		
K09016	3	putative pyrimidine permease RutG		
K09017	38	TetR/AcrR family transcriptional regulator		
K09018	1	putative monooxygenase RutA [EC:1.14.-.-]		
K09019	4	putative NADH dehydrogenase/NAD(P)H nitroreductase RutE [EC:1.-.-.-]		
K09020	6	putative isochorismatase family protein RutB [EC:3.-.-.-]		
K09022	1	UPF0076 protein YjgF		
K09023	5	protein RutD		
K09024	2	putative flavin reductase RutF [EC:1.5.1.-]		
K09065	3	N-acetylornithine carbamoyltransferase [EC:2.1.3.9]		
K09116	3	hypothetical protein		
K09117	10	hypothetical protein		
K09118	29	hypothetical protein		
K09120	2	hypothetical protein		
K09121	25	hypothetical protein		
K09122	9	hypothetical protein		
K09123	12	hypothetical protein		
K09125	6	hypothetical protein		
K09128	3	hypothetical protein		
K09129	5	hypothetical protein		
K09131	12	hypothetical protein		
K09132	1	hypothetical protein		
K09134	98	hypothetical protein		
K09136	1	hypothetical protein		
K09137	13	hypothetical protein		
K09141	10	hypothetical protein		
K09143	3	hypothetical protein		
K09144	1	hypothetical protein		
K09146	2	hypothetical protein		
K09151	9	hypothetical protein		
K09153	4	hypothetical protein		
K09155	3	hypothetical protein		
K09157	3	hypothetical protein		
K09158	2	hypothetical protein		
K09159	2	hypothetical protein		
K09160	3	hypothetical protein		
K09162	15	hypothetical protein		
K09163	2	hypothetical protein		
K09164	7	hypothetical protein		
K09165	6	hypothetical protein		
K09166	8	hypothetical protein		
K09167	1	hypothetical protein		
K09181	129	hypothetical protein		
K09190	1	hypothetical protein		
K09251	10	putrescine aminotransferase [EC:2.6.1.82]		
K09252	3	feruloyl esterase [EC:3.1.1.73]		
K09384	1	hypothetical protein		
K09386	19	hypothetical protein		
K09456	23	putative acyl-CoA dehydrogenase		
K09457	12	7-cyano-7-deazaguanine reductase [EC:1.7.1.13]		
K09458	82	3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]		
K09459	5	phosphonopyruvate decarboxylase [EC:4.1.1.82]		
K09461	29	anthraniloyl-CoA monooxygenase [EC:1.14.13.40]		
K09471	25	gamma-glutamylputrescine oxidase [EC:1.4.3.-]		
K09472	7	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase [EC:1.2.1.-]		
K09474	2	acid phosphatase (class A) [EC:3.1.3.2]		
K09477	5	citrate:succinate antiporter		

K09516	1	all-trans-retinol 13,14-reductase [EC:1.3.99.23]		
K09607	31	immune inhibitor A [EC:3.4.24.-]		
K09680	3	type II pantothenate kinase [EC:2.7.1.33]		
K09681	11	LysR family transcriptional regulator, transcription activator of		
K09684	10	purine catabolism regulatory protein		
K09686	142	antibiotic transport system permease protein		
K09687	115	antibiotic transport system ATP-binding protein		
K09688	3	capsular polysaccharide transport system permease protein		
K09689	1	capsular polysaccharide transport system ATP-binding protein		
K09690	46	lipopolysaccharide transport system permease protein		
K09691	27	lipopolysaccharide transport system ATP-binding protein		
K09693	8	teichoic acid transport system ATP-binding protein [EC:3.6.3.40]		
K09694	20	lipooligosaccharide transport system permease protein		
K09695	6	lipooligosaccharide transport system ATP-binding protein		
K09697	5	sodium transport system ATP-binding protein		
K09698	20	nondiscriminating glutamyl-tRNA synthetase [EC:6.1.1.24]		
K09699	12	2-oxoisovalerate dehydrogenase E2 component (dihydrolipoyl		
K09700	2	hypothetical protein		
K09701	10	hypothetical protein		
K09702	2	hypothetical protein		
K09703	2	hypothetical protein		
K09704	1	hypothetical protein		
K09707	3	hypothetical protein		
K09709	9	hypothetical protein		
K09710	20	hypothetical protein		
K09711	3	hypothetical protein		
K09726	3	hypothetical protein		
K09729	2	hypothetical protein		
K09740	1	hypothetical protein		
K09747	16	hypothetical protein		
K09748	32	hypothetical protein		
K09749	6	hypothetical protein		
K09758	10	aspartate 4-decarboxylase [EC:4.1.1.12]		
K09759	2	nondiscriminating aspartyl-tRNA synthetase [EC:6.1.1.23]		
K09760	28	DNA recombination protein RmuC		
K09761	46	ribosomal RNA small subunit methyltransferase E [EC:2.1.1.-]		
K09762	5	hypothetical protein		
K09763	4	hypothetical protein		
K09764	6	hypothetical protein		
K09765	1	hypothetical protein		
K09766	3	hypothetical protein		
K09767	15	hypothetical protein		
K09768	8	hypothetical protein		
K09769	27	hypothetical protein		
K09770	9	hypothetical protein		
K09772	3	cell division inhibitor SepF		
K09773	10	hypothetical protein		
K09774	441	lipopolysaccharide export system protein LptA		
K09775	19	hypothetical protein		
K09776	1	hypothetical protein		
K09777	2	hypothetical protein		
K09778	5	hypothetical protein		
K09779	5	hypothetical protein		
K09780	2	hypothetical protein		
K09781	3	hypothetical protein		
K09786	18	hypothetical protein		
K09787	1	hypothetical protein		
K09788	41	hypothetical protein		
K09790	2	hypothetical protein		

K09791	3	hypothetical protein		
K09792	7	hypothetical protein		
K09793	1	hypothetical protein		
K09795	3	hypothetical protein		
K09796	6	hypothetical protein		
K09798	3	hypothetical protein		
K09799	2	hypothetical protein		
K09800	10	hypothetical protein		
K09801	2	hypothetical protein		
K09802	1	hypothetical protein		
K09803	7	hypothetical protein		
K09806	1	hypothetical protein		
K09807	9	hypothetical protein		
K09808	44	lipoprotein-releasing system permease protein		
K09809	13	CDP-glycerol glycerophosphotransferase [EC:2.7.8.12]		
K09810	59	lipoprotein-releasing system ATP-binding protein [EC:3.6.3.-]		
K09811	32	cell division transport system permease protein		
K09812	13	cell division transport system ATP-binding protein		
K09815	10	zinc transport system substrate-binding protein		
K09816	9	zinc transport system permease protein		
K09817	8	zinc transport system ATP-binding protein [EC:3.6.3.-]		
K09818	5	manganese/iron transport system substrate-binding protein		
K09819	8	manganese/iron transport system permease protein		
K09820	12	manganese/iron transport system ATP-binding protein		
K09822	6	hypothetical protein		
K09825	6	Fur family transcriptional regulator, peroxide stress response		
K09826	4	Fur family transcriptional regulator, iron response regulator		
K09833	1	homogenitisate phytyltransferase		
K09835	2	carotenoid isomerase [EC:5.-.-.-]		
K09845	3	methoxyneurosporene dehydrogenase [EC:1.14.99.-]		
K09846	18	hydroxyneurosporene methyltransferase [EC:2.1.1.-]		
K09858	1	SEC-C motif domain protein		
K09859	1	hypothetical protein		
K09862	6	hypothetical protein		
K09879	1	isorenieratene synthase		
K09882	3	cobaltochelatase CobS [EC:6.6.1.2]		
K09883	6	cobaltochelatase CobT [EC:6.6.1.2]		
K09888	10	cell division protein ZapA		
K09889	3	hypothetical protein		
K09891	1	hypothetical protein		
K09895	4	hypothetical protein		
K09903	23	uridylate kinase [EC:2.7.4.22]		
K09906	1	hypothetical protein		
K09909	2	hypothetical protein		
K09913	1	hypothetical protein		
K09914	4	putative lipoprotein		
K09915	12	hypothetical protein		
K09916	5	hypothetical protein		
K09917	1	hypothetical protein		
K09918	2	hypothetical protein		
K09919	9	hypothetical protein		
K09921	6	hypothetical protein		
K09922	3	hypothetical protein		
K09923	1	hypothetical protein		
K09924	5	hypothetical protein		
K09926	2	hypothetical protein		
K09927	30	hypothetical protein		
K09928	3	hypothetical protein		
K09930	9	hypothetical protein		

K09931	19	hypothetical protein		
K09933	8	hypothetical protein		
K09934	3	hypothetical protein		
K09935	1	hypothetical protein		
K09936	3	hypothetical protein		
K09937	2	hypothetical protein		
K09939	1	hypothetical protein		
K09941	1	hypothetical protein		
K09942	1	hypothetical protein		
K09949	15	hypothetical protein		
K09950	1	hypothetical protein		
K09951	1	CRISPR-associated protein Cas2		
K09952	6	hypothetical protein		
K09953	2	lipid A 3-O-deacylase		
K09955	22	hypothetical protein		
K09958	8	hypothetical protein		
K09959	1	hypothetical protein		
K09962	1	hypothetical protein		
K09966	6	hypothetical protein		
K09967	7	hypothetical protein		
K09969	7	general L-amino acid transport system substrate-binding protein		
K09970	2	general L-amino acid transport system permease protein		
K09971	7	general L-amino acid transport system permease protein		
K09972	2	general L-amino acid transport system ATP-binding protein		
K09973	11	hypothetical protein		
K09974	1	hypothetical protein		
K09978	1	hypothetical protein		
K09979	1	hypothetical protein		
K09981	4	hypothetical protein		
K09983	6	hypothetical protein		
K09984	4	hypothetical protein		
K09986	2	hypothetical protein		
K09988	2	hypothetical protein		
K09989	5	hypothetical protein		
K09990	7	hypothetical protein		
K09992	5	hypothetical protein		
K09994	1	PhnO protein [EC:2.3.1.-]		
K09996	9	arginine transport system substrate-binding protein		
K09999	2	arginine transport system permease protein		
K10001	14	glutamate/aspartate transport system substrate-binding protein		
K10002	5	glutamate/aspartate transport system permease protein		
K10003	8	glutamate/aspartate transport system permease protein		
K10004	3	glutamate/aspartate transport system ATP-binding protein		
K10005	1	glutamate transport system substrate-binding protein		
K10006	2	glutamate transport system permease protein		
K10007	2	glutamate transport system permease protein		
K10009	4	cystine transport system permease protein		
K10010	1	cystine transport system ATP-binding protein [EC:3.6.3.-]		
K10011	7	UDP-GlcUA decarboxylase/UDP-L-Ara4N formyltransferase		
K10012	8	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase		
K10014	1	histidine transport system substrate-binding protein		
K10017	1	histidine transport system ATP-binding protein [EC:3.6.3.21]		
K10026	15	queuosine biosynthesis protein QueE		
K10027	11	phytoene dehydrogenase [EC:1.14.99.-]		
K10036	2	glutamine transport system substrate-binding protein		
K10037	3	glutamine transport system permease protein		
K10039	6	putative glutamine transport system substrate-binding protein		
K10040	3	putative glutamine transport system permease protein		
K10041	2	putative glutamine transport system ATP-binding protein [EC:3.6.3.-]		

K10108	11	maltose/maltodextrin transport system substrate-binding protein		
K10109	5	maltose/maltodextrin transport system permease protein		
K10110	13	maltose/maltodextrin transport system permease protein		
K10111	2	maltose/maltodextrin transport system ATP-binding protein		
K10112	10	maltose/maltodextrin transport system ATP-binding protein		
K10117	1	multiple sugar transport system substrate-binding protein		
K10118	3	multiple sugar transport system permease protein		
K10119	3	multiple sugar transport system permease protein		
K10120	2	putative sugar transport system substrate-binding protein		
K10121	12	putative sugar transport system permease protein		
K10122	6	putative sugar transport system permease protein		
K10125	16	two-component system, NtrC family, C4-dicarboxylate transport sensor		
K10126	65	two-component system, NtrC family, C4-dicarboxylate transport		
K10188	9	lactose/L-arabinose transport system substrate-binding protein		
K10189	8	lactose/L-arabinose transport system permease protein		
K10190	19	lactose/L-arabinose transport system permease protein		
K10191	1	lactose/L-arabinose transport system ATP-binding protein		
K10193	2	oligogalacturonide transport system permease protein		
K10200	3	N-acetylglucosamine transport system substrate-binding protein		
K10201	3	N-acetylglucosamine transport system permease protein		
K10206	25	LL-diaminopimelate aminotransferase [EC:2.6.1.83]		
K10209	1	dehydrosqualene desaturase [EC:1.14.99.-]		
K10210	3	4,4'-diaponeurosporene oxidase [EC:1.-.-.-]		
K10215	11	monooxygenase [EC:1.14.13.-]		
K10217	4	aminomuconate-semialdehyde dehydrogenase [EC:1.2.1.32]		
K10218	5	4-hydroxy-4-methyl-2-oxoglutarate aldolase [EC:4.1.3.17]		
K10219	34	4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase		
K10220	52	4-oxalmesaconate hydratase [EC:4.2.1.83]		
K10221	17	2-pyrone-4,6-dicarboxylate lactonase [EC:3.1.1.57]		
K10227	10	sorbitol/mannitol transport system substrate-binding protein		
K10228	1	sorbitol/mannitol transport system permease protein		
K10229	2	sorbitol/mannitol transport system permease protein		
K10230	1	sorbitol/mannitol transport system ATP-binding protein		
K10231	10	kojibiose phosphorylase [EC:2.4.1.230]		
K10232	15	alpha-glucoside transport system substrate-binding protein		
K10233	5	alpha-glucoside transport system permease protein		
K10234	8	alpha-glucoside transport system permease protein		
K10236	6	trehalose/maltose transport system substrate-binding protein		
K10237	4	trehalose/maltose transport system permease protein		
K10238	3	trehalose/maltose transport system permease protein		
K10239	1	trehalose/maltose transport system ATP-binding protein		
K10240	2	cellobiose transport system substrate-binding protein		
K10241	1	cellobiose transport system permease protein		
K10242	1	cellobiose transport system permease protein		
K10243	2	cellobiose transport system ATP-binding protein		
K10253	2	DOPA 4,5-dioxygenase [EC:1.14.99.-]		
K10254	1	myosin-crossreactive antigen		
K10255	15	omega-6 fatty acid desaturase (delta-12 desaturase) [EC:1.14.19.-]		
K10353	5	deoxyadenosine kinase [EC:2.7.1.76]		
K10439	21	ribose transport system substrate-binding protein		
K10440	29	ribose transport system permease protein		
K10441	27	ribose transport system ATP-binding protein [EC:3.6.3.17]		
K10533	3	limonene-1,2-epoxide hydrolase [EC:3.3.2.8]		
K10536	12	agmatine deiminase [EC:3.5.3.12]		
K10538	1	L-arabinose transport system permease protein		
K10541	3	methyl-galactoside transport system permease protein		
K10542	1	methyl-galactoside transport system ATP-binding protein		
K10543	5	D-xylose transport system substrate-binding protein		
K10544	14	D-xylose transport system permease protein		

K10545	1	D-xylose transport system ATP-binding protein [EC:3.6.3.17]		
K10547	1	putative multiple sugar transport system permease protein		
K10549	2	D-allose transport system substrate-binding protein		
K10552	6	fructose transport system substrate-binding protein		
K10553	2	fructose transport system permease protein		
K10554	2	fructose transport system ATP-binding protein		
K10555	9	AI-2 transport system substrate-binding protein		
K10556	4	AI-2 transport system permease protein		
K10557	2	AI-2 transport system permease protein		
K10559	7	rhamnose transport system substrate-binding protein		
K10560	3	rhamnose transport system permease protein		
K10561	1	rhamnose transport system permease protein		
K10563	62	formamidopyrimidine-DNA glycosylase [EC:3.2.2.23 4.2.99.18]		
K10616	19	p-cymene monooxygenase [EC:1.14.13.-]		
K10617	7	p-cumic alcohol dehydrogenase		
K10618	7	p-cumic aldehyde dehydrogenase		
K10619	17	p-cumate dioxygenase [EC:1.14.12.-]		
K10620	1	2,3-dihydroxy-2,3-dihydro-p-cumate dehydrogenase [EC:1.3.1.58]		
K10621	5	2,3-dihydroxy-p-cumate-3,4-dioxygenase [EC:1.13.11.-]		
K10622	2	HCOMODA decarboxylase [EC:4.1.1.-]		
K10674	2	ectoine hydroxylase [EC:1.14.11.-]		
K10676	13	2,4-dichlorophenol 6-monooxygenase [EC:1.14.13.20]		
K10678	1	nitroreductase [EC:1.-.-.-]		
K10679	1	nitroreductase / dihydropteridine reductase [EC:1.-.-.- 1.5.1.34]		
K10680	11	N-ethylmaleimide reductase [EC:1.-.-.-]		
K10697	6	two-component system, OmpR family, response regulator RpaA		
K10700	13	ethylbenzene hydroxylase [EC:1.17.99.2]		
K10701	20	acetophenone carboxylase [EC:6.4.1.-]		
K10708	1	fructoselysine 6-phosphate deglycase [EC:3.5.-.-]		
K10711	1	GntR family transcriptional regulator, frlABCD operon		
K10713	1	formaldehyde-activating enzyme [EC:4.3.-.-]		
K10715	7	two-component system, sensor histidine kinase RpfC [EC:2.7.13.3]		
K10716	1	voltage-gated potassium channel		
K10747	4	DNA ligase 1 [EC:6.5.1.1]		
K10754	4	replication factor C subunit 1		
K10763	2	DnaA-homolog protein		
K10764	12	O-succinylhomoserine sulfhydrylase [EC:2.5.1.-]		
K10773	24	endonuclease III [EC:4.2.99.18]		
K10774	6	tyrosine ammonia-lyase [EC:4.3.1.23]		
K10775	1	phenylalanine ammonia-lyase [EC:4.3.1.24]		
K10778	19	AraC family transcriptional regulator, regulatory protein of		
K10780	3	enoyl-[acyl carrier protein] reductase III [EC:1.3.1.-]		
K10799	18	tankyrase [EC:2.4.2.30]		
K10804	10	acyl-CoA thioesterase I [EC:3.1.2.- 3.1.1.5]		
K10805	10	acyl-CoA thioesterase II [EC:3.1.2.-]		
K10806	4	acyl-CoA thioesterase YciA [EC:3.1.2.-]		
K10807	1	ribonucleoside-diphosphate reductase subunit M1 [EC:1.17.4.1]		
K10810	1	transcriptional regulator TenI		
K10815	1	hydrogen cyanide synthase HcnB [EC:1.4.99.5]		
K10816	2	hydrogen cyanide synthase HcnC [EC:1.4.99.5]		
K10817	32	erythronolide synthase [EC:2.3.1.94]		
K10819	143	histidine kinase		
K10820	13	monosaccharide-transporting ATPase [EC:3.6.3.17]		
K10822	21	nonpolar-amino-acid-transporting ATPase [EC:3.6.3.22]		
K10826	34	Fe3+-transporting ATPase [EC:3.6.3.30]		
K10828	1	quaternary-amine-transporting ATPase [EC:3.6.3.32]		
K10829	1	iron-chelate-transporting ATPase [EC:3.6.3.34]		
K10834	7	heme-transporting ATPase [EC:3.6.3.41]		
K10843	12	DNA excision repair protein ERCC-3 [EC:3.6.1.-]		

K10844	3	DNA excision repair protein ERCC-2 [EC:3.6.1.-]		
K10855	1	acetone carboxylase, beta subunit [EC:6.4.1.6]		
K10857	1	exodeoxyribonuclease X [EC:3.1.11.-]		
K10907	72	aminotransferase [EC:2.6.1.-]		
K10908	1	DNA-directed RNA polymerase, mitochondrial [EC:2.7.7.6]		
K10912	2	two-component system, repressor protein LuxO		
K10914	3	CRP/FNR family transcriptional regulator, cyclic AMP receptor		
K10915	1	CAI-1 autoinducer synthase [EC:2.3.-.-]		
K10917	8	PadR family transcriptional regulator, regulatory protein AphA		
K10918	14	LysR family transcriptional regulator, transcriptional activator		
K10941	18	sigma-54 specific transcriptional regulator, flagellar regulatory		
K10942	29	two-component system, sensor histidine kinase FlrB [EC:2.7.13.3]		
K10943	57	two component system, response regulator FlrC		
K10947	19	PadR family transcriptional regulator, regulatory protein PadR		
K10972	1	LysR family transcriptional regulator, transcriptional activator of		
K10979	36	DNA end-binding protein Ku		
K11003	4	hemolysin D		
K11004	5	ATP-binding cassette, subfamily B, bacterial HlyB/CyaB		
K11005	15	hemolysin A		
K11016	4	hemolysin		
K11017	8	hemolysin activation/secretion protein??		
K11029	4	anthrax edema toxin adenylate cyclase [EC:4.6.1.1]		
K11031	2	thiol-activated cytolysin		
K11041	2	exfoliative toxin A/B		
K11049	16	CylG protein		
K11053	3	CylF protein		
K11060	5	probable enterotoxin B		
K11062	1	probable enterotoxin D		
K11065	10	thiol peroxidase, atypical 2-Cys peroxiredoxin [EC:1.11.1.15]		
K11066	3	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]		
K11068	27	hemolysin III		
K11069	17	spermidine/putrescine transport system substrate-binding protein		
K11070	19	spermidine/putrescine transport system permease protein		
K11071	27	spermidine/putrescine transport system permease protein		
K11072	19	spermidine/putrescine transport system ATP-binding protein		
K11073	4	putrescine transport system substrate-binding protein		
K11074	10	putrescine transport system permease protein		
K11075	10	putrescine transport system permease protein		
K11076	10	putrescine transport system ATP-binding protein		
K11079	3	mannopine transport system permease protein		
K11082	1	2-aminoethylphosphonate transport system permease protein		
K11085	118	ATP-binding cassette, subfamily B, bacterial MsbA [EC:3.6.3.-]		
K11102	12	proton glutamate symport protein		
K11103	9	aerobic C4-dicarboxylate transport protein		
K11105	21	cell volume regulation protein A		
K11106	6	L-tartrate/succinate antiporter		
K11144	8	primosomal protein DnaI		
K11145	2	ribonuclease III family protein		
K11159	3	carotenoid cleavage dioxygenase		
K11173	9	hydroxyacid-oxoacid transhydrogenase [EC:1.1.99.24]		
K11174	8	carbon-monoxide dehydrogenase (ferredoxin) [EC:1.2.7.4]		
K11175	32	phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]		
K11177	61	xanthine dehydrogenase YagR molybdenum-binding subunit [EC:1.17.1.4]		
K11178	19	xanthine dehydrogenase YagS FAD-binding subunit [EC:1.17.1.4]		
K11179	14	tRNA 2-thiouridine synthesizing protein E [EC:2.8.1.-]		
K11180	3	sulfite reductase, dissimilatory-type alpha subunit [EC:1.8.99.3]		
K11181	3	sulfite reductase, dissimilatory-type beta subunit [EC:1.8.99.3]		
K11183	16	phosphocarrier protein FPr		
K11189	29	phosphocarrier protein		

K11192	1	PTS system, N-acetylmuramic acid-specific IIC component		
K11201	2	PTS system, fructose-specific IIA-like component [EC:2.7.1.69]		
K11209	5	GST-like protein		
K11212	20	LPPG:FO 2-phospho-L-lactate transferase [EC:2.7.8.-]		
K11216	1	autoinducer 2 (AI-2) kinase [EC:2.7.1.-]		
K11249	1	cysteine/O-acetylserine efflux protein		
K11250	1	leucine efflux protein		
K11258	2	acetolactate synthase II small subunit [EC:2.2.1.6]		
K11261	6	formylmethanofuran dehydrogenase subunit E [EC:1.2.99.5]		
K11263	26	acetyl-/propionyl-CoA carboxylase, biotin carboxylase, biotin		
K11264	2	methylmalonyl-CoA decarboxylase [EC:4.1.1.41]		
K11311	2	anthranilate dioxygenase reductase		
K11312	6	cupin 2 domain-containing protein		
K11325	6	L-cysteine/cystine lyase		
K11326	7	cation efflux system protein involved in nickel and cobalt tolerance		
K11329	27	two-component system, OmpR family, response regulator RpaB		
K11333	1	chlorophyllide reductase iron protein subunit X [EC:1.18.6.1]		
K11337	3	3-hydroxyethyl bacteriochlorophyllide a dehydrogenase [EC:1.-.-.-]		
K11354	3	two-component system, chemotaxis family, sensor kinase Cph1		
K11355	3	two-component system, chemotaxis family, response regulator Rcp1		
K11356	2	two-component system, sensor histidine kinase and response regulator		
K11357	7	two-component system, cell cycle sensor histidine kinase DivJ		
K11358	4	aspartate aminotransferase [EC:2.6.1.1]		
K11381	62	2-oxoisovalerate dehydrogenase E1 component [EC:1.2.4.4]		
K11383	3	two-component system, NtrC family, sensor histidine kinase KinB		
K11384	7	two-component system, NtrC family, response regulator AlgB		
K11418	13	histone deacetylase 11 [EC:3.5.1.98]		
K11443	7	two-component system, cell cycle response regulator DivK		
K11444	8	two-component system, chemotaxis family, response regulator WspR		
K11472	15	glycolate oxidase FAD binding subunit		
K11473	36	glycolate oxidase iron-sulfur subunit		
K11475	15	GntR family transcriptional regulator, vanillate catabolism		
K11476	4	GntR family transcriptional regulator, gluconate operon		
K11477	13	glc operon protein GlcG		
K11523	4	two-component system, chemotaxis family, response regulator PixH		
K11525	1	methyl-accepting chemotaxis protein PixJ		
K11526	1	two-component system, chemotaxis family, sensor histidine kinase and		
K11527	58	two-component system, unclassified family, sensor histidine kinase		
K11528	4	UDP-N-acetylglucosamine pyrophosphorylase [EC:2.7.7.23]		
K11531	1	lsr operon transcriptional repressor		
K11532	1	fructose-1,6-bisphosphatase II / sedoheptulose-1,7-bisphosphatase		
K11533	1	fatty acid synthase, bacteria type [EC:2.3.1.-]		
K11537	6	MFS transporter, NHS family, xanthosine permease		
K11603	1	manganese transport system ATP-binding protein		
K11604	1	manganese/iron transport system substrate-binding protein		
K11606	3	manganese/iron transport system permease protein		
K11608	1	beta-ketoacyl ACP synthase [EC:2.3.1.-]		
K11609	1	beta-ketoacyl ACP synthase [EC:2.3.1.-]		
K11610	1	beta-ketoacyl ACP reductase [EC:1.1.1.100]		
K11611	8	enoyl ACP reductase [EC:1.3.1.9]		
K11615	3	two-component system, CitB family, response regulator MalR		
K11616	1	malate:Na+ symporter		
K11617	3	two-component system, NarL family, sensor histidine kinase LiaS		
K11618	39	two-component system, NarL family, response regulator LiaR		
K11619	11	lia operon protein LiaI		
K11621	1	lia operon protein LiaG		
K11624	2	two-component system, NarL family, response regulator YdfI		
K11625	9	membrane protein YdfJ		
K11634	1	two-component system, OmpR family, response regulator YxdJ		

K11646	1	dehydroquinate synthase II [EC:1.4.1.-]		
K11688	92	C4-dicarboxylate-binding protein DctP		
K11689	12	C4-dicarboxylate transporter, DctQ subunit		
K11690	144	C4-dicarboxylate transporter, DctM subunit		
K11693	2	peptidoglycan pentaglycine glycine transferase (the first glycine)		
K11710	3	manganese/zinc/iron transport system ATP- binding protein		
K11711	16	two-component system, LuxR family, sensor histidine kinase DctS		
K11712	12	two-component system, LuxR family, response regulator DctR		
K11717	72	cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]		
K11719	2	lipopolysaccharide export system protein LptC		
K11720	14	lipopolysaccharide export system permease protein		
K11731	6	citronellyl-CoA dehydrogenase [EC:1.3.99.-]		
K11740	2	bacteriophage N4 adsorption protein B		
K11741	6	quaternary ammonium compound-resistance protein SugE		
K11744	5	AI-2 transport protein TqsA		
K11745	10	glutathione-regulated potassium-efflux system ancillary protein KefC		
K11746	1	glutathione-regulated potassium-efflux system ancillary protein KefF		
K11747	9	glutathione-regulated potassium-efflux system protein KefB		
K11748	1	glutathione-regulated potassium-efflux system ancillary protein KefG		
K11749	54	regulator of sigma E protease [EC:3.4.24.-]		
K11750	11	esterase FrsA [EC:3.1.-.-]		
K11751	4	5'-nucleotidase / UDP-sugar diphosphatase [EC:3.1.3.5 3.6.1.45]		
K11752	32	diaminohydroxyphosphoribosylaminopyrimidine deaminase /		
K11753	31	riboflavin kinase / FMN adenylyltransferase [EC:2.7.1.26 2.7.7.2]		
K11754	47	dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12		
K11755	12	phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP		
K11777	1	HAD superfamily phosphatase		
K11779	20	FO synthase [EC:2.5.1.-]		
K11781	1	FO synthase subunit 2 [EC:2.5.1.-]		
K11782	5	chorismate futalosine-lyase [EC:4.1.99.-]		
K11784	17	de-hypoxanthine futalosine synthase [EC:1.21.-.-]		
K11785	2	1,4-dihydroxy-6-naphthoate synthase [EC:1.14.-.-]		
K11890	5	type VI secretion system protein ImpM		
K11891	8	type VI secretion system protein ImpL		
K11892	8	type VI secretion system protein ImpK		
K11893	9	type VI secretion system protein ImpJ		
K11894	3	type VI secretion system protein ImpI		
K11895	4	type VI secretion system protein ImpH		
K11896	7	type VI secretion system protein ImpG		
K11897	2	type VI secretion system protein ImpF		
K11898	1	type VI secretion system protein ImpE		
K11899	2	type VI secretion system protein ImpD		
K11900	10	type VI secretion system protein ImpC		
K11901	8	type VI secretion system protein ImpB		
K11902	6	type VI secretion system protein ImpA		
K11903	1	type VI secretion system secreted protein Hcp		
K11904	9	type VI secretion system secreted protein VgrG		
K11905	1	type VI secretion system protein		
K11906	7	type VI secretion system protein VasD		
K11907	13	type VI secretion system protein VasG		
K11910	2	type VI secretion system protein VasJ		
K11911	1	type VI secretion system protein VasL		
K11912	28	serine/threonine-protein kinase PpkA [EC:2.7.11.1]		
K11913	3	type VI secretion system protein		
K11914	2	sigma-54 dependent transcriptional regulator		
K11916	1	serine/threonine-protein kinase Stk1 [EC:2.7.11.-]		
K11917	3	sigma-54 specific transcriptional regulator		
K11921	10	LysR family transcriptional regulator		
K11922	1	GntR family transcriptional regulator, mannosyl-D-glycerate		

K11923	3	MerR family transcriptional regulator, copper efflux regulator		
K11924	4	DtxR family transcriptional regulator, manganese transport regulator		
K11925	1	SgrR family transcriptional regulator		
K11926	1	sigma factor-binding protein Crl		
K11927	27	ATP-dependent RNA helicase RhlE [EC:3.6.4.13]		
K11928	6	sodium/proline symporter		
K11930	1	periplasmic protein TorT		
K11931	5	biofilm PGA synthesis lipoprotein PgaB [EC:3.-.-.-]		
K11933	4	NADH oxidoreductase Hcr [EC:1.-.-.-]		
K11936	26	biofilm PGA synthesis N-glycosyltransferase PgaC [EC:2.4.-.-]		
K11938	1	HMP-PP phosphatase [EC:3.6.1.-]		
K11939	8	inner membrane transporter RhtA		
K11940	2	heat shock protein HspQ		
K11942	14	methylmalonyl-CoA mutase [EC:5.4.99.2]		
K11948	2	1-hydroxy-2-naphthoate dioxygenase [EC:1.13.11.38]		
K11949	1	4-(2-carboxyphenyl)-2-oxobut-3-enoate aldolase [EC:4.1.2.34]		
K11953	1	bicarbonate transport system ATP-binding protein [EC:3.6.3.-]		
K11954	2	neutral amino acid transport system substrate-binding protein		
K11955	1	neutral amino acid transport system permease protein		
K11956	1	neutral amino acid transport system permease protein		
K11957	2	neutral amino acid transport system ATP-binding protein		
K11958	2	neutral amino acid transport system ATP-binding protein		
K11959	4	urea transport system substrate-binding protein		
K11960	1	urea transport system permease protein		
K11961	2	urea transport system permease protein		
K11963	1	urea transport system ATP-binding protein		
K11987	1	prostaglandin-endoperoxide synthase 2 [EC:1.14.99.1]		
K11991	12	tRNA-specific adenosine deaminase [EC:3.5.4.-]		
K12059	1	conjugal transfer pilus assembly protein TrbC		
K12063	2	conjugal transfer ATP-binding protein TraC		
K12065	1	conjugal transfer pilus assembly protein TraB		
K12073	3	1,4-dihydroxy-2-naphthoyl-CoA thioesterase [EC:3.1.2.-]		
K12111	2	evolved beta-galactosidase subunit alpha [EC:3.2.1.23]		
K12137	9	hydrogenase-4 component B [EC:1.-.-.-]		
K12138	10	hydrogenase-4 component C [EC:1.-.-.-]		
K12139	6	hydrogenase-4 component D [EC:1.-.-.-]		
K12140	6	hydrogenase-4 component E [EC:1.-.-.-]		
K12141	14	hydrogenase-4 component F [EC:1.-.-.-]		
K12142	1	hydrogenase-4 component G [EC:1.-.-.-]		
K12143	4	hydrogenase-4 component H		
K12146	16	hydrogenase-4 transcriptional activator		
K12148	3	biofilm regulator BssS		
K12150	1	HIT-like protein HinT		
K12152	3	phosphatase NudJ [EC:3.6.1.-]		
K12203	34	defect in organelle trafficking protein DotB		
K12206	6	intracellular multiplication protein IcmB		
K12209	3	intracellular multiplication protein IcmE		
K12210	6	intracellular multiplication protein IcmF		
K12213	10	intracellular multiplication protein IcmK		
K12214	5	intracellular multiplication protein IcmL		
K12216	1	intracellular multiplication protein IcmN		
K12234	9	F420-0:gamma-glutamyl ligase [EC:6.3.2.-]		
K12238	5	pyochelin biosynthesis protein PchD		
K12240	1	pyochelin synthetase		
K12251	28	N-carbamoylputrescine amidase [EC:3.5.1.53]		
K12252	2	arginine:pyruvate transaminase [EC:2.6.1.84]		
K12253	4	5-guanidino-2-oxopentanoate decarboxylase [EC:4.1.1.75]		
K12254	3	4-guanidinobutyraldehyde dehydrogenase / NAD-dependent aldehyde		
K12255	4	guanidinobutyrase [EC:3.5.3.7]		

K12256	7	putrescine aminotransferase [EC:2.6.1.-]		
K12257	30	SecD/SecF fusion protein		
K12262	5	cytochrome b561		
K12264	2	anaerobic nitric oxide reductase flavorubredoxin		
K12265	1	nitric oxide reductase FlRd-NAD(+) reductase [EC:1.18.1.-]		
K12266	6	anaerobic nitric oxide reductase transcription regulator		
K12267	22	peptide methionine sulfoxide reductase msrA/msrB [EC:1.8.4.11		
K12276	10	MSHA biogenesis protein MshE		
K12278	8	MSHA biogenesis protein MshG		
K12282	9	MSHA biogenesis protein MshL		
K12283	7	MSHA biogenesis protein MshM		
K12287	4	MSHA biogenesis protein MshQ		
K12297	4	ribosomal RNA large subunit methyltransferase L [EC:2.1.1.52]		
K12299	1	MFS transporter, ACS family, probable galactarate transporter		
K12308	35	beta-galactosidase [EC:3.2.1.23]		
K12339	16	cysteine synthase B [EC:2.5.1.47]		
K12340	36	outer membrane channel protein TolC		
K12343	4	3-oxo-5-alpha-steroid 4-dehydrogenase 1 [EC:1.3.99.5]		
K12344	4	3-oxo-5-alpha-steroid 4-dehydrogenase 2 [EC:1.3.99.5]		
K12368	17	dipeptide transport system substrate-binding protein		
K12369	12	dipeptide transport system permease protein		
K12370	10	dipeptide transport system permease protein		
K12371	6	dipeptide transport system ATP-binding protein		
K12372	1	dipeptide transport system ATP-binding protein		
K12373	31	beta-hexosaminidase [EC:3.2.1.52]		
K12410	28	NAD-dependent deacetylase [EC:3.5.1.-]		
K12420	16	ketoacyl reductase [EC:1.3.1.-]		
K12421	1	fatty acid CoA ligase FadD9		
K12423	2	fatty acid CoA ligase FadD21		
K12424	2	fatty acid CoA ligase FadD22		
K12427	1	fatty acid CoA ligase FadD28		
K12428	1	fatty acid CoA ligase FadD32		
K12429	5	fatty acid CoA ligase FadD36		
K12430	3	polyketide synthase 1/15		
K12432	1	polyketide synthase 3/4		
K12436	22	polyketide synthase 12		
K12437	1	polyketide synthase 13		
K12441	1	phenolpthiocerol synthesis type-I polyketide synthase B		
K12442	1	phenolpthiocerol synthesis type-I polyketide synthase C		
K12444	3	phenolpthiocerol synthesis type-I polyketide synthase E		
K12445	2	trans enoyl reductase [EC:1.3.1.-]		
K12452	6	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase		
K12454	22	CDP-paratose 2-epimerase [EC:5.1.3.10]		
K12500	1	thioesterase III [EC:3.1.2.-]		
K12503	5	short-chain Z-isoprenyl diphosphate synthase [EC:2.5.1.68]		
K12506	29	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase /		
K12507	2	acyl-CoA synthetase [EC:6.2.1.-]		
K12508	42	feruloyl-CoA synthase [EC:6.2.1.34]		
K12510	17	tight adherence protein B		
K12511	16	tight adherence protein C		
K12524	14	bifunctional aspartokinase/homoserine dehydrogenase 1 [EC:2.7.2.4		
K12525	1	bifunctional aspartokinase/homoserine dehydrogenase 2 [EC:2.7.2.4		
K12526	1	bifunctional diaminopimelate decarboxylase/aspartate kinase		
K12527	2	putative selenate reductase [EC:1.97.1.9]		
K12528	2	putative selenate reductase molybdopterin-binding subunit		
K12536	4	ATP-binding cassette, subfamily C, bacterial HasD		
K12537	2	protease secretion protein HasE		
K12538	1	outer membrane protein HasF		
K12541	3	ATP-binding cassette, subfamily C, bacterial LapB		

K12542	1	membrane fusion protein LapC		
K12543	1	outer membrane protein LapE		
K12544	1	S-layer protein		
K12549	12	surface adhesion protein		
K12555	1	penicillin-binding protein 2A [EC:2.4.1.129 2.3.2.-]		
K12573	53	ribonuclease R [EC:3.1.-.-]		
K12574	39	ribonuclease J [EC:3.1.-.-]		
K12583	6	phosphatidylinositol alpha 1,6-mannosyltransferase [EC:2.4.1.-]		
K12645	13	epi-isozizaene 5-monooxygenase [EC:1.14.13.106]		
K12658	5	4-hydroxyproline epimerase [EC:5.1.1.8]		
K12660	5	2-dehydro-3-deoxy-L-rhamnonate aldolase [EC:4.1.2.-]		
K12661	1	L-rhamnonate dehydratase [EC:4.2.1.90]		
K12673	2	N2-(2-carboxyethyl)arginine synthase [EC:2.5.1.66]		
K12686	2	outer membrane lipase/esterase		
K12688	2	autotransporter serine protease [EC:3.4.21.-]		
K12941	17	aminobenzoyl-glutamate utilization protein B		
K12942	5	aminobenzoyl-glutamate transport protein		
K12943	2	lipoprotein YgeR		
K12949	13	cation-transporting P-type ATPase A/B [EC:3.6.3.-]		
K12950	1	cation-transporting P-type ATPase C [EC:3.6.3.-]		
K12952	7	cation-transporting ATPase E [EC:3.6.3.-]		
K12953	6	cation-transporting ATPase F [EC:3.6.3.-]		
K12956	10	cation-transporting ATPase V [EC:3.6.3.-]		
K12960	17	5-methylthioadenosine/S-adenosylhomocysteine deaminase		
K12961	2	DnaA initiator-associating protein		
K12972	5	gyoxylate/hydroxypyruvate reductase A [EC:1.1.1.79 1.1.1.81]		
K12979	2	beta-hydroxylase [EC:1.14.11.-]		
K12982	2	heptosyltransferase I [EC:2.4.-.-]		
K12984	12	(heptosyl)LPS beta-1,4-glucosyltransferase [EC:2.4.1.-]		
K12987	3	alpha-1,6-rhamnosyltransferase [EC:2.4.1.-]		
K12988	2	alpha-1,3-rhamnosyltransferase [EC:2.4.1.-]		
K12989	2	mannosyltransferase [EC:2.4.1.-]		
K12990	3	rhamnosyltransferase [EC:2.4.1.-]		
K12992	1	rhamnosyltransferase [EC:2.4.1.-]		
K12994	6	alpha-1,3-rhamnosyltransferase [EC:2.4.1.-]		
K12995	3	rhamnosyltransferase [EC:2.4.1.-]		
K12996	4	rhamnosyltransferase [EC:2.4.1.-]		
K12997	1	rhamnosyltransferase [EC:2.4.1.-]		
K13001	4	mannosyltransferase [EC:2.4.1.-]		
K13002	3	glycosyltransferase [EC:2.4.1.-]		
K13004	5	galacturonosyltransferase [EC:2.4.1.-]		
K13006	4	UDP-perosamine 4-acetyltransferase [EC:2.3.1.-]		
K13007	1	Fuc2NAc and GlcNAc transferase [EC:2.4.1.-]		
K13010	16	perosamine synthetase		
K13013	17	O-antigen biosynthesis protein WbqV		
K13014	2	undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]		
K13015	28	UDP-N-acetyl-D-glucosamine dehydrogenase [EC:1.1.1.-]		
K13016	1	UDP-D-GlcNAcA oxidase [EC:1.1.1.-]		
K13017	16	UDP-3-keto-D-GlcNAcA aminotransferase [EC:2.6.1.-]		
K13018	4	UDP-D-GlcNAc3NA acetyltransferase [EC:2.3.1.-]		
K13019	9	UDP-GlcNAc3NAcA epimerase [EC:5.1.3.23]		
K13020	21	UDP-D-GlcNAcA oxidase [EC:1.1.1.-]		
K13021	6	MFS transporter, ACS family, tartrate transporter		
K13038	42	phosphopantothenoylcysteine decarboxylase /		
K13039	5	sulfopyruvate decarboxylase subunit beta [EC:4.1.1.79]		
K13041	1	two-component system, LuxR family, response regulator TtrR		
K13042	2	dimethylglycine N-methyltransferase [EC:2.1.1.161]		
K13043	3	N-succinyl-L-ornithine transcarbamylase [EC:2.1.3.11]		
K13049	48	carboxypeptidase PM20D1 [EC:3.4.17.-]		

K13051	19	beta-aspartyl-peptidase (threonine type) [EC:3.4.19.5]		
K13052	1	cell division protein DivIC		
K13057	14	trehalose synthase [EC:2.4.1.245]		
K13058	1	mannosylfructose-phosphate synthase [EC:2.4.1.246]		
K13063	1	phenazine biosynthesis protein phzE [EC:2.6.1.86]		
K13069	3	diguanylate cyclase [EC:2.7.7.65]		
K13074	8	biflaviolin synthase [EC:1.14.21.7]		
K13075	16	N-acyl homoserine lactone hydrolase [EC:3.1.1.81]		
K13237	3	peroxisomal 2,4-dienoyl-CoA reductase [EC:1.3.1.34]		
K13243	2	c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]		
K13244	1	c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]		
K13245	7	c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]		
K13252	1	putrescine carbamoyltransferase [EC:2.1.3.6]		
K13256	3	protein PsiE		
K13274	5	cell wall-associated protease [EC:3.4.21.-]		
K13275	2	major intracellular serine protease [EC:3.4.21.-]		
K13276	3	bacillopeptidase F [EC:3.4.21.-]		
K13277	3	minor extracellular protease Epr [EC:3.4.21.-]		
K13280	2	signal peptidase, endoplasmic reticulum-type [EC:3.4.-.-]		
K13281	2	UV DNA damage endonuclease [EC:3.-.-.-]		
K13282	2	cyanophycinase [EC:3.4.15.6]		
K13283	57	ferrous-iron efflux pump FieF		
K13285	1	invasin B		
K13288	10	oligoribonuclease [EC:3.1.-.-]		
K13292	27	phosphatidylglycerol:prolipoprotein diacylglycerol transferase		
K13317	3	NDP-4-keto-2,6-dideoxyhexose 3-C-methyltransferase		
K13318	6	dTDP-4-keto-6-deoxy-L-hexose 4-reductase		
K13378	29	NADH dehydrogenase I subunit C/D [EC:1.6.5.3]		
K13380	1	NADH dehydrogenase I subunit B/C/D [EC:1.6.5.3]		
K13408	2	membrane fusion protein RaxA		
K13409	1	ATP-binding cassette, subfamily B, bacterial RaxB		
K13419	13	serine/threonine-protein kinase PknK [EC:2.7.11.1]		
K13421	1	uridine monophosphate synthetase [EC:2.4.2.10 4.1.1.23]		
K13479	1	xanthine dehydrogenase FAD-binding subunit [EC:1.17.1.4]		
K13481	2	xanthine dehydrogenase small subunit [EC:1.17.1.4]		
K13482	10	xanthine dehydrogenase large subunit [EC:1.17.1.4]		
K13483	14	xanthine dehydrogenase YagT iron-sulfur-binding subunit		
K13486	2	chemotaxis protein methyltransferase WspC		
K13490	5	two-component system, chemotaxis family, sensor histidine kinase and		
K13491	1	two-component system, chemotaxis family, response regulator WspF		
K13497	7	anthranilate synthase/phosphoribosyltransferase [EC:4.1.3.27		
K13498	7	indole-3-glycerol phosphate synthase / phosphoribosylanthranilate		
K13500	1	chondroitin synthase [EC:2.4.1.175 2.4.1.226]		
K13503	3	anthranilate synthase [EC:4.1.3.27]		
K13522	2	bifunctional NMN adenylyltransferase/nudix hydrolase [EC:2.7.7.1		
K13525	23	transitional endoplasmic reticulum ATPase		
K13527	10	proteasome-associated ATPase		
K13529	16	AraC family transcriptional regulator, regulatory protein of		
K13530	4	AraC family transcriptional regulator, regulatory protein of		
K13531	1	methylated-DNA-[protein]-cysteine S-methyltransferase [EC:2.1.1.63]		
K13532	2	two-component system, sporulation sensor kinase D [EC:2.7.13.3]		
K13533	7	two-component system, sporulation sensor kinase E [EC:2.7.13.3]		
K13540	2	precorrin-2 C20-methyltransferase / precorrin-3B		
K13541	3	cobalamin biosynthesis protein CbiG / precorrin-3B		
K13542	25	uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107		
K13543	6	uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107		
K13571	4	proteasome accessory factor A [EC:6.3.2.-]		
K13572	7	proteasome accessory factor B		
K13573	11	proteasome accessory factor C		

K13574	10	uncharacterized oxidoreductase [EC:1.1.1.-]		
K13581	4	modification methylase [EC:2.1.1.72]		
K13582	2	localization factor PodJL		
K13583	3	GcrA cell cycle regulator		
K13584	1	two-component system, cell cycle response regulator CtrA		
K13587	41	two-component system, cell cycle sensor histidine kinase and		
K13588	1	histidine phosphotransferase ChpT		
K13589	2	two-component system, cell cycle response regulator CpdR		
K13590	30	diguanylate cyclase		
K13592	1	regulator of CtrA degradation		
K13593	1	cyclic-di-GMP phosphodiesterase, flagellum assembly factor TipF		
K13598	35	two-component system, NtrC family, nitrogen regulation sensor		
K13599	57	two-component system, NtrC family, nitrogen regulation response		
K13601	26	bacteriochlorophyll C8 methyltransferase [EC:2.1.1.-]		
K13602	20	bacteriochlorophyll C12 methyltransferase [EC:2.1.1.-]		
K13604	7	bacteriochlorophyll C20 methyltransferase [EC:2.1.1.-]		
K13607	4	cinnamoyl-CoA:phenyllactate CoA-transferase [EC:2.8.3.17]		
K13611	6	polyketide synthase PksJ		
K13612	1	polyketide synthase PksL		
K13614	6	polyketide synthase PksN		
K13628	22	iron-sulfur cluster assembly protein		
K13633	20	AraC family transcriptional regulator, transcriptional activator		
K13634	7	LysR family transcriptional regulator, cys regulon transcriptional		
K13635	7	LysR family transcriptional regulator, cys regulon transcriptional		
K13637	1	GntR family transcriptional regulator, uxuAB operon transcriptional		
K13638	4	MerR family transcriptional regulator, Zn(II)-responsive regulator		
K13639	5	MerR family transcriptional regulator, redox-sensitive		
K13640	10	MerR family transcriptional regulator, heat shock protein HspR		
K13641	40	IclR family transcriptional regulator, acetate operon repressor		
K13642	7	CRP/FNR family transcriptional regulator, transcriptional activator		
K13643	24	Rrf2 family transcriptional regulator, iron-sulfur cluster assembly		
K13652	4	AraC family transcriptional regulator		
K13653	3	AraC family transcriptional regulator		
K13654	5	GntR family transcriptional regulator, colanic acid and biofilm gene		
K13660	1	beta-1,4-glucosyltransferase [EC:2.4.1.-]		
K13661	9	GumC protein		
K13668	21	phosphatidylinositol alpha-1,6-mannosyltransferase [EC:2.4.1.-]		
K13670	1	alpha-1,6-mannosyltransferase [EC:2.4.1.-]		
K13678	1	monoglucosyldiacylglycerol glycosyltransferase [EC:2.4.1.-]		
K13683	1	putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]		
K13684	1	putative colanic acid biosynthesis glycosyltransferase [EC:2.4.-.-]		
K13685	27	UDP-N-acetylglucosamine:undecaprenyl-P N-acetylglucosaminyl 1-P		
K13688	38	cyclic beta-1,2-glucan synthetase [EC:2.4.1.-]		
K13693	8	glucosyl-3-phosphoglycerate synthase [EC:2.4.1.-]		
K13694	3	lipoprotein Spr		
K13695	3	probable lipoprotein NlpC		
K13730	107	internalin A		
K13735	100	adhesin/invasin		
K13741	1	guanine nucleotide exchange factor SopE		
K13742	1	protein IpgB1		
K13745	5	L-2,4-diaminobutyrate decarboxylase [EC:4.1.1.86]		
K13746	1	carboxynorspermidine dehydrogenase		
K13747	2	carboxynorspermidine decarboxylase [EC:4.1.1.-]		
K13766	13	methylglutaconyl-CoA hydratase [EC:4.2.1.18]		
K13767	5	enoyl-CoA hydratase [EC:4.2.1.17]		
K13770	16	TetR/AcrR family transcriptional regulator, fatty acid metabolism		
K13771	2	Rrf2 family transcriptional regulator, nitric oxide-sensitive		
K13774	3	citronellol/citronellal dehydrogenase		
K13775	5	citronellol/citronellal dehydrogenase		

K13776	1	citronellyl-CoA synthetase [EC:6.2.1.-]		
K13777	1	geranyl-CoA carboxylase alpha subunit [EC:6.4.1.5]		
K13778	4	geranyl-CoA carboxylase beta subunit [EC:6.4.1.5]		
K13787	9	geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10		
K13788	5	phosphate acetyltransferase [EC:2.3.1.8]		
K13789	15	geranylgeranyl diphosphate synthase, type II [EC:2.5.1.1 2.5.1.10		
K13794	1	LysR family transcriptional regulator, regulatory protein for tcuABC		
K13795	4	citrate/tricarballylate utilization protein		
K13796	11	tricarballylate dehydrogenase		
K13797	2	DNA-directed RNA polymerase subunit beta-beta' [EC:2.7.7.6]		
K13799	8	pantoate ligase / cytidylate kinase [EC:6.3.2.1 2.7.4.14]		
K13810	14	transaldolase / glucose-6-phosphate isomerase [EC:2.2.1.2 5.3.1.9]		
K13811	3	3'-phosphoadenosine 5'-phosphosulfate synthase [EC:2.7.7.4 2.7.1.25]		
K13815	21	two-component system, response regulator RpfG		
K13816	7	DSF synthase		
K13819	3	NifU-like protein		
K13820	1	flagellar biosynthetic protein FliR/FlhB		
K13821	28	proline dehydrogenase / delta 1-pyrroline-5-carboxylate		
K13829	16	shikimate kinase / 3-dehydroquinate synthase [EC:2.7.1.71 4.2.3.4]		
K13832	9	3-dehydroquinate dehydratase / shikimate dehydrogenase [EC:4.2.1.10		
K13874	3	L-arabinonolactonase [EC:3.1.1.15]		
K13875	7	L-arabonate dehydrase [EC:4.2.1.25]		
K13876	5	2-keto-3-deoxy-L-arabinonate dehydratase [EC:4.2.1.43]		
K13888	53	macrolide-specific efflux protein MacA		
K13889	13	glutathione transport system substrate-binding protein		
K13890	6	glutathione transport system permease protein		
K13891	2	glutathione transport system permease protein		
K13892	4	glutathione transport system ATP-binding protein		
K13893	9	microcin C transport system substrate-binding protein		
K13894	2	microcin C transport system permease protein		
K13895	4	microcin C transport system permease protein		
K13896	3	microcin C transport system ATP-binding protein		
K13919	1	propanediol dehydratase medium subunit [EC:4.2.1.28]		
K13922	1	propionaldehyde dehydrogenase		
K13924	124	two-component system, chemotaxis family, CheB/CheR fusion protein		
K13926	4	ribosome-dependent ATPase		
K13940	13	dihydroneopterin aldolase /		
K13950	9	para-aminobenzoate synthetase [EC:2.6.1.85]		
K13953	52	alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]		
K13954	5	alcohol dehydrogenase [EC:1.1.1.1]		
K13955	7	zinc-binding alcohol dehydrogenase/oxidoreductase		
K13963	11	serpin B		
K13979	9	uncharacterized zinc-type alcohol dehydrogenase-like protein		
K13990	19	glutamate formiminotransferase / formiminotetrahydrofolate		
K13993	58	HSP20 family protein		
K13995	2	maleamate amidohydrolase [EC:3.5.1.107]		

KEGG ID	Sequences	KEGG pathway	KEGG category	
K00001	181	alcohol dehydrogenase [EC:1.1.1.1]	Metabolism	
K00002	3	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	Metabolism	
K00003	74	homoserine dehydrogenase [EC:1.1.1.3]	Metabolism	
K00004	3	(R,R)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4	Metabolism	
K00005	10	glycerol dehydrogenase [EC:1.1.1.6]	Metabolism	
K00008	37	L-iditol 2-dehydrogenase [EC:1.1.1.14]	Metabolism	
K00009	4	mannitol-1-phosphate 5-dehydrogenase [EC:1.1.1.17]	Metabolism	
K00010	96	myo-inositol 2-dehydrogenase [EC:1.1.1.18]	Metabolism	
K00011	4	aldehyde reductase [EC:1.1.1.21]	Metabolism	
K00012	45	UDPglucose 6-dehydrogenase [EC:1.1.1.22]	Metabolism	
K00013	43	histidinol dehydrogenase [EC:1.1.1.23]	Metabolism	
K00014	37	shikimate dehydrogenase [EC:1.1.1.25]	Metabolism	
K00015	39	glyoxylate reductase [EC:1.1.1.26]	Metabolism	
K00016	26	L-lactate dehydrogenase [EC:1.1.1.27]	Metabolism	
K00018	11	glycerate dehydrogenase [EC:1.1.1.29]	Metabolism	
K00019	33	3-hydroxybutyrate dehydrogenase [EC:1.1.1.30]	Metabolism	
K00020	92	3-hydroxyisobutyrate dehydrogenase [EC:1.1.1.31]	Metabolism	
K00021	14	3-hydroxy-3-methylglutaryl-CoA reductase [EC:1.1.1.34]	Metabolism	
K00023	24	acetoacetyl-CoA reductase [EC:1.1.1.36]	Metabolism	
K00024	35	malate dehydrogenase [EC:1.1.1.37]	Metabolism	
K00027	40	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]	Metabolism	
K00028	4	malate dehydrogenase (decarboxylating) [EC:1.1.1.39]	Metabolism	
K00029	39	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)	Metabolism	
K00030	19	isocitrate dehydrogenase (NAD+) [EC:1.1.1.41]	Metabolism	
K00031	37	isocitrate dehydrogenase [EC:1.1.1.42]	Metabolism	
K00032	1	phosphogluconate 2-dehydrogenase [EC:1.1.1.43]	Metabolism	
K00033	37	6-phosphogluconate dehydrogenase [EC:1.1.1.44]	Metabolism	
K00034	25	glucose 1-dehydrogenase [EC:1.1.1.47]	Metabolism	
K00035	1	D-galactose 1-dehydrogenase [EC:1.1.1.48]	Metabolism	
K00036	118	glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49]	Metabolism	
K00037	2	3-alpha-hydroxysteroid dehydrogenase [EC:1.1.1.50]	Metabolism	
K00038	6	3alpha(or 20beta)-hydroxysteroid dehydrogenase [EC:1.1.1.53]	Metabolism	
K00040	4	fructuronate reductase [EC:1.1.1.57]	Metabolism	
K00042	60	2-hydroxy-3-oxopropionate reductase [EC:1.1.1.60]	Metabolism	
K00043	6	4-hydroxybutyrate dehydrogenase [EC:1.1.1.61]	Metabolism	
K00044	10	estradiol 17beta-dehydrogenase [EC:1.1.1.62]	Metabolism	
K00045	4	mannitol 2-dehydrogenase [EC:1.1.1.67]	Metabolism	
K00048	20	lactaldehyde reductase [EC:1.1.1.77]	Metabolism	
K00050	46	hydroxypyruvate reductase [EC:1.1.1.81]	Metabolism	
K00051	10	malate dehydrogenase (NADP+) [EC:1.1.1.82]	Metabolism	
K00052	66	3-isopropylmalate dehydrogenase [EC:1.1.1.85]	Metabolism	
K00053	17	ketol-acid reductoisomerase [EC:1.1.1.86]	Metabolism	
K00054	7	hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]	Metabolism	
K00055	2	aryl-alcohol dehydrogenase [EC:1.1.1.90]	Metabolism	
K00057	38	glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94]	Metabolism	
K00058	145	D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	Metabolism	
K00059	312	3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	Metabolism	
K00060	50	threonine 3-dehydrogenase [EC:1.1.1.103]	Metabolism	
K00064	7	D-threo-aldose 1-dehydrogenase [EC:1.1.1.122]	Metabolism	
K00065	29	2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]	Metabolism	
K00066	25	GDP-mannose 6-dehydrogenase [EC:1.1.1.132]	Metabolism	
K00067	36	dTDP-4-dehydrorhamnose reductase [EC:1.1.1.133]	Metabolism	
K00068	7	sorbitol-6-phosphate 2-dehydrogenase [EC:1.1.1.140]	Metabolism	
K00071	3	11beta-hydroxysteroid dehydrogenase [EC:1.1.1.146]	Metabolism	
K00073	35	ureidoglycolate dehydrogenase [EC:1.1.1.154]	Metabolism	
K00074	63	3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]	Metabolism	

K00075	37	UDP-N-acetylmuramate dehydrogenase [EC:1.1.1.158]	Metabolism	
K00077	44	2-dehydropantoate 2-reductase [EC:1.1.1.169]	Metabolism	
K00079	12	carbonyl reductase (NADPH) [EC:1.1.1.184]	Metabolism	
K00082	9	5-amino-6-(5-phosphoribosylamino)uracil reductase [EC:1.1.1.193]	Metabolism	
K00083	2	cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	Metabolism	
K00086	5	1,3-propanediol dehydrogenase [EC:1.1.1.202]	Metabolism	
K00087	105	xanthine dehydrogenase molybdenum-binding subunit [EC:1.17.1.4]	Metabolism	
K00088	84	IMP dehydrogenase [EC:1.1.1.205]	Metabolism	
K00090	13	gluconate 2-dehydrogenase [EC:1.1.1.215]	Metabolism	
K00094	1	galactitol-1-phosphate 5-dehydrogenase [EC:1.1.1.251]	Metabolism	
K00096	3	glycerol-1-phosphate dehydrogenase [NAD(P)] [EC:1.1.1.261]	Metabolism	
K00097	42	4-hydroxythreonine-4-phosphate dehydrogenase [EC:1.1.1.262]	Metabolism	
K00099	51	1-deoxy-D-xylulose-5-phosphate reductoisomerase [EC:1.1.1.267]	Metabolism	
K00100	439	Unclassified; E1.1.1.-	Metabolism	
K00101	50	L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]	Metabolism	
K00102	85	D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]	Metabolism	
K00103	10	L-gulonolactone oxidase [EC:1.1.3.8]	Metabolism	
K00104	91	glycolate oxidase [EC:1.1.3.15]	Metabolism	
K00105	3	alpha-glycerophosphate oxidase [EC:1.1.3.21]	Metabolism	
K00108	51	choline dehydrogenase [EC:1.1.99.1]	Metabolism	
K00109	14	2-hydroxyglutarate dehydrogenase [EC:1.1.99.2]	Metabolism	
K00111	53	glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]	Metabolism	
K00112	2	glycerol-3-phosphate dehydrogenase subunit B [EC:1.1.5.3]	Metabolism	
K00113	10	glycerol-3-phosphate dehydrogenase subunit C [EC:1.1.5.3]	Metabolism	
K00114	80	alcohol dehydrogenase (acceptor) [EC:1.1.99.8]	Metabolism	
K00116	24	malate dehydrogenase (quinone) [EC:1.1.5.4]	Metabolism	
K00117	55	quinoprotein glucose dehydrogenase [EC:1.1.5.2]	Metabolism	
K00121	49	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	Metabolism	
K00122	100	formate dehydrogenase [EC:1.2.1.2]	Metabolism	
K00123	164	formate dehydrogenase, alpha subunit [EC:1.2.1.2]	Metabolism	
K00124	24	formate dehydrogenase, beta subunit [EC:1.2.1.2]	Metabolism	
K00127	21	formate dehydrogenase, gamma subunit [EC:1.2.1.2]	Metabolism	
K00128	152	aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]	Metabolism	
K00129	2	aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]	Metabolism	
K00130	60	betaine-aldehyde dehydrogenase [EC:1.2.1.8]	Metabolism	
K00131	21	glyceraldehyde-3-phosphate dehydrogenase (NADP) [EC:1.2.1.9]	Metabolism	
K00132	6	acetaldehyde dehydrogenase (acetylating) [EC:1.2.1.10]	Metabolism	
K00133	35	aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	Metabolism	
K00134	29	glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	Metabolism	
K00135	94	succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]	Metabolism	
K00137	5	aminobutyraldehyde dehydrogenase [EC:1.2.1.19]	Metabolism	
K00138	6	aldehyde dehydrogenase [EC:1.2.1.-]	Metabolism	
K00140	32	methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.27]	Metabolism	
K00141	6	benzaldehyde dehydrogenase (NAD) [EC:1.2.1.28]	Metabolism	
K00145	50	N-acetyl-gamma-glutamyl-phosphate reductase [EC:1.2.1.38]	Metabolism	
K00146	17	phenylacetaldehyde dehydrogenase [EC:1.2.1.39]	Metabolism	
K00147	25	glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41]	Metabolism	
K00148	5	glutathione-independent formaldehyde dehydrogenase [EC:1.2.1.46]	Metabolism	
K00150	2	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]	Metabolism	
K00151	15	5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase	Metabolism	
K00152	5	salicylaldehyde dehydrogenase [EC:1.2.1.65]	Metabolism	
K00156	27	pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]	Metabolism	
K00157	22	aldehyde oxidase [EC:1.2.3.1]	Metabolism	
K00158	6	pyruvate oxidase [EC:1.2.3.3]	Metabolism	
K00161	65	pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	Metabolism	
K00162	66	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]	Metabolism	
K00163	45	pyruvate dehydrogenase E1 component [EC:1.2.4.1]	Metabolism	

K00164	41	2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]	Metabolism	
K00166	32	2-oxoisovalerate dehydrogenase E1 component, alpha subunit	Metabolism	
K00167	31	2-oxoisovalerate dehydrogenase E1 component, beta subunit	Metabolism	
K00169	37	pyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.1]	Metabolism	
K00170	17	pyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.1]	Metabolism	
K00171	15	pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]	Metabolism	
K00172	16	pyruvate ferredoxin oxidoreductase, gamma subunit [EC:1.2.7.1]	Metabolism	
K00174	70	2-oxoglutarate ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3]	Metabolism	
K00175	41	2-oxoglutarate ferredoxin oxidoreductase subunit beta [EC:1.2.7.3]	Metabolism	
K00176	10	2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7.3]	Metabolism	
K00177	12	2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3]	Metabolism	
K00186	10	2-oxoisovalerate ferredoxin oxidoreductase, alpha subunit	Metabolism	
K00187	7	2-oxoisovalerate ferredoxin oxidoreductase, beta subunit	Metabolism	
K00194	1	carbon-monoxide dehydrogenase delta subunit [EC:1.2.99.2]	Metabolism	
K00197	5	carbon-monoxide dehydrogenase gamma subunit [EC:1.2.99.2]	Metabolism	
K00198	3	carbon-monoxide dehydrogenase catalytic subunit [EC:1.2.99.2]	Metabolism	
K00200	8	formylmethanofuran dehydrogenase subunit A [EC:1.2.99.5]	Metabolism	
K00201	1	formylmethanofuran dehydrogenase subunit B [EC:1.2.99.5]	Metabolism	
K00202	2	formylmethanofuran dehydrogenase subunit C [EC:1.2.99.5]	Metabolism	
K00207	10	dihydropyrimidine dehydrogenase (NADP+) [EC:1.3.1.2]	Metabolism	
K00208	71	enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9]	Metabolism	
K00209	3	enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific)	Metabolism	
K00210	23	prephenate dehydrogenase [EC:1.3.1.12]	Metabolism	
K00214	1	biliverdin reductase [EC:1.3.1.24]	Metabolism	
K00215	29	dihydrodipicolinate reductase [EC:1.3.1.26]	Metabolism	
K00216	2	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [EC:1.3.1.28]	Metabolism	
K00217	4	maleylacetate reductase [EC:1.3.1.32]	Metabolism	
K00218	9	protochlorophyllide reductase [EC:1.3.1.33]	Metabolism	
K00220	4	cyclohexadienyl dehydrogenase [EC:1.3.1.43]	Metabolism	
K00226	72	dihydroorotate oxidase [EC:1.3.3.1]	Metabolism	
K00227	3	lathosterol oxidase [EC:1.14.21.6]	Metabolism	
K00228	17	coproporphyrinogen III oxidase [EC:1.3.3.3]	Metabolism	
K00230	8	protoporphyrinogen oxidase [EC:1.3.3.4]	Metabolism	
K00231	27	protoporphyrinogen oxidase [EC:1.3.3.4]	Metabolism	
K00232	1	acyl-CoA oxidase [EC:1.3.3.6]	Metabolism	
K00239	70	succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]	Metabolism	
K00240	31	succinate dehydrogenase iron-sulfur protein [EC:1.3.99.1]	Metabolism	
K00241	21	succinate dehydrogenase cytochrome b-556 subunit [EC:1.3.99.1]	Metabolism	
K00242	5	succinate dehydrogenase hydrophobic membrane anchor protein	Metabolism	
K00244	39	fumarate reductase flavoprotein subunit [EC:1.3.99.1]	Metabolism	
K00245	7	fumarate reductase iron-sulfur protein [EC:1.3.99.1]	Metabolism	
K00246	13	fumarate reductase subunit C [EC:1.3.99.1]	Metabolism	
K00247	5	fumarate reductase subunit D [EC:1.3.99.1]	Metabolism	
K00248	107	butyryl-CoA dehydrogenase [EC:1.3.99.2]	Metabolism	
K00249	223	acyl-CoA dehydrogenase [EC:1.3.99.3]	Metabolism	
K00252	32	glutaryl-CoA dehydrogenase [EC:1.3.99.7]	Metabolism	
K00253	67	isovaleryl-CoA dehydrogenase [EC:1.3.99.10]	Metabolism	
K00255	14	long-chain-acyl-CoA dehydrogenase [EC:1.3.99.13]	Metabolism	
K00257	333	Unclassified; E1.3.99.-	Metabolism	
K00259	29	alanine dehydrogenase [EC:1.4.1.1]	Metabolism	
K00260	63	glutamate dehydrogenase [EC:1.4.1.2]	Metabolism	
K00261	38	glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]	Metabolism	
K00262	26	glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	Metabolism	
K00263	17	leucine dehydrogenase [EC:1.4.1.9]	Metabolism	
K00265	89	glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14]	Metabolism	
K00266	101	glutamate synthase (NADPH/NADH) small chain [EC:1.4.1.13 1.4.1.14]	Metabolism	
K00271	14	valine dehydrogenase [EC:1.4.1.-]	Metabolism	

K00273	15	D-amino-acid oxidase [EC:1.4.3.3]	Metabolism	
K00274	21	monoamine oxidase [EC:1.4.3.4]	Metabolism	
K00275	18	pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]	Metabolism	
K00276	60	primary-amine oxidase [EC:1.4.3.21]	Metabolism	
K00278	44	L-aspartate oxidase [EC:1.4.3.16]	Metabolism	
K00279	15	cytokinin dehydrogenase [EC:1.5.99.12]	Metabolism	
K00281	24	glycine dehydrogenase [EC:1.4.4.2]	Metabolism	
K00282	30	glycine dehydrogenase subunit 1 [EC:1.4.4.2]	Metabolism	
K00283	25	glycine dehydrogenase subunit 2 [EC:1.4.4.2]	Metabolism	
K00284	28	glutamate synthase (ferredoxin) [EC:1.4.7.1]	Metabolism	
K00285	34	D-amino-acid dehydrogenase [EC:1.4.99.1]	Metabolism	
K00286	27	pyrroline-5-carboxylate reductase [EC:1.5.1.2]	Metabolism	
K00287	56	dihydrofolate reductase [EC:1.5.1.3]	Metabolism	
K00290	30	saccharopine dehydrogenase (NAD+, L-lysine forming) [EC:1.5.1.7]	Metabolism	
K00294	69	1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	Metabolism	
K00297	67	methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]	Metabolism	
K00299	34	FMN reductase [EC:1.5.1.29]	Metabolism	
K00301	35	sarcosine oxidase [EC:1.5.3.1]	Metabolism	
K00302	11	sarcosine oxidase, subunit alpha [EC:1.5.3.1]	Metabolism	
K00303	37	sarcosine oxidase, subunit beta [EC:1.5.3.1]	Metabolism	
K00304	2	sarcosine oxidase, subunit delta [EC:1.5.3.1]	Metabolism	
K00305	1	sarcosine oxidase, subunit gamma [EC:1.5.3.1]	Metabolism	
K00314	44	sarcosine dehydrogenase [EC:1.5.99.1]	Metabolism	
K00315	21	dimethylglycine dehydrogenase [EC:1.5.99.2]	Metabolism	
K00317	11	trimethylamine dehydrogenase [EC:1.5.8.2]	Metabolism	
K00318	21	proline dehydrogenase [EC:1.5.99.8]	Metabolism	
K00320	25	coenzyme F420-dependent N5,N10-methenyltetrahydromethanopterin	Metabolism	
K00322	12	NAD(P) transhydrogenase [EC:1.6.1.1]	Metabolism	
K00324	34	NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]	Metabolism	
K00325	18	NAD(P) transhydrogenase subunit beta [EC:1.6.1.2]	Metabolism	
K00326	1	cytochrome-b5 reductase [EC:1.6.2.2]	Metabolism	
K00329	36	NADH dehydrogenase [EC:1.6.5.3]	Metabolism	
K00330	25	NADH dehydrogenase I subunit A [EC:1.6.5.3]	Metabolism	
K00331	27	NADH dehydrogenase I subunit B [EC:1.6.5.3]	Metabolism	
K00332	21	NADH dehydrogenase I subunit C [EC:1.6.5.3]	Metabolism	
K00333	64	NADH dehydrogenase I subunit D [EC:1.6.5.3]	Metabolism	
K00334	43	NADH dehydrogenase I subunit E [EC:1.6.5.3]	Metabolism	
K00335	80	NADH dehydrogenase I subunit F [EC:1.6.5.3]	Metabolism	
K00336	63	NADH dehydrogenase I subunit G [EC:1.6.5.3]	Metabolism	
K00337	55	NADH dehydrogenase I subunit H [EC:1.6.5.3]	Metabolism	
K00338	26	NADH dehydrogenase I subunit I [EC:1.6.5.3]	Metabolism	
K00339	20	NADH dehydrogenase I subunit J [EC:1.6.5.3]	Metabolism	
K00340	15	NADH dehydrogenase I subunit K [EC:1.6.5.3]	Metabolism	
K00341	57	NADH dehydrogenase I subunit L [EC:1.6.5.3]	Metabolism	
K00342	63	NADH dehydrogenase I subunit M [EC:1.6.5.3]	Metabolism	
K00343	62	NADH dehydrogenase I subunit N [EC:1.6.5.3]	Metabolism	
K00355	4	NAD(P)H dehydrogenase (quinone) [EC:1.6.5.2]	Metabolism	
K00356	59	NADH dehydrogenase [EC:1.6.99.3]	Metabolism	
K00360	39	nitrate reductase (NADH) [EC:1.7.1.1]	Metabolism	
K00362	26	nitrite reductase (NAD(P)H) large subunit [EC:1.7.1.4]	Metabolism	
K00363	13	nitrite reductase (NAD(P)H) small subunit [EC:1.7.1.4]	Metabolism	
K00364	4	GMP reductase [EC:1.7.1.7]	Metabolism	
K00365	9	urate oxidase [EC:1.7.3.3]	Metabolism	
K00366	23	ferredoxin-nitrite reductase [EC:1.7.7.1]	Metabolism	
K00367	5	ferredoxin-nitrate reductase [EC:1.7.7.2]	Metabolism	
K00368	53	nitrite reductase (NO-forming) [EC:1.7.2.1]	Metabolism	
K00370	34	nitrate reductase 1, alpha subunit [EC:1.7.99.4]	Metabolism	

K00371	12	nitrate reductase 1, beta subunit [EC:1.7.99.4]	Metabolism	
K00372	36	nitrate reductase catalytic subunit [EC:1.7.99.4]	Metabolism	
K00373	4	nitrate reductase 1, delta subunit [EC:1.7.99.4]	Metabolism	
K00374	4	nitrate reductase 1, gamma subunit [EC:1.7.99.4]	Metabolism	
K00376	14	nitrous-oxide reductase [EC:1.7.99.6]	Metabolism	
K00380	19	sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]	Metabolism	
K00381	24	sulfite reductase (NADPH) hemoprotein beta-component [EC:1.8.1.2]	Metabolism	
K00382	97	dihydrolipoamide dehydrogenase [EC:1.8.1.4]	Metabolism	
K00383	19	glutathione reductase (NADPH) [EC:1.8.1.7]	Metabolism	
K00384	111	thioredoxin reductase (NADPH) [EC:1.8.1.9]	Metabolism	
K00385	1	anaerobic sulfite reductase subunit C [EC:1.8.1.-]	Metabolism	
K00387	22	sulfite oxidase [EC:1.8.3.1]	Metabolism	
K00390	17	phosphoadenosine phosphosulfate reductase [EC:1.8.4.8]	Metabolism	
K00392	14	sulfite reductase (ferredoxin) [EC:1.8.7.1]	Metabolism	
K00394	11	adenylylsulfate reductase, subunit A [EC:1.8.99.2]	Metabolism	
K00395	3	adenylylsulfate reductase, subunit B [EC:1.8.99.2]	Metabolism	
K00404	16	cb-type cytochrome c oxidase subunit I [EC:1.9.3.1]	Metabolism	
K00405	17	cb-type cytochrome c oxidase subunit II [EC:1.9.3.1]	Metabolism	
K00406	34	cb-type cytochrome c oxidase subunit III [EC:1.9.3.1]	Metabolism	
K00407	6	cb-type cytochrome c oxidase subunit IV [EC:1.9.3.1]	Metabolism	
K00411	10	ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.2]	Metabolism	
K00412	35	ubiquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.2]	Metabolism	
K00413	8	ubiquinol-cytochrome c reductase cytochrome c1 subunit [EC:1.10.2.2]	Metabolism	
K00423	22	L-ascorbate oxidase [EC:1.10.3.3]	Metabolism	
K00425	39	cytochrome bd-I oxidase subunit I [EC:1.10.3.-]	Metabolism	
K00426	23	cytochrome bd-I oxidase subunit II [EC:1.10.3.-]	Metabolism	
K00432	7	glutathione peroxidase [EC:1.11.1.9]	Metabolism	
K00441	4	coenzyme F420 hydrogenase beta subunit [EC:1.12.98.1]	Metabolism	
K00442	3	coenzyme F420 hydrogenase delta subunit	Metabolism	
K00446	7	catechol 2,3-dioxygenase [EC:1.13.11.2]	Metabolism	
K00448	10	protocatechuate 3,4-dioxygenase, alpha subunit [EC:1.13.11.3]	Metabolism	
K00449	6	protocatechuate 3,4-dioxygenase, beta subunit [EC:1.13.11.3]	Metabolism	
K00450	24	gentisate 1,2-dioxygenase [EC:1.13.11.4]	Metabolism	
K00451	27	homogentisate 1,2-dioxygenase [EC:1.13.11.5]	Metabolism	
K00453	11	tryptophan 2,3-dioxygenase [EC:1.13.11.11]	Metabolism	
K00455	1	3,4-dihydroxyphenylacetate 2,3-dioxygenase [EC:1.13.11.15]	Metabolism	
K00457	19	4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]	Metabolism	
K00459	54	nitronate monooxygenase [EC:1.13.12.16]	Metabolism	
K00462	4	biphenyl-2,3-diol 1,2-dioxygenase [EC:1.13.11.39]	Metabolism	
K00466	5	tryptophan 2-monooxygenase [EC:1.13.12.3]	Metabolism	
K00467	12	lactate 2-monooxygenase [EC:1.13.12.4]	Metabolism	
K00480	28	salicylate hydroxylase [EC:1.14.13.1]	Metabolism	
K00481	6	p-hydroxybenzoate 3-monooxygenase [EC:1.14.13.2]	Metabolism	
K00483	31	4-hydroxyphenylacetate-3-hydroxylase large chain [EC:1.14.13.3]	Metabolism	
K00484	2	4-hydroxyphenylacetate-3-hydroxylase small chain [EC:1.14.13.3]	Metabolism	
K00485	11	dimethylaniline monooxygenase (N-oxide forming) [EC:1.14.13.8]	Metabolism	
K00491	2	nitric-oxide synthase, bacterial [EC:1.14.13.39]	Metabolism	
K00493	46	unspecific monooxygenase [EC:1.14.14.1]	Metabolism	
K00499	10	choline monooxygenase [EC:1.14.15.7]	Metabolism	
K00500	17	phenylalanine-4-hydroxylase [EC:1.14.16.1]	Metabolism	
K00507	40	stearoyl-CoA desaturase (delta-9 desaturase) [EC:1.14.19.1]	Metabolism	
K00508	4	linoleoyl-CoA desaturase [EC:1.14.19.3]	Metabolism	
K00514	1	zeta-carotene desaturase [EC:1.14.99.30]	Metabolism	
K00517	179	Unclassified; E1.14.-.-	Metabolism	
K00523	25	CDP-4-dehydro-6-deoxyglucose reductase [EC:1.17.1.1]	Metabolism	
K00525	87	ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]	Metabolism	
K00526	14	ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1]	Metabolism	

K00527	5	ribonucleoside-triphosphate reductase [EC:1.17.4.2]	Metabolism	
K00529	61	ferredoxin--NAD+ reductase [EC:1.18.1.3]	Metabolism	
K00544	5	betaine-homocysteine S-methyltransferase [EC:2.1.1.5]	Metabolism	
K00547	33	homocysteine S-methyltransferase [EC:2.1.1.10]	Metabolism	
K00548	117	5-methyltetrahydrofolate--homocysteine methyltransferase	Metabolism	
K00549	72	5-methyltetrahydropteroyltriglutamate--homocysteine	Metabolism	
K00551	21	phosphatidylethanolamine N-methyltransferase [EC:2.1.1.17]	Metabolism	
K00558	15	DNA (cytosine-5-)-methyltransferase [EC:2.1.1.37]	Metabolism	
K00559	1	sterol 24-C-methyltransferase [EC:2.1.1.41]	Metabolism	
K00560	9	thymidylate synthase [EC:2.1.1.45]	Metabolism	
K00568	65	3-demethylubiquinone-9 3-methyltransferase [EC:2.1.1.- 2.1.1.64]	Metabolism	
K00569	4	thiopurine S-methyltransferase [EC:2.1.1.67]	Metabolism	
K00570	5	phosphatidyl-N-methylethanolamine N-methyltransferase [EC:2.1.1.71]	Metabolism	
K00584	1	tetrahydromethanopterin S-methyltransferase subunit H [EC:2.1.1.86]	Metabolism	
K00587	7	protein-S-isoprenylcysteine O-methyltransferase [EC:2.1.1.100]	Metabolism	
K00588	15	caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]	Metabolism	
K00595	6	precorrin-6Y C5,15-methyltransferase / precorrin-8W decarboxylase	Metabolism	
K00600	49	glycine hydroxymethyltransferase [EC:2.1.2.1]	Metabolism	
K00602	28	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP	Metabolism	
K00603	20	glutamate formiminotransferase [EC:2.1.2.5]	Metabolism	
K00604	50	methionyl-tRNA formyltransferase [EC:2.1.2.9]	Metabolism	
K00605	69	aminomethyltransferase [EC:2.1.2.10]	Metabolism	
K00606	26	3-methyl-2-oxobutanoate hydroxymethyltransferase [EC:2.1.2.11]	Metabolism	
K00609	35	aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]	Metabolism	
K00610	12	aspartate carbamoyltransferase regulatory subunit	Metabolism	
K00611	50	ornithine carbamoyltransferase [EC:2.1.3.3]	Metabolism	
K00613	1	glycine amidinotransferase [EC:2.1.4.1]	Metabolism	
K00615	102	transketolase [EC:2.2.1.1]	Metabolism	
K00616	40	transaldolase [EC:2.2.1.2]	Metabolism	
K00619	22	amino-acid N-acetyltransferase [EC:2.3.1.1]	Metabolism	
K00620	31	glutamate N-acetyltransferase / amino-acid N-acetyltransferase	Metabolism	
K00622	5	arylamine N-acetyltransferase [EC:2.3.1.5]	Metabolism	
K00625	21	phosphate acetyltransferase [EC:2.3.1.8]	Metabolism	
K00626	211	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	Metabolism	
K00627	68	pyruvate dehydrogenase E2 component (dihydrolipoamide	Metabolism	
K00631	12	glycerol-3-phosphate O-acyltransferase [EC:2.3.1.15]	Metabolism	
K00632	93	acetyl-CoA acyltransferase [EC:2.3.1.16]	Metabolism	
K00634	11	phosphate butyryltransferase [EC:2.3.1.19]	Metabolism	
K00639	42	glycine C-acetyltransferase [EC:2.3.1.29]	Metabolism	
K00640	27	serine O-acetyltransferase [EC:2.3.1.30]	Metabolism	
K00641	37	homoserine O-acetyltransferase [EC:2.3.1.31]	Metabolism	
K00643	12	5-aminolevulinate synthase [EC:2.3.1.37]	Metabolism	
K00645	48	[acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]	Metabolism	
K00647	39	3-oxoacyl-[acyl-carrier-protein] synthase I [EC:2.3.1.41]	Metabolism	
K00648	79	3-oxoacyl-[acyl-carrier-protein] synthase III [EC:2.3.1.180]	Metabolism	
K00651	3	homoserine O-succinyltransferase [EC:2.3.1.46]	Metabolism	
K00652	51	8-amino-7-oxononanoate synthase [EC:2.3.1.47]	Metabolism	
K00654	7	serine palmitoyltransferase [EC:2.3.1.50]	Metabolism	
K00655	121	1-acyl-sn-glycerol-3-phosphate acyltransferase [EC:2.3.1.51]	Metabolism	
K00656	38	formate C-acetyltransferase [EC:2.3.1.54]	Metabolism	
K00657	13	diamine N-acetyltransferase [EC:2.3.1.57]	Metabolism	
K00658	41	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide	Metabolism	
K00660	12	chalcone synthase [EC:2.3.1.74]	Metabolism	
K00672	6	formylmethanofuran--tetrahydromethanopterin N-formyltransferase	Metabolism	
K00673	3	arginine N-succinyltransferase [EC:2.3.1.109]	Metabolism	
K00674	18	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	Metabolism	
K00677	32	UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]	Metabolism	

K00681	137	gamma-glutamyltranspeptidase [EC:2.3.2.2]	Metabolism	
K00688	90	starch phosphorylase [EC:2.4.1.1]	Metabolism	
K00690	3	sucrose phosphorylase [EC:2.4.1.7]	Metabolism	
K00691	17	maltose phosphorylase [EC:2.4.1.8]	Metabolism	
K00693	14	glycogen(starch) synthase [EC:2.4.1.11]	Metabolism	
K00694	12	cellulose synthase (UDP-forming) [EC:2.4.1.12]	Metabolism	
K00695	2	sucrose synthase [EC:2.4.1.13]	Metabolism	
K00696	1	sucrose-phosphate synthase [EC:2.4.1.14]	Metabolism	
K00697	44	alpha,alpha-trehalose-phosphate synthase (UDP-forming) [EC:2.4.1.15]	Metabolism	
K00700	62	1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	Metabolism	
K00702	10	cellobiose phosphorylase [EC:2.4.1.20]	Metabolism	
K00703	39	starch synthase [EC:2.4.1.21]	Metabolism	
K00705	74	4-alpha-glucanotransferase [EC:2.4.1.25]	Metabolism	
K00720	5	ceramide glucosyltransferase [EC:2.4.1.80]	Metabolism	
K00721	123	dolichol-phosphate mannosyltransferase [EC:2.4.1.83]	Metabolism	
K00743	2	N-acetyllactosaminide 3-alpha-galactosyltransferase [EC:2.4.1.87]	Metabolism	
K00748	28	lipid-A-disaccharide synthase [EC:2.4.1.182]	Metabolism	
K00756	8	pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]	Metabolism	
K00757	2	uridine phosphorylase [EC:2.4.2.3]	Metabolism	
K00758	21	thymidine phosphorylase [EC:2.4.2.4]	Metabolism	
K00759	26	adenine phosphoribosyltransferase [EC:2.4.2.7]	Metabolism	
K00760	33	hypoxanthine phosphoribosyltransferase [EC:2.4.2.8]	Metabolism	
K00761	13	uracil phosphoribosyltransferase [EC:2.4.2.9]	Metabolism	
K00762	22	orotate phosphoribosyltransferase [EC:2.4.2.10]	Metabolism	
K00763	180	nicotinate phosphoribosyltransferase [EC:2.4.2.11]	Metabolism	
K00764	58	amidophosphoribosyltransferase [EC:2.4.2.14]	Metabolism	
K00765	31	ATP phosphoribosyltransferase [EC:2.4.2.17]	Metabolism	
K00766	31	anthranilate phosphoribosyltransferase [EC:2.4.2.18]	Metabolism	
K00767	54	nicotinate-nucleotide pyrophosphorylase (carboxylating)	Metabolism	
K00768	8	nicotinate-nucleotide--dimethylbenzimidazole	Metabolism	
K00772	30	5'-methylthioadenosine phosphorylase [EC:2.4.2.28]	Metabolism	
K00788	35	thiamine-phosphate pyrophosphorylase [EC:2.5.1.3]	Metabolism	
K00789	31	S-adenosylmethionine synthetase [EC:2.5.1.6]	Metabolism	
K00790	50	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7]	Metabolism	
K00791	29	tRNA dimethylallyltransferase [EC:2.5.1.75]	Metabolism	
K00793	31	riboflavin synthase alpha chain [EC:2.5.1.9]	Metabolism	
K00794	15	riboflavin synthase beta chain [EC:2.5.1.-]	Metabolism	
K00795	8	farnesyl diphosphate synthase [EC:2.5.1.1 2.5.1.10]	Metabolism	
K00796	35	dihydropteroate synthase [EC:2.5.1.15]	Metabolism	
K00797	37	spermidine synthase [EC:2.5.1.16]	Metabolism	
K00798	27	cob(I)alamin adenosyltransferase [EC:2.5.1.17]	Metabolism	
K00799	108	glutathione S-transferase [EC:2.5.1.18]	Metabolism	
K00800	62	3-phosphoshikimate 1-carboxyvinyltransferase [EC:2.5.1.19]	Metabolism	
K00801	13	farnesyl-diphosphate farnesyltransferase [EC:2.5.1.21]	Metabolism	
K00802	3	spermine synthase [EC:2.5.1.22]	Metabolism	
K00803	23	alkyldihydroxyacetonephosphate synthase [EC:2.5.1.26]	Metabolism	
K00805	9	heptaprenyl diphosphate synthase [EC:2.5.1.30]	Metabolism	
K00806	20	undecaprenyl diphosphate synthase [EC:2.5.1.31]	Metabolism	
K00808	4	homospermidine synthase [EC:2.5.1.44]	Metabolism	
K00811	2	aspartate aminotransferase [EC:2.6.1.1]	Metabolism	
K00812	46	aspartate aminotransferase [EC:2.6.1.1]	Metabolism	
K00813	7	aspartate aminotransferase [EC:2.6.1.1]	Metabolism	
K00814	3	alanine transaminase [EC:2.6.1.2]	Metabolism	
K00817	59	histidinol-phosphate aminotransferase [EC:2.6.1.9]	Metabolism	
K00818	49	acetylornithine aminotransferase [EC:2.6.1.11]	Metabolism	
K00819	14	ornithine--oxo-acid transaminase [EC:2.6.1.13]	Metabolism	
K00820	67	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	Metabolism	

K00821	47	acetylornithine/N-succinyldiaminopimelate aminotransferase	Metabolism	
K00822	14	beta-alanine--pyruvate transaminase [EC:2.6.1.18]	Metabolism	
K00823	47	4-aminobutyrate aminotransferase [EC:2.6.1.19]	Metabolism	
K00824	14	D-alanine transaminase [EC:2.6.1.21]	Metabolism	
K00825	17	2-aminoadipate transaminase [EC:2.6.1.39]	Metabolism	
K00826	73	branched-chain amino acid aminotransferase [EC:2.6.1.42]	Metabolism	
K00831	23	phosphoserine aminotransferase [EC:2.6.1.52]	Metabolism	
K00832	8	aromatic-amino-acid transaminase [EC:2.6.1.57]	Metabolism	
K00833	19	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	Metabolism	
K00835	12	valine--pyruvate aminotransferase [EC:2.6.1.66]	Metabolism	
K00836	5	diaminobutyrate-2-oxoglutarate transaminase [EC:2.6.1.76]	Metabolism	
K00839	38	aminotransferase [EC:2.6.1.-]	Metabolism	
K00840	1	succinylornithine aminotransferase [EC:2.6.1.81]	Metabolism	
K00841	1	aminotransferase [EC:2.6.1.-]	Metabolism	
K00845	73	glucokinase [EC:2.7.1.2]	Metabolism	
K00846	2	ketohexokinase [EC:2.7.1.3]	Metabolism	
K00847	33	fructokinase [EC:2.7.1.4]	Metabolism	
K00848	14	rhamnulokinase [EC:2.7.1.5]	Metabolism	
K00849	14	galactokinase [EC:2.7.1.6]	Metabolism	
K00850	56	6-phosphofructokinase [EC:2.7.1.11]	Metabolism	
K00851	14	gluconokinase [EC:2.7.1.12]	Metabolism	
K00852	25	ribokinase [EC:2.7.1.15]	Metabolism	
K00853	8	L-ribulokinase [EC:2.7.1.16]	Metabolism	
K00854	34	xylulokinase [EC:2.7.1.17]	Metabolism	
K00855	13	phosphoribulokinase [EC:2.7.1.19]	Metabolism	
K00856	21	adenosine kinase [EC:2.7.1.20]	Metabolism	
K00857	8	thymidine kinase [EC:2.7.1.21]	Metabolism	
K00858	35	NAD+ kinase [EC:2.7.1.23]	Metabolism	
K00859	35	dephospho-CoA kinase [EC:2.7.1.24]	Metabolism	
K00860	18	adenylylsulfate kinase [EC:2.7.1.25]	Metabolism	
K00861	3	riboflavin kinase [EC:2.7.1.26]	Metabolism	
K00863	8	dihydroxyacetone kinase [EC:2.7.1.29]	Metabolism	
K00864	41	glycerol kinase [EC:2.7.1.30]	Metabolism	
K00865	12	glycerate kinase [EC:2.7.1.31]	Metabolism	
K00866	1	choline kinase [EC:2.7.1.32]	Metabolism	
K00867	2	type I pantothenate kinase [EC:2.7.1.33]	Metabolism	
K00868	445	pyridoxine kinase [EC:2.7.1.35]	Metabolism	
K00869	1	mevalonate kinase [EC:2.7.1.36]	Metabolism	
K00872	9	homoserine kinase [EC:2.7.1.39]	Metabolism	
K00873	44	pyruvate kinase [EC:2.7.1.40]	Metabolism	
K00874	20	2-dehydro-3-deoxygluconokinase [EC:2.7.1.45]	Metabolism	
K00875	2	D-ribulokinase [EC:2.7.1.47]	Metabolism	
K00876	12	uridine kinase [EC:2.7.1.48]	Metabolism	
K00877	3	hydroxymethylpyrimidine kinase [EC:2.7.1.49]	Metabolism	
K00878	3	hydroxyethylthiazole kinase [EC:2.7.1.50]	Metabolism	
K00879	4	L-fuculokinase [EC:2.7.1.51]	Metabolism	
K00880	1	L-xylulokinase [EC:2.7.1.53]	Metabolism	
K00882	14	1-phosphofructokinase [EC:2.7.1.56]	Metabolism	
K00883	1	2-dehydro-3-deoxygalactonokinase [EC:2.7.1.58]	Metabolism	
K00884	7	N-acetylglucosamine kinase [EC:2.7.1.59]	Metabolism	
K00885	1	N-acylmannosamine kinase [EC:2.7.1.60]	Metabolism	
K00886	9	polyphosphate glucokinase [EC:2.7.1.63]	Metabolism	
K00887	10	undecaprenol kinase [EC:2.7.1.66]	Metabolism	
K00891	31	shikimate kinase [EC:2.7.1.71]	Metabolism	
K00894	3	ethanolamine kinase [EC:2.7.1.82]	Metabolism	
K00895	22	pyrophosphate--fructose-6-phosphate 1-phosphotransferase	Metabolism	
K00901	6	diacylglycerol kinase [EC:2.7.1.107]	Metabolism	

K00904	18	deoxyguanosine kinase [EC:2.7.1.113]	Metabolism	
K00912	13	tetraacyldisaccharide 4'-kinase [EC:2.7.1.130]	Metabolism	
K00917	9	tagatose 6-phosphate kinase [EC:2.7.1.144]	Metabolism	
K00919	25	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [EC:2.7.1.148]	Metabolism	
K00925	31	acetate kinase [EC:2.7.2.1]	Metabolism	
K00926	18	carbamate kinase [EC:2.7.2.2]	Metabolism	
K00927	35	phosphoglycerate kinase [EC:2.7.2.3]	Metabolism	
K00928	33	aspartate kinase [EC:2.7.2.4]	Metabolism	
K00929	3	butyrate kinase [EC:2.7.2.7]	Metabolism	
K00930	23	acetylglutamate kinase [EC:2.7.2.8]	Metabolism	
K00931	54	glutamate 5-kinase [EC:2.7.2.11]	Metabolism	
K00932	1	propionate kinase [EC:2.7.2.15]	Metabolism	
K00933	1	creatine kinase [EC:2.7.3.2]	Metabolism	
K00934	4	arginine kinase [EC:2.7.3.3]	Metabolism	
K00937	60	polyphosphate kinase [EC:2.7.4.1]	Metabolism	
K00938	5	phosphomevalonate kinase [EC:2.7.4.2]	Metabolism	
K00939	34	adenylate kinase [EC:2.7.4.3]	Metabolism	
K00940	20	nucleoside-diphosphate kinase [EC:2.7.4.6]	Metabolism	
K00941	29	phosphomethylpyrimidine kinase [EC:2.7.4.7]	Metabolism	
K00942	26	guanylate kinase [EC:2.7.4.8]	Metabolism	
K00943	33	dTMP kinase [EC:2.7.4.9]	Metabolism	
K00945	33	cytidylate kinase [EC:2.7.4.14]	Metabolism	
K00946	33	thiamine-monophosphate kinase [EC:2.7.4.16]	Metabolism	
K00948	177	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	Metabolism	
K00950	17	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	Metabolism	
K00951	90	GTP pyrophosphokinase [EC:2.7.6.5]	Metabolism	
K00954	23	pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]	Metabolism	
K00955	28	bifunctional enzyme CysN/CysC [EC:2.7.7.4 2.7.1.25]	Metabolism	
K00956	29	sulfate adenylyltransferase subunit 1 [EC:2.7.7.4]	Metabolism	
K00957	10	sulfate adenylyltransferase subunit 2 [EC:2.7.7.4]	Metabolism	
K00958	25	sulfate adenylyltransferase [EC:2.7.7.4]	Metabolism	
K00962	39	polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]	Metabolism	
K00963	23	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]	Metabolism	
K00965	24	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]	Metabolism	
K00966	49	mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]	Metabolism	
K00969	56	nicotinate-nucleotide adenylyltransferase [EC:2.7.7.18]	Metabolism	
K00971	42	mannose-1-phosphate guanylyltransferase [EC:2.7.7.22]	Metabolism	
K00972	3	UDP-N-acetylglucosamine pyrophosphorylase [EC:2.7.7.23]	Metabolism	
K00973	45	glucose-1-phosphate thymidylyltransferase [EC:2.7.7.24]	Metabolism	
K00975	42	glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]	Metabolism	
K00978	15	glucose-1-phosphate cytidylyltransferase [EC:2.7.7.33]	Metabolism	
K00979	26	3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase)	Metabolism	
K00980	8	glycerol-3-phosphate cytidylyltransferase [EC:2.7.7.39]	Metabolism	
K00981	27	phosphatidate cytidylyltransferase [EC:2.7.7.41]	Metabolism	
K00983	2	N-acylneuraminate cytidylyltransferase [EC:2.7.7.43]	Metabolism	
K00991	20	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	Metabolism	
K00992	28	Unclassified; E2.7.7.-	Metabolism	
K00995	115	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Metabolism	
K00997	15	holo-[acyl-carrier protein] synthase [EC:2.7.8.7]	Metabolism	
K00998	20	phosphatidylserine synthase [EC:2.7.8.8]	Metabolism	
K00999	4	CDP-diacylglycerol--inositol 3-phosphatidyltransferase [EC:2.7.8.11]	Metabolism	
K01000	52	phospho-N-acetylmuramoyl-pentapeptide-transferase [EC:2.7.8.13]	Metabolism	
K01003	30	carboxyvinyl-carboxyphosphonate phosphorylmutase [EC:2.7.8.23]	Metabolism	
K01006	55	pyruvate,orthophosphate dikinase [EC:2.7.9.1]	Metabolism	
K01007	80	pyruvate, water dikinase [EC:2.7.9.2]	Metabolism	
K01008	29	selenide, water dikinase [EC:2.7.9.3]	Metabolism	
K01011	21	3-mercaptopyruvate sulfurtransferase [EC:2.8.1.2]	Metabolism	

K01012	22	biotin synthetase [EC:2.8.1.6]	Metabolism	
K01026	7	propionate CoA-transferase [EC:2.8.3.1]	Metabolism	
K01027	3	3-oxoacid CoA-transferase [EC:2.8.3.5]	Metabolism	
K01028	6	3-oxoacid CoA-transferase subunit A [EC:2.8.3.5]	Metabolism	
K01029	3	3-oxoacid CoA-transferase subunit B [EC:2.8.3.5]	Metabolism	
K01031	3	3-oxoadipate CoA-transferase, alpha subunit [EC:2.8.3.6]	Metabolism	
K01032	3	3-oxoadipate CoA-transferase, beta subunit [EC:2.8.3.6]	Metabolism	
K01035	2	acetate CoA-transferase beta subunit [EC:2.8.3.8]	Metabolism	
K01039	25	glutaconate CoA-transferase, subunit A [EC:2.8.3.12]	Metabolism	
K01040	18	glutaconate CoA-transferase, subunit B [EC:2.8.3.12]	Metabolism	
K01042	37	L-seryl-tRNA(Ser) seleniumtransferase [EC:2.9.1.1]	Metabolism	
K01044	56	carboxylesterase [EC:3.1.1.1]	Metabolism	
K01046	68	triacylglycerol lipase [EC:3.1.1.3]	Metabolism	
K01048	6	lysophospholipase [EC:3.1.1.5]	Metabolism	
K01051	2	pectinesterase [EC:3.1.1.11]	Metabolism	
K01053	63	gluconolactonase [EC:3.1.1.17]	Metabolism	
K01054	3	acylglycerol lipase [EC:3.1.1.23]	Metabolism	
K01055	56	3-oxoadipate enol-lactonase [EC:3.1.1.24]	Metabolism	
K01057	24	6-phosphogluconolactonase [EC:3.1.1.31]	Metabolism	
K01058	8	phospholipase A1 [EC:3.1.1.32]	Metabolism	
K01060	3	cephalosporin-C deacetylase [EC:3.1.1.41]	Metabolism	
K01061	68	carboxymethylenebutenolidase [EC:3.1.1.45]	Metabolism	
K01062	1	1-alkyl-2-acetylglycerophosphocholine esterase [EC:3.1.1.47]	Metabolism	
K01067	12	acetyl-CoA hydrolase [EC:3.1.2.1]	Metabolism	
K01068	5	palmitoyl-CoA hydrolase [EC:3.1.2.2]	Metabolism	
K01069	110	hydroxyacylglutathione hydrolase [EC:3.1.2.6]	Metabolism	
K01070	5	S-formylglutathione hydrolase [EC:3.1.2.12]	Metabolism	
K01071	2	oleoyl-[acyl-carrier-protein] hydrolase [EC:3.1.2.14]	Metabolism	
K01075	12	4-hydroxybenzoyl-CoA thioesterase [EC:3.1.2.23]	Metabolism	
K01077	90	alkaline phosphatase [EC:3.1.3.1]	Metabolism	
K01078	17	acid phosphatase [EC:3.1.3.2]	Metabolism	
K01079	34	phosphoserine phosphatase [EC:3.1.3.3]	Metabolism	
K01081	32	5'-nucleotidase [EC:3.1.3.5]	Metabolism	
K01083	1	3-phytase [EC:3.1.3.8]	Metabolism	
K01087	73	trehalose-phosphatase [EC:3.1.3.12]	Metabolism	
K01091	72	phosphoglycolate phosphatase [EC:3.1.3.18]	Metabolism	
K01092	58	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]	Metabolism	
K01093	4	4-phytase / acid phosphatase [EC:3.1.3.26 3.1.3.2]	Metabolism	
K01095	8	phosphatidylglycerophosphatase A [EC:3.1.3.27]	Metabolism	
K01096	4	phosphatidylglycerophosphatase B [EC:3.1.3.27]	Metabolism	
K01101	7	4-nitrophenyl phosphatase [EC:3.1.3.41]	Metabolism	
K01103	1	fructose-2,6-bisphosphatase [EC:3.1.3.46]	Metabolism	
K01113	42	phosphodiesterase/alkaline phosphatase D [EC:3.1.4.1]	Metabolism	
K01114	33	phospholipase C [EC:3.1.4.3]	Metabolism	
K01115	8	phospholipase D [EC:3.1.4.4]	Metabolism	
K01119	13	2',3'-cyclic-nucleotide 2'-phosphodiesterase [EC:3.1.4.16]	Metabolism	
K01120	22	3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]	Metabolism	
K01126	47	glycerophosphoryl diester phosphodiesterase [EC:3.1.4.46]	Metabolism	
K01129	24	dGTPase [EC:3.1.5.1]	Metabolism	
K01130	86	arylsulfatase [EC:3.1.6.1]	Metabolism	
K01131	7	steryl-sulfatase [EC:3.1.6.2]	Metabolism	
K01132	17	N-acetylgalactosamine-6-sulfatase [EC:3.1.6.4]	Metabolism	
K01134	23	arylsulfatase A [EC:3.1.6.8]	Metabolism	
K01135	17	arylsulfatase B [EC:3.1.6.12]	Metabolism	
K01136	8	iduronate 2-sulfatase [EC:3.1.6.13]	Metabolism	
K01137	10	N-acetylglucosamine-6-sulfatase [EC:3.1.6.14]	Metabolism	
K01139	45	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	Metabolism	

K01176	36	alpha-amylase [EC:3.2.1.1]	Metabolism	
K01178	57	glucoamylase [EC:3.2.1.3]	Metabolism	
K01179	39	endoglucanase [EC:3.2.1.4]	Metabolism	
K01182	13	oligo-1,6-glucosidase [EC:3.2.1.10]	Metabolism	
K01183	28	chitinase [EC:3.2.1.14]	Metabolism	
K01184	1	polygalacturonase [EC:3.2.1.15]	Metabolism	
K01186	2	sialidase-1 [EC:3.2.1.18]	Metabolism	
K01187	42	alpha-glucosidase [EC:3.2.1.20]	Metabolism	
K01188	77	beta-glucosidase [EC:3.2.1.21]	Metabolism	
K01190	51	beta-galactosidase [EC:3.2.1.23]	Metabolism	
K01191	17	alpha-mannosidase [EC:3.2.1.24]	Metabolism	
K01192	9	beta-mannosidase [EC:3.2.1.25]	Metabolism	
K01193	2	beta-fructofuranosidase [EC:3.2.1.26]	Metabolism	
K01194	6	alpha,alpha-trehalase [EC:3.2.1.28]	Metabolism	
K01195	8	beta-glucuronidase [EC:3.2.1.31]	Metabolism	
K01197	1	hyaluronoglucosaminidase [EC:3.2.1.35]	Metabolism	
K01198	9	xylan 1,4-beta-xylosidase [EC:3.2.1.37]	Metabolism	
K01199	9	glucan endo-1,3-beta-D-glucosidase [EC:3.2.1.39]	Metabolism	
K01201	13	glucosylceramidase [EC:3.2.1.45]	Metabolism	
K01206	21	alpha-L-fucosidase [EC:3.2.1.51]	Metabolism	
K01207	53	beta-N-acetylhexosaminidase [EC:3.2.1.52]	Metabolism	
K01208	1	cyclomaltodextrinase [EC:3.2.1.54]	Metabolism	
K01209	22	alpha-N-arabinofuranosidase [EC:3.2.1.55]	Metabolism	
K01210	10	glucan 1,3-beta-glucosidase [EC:3.2.1.58]	Metabolism	
K01212	11	levanase [EC:3.2.1.65]	Metabolism	
K01213	6	galacturan 1,4-alpha-galacturonidase [EC:3.2.1.67]	Metabolism	
K01218	6	mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]	Metabolism	
K01220	15	6-phospho-beta-galactosidase [EC:3.2.1.85]	Metabolism	
K01222	6	6-phospho-beta-glucosidase [EC:3.2.1.86]	Metabolism	
K01223	1	6-phospho-beta-glucosidase [EC:3.2.1.86]	Metabolism	
K01225	25	cellulose 1,4-beta-cellobiosidase [EC:3.2.1.91]	Metabolism	
K01226	3	trehalose-6-phosphate hydrolase [EC:3.2.1.93]	Metabolism	
K01236	28	maltooligosyltrehalose trehalohydrolase [EC:3.2.1.141]	Metabolism	
K01239	17	purine nucleosidase [EC:3.2.2.1]	Metabolism	
K01241	4	AMP nucleosidase [EC:3.2.2.4]	Metabolism	
K01243	6	S-adenosylhomocysteine/5'-methylthioadenosine nucleosidase	Metabolism	
K01251	29	adenosylhomocysteinase [EC:3.3.1.1]	Metabolism	
K01253	35	microsomal epoxide hydrolase [EC:3.3.2.9]	Metabolism	
K01255	52	leucyl aminopeptidase [EC:3.4.11.1]	Metabolism	
K01256	102	aminopeptidase N [EC:3.4.11.2]	Metabolism	
K01259	49	proline iminopeptidase [EC:3.4.11.5]	Metabolism	
K01270	3	aminoacylhistidine dipeptidase [EC:3.4.13.3]	Metabolism	
K01424	54	L-asparaginase [EC:3.5.1.1]	Metabolism	
K01425	10	glutaminase [EC:3.5.1.2]	Metabolism	
K01426	156	amidase [EC:3.5.1.4]	Metabolism	
K01428	11	urease alpha subunit [EC:3.5.1.5]	Metabolism	
K01429	3	urease beta subunit [EC:3.5.1.5]	Metabolism	
K01430	6	urease gamma subunit [EC:3.5.1.5]	Metabolism	
K01431	27	beta-ureidopropionase [EC:3.5.1.6]	Metabolism	
K01433	7	formyltetrahydrofolate deformylase [EC:3.5.1.10]	Metabolism	
K01434	69	penicillin amidase [EC:3.5.1.11]	Metabolism	
K01438	28	acetylornithine deacetylase [EC:3.5.1.16]	Metabolism	
K01439	82	succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]	Metabolism	
K01443	68	N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]	Metabolism	
K01444	9	N4-(beta-N-acetylglucosaminyl)-L-asparaginase [EC:3.5.1.26]	Metabolism	
K01451	45	hippurate hydrolase [EC:3.5.1.32]	Metabolism	
K01452	38	chitin deacetylase [EC:3.5.1.41]	Metabolism	

K01453	19	Unclassified; E3.5.1.46	Metabolism	
K01455	26	formamidase [EC:3.5.1.49]	Metabolism	
K01457	9	allophanate hydrolase [EC:3.5.1.54]	Metabolism	
K01458	6	N-formylglutamate deformylase [EC:3.5.1.68]	Metabolism	
K01464	42	dihydropyrimidinase [EC:3.5.2.2]	Metabolism	
K01465	147	dihydroorotase [EC:3.5.2.3]	Metabolism	
K01466	28	allantoinase [EC:3.5.2.5]	Metabolism	
K01468	45	imidazolonepropionase [EC:3.5.2.7]	Metabolism	
K01469	35	5-oxoprolinase (ATP-hydrolysing) [EC:3.5.2.9]	Metabolism	
K01470	24	creatinine amidohydrolase [EC:3.5.2.10]	Metabolism	
K01471	12	Unclassified; E3.5.2.12	Metabolism	
K01473	68	N-methylhydantoinase A [EC:3.5.2.14]	Metabolism	
K01474	76	N-methylhydantoinase B [EC:3.5.2.14]	Metabolism	
K01476	13	arginase [EC:3.5.3.1]	Metabolism	
K01477	8	allantoicase [EC:3.5.3.4]	Metabolism	
K01478	10	arginine deiminase [EC:3.5.3.6]	Metabolism	
K01479	4	formiminoglutamase [EC:3.5.3.8]	Metabolism	
K01480	40	agmatinase [EC:3.5.3.11]	Metabolism	
K01483	1	ureidoglycolate hydrolase [EC:3.5.3.19]	Metabolism	
K01484	1	succinylarginine dihydrolase [EC:3.5.3.23]	Metabolism	
K01485	25	cytosine deaminase [EC:3.5.4.1]	Metabolism	
K01486	15	adenine deaminase [EC:3.5.4.2]	Metabolism	
K01487	12	guanine deaminase [EC:3.5.4.3]	Metabolism	
K01488	35	adenosine deaminase [EC:3.5.4.4]	Metabolism	
K01489	21	cytidine deaminase [EC:3.5.4.5]	Metabolism	
K01491	34	methylenetetrahydrofolate dehydrogenase (NADP+) /	Metabolism	
K01492	2	phosphoribosylaminoimidazolecarboxamide formyltransferase	Metabolism	
K01493	13	dCMP deaminase [EC:3.5.4.12]	Metabolism	
K01494	20	dCTP deaminase [EC:3.5.4.13]	Metabolism	
K01495	28	GTP cyclohydrolase I [EC:3.5.4.16]	Metabolism	
K01496	6	phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]	Metabolism	
K01497	24	GTP cyclohydrolase II [EC:3.5.4.25]	Metabolism	
K01498	1	diaminohydroxyphosphoribosylaminopyrimidine deaminase [EC:3.5.4.26]	Metabolism	
K01499	3	methenyltetrahydromethanopterin cyclohydrolase [EC:3.5.4.27]	Metabolism	
K01501	28	nitrilase [EC:3.5.5.1]	Metabolism	
K01502	12	aliphatic nitrilase [EC:3.5.5.7]	Metabolism	
K01505	4	1-aminocyclopropane-1-carboxylate deaminase [EC:3.5.99.7]	Metabolism	
K01507	54	inorganic pyrophosphatase [EC:3.6.1.1]	Metabolism	
K01512	16	acylphosphatase [EC:3.6.1.7]	Metabolism	
K01514	57	exopolyphosphatase [EC:3.6.1.11]	Metabolism	
K01515	41	ADP-ribose pyrophosphatase [EC:3.6.1.13]	Metabolism	
K01518	13	bis(5'-nucleosidyl)-tetraphosphatase [EC:3.6.1.17]	Metabolism	
K01520	14	dUTP pyrophosphatase [EC:3.6.1.23]	Metabolism	
K01523	4	phosphoribosyl-ATP pyrophosphohydrolase [EC:3.6.1.31]	Metabolism	
K01524	18	guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	Metabolism	
K01525	13	bis(5'-nucleosyl)-tetraphosphatase (symmetrical) [EC:3.6.1.41]	Metabolism	
K01535	2	H+-transporting ATPase [EC:3.6.3.6]	Metabolism	
K01555	12	fumarylacetoacetase [EC:3.7.1.2]	Metabolism	
K01556	30	kynureninase [EC:3.7.1.3]	Metabolism	
K01557	5	acylpyruvate hydrolase [EC:3.7.1.5]	Metabolism	
K01560	34	2-haloacid dehalogenase [EC:3.8.1.2]	Metabolism	
K01561	20	haloacetate dehalogenase [EC:3.8.1.3]	Metabolism	
K01563	44	haloalkane dehalogenase [EC:3.8.1.5]	Metabolism	
K01568	1	pyruvate decarboxylase [EC:4.1.1.1]	Metabolism	
K01571	11	oxaloacetate decarboxylase, alpha subunit [EC:4.1.1.3]	Metabolism	
K01572	9	oxaloacetate decarboxylase, beta subunit [EC:4.1.1.3]	Metabolism	
K01576	25	benzoylformate decarboxylase [EC:4.1.1.7]	Metabolism	

K01577	9	oxalyl-CoA decarboxylase [EC:4.1.1.8]	Metabolism	
K01578	19	malonyl-CoA decarboxylase [EC:4.1.1.9]	Metabolism	
K01579	12	aspartate 1-decarboxylase [EC:4.1.1.11]	Metabolism	
K01580	8	glutamate decarboxylase [EC:4.1.1.15]	Metabolism	
K01581	17	ornithine decarboxylase [EC:4.1.1.17]	Metabolism	
K01582	22	lysine decarboxylase [EC:4.1.1.18]	Metabolism	
K01583	17	arginine decarboxylase [EC:4.1.1.19]	Metabolism	
K01584	17	arginine decarboxylase [EC:4.1.1.19]	Metabolism	
K01585	30	arginine decarboxylase [EC:4.1.1.19]	Metabolism	
K01586	61	diaminopimelate decarboxylase [EC:4.1.1.20]	Metabolism	
K01588	20	5-(carboxyamino)imidazole ribonucleotide mutase [EC:5.4.99.18]	Metabolism	
K01589	16	5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]	Metabolism	
K01591	30	orotidine-5'-phosphate decarboxylase [EC:4.1.1.23]	Metabolism	
K01592	14	tyrosine decarboxylase [EC:4.1.1.25]	Metabolism	
K01593	61	aromatic-L-amino-acid decarboxylase [EC:4.1.1.28]	Metabolism	
K01594	14	sulfinoalanine decarboxylase [EC:4.1.1.29]	Metabolism	
K01595	40	phosphoenolpyruvate carboxylase [EC:4.1.1.31]	Metabolism	
K01596	30	phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]	Metabolism	
K01598	9	phosphopantothenoylcysteine decarboxylase [EC:4.1.1.36]	Metabolism	
K01599	38	uroporphyrinogen decarboxylase [EC:4.1.1.37]	Metabolism	
K01601	7	ribulose-bisphosphate carboxylase large chain [EC:4.1.1.39]	Metabolism	
K01602	3	ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]	Metabolism	
K01607	55	4-carboxymuconolactone decarboxylase [EC:4.1.1.44]	Metabolism	
K01608	8	tartronate-semialdehyde synthase [EC:4.1.1.47]	Metabolism	
K01609	19	indole-3-glycerol phosphate synthase [EC:4.1.1.48]	Metabolism	
K01610	22	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	Metabolism	
K01611	4	S-adenosylmethionine decarboxylase [EC:4.1.1.50]	Metabolism	
K01612	5	4-hydroxybenzoate decarboxylase [EC:4.1.1.61]	Metabolism	
K01613	14	phosphatidylserine decarboxylase [EC:4.1.1.65]	Metabolism	
K01615	12	glutaconyl-CoA decarboxylase [EC:4.1.1.70]	Metabolism	
K01617	5	4-oxalocrotonate decarboxylase [EC:4.1.1.77]	Metabolism	
K01619	13	deoxyribose-phosphate aldolase [EC:4.1.2.4]	Metabolism	
K01620	32	threonine aldolase [EC:4.1.2.5]	Metabolism	
K01621	20	phosphoketolase [EC:4.1.2.9]	Metabolism	
K01623	28	fructose-bisphosphate aldolase, class I [EC:4.1.2.13]	Metabolism	
K01624	8	fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	Metabolism	
K01625	11	2-dehydro-3-deoxyphosphogluconate aldolase /	Metabolism	
K01626	26	3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]	Metabolism	
K01627	29	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase)	Metabolism	
K01628	51	L-fuculose-phosphate aldolase [EC:4.1.2.17]	Metabolism	
K01629	6	rhamnulose-1-phosphate aldolase [EC:4.1.2.19]	Metabolism	
K01630	13	2-dehydro-3-deoxyglucarate aldolase [EC:4.1.2.20]	Metabolism	
K01631	11	2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]	Metabolism	
K01633	13	dihydroneopterin aldolase [EC:4.1.2.25]	Metabolism	
K01634	7	sphinganine-1-phosphate aldolase [EC:4.1.2.27]	Metabolism	
K01635	10	tagatose 1,6-diphosphate aldolase [EC:4.1.2.40]	Metabolism	
K01637	13	isocitrate lyase [EC:4.1.3.1]	Metabolism	
K01638	23	malate synthase [EC:2.3.3.9]	Metabolism	
K01639	16	N-acetylneuraminate lyase [EC:4.1.3.3]	Metabolism	
K01640	23	hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]	Metabolism	
K01641	3	hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]	Metabolism	
K01647	50	citrate synthase [EC:2.3.3.1]	Metabolism	
K01648	1	ATP citrate (pro-S)-lyase [EC:2.3.3.8]	Metabolism	
K01649	82	2-isopropylmalate synthase [EC:2.3.3.13]	Metabolism	
K01652	178	acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	Metabolism	
K01653	22	acetolactate synthase I/III small subunit [EC:2.2.1.6]	Metabolism	
K01654	14	N-acetylneuraminate synthase [EC:2.5.1.56]	Metabolism	

K01655	8	homocitrate synthase [EC:2.3.3.14]	Metabolism	
K01657	59	anthranilate synthase component I [EC:4.1.3.27]	Metabolism	
K01658	28	anthranilate synthase component II [EC:4.1.3.27]	Metabolism	
K01659	6	2-methylcitrate synthase [EC:2.3.3.5]	Metabolism	
K01661	17	naphthoate synthase [EC:4.1.3.36]	Metabolism	
K01662	55	1-deoxy-D-xylulose-5-phosphate synthase [EC:2.2.1.7]	Metabolism	
K01664	14	para-aminobenzoate synthetase component II [EC:2.6.1.85]	Metabolism	
K01665	22	para-aminobenzoate synthetase component I [EC:2.6.1.85]	Metabolism	
K01666	4	4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]	Metabolism	
K01667	15	tryptophanase [EC:4.1.99.1]	Metabolism	
K01668	12	tyrosine phenol-lyase [EC:4.1.99.2]	Metabolism	
K01673	27	carbonic anhydrase [EC:4.2.1.1]	Metabolism	
K01676	23	fumarate hydratase, class I [EC:4.2.1.2]	Metabolism	
K01677	4	fumarate hydratase subunit alpha [EC:4.2.1.2]	Metabolism	
K01679	37	fumarate hydratase, class II [EC:4.2.1.2]	Metabolism	
K01681	81	aconitate hydratase 1 [EC:4.2.1.3]	Metabolism	
K01682	7	aconitate hydratase 2 [EC:4.2.1.3]	Metabolism	
K01684	33	galactonate dehydratase [EC:4.2.1.6]	Metabolism	
K01685	24	altronate hydrolase [EC:4.2.1.7]	Metabolism	
K01686	9	mannonate dehydratase [EC:4.2.1.8]	Metabolism	
K01687	73	dihydroxy-acid dehydratase [EC:4.2.1.9]	Metabolism	
K01689	42	enolase [EC:4.2.1.11]	Metabolism	
K01690	2	phosphogluconate dehydratase [EC:4.2.1.12]	Metabolism	
K01692	266	enoyl-CoA hydratase [EC:4.2.1.17]	Metabolism	
K01693	14	imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]	Metabolism	
K01695	29	tryptophan synthase alpha chain [EC:4.2.1.20]	Metabolism	
K01696	29	tryptophan synthase beta chain [EC:4.2.1.20]	Metabolism	
K01697	25	cystathionine beta-synthase [EC:4.2.1.22]	Metabolism	
K01698	18	porphobilinogen synthase [EC:4.2.1.24]	Metabolism	
K01699	4	propanediol dehydratase large subunit [EC:4.2.1.28]	Metabolism	
K01703	59	3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit	Metabolism	
K01704	24	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit	Metabolism	
K01705	1	homoaconitate hydratase [EC:4.2.1.36]	Metabolism	
K01706	7	glucarate dehydratase [EC:4.2.1.40]	Metabolism	
K01708	22	galactarate dehydratase [EC:4.2.1.42]	Metabolism	
K01709	15	CDP-glucose 4,6-dehydratase [EC:4.2.1.45]	Metabolism	
K01710	121	dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]	Metabolism	
K01711	34	GDPmannose 4,6-dehydratase [EC:4.2.1.47]	Metabolism	
K01712	17	urocanate hydratase [EC:4.2.1.49]	Metabolism	
K01713	19	prephenate dehydratase [EC:4.2.1.51]	Metabolism	
K01714	67	dihydrodipicolinate synthase [EC:4.2.1.52]	Metabolism	
K01715	61	3-hydroxybutyryl-CoA dehydratase [EC:4.2.1.55]	Metabolism	
K01716	1	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.60]	Metabolism	
K01719	22	uroporphyrinogen-III synthase [EC:4.2.1.75]	Metabolism	
K01720	63	2-methylcitrate dehydratase [EC:4.2.1.79]	Metabolism	
K01725	1	cyanate lyase [EC:4.2.1.104]	Metabolism	
K01728	1	pectate lyase [EC:4.2.2.2]	Metabolism	
K01733	66	threonine synthase [EC:4.2.3.1]	Metabolism	
K01734	6	methylglyoxal synthase [EC:4.2.3.3]	Metabolism	
K01735	30	3-dehydroquinate synthase [EC:4.2.3.4]	Metabolism	
K01736	40	chorismate synthase [EC:4.2.3.5]	Metabolism	
K01737	25	6-pyruvoyl tetrahydrobiopterin synthase [EC:4.2.3.12]	Metabolism	
K01738	73	cysteine synthase A [EC:2.5.1.47]	Metabolism	
K01739	49	cystathionine gamma-synthase [EC:2.5.1.48]	Metabolism	
K01740	36	O-acetylhomoserine (thiol)-lyase [EC:2.5.1.49]	Metabolism	
K01744	18	aspartate ammonia-lyase [EC:4.3.1.1]	Metabolism	
K01745	32	histidine ammonia-lyase [EC:4.3.1.3]	Metabolism	

K01746	14	formiminotetrahydrofolate cyclodeaminase [EC:4.3.1.4]	Metabolism	
K01749	28	hydroxymethylbilane synthase [EC:2.5.1.61]	Metabolism	
K01750	39	ornithine cyclodeaminase [EC:4.3.1.12]	Metabolism	
K01752	8	L-serine dehydratase [EC:4.3.1.17]	Metabolism	
K01754	80	threonine dehydratase [EC:4.3.1.19]	Metabolism	
K01755	59	argininosuccinate lyase [EC:4.3.2.1]	Metabolism	
K01756	53	adenylosuccinate lyase [EC:4.3.2.2]	Metabolism	
K01757	6	strictosidine synthase [EC:4.3.3.2]	Metabolism	
K01758	28	cystathionine gamma-lyase [EC:4.4.1.1]	Metabolism	
K01759	62	lactoylglutathione lyase [EC:4.4.1.5]	Metabolism	
K01760	59	cystathionine beta-lyase [EC:4.4.1.8]	Metabolism	
K01761	21	methionine-gamma-lyase [EC:4.4.1.11]	Metabolism	
K01768	403	adenylate cyclase [EC:4.6.1.1]	Metabolism	
K01769	7	guanylate cyclase, other [EC:4.6.1.2]	Metabolism	
K01770	23	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:4.6.1.12]	Metabolism	
K01772	32	ferrochelatase [EC:4.99.1.1]	Metabolism	
K01775	45	alanine racemase [EC:5.1.1.1]	Metabolism	
K01776	47	glutamate racemase [EC:5.1.1.3]	Metabolism	
K01777	12	proline racemase [EC:5.1.1.4]	Metabolism	
K01778	33	diaminopimelate epimerase [EC:5.1.1.7]	Metabolism	
K01779	30	aspartate racemase [EC:5.1.1.13]	Metabolism	
K01781	68	mandelate racemase [EC:5.1.2.2]	Metabolism	
K01782	36	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase /	Metabolism	
K01783	21	ribulose-phosphate 3-epimerase [EC:5.1.3.1]	Metabolism	
K01784	233	UDP-glucose 4-epimerase [EC:5.1.3.2]	Metabolism	
K01785	23	aldose 1-epimerase [EC:5.1.3.3]	Metabolism	
K01786	5	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]	Metabolism	
K01787	7	N-acylglucosamine 2-epimerase [EC:5.1.3.8]	Metabolism	
K01790	33	dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13]	Metabolism	
K01791	43	UDP-N-acetylglucosamine 2-epimerase [EC:5.1.3.14]	Metabolism	
K01792	3	glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	Metabolism	
K01795	128	Unclassified; E5.1.3.-	Metabolism	
K01796	35	alpha-methylacyl-CoA racemase [EC:5.1.99.4]	Metabolism	
K01799	14	maleate isomerase [EC:5.2.1.1]	Metabolism	
K01800	11	maleylacetoacetate isomerase [EC:5.2.1.2]	Metabolism	
K01801	8	maleylpyruvate isomerase [EC:5.2.1.4]	Metabolism	
K01803	29	triosephosphate isomerase (TIM) [EC:5.3.1.1]	Metabolism	
K01804	10	L-arabinose isomerase [EC:5.3.1.4]	Metabolism	
K01805	13	xylose isomerase [EC:5.3.1.5]	Metabolism	
K01807	12	ribose 5-phosphate isomerase A [EC:5.3.1.6]	Metabolism	
K01808	26	ribose 5-phosphate isomerase B [EC:5.3.1.6]	Metabolism	
K01809	44	mannose-6-phosphate isomerase [EC:5.3.1.8]	Metabolism	
K01810	53	glucose-6-phosphate isomerase [EC:5.3.1.9]	Metabolism	
K01812	7	glucuronate isomerase [EC:5.3.1.12]	Metabolism	
K01813	9	L-rhamnose isomerase [EC:5.3.1.14]	Metabolism	
K01814	30	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide	Metabolism	
K01816	12	hydroxypyruvate isomerase [EC:5.3.1.22]	Metabolism	
K01817	27	phosphoribosylanthranilate isomerase [EC:5.3.1.24]	Metabolism	
K01818	6	L-fucose isomerase [EC:5.3.1.25]	Metabolism	
K01820	9	Unclassified; E5.3.1.-	Metabolism	
K01821	5	4-oxalocrotonate tautomerase [EC:5.3.2.-]	Metabolism	
K01822	1	steroid delta-isomerase [EC:5.3.3.1]	Metabolism	
K01823	12	isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]	Metabolism	
K01825	4	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase /	Metabolism	
K01826	20	5-carboxymethyl-2-hydroxymuconate isomerase [EC:5.3.3.10]	Metabolism	
K01834	100	phosphoglycerate mutase [EC:5.4.2.1]	Metabolism	
K01835	41	phosphoglucomutase [EC:5.4.2.2]	Metabolism	

K01838	4	beta-phosphoglucomutase [EC:5.4.2.6]	Metabolism	
K01839	18	phosphopentomutase [EC:5.4.2.7]	Metabolism	
K01840	87	phosphomannomutase [EC:5.4.2.8]	Metabolism	
K01841	3	phosphoenolpyruvate phosphomutase [EC:5.4.2.9]	Metabolism	
K01843	25	lysine 2,3-aminomutase [EC:5.4.3.2]	Metabolism	
K01844	3	beta-lysine 5,6-aminomutase [EC:5.4.3.3]	Metabolism	
K01845	65	glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]	Metabolism	
K01846	4	methylaspartate mutase [EC:5.4.99.1]	Metabolism	
K01847	14	methylmalonyl-CoA mutase [EC:5.4.99.2]	Metabolism	
K01848	52	methylmalonyl-CoA mutase, N-terminal domain [EC:5.4.99.2]	Metabolism	
K01849	12	methylmalonyl-CoA mutase, C-terminal domain [EC:5.4.99.2]	Metabolism	
K01851	1	salicylate biosynthesis isochorismate synthase [EC:5.4.4.2]	Metabolism	
K01854	46	UDP-galactopyranose mutase [EC:5.4.99.9]	Metabolism	
K01856	36	muconate cycloisomerase [EC:5.5.1.1]	Metabolism	
K01857	15	3-carboxy-cis,cis-muconate cycloisomerase [EC:5.5.1.2]	Metabolism	
K01858	12	myo-inositol-1-phosphate synthase [EC:5.5.1.4]	Metabolism	
K01860	15	chloromuconate cycloisomerase [EC:5.5.1.7]	Metabolism	
K01874	56	methionyl-tRNA synthetase [EC:6.1.1.10]	Metabolism	
K01885	74	glutamyl-tRNA synthetase [EC:6.1.1.17]	Metabolism	
K01895	175	acetyl-CoA synthetase [EC:6.2.1.1]	Metabolism	
K01897	294	long-chain acyl-CoA synthetase [EC:6.2.1.3]	Metabolism	
K01902	19	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]	Metabolism	
K01903	30	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]	Metabolism	
K01904	37	4-coumarate--CoA ligase [EC:6.2.1.12]	Metabolism	
K01905	37	acetyl-CoA synthetase (ADP-forming) [EC:6.2.1.13]	Metabolism	
K01906	43	6-carboxyhexanoate--CoA ligase [EC:6.2.1.14]	Metabolism	
K01907	38	acetoacetyl-CoA synthetase [EC:6.2.1.16]	Metabolism	
K01908	12	propionyl-CoA synthetase [EC:6.2.1.17]	Metabolism	
K01911	22	O-succinylbenzoic acid--CoA ligase [EC:6.2.1.26]	Metabolism	
K01912	88	phenylacetate-CoA ligase [EC:6.2.1.30]	Metabolism	
K01914	7	aspartate--ammonia ligase [EC:6.3.1.1]	Metabolism	
K01915	141	glutamine synthetase [EC:6.3.1.2]	Metabolism	
K01916	33	NAD+ synthase [EC:6.3.1.5]	Metabolism	
K01917	15	glutathionylspermidine synthase [EC:6.3.1.8]	Metabolism	
K01918	21	pantoate--beta-alanine ligase [EC:6.3.2.1]	Metabolism	
K01919	16	glutamate--cysteine ligase [EC:6.3.2.2]	Metabolism	
K01920	20	glutathione synthase [EC:6.3.2.3]	Metabolism	
K01921	88	D-alanine-D-alanine ligase [EC:6.3.2.4]	Metabolism	
K01922	6	phosphopantothenate-cysteine ligase [EC:6.3.2.5]	Metabolism	
K01923	35	phosphoribosylaminoimidazole-succinocarboxamide synthase	Metabolism	
K01924	35	UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8]	Metabolism	
K01925	33	UDP-N-acetylmuramoylalanine--D-glutamate ligase [EC:6.3.2.9]	Metabolism	
K01928	42	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	Metabolism	
K01929	58	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-	Metabolism	
K01933	32	phosphoribosylformylglycinamidine cyclo-ligase [EC:6.3.3.1]	Metabolism	
K01934	15	5-formyltetrahydrofolate cyclo-ligase [EC:6.3.3.2]	Metabolism	
K01935	11	dethiobiotin synthetase [EC:6.3.3.3]	Metabolism	
K01937	42	CTP synthase [EC:6.3.4.2]	Metabolism	
K01938	23	formate--tetrahydrofolate ligase [EC:6.3.4.3]	Metabolism	
K01939	47	adenylosuccinate synthase [EC:6.3.4.4]	Metabolism	
K01940	34	argininosuccinate synthase [EC:6.3.4.5]	Metabolism	
K01941	8	urea carboxylase [EC:6.3.4.6]	Metabolism	
K01945	31	phosphoribosylamine--glycine ligase [EC:6.3.4.13]	Metabolism	
K01947	4	biotin-[acetyl-CoA-carboxylase] ligase / type III pantothenate	Metabolism	
K01950	63	NAD+ synthase (glutamine-hydrolysing) [EC:6.3.5.1]	Metabolism	
K01951	50	GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]	Metabolism	
K01952	89	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]	Metabolism	

K01953	160	asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]	Metabolism	
K01955	66	carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]	Metabolism	
K01956	39	carbamoyl-phosphate synthase small subunit [EC:6.3.5.5]	Metabolism	
K01958	22	pyruvate carboxylase [EC:6.4.1.1]	Metabolism	
K01959	2	pyruvate carboxylase subunit A [EC:6.4.1.1]	Metabolism	
K01960	23	pyruvate carboxylase subunit B [EC:6.4.1.1]	Metabolism	
K01961	38	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2	Metabolism	
K01962	21	acetyl-CoA carboxylase carboxyl transferase subunit alpha	Metabolism	
K01963	31	acetyl-CoA carboxylase carboxyl transferase subunit beta	Metabolism	
K01965	36	propionyl-CoA carboxylase alpha chain [EC:6.4.1.3]	Metabolism	
K01966	69	propionyl-CoA carboxylase beta chain [EC:6.4.1.3]	Metabolism	
K01968	21	3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4]	Metabolism	
K01969	19	3-methylcrotonyl-CoA carboxylase beta subunit [EC:6.4.1.4]	Metabolism	
K02045	11	sulfate transport system ATP-binding protein [EC:3.6.3.25]	Metabolism	
K02046	14	sulfate transport system permease protein	Metabolism	
K02047	9	sulfate transport system permease protein	Metabolism	
K02048	16	sulfate transport system substrate-binding protein	Metabolism	
K02079	2	N-acetylgalactosamine-6-phosphate deacetylase [EC:3.5.1.25]	Metabolism	
K02083	5	allantoate deiminase [EC:3.5.3.9]	Metabolism	
K02108	50	F-type H+-transporting ATPase subunit a [EC:3.6.3.14]	Metabolism	
K02109	12	F-type H+-transporting ATPase subunit b [EC:3.6.3.14]	Metabolism	
K02110	10	F-type H+-transporting ATPase subunit c [EC:3.6.3.14]	Metabolism	
K02111	32	F-type H+-transporting ATPase subunit alpha [EC:3.6.3.14]	Metabolism	
K02112	21	F-type H+-transporting ATPase subunit beta [EC:3.6.3.14]	Metabolism	
K02113	26	F-type H+-transporting ATPase subunit delta [EC:3.6.3.14]	Metabolism	
K02114	7	F-type H+-transporting ATPase subunit epsilon [EC:3.6.3.14]	Metabolism	
K02115	35	F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]	Metabolism	
K02117	20	V-type H+-transporting ATPase subunit A [EC:3.6.3.14]	Metabolism	
K02118	13	V-type H+-transporting ATPase subunit B [EC:3.6.3.14]	Metabolism	
K02120	3	V-type H+-transporting ATPase subunit D [EC:3.6.3.14]	Metabolism	
K02121	2	V-type H+-transporting ATPase subunit E [EC:3.6.3.14]	Metabolism	
K02123	15	V-type H+-transporting ATPase subunit I [EC:3.6.3.14]	Metabolism	
K02124	4	V-type H+-transporting ATPase subunit K [EC:3.6.3.14]	Metabolism	
K02160	11	acetyl-CoA carboxylase biotin carboxyl carrier protein	Metabolism	
K02169	17	biotin synthesis protein BioC	Metabolism	
K02170	4	biotin biosynthesis protein BioH	Metabolism	
K02188	4	cobalamin biosynthesis protein CbiD	Metabolism	
K02189	1	cobalamin biosynthesis protein CbiG	Metabolism	
K02203	6	phosphoserine / homoserine phosphotransferase [EC:3.1.3.3 2.7.1.39]	Metabolism	
K02204	5	homoserine kinase type II [EC:2.7.1.39]	Metabolism	
K02224	18	cobyrinic acid a,c-diamide synthase [EC:6.3.5.9 6.3.1.-]	Metabolism	
K02226	2	alpha-ribazole phosphatase [EC:3.1.3.73]	Metabolism	
K02227	11	adenosylcobinamide-phosphate synthase CobD [EC:6.3.1.10]	Metabolism	
K02229	1	precorrin-3B synthase [EC:1.14.13.83]	Metabolism	
K02230	13	cobaltochelatase CobN [EC:6.6.1.2]	Metabolism	
K02231	13	adenosylcobinamide kinase / adenosylcobinamide-phosphate	Metabolism	
K02232	9	adenosylcobyric acid synthase [EC:6.3.5.10]	Metabolism	
K02233	2	adenosylcobinamide-GDP ribazoletransferase [EC:2.7.8.26]	Metabolism	
K02234	13	cobalamin biosynthesis protein CobW	Metabolism	
K02258	6	cytochrome c oxidase subunit XI assembly protein	Metabolism	
K02259	27	cytochrome c oxidase subunit XV assembly protein	Metabolism	
K02274	88	cytochrome c oxidase subunit I [EC:1.9.3.1]	Metabolism	
K02275	66	cytochrome c oxidase subunit II [EC:1.9.3.1]	Metabolism	
K02276	37	cytochrome c oxidase subunit III [EC:1.9.3.1]	Metabolism	
K02287	2	phycocyanin-associated, rod	Metabolism	
K02288	2	phycocyanobilin lyase alpha subunit [EC:4.-.-.-]	Metabolism	
K02291	30	phytoene synthase [EC:2.5.1.32]	Metabolism	

K02292	50	beta-carotene ketolase (CrtO type)	Metabolism	
K02293	3	phytoene dehydrogenase, phytoene desaturase [EC:1.14.99.-]	Metabolism	
K02297	3	cytochrome o ubiquinol oxidase subunit II [EC:1.10.3.-]	Metabolism	
K02298	6	cytochrome o ubiquinol oxidase subunit I [EC:1.10.3.-]	Metabolism	
K02299	4	cytochrome o ubiquinol oxidase subunit III [EC:1.10.3.-]	Metabolism	
K02301	31	protoheme IX farnesyltransferase [EC:2.5.1.-]	Metabolism	
K02302	27	uroporphyrin-III C-methyltransferase / precorrin-2 dehydrogenase /	Metabolism	
K02303	22	uroporphyrin-III C-methyltransferase [EC:2.1.1.107]	Metabolism	
K02304	6	precorrin-2 dehydrogenase / sirohydrochlorin ferrochelatase	Metabolism	
K02305	3	nitric-oxide reductase, cytochrome c-containing subunit II	Metabolism	
K02319	11	DNA polymerase I [EC:2.7.7.7]	Metabolism	
K02335	90	DNA polymerase I [EC:2.7.7.7]	Metabolism	
K02337	211	DNA polymerase III subunit alpha [EC:2.7.7.7]	Metabolism	
K02338	59	DNA polymerase III subunit beta [EC:2.7.7.7]	Metabolism	
K02339	6	DNA polymerase III subunit chi [EC:2.7.7.7]	Metabolism	
K02340	11	DNA polymerase III subunit delta [EC:2.7.7.7]	Metabolism	
K02341	35	DNA polymerase III subunit delta' [EC:2.7.7.7]	Metabolism	
K02342	60	DNA polymerase III subunit epsilon [EC:2.7.7.7]	Metabolism	
K02343	65	DNA polymerase III subunit gamma/tau [EC:2.7.7.7]	Metabolism	
K02345	1	DNA polymerase III subunit theta [EC:2.7.7.7]	Metabolism	
K02361	19	isochorismate synthase [EC:5.4.4.2]	Metabolism	
K02363	1	enterobactin 2,3-dihydroxybenzoate-AMP ligase /	Metabolism	
K02364	7	enterobactin synthetase component F [EC:2.7.7.-]	Metabolism	
K02371	8	enoyl-[acyl carrier protein] reductase II [EC:1.3.1.-]	Metabolism	
K02372	22	3R-hydroxymyristoyl ACP dehydrase [EC:4.2.1.-]	Metabolism	
K02377	24	GDP-L-fucose synthase [EC:1.1.1.271]	Metabolism	
K02428	30	nucleoside-triphosphate pyrophosphatase [EC:3.6.1.19]	Metabolism	
K02437	29	glycine cleavage system H protein	Metabolism	
K02438	33	glycogen operon protein GlgX [EC:3.2.1.-]	Metabolism	
K02439	2	thiosulfate sulfurtransferase [EC:2.8.1.1]	Metabolism	
K02446	28	fructose-1,6-bisphosphatase II [EC:3.1.3.11]	Metabolism	
K02472	10	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.-]	Metabolism	
K02473	35	UDP-N-acetylglucosamine 4-epimerase [EC:5.1.3.7]	Metabolism	
K02474	11	UDP-N-acetyl-D-galactosamine dehydrogenase [EC:1.1.1.-]	Metabolism	
K02492	42	glutamyl-tRNA reductase [EC:1.2.1.70]	Metabolism	
K02495	53	oxygen-independent coproporphyrinogen III oxidase [EC:1.3.99.22]	Metabolism	
K02496	3	uroporphyrin-III C-methyltransferase [EC:2.1.1.107]	Metabolism	
K02500	27	cyclase HisF [EC:4.1.3.-]	Metabolism	
K02501	31	glutamine amidotransferase [EC:2.4.2.-]	Metabolism	
K02502	22	ATP phosphoribosyltransferase regulatory subunit	Metabolism	
K02509	7	2-oxo-hept-3-ene-1,7-dioate hydratase [EC:4.2.1.-]	Metabolism	
K02510	35	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [EC:4.1.2.-]	Metabolism	
K02517	28	lipid A biosynthesis lauroyl acyltransferase [EC:2.3.1.-]	Metabolism	
K02523	22	octaprenyl diphosphate synthase [EC:2.5.1.-]	Metabolism	
K02527	16	3-deoxy-D-manno-octulosonic-acid transferase [EC:2.-.-.-]	Metabolism	
K02535	25	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	Metabolism	
K02536	33	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	Metabolism	
K02548	10	1,4-dihydroxy-2-naphthoate octaprenyltransferase [EC:2.5.1.-]	Metabolism	
K02549	20	O-succinylbenzoate synthase [EC:4.2.1.113]	Metabolism	
K02551	32	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate	Metabolism	
K02552	12	menaquinone-specific isochorismate synthase [EC:5.4.4.2]	Metabolism	
K02554	5	2-keto-4-pentenoate hydratase [EC:4.2.1.80]	Metabolism	
K02563	30	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)	Metabolism	
K02564	23	glucosamine-6-phosphate deaminase [EC:3.5.99.6]	Metabolism	
K02567	28	periplasmic nitrate reductase NapA [EC:1.7.99.4]	Metabolism	
K02568	8	cytochrome c-type protein NapB	Metabolism	
K02575	27	MFS transporter, NNP family, nitrate/nitrite transporter	Metabolism	

K02586	4	nitrogenase molybdenum-iron protein alpha chain [EC:1.18.6.1]	Metabolism	
K02588	1	nitrogenase iron protein NifH [EC:1.18.6.1]	Metabolism	
K02591	3	nitrogenase molybdenum-iron protein beta chain [EC:1.18.6.1]	Metabolism	
K02594	3	homocitrate synthase NifV	Metabolism	
K02609	16	phenylacetic acid degradation protein	Metabolism	
K02610	4	phenylacetic acid degradation protein	Metabolism	
K02611	10	phenylacetic acid degradation protein	Metabolism	
K02612	14	phenylacetic acid degradation protein	Metabolism	
K02613	11	phenylacetic acid degradation NADH oxidoreductase	Metabolism	
K02614	21	phenylacetic acid degradation protein	Metabolism	
K02615	3	acetyl-CoA acetyltransferase [EC:2.3.1.-]	Metabolism	
K02618	19	phenylacetic acid degradation protein	Metabolism	
K02619	44	4-amino-4-deoxychorismate lyase [EC:4.1.3.38]	Metabolism	
K02626	5	arginine decarboxylase [EC:4.1.1.19]	Metabolism	
K02635	19	cytochrome b6	Metabolism	
K02636	14	cytochrome b6-f complex iron-sulfur subunit [EC:1.10.99.1]	Metabolism	
K02637	1	cytochrome b6-f complex subunit 4	Metabolism	
K02638	2	plastocyanin	Metabolism	
K02641	2	ferredoxin--NADP+ reductase [EC:1.18.1.2]	Metabolism	
K02690	1	photosystem I core protein Ib	Metabolism	
K02745	1	PTS system, N-acetylgalactosamine-specific IIB component	Metabolism	
K02765	3	PTS system, D-glucosamine-specific IIC component	Metabolism	
K02768	6	PTS system, fructose-specific IIA component [EC:2.7.1.69]	Metabolism	
K02769	1	PTS system, fructose-specific IIB component [EC:2.7.1.69]	Metabolism	
K02770	12	PTS system, fructose-specific IIC component	Metabolism	
K02774	5	PTS system, galactitol-specific IIB component [EC:2.7.1.69]	Metabolism	
K02775	2	PTS system, galactitol-specific IIC component	Metabolism	
K02777	109	PTS system, glucose-specific IIA component [EC:2.7.1.69]	Metabolism	
K02779	2	PTS system, glucose-specific IIC component	Metabolism	
K02793	6	PTS system, mannose-specific IIA component [EC:2.7.1.69]	Metabolism	
K02794	3	PTS system, mannose-specific IIB component [EC:2.7.1.69]	Metabolism	
K02795	3	PTS system, mannose-specific IIC component	Metabolism	
K02796	6	PTS system, mannose-specific IID component	Metabolism	
K02799	2	PTS system, mannitol-specific IIB component [EC:2.7.1.69]	Metabolism	
K02800	3	PTS system, mannitol-specific IIC component	Metabolism	
K02804	1	PTS system, N-acetylglucosamine-specific IIC component	Metabolism	
K02821	9	PTS system, ascorbate-specific IIA component [EC:2.7.1.69]	Metabolism	
K02823	18	dihydroorotate dehydrogenase electron transfer subunit	Metabolism	
K02825	13	pyrimidine operon attenuation protein / uracil	Metabolism	
K02826	1	quinol oxidase polypeptide II [EC:1.9.3.-]	Metabolism	
K02827	1	quinol oxidase polypeptide I [EC:1.9.3.-]	Metabolism	
K02828	1	quinol oxidase polypeptide III [EC:1.9.3.-]	Metabolism	
K02841	22	heptosyltransferase I [EC:2.4.-.-]	Metabolism	
K02843	38	heptosyltransferase II [EC:2.4.-.-]	Metabolism	
K02844	36	UDP-glucose:(heptosyl)LPS alpha-1,3-glucosyltransferase [EC:2.4.1.-]	Metabolism	
K02849	21	heptosyltransferase III [EC:2.4.-.-]	Metabolism	
K02858	40	3,4-dihydroxy 2-butanone 4-phosphate synthase [EC:4.1.99.12]	Metabolism	
K03040	34	DNA-directed RNA polymerase subunit alpha [EC:2.7.7.6]	Metabolism	
K03043	77	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]	Metabolism	
K03046	516	DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]	Metabolism	
K03060	10	DNA-directed RNA polymerase subunit omega [EC:2.7.7.6]	Metabolism	
K03077	3	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]	Metabolism	
K03080	2	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]	Metabolism	
K03119	43	taurine dioxygenase [EC:1.14.11.17]	Metabolism	
K03146	1	thiamine biosynthetic enzyme	Metabolism	
K03147	11	thiamine biosynthesis protein ThiC	Metabolism	
K03148	16	adenylyltransferase ThiF [EC:2.7.7.-]	Metabolism	

K03149	27	thiamine biosynthesis ThiG	Metabolism	
K03150	1	thiamine biosynthesis ThiH	Metabolism	
K03151	4	thiamine biosynthesis protein ThiI	Metabolism	
K03153	10	glycine oxidase [EC:1.4.3.19]	Metabolism	
K03179	26	4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]	Metabolism	
K03182	88	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiD [EC:4.1.1.-]	Metabolism	
K03183	77	ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.-]	Metabolism	
K03184	1	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	Metabolism	
K03185	16	2-octaprenyl-6-methoxyphenol hydroxylase [EC:1.14.13.-]	Metabolism	
K03186	20	3-octaprenyl-4-hydroxybenzoate carboxy-lyase UbiX [EC:4.1.1.-]	Metabolism	
K03269	5	UDP-2,3-diacylglucosamine hydrolase [EC:3.6.1.-]	Metabolism	
K03270	14	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (KDO 8-P	Metabolism	
K03271	12	phosphoheptose isomerase [EC:5.-.-.-]	Metabolism	
K03272	33	D-beta-D-heptose 7-phosphate kinase / D-beta-D-heptose 1-phosphate	Metabolism	
K03273	14	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.-]	Metabolism	
K03274	9	ADP-L-glycero-D-manno-heptose 6-epimerase [EC:5.1.3.20]	Metabolism	
K03280	1	UDP-N-acetylglucosamine:(glucosyl)LPS	Metabolism	
K03331	1	L-xylulose reductase [EC:1.1.1.10]	Metabolism	
K03332	2	fructan beta-fructosidase [EC:3.2.1.80]	Metabolism	
K03333	41	cholesterol oxidase [EC:1.1.3.6]	Metabolism	
K03335	20	inososе dehydratase [EC:4.2.1.44]	Metabolism	
K03336	12	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase [EC:3.7.1.-]	Metabolism	
K03337	2	5-deoxy-glucuronate isomerase [EC:5.3.1.-]	Metabolism	
K03338	5	5-dehydro-2-deoxygluconokinase [EC:2.7.1.92]	Metabolism	
K03339	1	6-phospho-5-dehydro-2-deoxy-D-gluconate aldolase [EC:4.1.2.29]	Metabolism	
K03342	7	para-aminobenzoate synthetase / 4-amino-4-deoxychorismate lyase	Metabolism	
K03343	8	putrescine oxidase [EC:1.4.3.10]	Metabolism	
K03366	4	(R,R)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4	Metabolism	
K03367	32	D-alanine-poly(phosphoribitol) ligase [EC:6.1.1.13]	Metabolism	
K03379	37	cyclohexanone monooxygenase [EC:1.14.13.22]	Metabolism	
K03380	35	phenol 2-monooxygenase [EC:1.14.13.7]	Metabolism	
K03381	13	catechol 1,2-dioxygenase [EC:1.13.11.1]	Metabolism	
K03382	5	hydroxyatrazine ethylaminohydrolase [EC:3.5.99.3]	Metabolism	
K03385	9	formate-dependent nitrite reductase, periplasmic cytochrome c552	Metabolism	
K03388	65	heterodisulfide reductase subunit A [EC:1.8.98.1]	Metabolism	
K03389	22	heterodisulfide reductase subunit B [EC:1.8.98.1]	Metabolism	
K03390	14	heterodisulfide reductase subunit C [EC:1.8.98.1]	Metabolism	
K03391	42	pentachlorophenol monooxygenase [EC:1.14.13.50]	Metabolism	
K03392	61	aminocarboxymuconate-semialdehyde decarboxylase [EC:4.1.1.45]	Metabolism	
K03394	1	precorrin-2 C20-methyltransferase / cobalt-factor-2	Metabolism	
K03396	1	S-(hydroxymethyl)glutathione synthase [EC:4.4.1.22]	Metabolism	
K03399	2	precorrin-6Y C5,15-methyltransferase [EC:2.1.1.132]	Metabolism	
K03403	4	magnesium chelatase subunit H [EC:6.6.1.1]	Metabolism	
K03404	10	magnesium chelatase subunit D [EC:6.6.1.1]	Metabolism	
K03405	29	magnesium chelatase subunit I [EC:6.6.1.1]	Metabolism	
K03416	11	methylmalonyl-CoA carboxyltransferase [EC:2.1.3.1]	Metabolism	
K03417	36	methylisocitrate lyase [EC:4.1.3.30]	Metabolism	
K03426	21	NAD+ diphosphatase [EC:3.6.1.22]	Metabolism	
K03429	22	1,2-diacylglycerol 3-glucosyltransferase [EC:2.4.1.157]	Metabolism	
K03430	5	2-aminoethylphosphonate-pyruvate transaminase [EC:2.6.1.37]	Metabolism	
K03431	33	phosphoglucosamine mutase [EC:5.4.2.10]	Metabolism	
K03434	14	N-acetylglucosaminylphosphatidylinositol deacetylase [EC:3.5.1.89]	Metabolism	
K03464	2	muconolactone D-isomerase [EC:5.3.3.4]	Metabolism	
K03465	12	thymidylate synthase (FAD) [EC:2.1.1.148]	Metabolism	
K03473	1	erythronate-4-phosphate dehydrogenase [EC:1.1.1.290]	Metabolism	
K03474	23	pyridoxine 5-phosphate synthase [EC:2.6.99.2]	Metabolism	
K03475	1	PTS system, ascorbate-specific IIC component	Metabolism	

K03476	18	L-ascorbate 6-phosphate lactonase [EC:3.1.1.-]	Metabolism	
K03517	23	quinolinate synthase [EC:2.5.1.72]	Metabolism	
K03518	27	carbon-monoxide dehydrogenase small subunit [EC:1.2.99.2]	Metabolism	
K03519	52	carbon-monoxide dehydrogenase medium subunit [EC:1.2.99.2]	Metabolism	
K03520	196	carbon-monoxide dehydrogenase large subunit [EC:1.2.99.2]	Metabolism	
K03524	31	BirA family transcriptional regulator, biotin operon repressor /	Metabolism	
K03525	31	type III pantothenate kinase [EC:2.7.1.33]	Metabolism	
K03526	24	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase [EC:1.17.7.1]	Metabolism	
K03527	34	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [EC:1.17.1.2]	Metabolism	
K03587	74	cell division protein FtsI (penicillin-binding protein 3)	Metabolism	
K03594	20	bacterioferritin	Metabolism	
K03621	30	glycerol-3-phosphate acyltransferase PlsX [EC:2.3.1.15]	Metabolism	
K03635	22	molybdenum cofactor biosynthesis protein E	Metabolism	
K03636	10	molybdenum cofactor biosynthesis protein D	Metabolism	
K03637	16	molybdenum cofactor biosynthesis protein C	Metabolism	
K03639	47	molybdenum cofactor biosynthesis protein A	Metabolism	
K03644	32	lipoic acid synthetase [EC:2.8.1.8]	Metabolism	
K03693	1	penicillin-binding protein	Metabolism	
K03707	6	transcriptional activator TenA [EC:3.5.99.2]	Metabolism	
K03715	6	1,2-diacylglycerol 3-beta-galactosyltransferase [EC:2.4.1.46]	Metabolism	
K03735	4	ethanolamine ammonia-lyase large subunit [EC:4.3.1.7]	Metabolism	
K03736	1	ethanolamine ammonia-lyase small subunit [EC:4.3.1.7]	Metabolism	
K03737	30	putative pyruvate-flavodoxin oxidoreductase [EC:1.2.7.-]	Metabolism	
K03738	68	aldehyde:ferredoxin oxidoreductase [EC:1.2.7.5]	Metabolism	
K03742	58	competence/damage-inducible protein CinA	Metabolism	
K03743	19	Unclassified; K03743	Metabolism	
K03763	10	DNA polymerase III subunit alpha, Gram-positive type [EC:2.7.7.7]	Metabolism	
K03777	7	D-lactate dehydrogenase [EC:1.1.1.28]	Metabolism	
K03778	7	D-lactate dehydrogenase [EC:1.1.1.28]	Metabolism	
K03779	2	L(+)-tartrate dehydratase alpha subunit [EC:4.2.1.32]	Metabolism	
K03780	3	L(+)-tartrate dehydratase beta subunit [EC:4.2.1.32]	Metabolism	
K03781	12	catalase [EC:1.11.1.6]	Metabolism	
K03782	24	catalase/peroxidase [EC:1.11.1.6 1.11.1.7]	Metabolism	
K03783	27	purine-nucleoside phosphorylase [EC:2.4.2.1]	Metabolism	
K03784	5	purine-nucleoside phosphorylase [EC:2.4.2.1]	Metabolism	
K03785	2	3-dehydroquinate dehydratase I [EC:4.2.1.10]	Metabolism	
K03786	17	3-dehydroquinate dehydratase II [EC:4.2.1.10]	Metabolism	
K03787	26	5'-nucleotidase [EC:3.1.3.5]	Metabolism	
K03795	10	sirohydrochlorin cobaltochelatase [EC:4.99.1.3]	Metabolism	
K03800	12	lipoate-protein ligase A [EC:2.7.7.63]	Metabolism	
K03801	27	lipoyl(octanoyl) transferase [EC:2.3.1.181]	Metabolism	
K03809	6	Trp repressor binding protein	Metabolism	
K03814	19	monofunctional biosynthetic peptidoglycan transglycosylase	Metabolism	
K03815	1	xanthosine phosphorylase [EC:2.4.2.-]	Metabolism	
K03821	52	polyhydroxyalkanoate synthase [EC:2.3.1.-]	Metabolism	
K03823	23	phosphinothricin acetyltransferase [EC:2.3.1.183]	Metabolism	
K03841	11	fructose-1,6-bisphosphatase I [EC:3.1.3.11]	Metabolism	
K03851	2	taurine-pyruvate aminotransferase [EC:2.6.1.77]	Metabolism	
K03852	6	sulfoacetaldehyde acetyltransferase [EC:2.3.3.15]	Metabolism	
K03856	30	3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]	Metabolism	
K03862	13	vanillate monooxygenase [EC:1.14.13.82]	Metabolism	
K03863	2	vanillate monooxygenase [EC:1.14.13.82]	Metabolism	
K03885	77	NADH dehydrogenase [EC:1.6.99.3]	Metabolism	
K03886	3	menaquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.-]	Metabolism	
K03887	9	menaquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.-]	Metabolism	
K03888	2	menaquinol-cytochrome c reductase cytochrome b/c subunit	Metabolism	
K03889	6	ubiquinol-cytochrome c reductase cytochrome c subunit	Metabolism	

K03890	3	ubiquinol-cytochrome c reductase iron-sulfur subunit	Metabolism	
K03891	15	ubiquinol-cytochrome c reductase cytochrome b subunit	Metabolism	
K03897	1	lysine N6-hydroxylase [EC:1.14.13.59]	Metabolism	
K03927	17	carboxylesterase type B [EC:3.1.1.1]	Metabolism	
K03943	6	NADH dehydrogenase (ubiquinone) flavoprotein 2 [EC:1.6.5.3 1.6.99.3]	Metabolism	
K03980	50	virulence factor	Metabolism	
K04019	11	ethanolamine utilization protein EutA	Metabolism	
K04020	4	phosphotransacetylase	Metabolism	
K04021	1	aldehyde dehydrogenase	Metabolism	
K04034	54	anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase	Metabolism	
K04035	62	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	Metabolism	
K04041	6	fructose-1,6-bisphosphatase III [EC:3.1.3.11]	Metabolism	
K04042	55	bifunctional protein GlmU [EC:2.7.7.23 2.3.1.157]	Metabolism	
K04072	15	acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10	Metabolism	
K04073	3	acetaldehyde dehydrogenase [EC:1.2.1.10]	Metabolism	
K04091	50	alkanesulfonate monooxygenase [EC:1.14.14.5]	Metabolism	
K04097	7	glutathione S-transferase [EC:2.5.1.18]	Metabolism	
K04098	2	hydroxyquinol 1,2-dioxygenase [EC:1.13.11.37]	Metabolism	
K04103	3	indolepyruvate decarboxylase [EC:4.1.1.74]	Metabolism	
K04107	6	4-hydroxybenzoyl-CoA reductase subunit 1 [EC:1.3.99.20]	Metabolism	
K04108	42	4-hydroxybenzoyl-CoA reductase subunit 2 [EC:1.3.99.20]	Metabolism	
K04110	22	benzoate-CoA ligase [EC:6.2.1.25]	Metabolism	
K04112	1	benzoyl-CoA reductase subunit [EC:1.3.99.15]	Metabolism	
K04113	10	benzoyl-CoA reductase subunit [EC:1.3.99.15]	Metabolism	
K04114	29	benzoyl-CoA reductase subunit [EC:1.3.99.15]	Metabolism	
K04115	16	benzoyl-CoA reductase subunit [EC:1.3.99.15]	Metabolism	
K04117	32	cyclohexanecarboxyl-CoA dehydrogenase [EC:1.3.99.-]	Metabolism	
K04118	4	pimeloyl-CoA dehydrogenase [EC:1.3.1.62]	Metabolism	
K04126	1	isopenicillin-N synthase [EC:1.21.3.1]	Metabolism	
K04127	15	isopenicillin-N epimerase [EC:5.1.1.17]	Metabolism	
K04128	1	hydroxymethyl cephem carbamoyltransferase [EC:2.1.3.-]	Metabolism	
K04340	1	scyllo-inosamine-4-phosphate amidinotransferase 1 [EC:2.1.4.2]	Metabolism	
K04486	6	histidinol-phosphatase (PHP family) [EC:3.1.3.15]	Metabolism	
K04487	57	cysteine desulfurase [EC:2.8.1.7]	Metabolism	
K04516	4	chorismate mutase [EC:5.4.99.5]	Metabolism	
K04517	16	prephenate dehydrogenase [EC:1.3.1.12]	Metabolism	
K04518	51	prephenate dehydratase [EC:4.2.1.51]	Metabolism	
K04561	21	nitric-oxide reductase, cytochrome b-containing subunit I	Metabolism	
K04719	4	5,6-dimethylbenzimidazole biosynthesis protein BluB	Metabolism	
K04780	19	nonribosomal peptide synthetase DhbF	Metabolism	
K04782	8	isochorismate pyruvate-lyase [EC:4.1.3.-]	Metabolism	
K04783	2	yersiniabactin salicyl-AMP ligase [EC:6.3.2.-]	Metabolism	
K04786	3	yersiniabactin nonribosomal peptide/polyketide synthase	Metabolism	
K04787	6	mycobactin salicyl-AMP ligase [EC:6.3.2.-]	Metabolism	
K05275	26	pyridoxine 4-dehydrogenase [EC:1.1.1.65]	Metabolism	
K05281	4	2'-hydroxyisoflavone reductase [EC:1.3.1.45]	Metabolism	
K05296	3	3(or 17)beta-hydroxysteroid dehydrogenase [EC:1.1.1.51]	Metabolism	
K05297	6	rubredoxin-NAD+ reductase [EC:1.18.1.1]	Metabolism	
K05299	10	formate dehydrogenase (NADP+) [EC:1.2.1.43]	Metabolism	
K05301	55	sulfite dehydrogenase [EC:1.8.2.1]	Metabolism	
K05306	2	phosphonoacetaldehyde hydrolase [EC:3.11.1.1]	Metabolism	
K05341	5	amylosucrase [EC:2.4.1.4]	Metabolism	
K05343	42	maltose alpha-D-glucosyltransferase [EC:5.4.99.16]	Metabolism	
K05344	1	glucose-1-phosphate phosphodismutase [EC:2.7.1.41]	Metabolism	
K05349	79	beta-glucosidase [EC:3.2.1.21]	Metabolism	
K05350	31	beta-glucosidase [EC:3.2.1.21]	Metabolism	
K05351	2	D-xylulose reductase [EC:1.1.1.9]	Metabolism	

K05358	3	quinate dehydrogenase (pyrroloquinoline-quinone) [EC:1.1.99.25]	Metabolism	
K05359	1	carboxycyclohexadienyl dehydratase [EC:4.2.1.91]	Metabolism	
K05362	1	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase	Metabolism	
K05363	1	serine/alanine adding enzyme [EC:2.3.2.10]	Metabolism	
K05364	58	peptidoglycan glycosyltransferase [EC:2.4.1.129]	Metabolism	
K05365	12	penicillin-binding protein 1B [EC:2.4.1.129 3.4.-.-]	Metabolism	
K05366	129	penicillin-binding protein 1A [EC:2.4.1.- 3.4.-.-]	Metabolism	
K05367	18	penicillin-binding protein 1C [EC:2.4.1.-]	Metabolism	
K05368	1	aquacobalamin reductase / NAD(P)H-flavin reductase [EC:1.16.1.3	Metabolism	
K05375	2	MbtH protein	Metabolism	
K05384	22	bilin biosynthesis protein	Metabolism	
K05386	8	bilin biosynthesis protein	Metabolism	
K05394	29	atrazine chlorohydrolase [EC:3.8.1.8]	Metabolism	
K05396	10	D-cysteine desulfhydrase [EC:4.4.1.15]	Metabolism	
K05515	85	penicillin-binding protein 2	Metabolism	
K05525	30	linalool 8-monooxygenase [EC:1.14.99.28]	Metabolism	
K05549	11	benzoate 1,2-dioxygenase alpha subunit [EC:1.14.12.10]	Metabolism	
K05550	4	benzoate 1,2-dioxygenase beta subunit [EC:1.14.12.10]	Metabolism	
K05551	24	3-oxoacyl-ACP synthase I [EC:2.3.1.-]	Metabolism	
K05552	22	3-oxoacyl-ACP synthase II [EC:2.3.1.-]	Metabolism	
K05555	12	cyclase [EC:4.-.-.-]	Metabolism	
K05556	3	hydroxylacyl-CoA dehydrogenase [EC:1.1.1.-]	Metabolism	
K05572	6	NADH dehydrogenase I subunit 1 [EC:1.6.5.3]	Metabolism	
K05573	9	NADH dehydrogenase I subunit 2 [EC:1.6.5.3]	Metabolism	
K05574	6	NADH dehydrogenase I subunit 3 [EC:1.6.5.3]	Metabolism	
K05575	8	NADH dehydrogenase I subunit 4 [EC:1.6.5.3]	Metabolism	
K05576	3	NADH dehydrogenase I subunit 4L [EC:1.6.5.3]	Metabolism	
K05577	7	NADH dehydrogenase I subunit 5 [EC:1.6.5.3]	Metabolism	
K05578	2	NADH dehydrogenase I subunit 6 [EC:1.6.5.3]	Metabolism	
K05579	2	NADH dehydrogenase I subunit 7 [EC:1.6.5.3]	Metabolism	
K05580	4	NADH dehydrogenase I subunit I [EC:1.6.5.3]	Metabolism	
K05586	3	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]	Metabolism	
K05587	6	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]	Metabolism	
K05588	3	diaphorase subunit of the bidirectional hydrogenase [EC:1.6.5.3]	Metabolism	
K05597	1	glutamin-(asparagin-)ase [EC:3.5.1.38]	Metabolism	
K05599	2	anthranilate 1,2-dioxygenase (deaminating, decarboxylating) large	Metabolism	
K05600	2	anthranilate 1,2-dioxygenase (deaminating, decarboxylating) small	Metabolism	
K05601	2	hydroxylamine reductase [EC:1.7.99.1]	Metabolism	
K05603	10	formimidoylglutamate deiminase [EC:3.5.3.13]	Metabolism	
K05606	12	methylmalonyl-CoA epimerase [EC:5.1.99.1]	Metabolism	
K05708	9	large terminal subunit of phenylpropionate dioxygenase	Metabolism	
K05709	3	small terminal subunit of phenylpropionate dioxygenase	Metabolism	
K05710	16	ferredoxin subunit of phenylpropionate dioxygenase	Metabolism	
K05712	33	3-(3-hydroxy-phenyl)propionate hydroxylase [EC:1.14.13.-]	Metabolism	
K05714	5	2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase [EC:3.7.1.-]	Metabolism	
K05780	2	putative phosphonate transport system ATP-binding protein	Metabolism	
K05783	1	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	Metabolism	
K05784	3	benzoate 1,2-dioxygenase electron transfer component	Metabolism	
K05797	3	4-cresol dehydrogenase (hydroxylating) [EC:1.17.99.1]	Metabolism	
K05823	1	N-acetyldiaminopimelate deacetylase [EC:3.5.1.47]	Metabolism	
K05825	2	2-aminoadipate transaminase [EC:2.6.1.-]	Metabolism	
K05827	5	lysine biosynthesis protein LysX	Metabolism	
K05829	4	N-acetyl-gamma-aminoadipyl-phosphate reductase [EC:1.2.1.-]	Metabolism	
K05830	3	acetylornithine/acetyl-lysine aminotransferase [EC:2.6.1.11 2.6.1.-]	Metabolism	
K05831	2	acetyl-lysine deacetylase [EC:3.5.1.-]	Metabolism	
K05873	1	adenylate cyclase, class 2 [EC:4.6.1.1]	Metabolism	
K05878	8	dihydroxyacetone kinase, N-terminal domain [EC:2.7.1.-]	Metabolism	

K05879	5	dihydroxyacetone kinase, C-terminal domain [EC:2.7.1.-]	Metabolism	
K05895	2	precorrin-6X reductase [EC:1.3.1.54]	Metabolism	
K05898	2	3-oxosteroid 1-dehydrogenase [EC:1.3.99.4]	Metabolism	
K05917	1	cytochrome P450, family 51 (sterol 14-demethylase) [EC:1.14.13.70]	Metabolism	
K05921	16	5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase /	Metabolism	
K05928	8	tocopherol O-methyltransferase [EC:2.1.1.95]	Metabolism	
K05929	6	phosphoethanolamine N-methyltransferase [EC:2.1.1.103]	Metabolism	
K05934	6	precorrin-3B C17-methyltransferase [EC:2.1.1.131]	Metabolism	
K05936	4	precorrin-4 C11-methyltransferase [EC:2.1.1.133]	Metabolism	
K05939	12	acyl-[acyl-carrier-protein]-phospholipid O-acyltransferase /	Metabolism	
K05957	4	L-glutamine:scyllo-inosose aminotransferase [EC:2.6.1.50]	Metabolism	
K05973	12	poly(3-hydroxybutyrate) depolymerase [EC:3.1.1.75]	Metabolism	
K05979	11	2-phosphosulfolactate phosphatase [EC:3.1.3.71]	Metabolism	
K06001	31	tryptophan synthase beta chain [EC:4.2.1.20]	Metabolism	
K06013	29	STE24 endopeptidase [EC:3.4.24.84]	Metabolism	
K06016	27	N-carbamoyl-L-amino-acid hydrolase [EC:3.5.1.87]	Metabolism	
K06019	4	pyrophosphatase PpaX [EC:3.6.1.1]	Metabolism	
K06034	5	sulfopyruvate decarboxylase subunit alpha [EC:4.1.1.79]	Metabolism	
K06041	24	arabinose-5-phosphate isomerase [EC:5.3.1.13]	Metabolism	
K06042	8	precorrin-8X methylmutase [EC:5.4.1.2]	Metabolism	
K06044	33	(1->4)-alpha-D-glucan 1-alpha-D-glucosylmutase [EC:5.4.99.15]	Metabolism	
K06045	23	squalene-hopene cyclase [EC:5.4.99.17]	Metabolism	
K06118	5	UDP-sulfoquinovose synthase [EC:3.13.1.1]	Metabolism	
K06120	2	glycerol dehydratase large subunit [EC:4.2.1.30]	Metabolism	
K06121	1	glycerol dehydratase medium subunit [EC:4.2.1.30]	Metabolism	
K06131	35	cardiolipin synthase [EC:2.7.8.-]	Metabolism	
K06132	18	putative cardiolipin synthase [EC:2.7.8.-]	Metabolism	
K06134	3	ubiquinone biosynthesis monooxygenase Coq7 [EC:1.14.13.-]	Metabolism	
K06151	40	gluconate 2-dehydrogenase alpha chain [EC:1.1.99.3]	Metabolism	
K06153	39	undecaprenyl-diphosphatase [EC:3.6.1.27]	Metabolism	
K06162	1	PhnM protein	Metabolism	
K06163	1	PhnJ protein	Metabolism	
K06164	3	PhnI protein	Metabolism	
K06167	14	PhnP protein	Metabolism	
K06208	12	chorismate mutase [EC:5.4.99.5]	Metabolism	
K06211	1	HipB family transcriptional regulator, involved in the regulation of	Metabolism	
K06215	8	pyridoxine biosynthesis protein [EC:4.-.-.-]	Metabolism	
K06281	38	hydrogenase large subunit [EC:1.12.99.6]	Metabolism	
K06282	22	hydrogenase small subunit [EC:1.12.99.6]	Metabolism	
K06445	16	acyl-CoA dehydrogenase [EC:1.3.99.-]	Metabolism	
K06446	6	acyl-CoA dehydrogenase [EC:1.3.99.-]	Metabolism	
K06447	2	succinylglutamic semialdehyde dehydrogenase [EC:1.2.1.71]	Metabolism	
K06606	2	inosose isomerase [EC:5.3.99.-]	Metabolism	
K06718	2	L-2,4-diaminobutyric acid acetyltransferase [EC:2.3.1.178]	Metabolism	
K06859	1	glucose-6-phosphate isomerase, archaeal [EC:5.3.1.9]	Metabolism	
K06881	34	Unclassified; K06881	Metabolism	
K06896	21	Unclassified; K06896	Metabolism	
K06912	17	alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate dioxygenase	Metabolism	
K06920	21	queuosine biosynthesis protein QueC	Metabolism	
K06981	1	Unclassified; K06981	Metabolism	
K06989	7	aspartate dehydrogenase [EC:1.4.1.21]	Metabolism	
K07008	22	Unclassified; K07008	Metabolism	
K07029	47	Unclassified; K07029	Metabolism	
K07031	8	Unclassified; K07031	Metabolism	
K07046	35	Unclassified; K07046	Metabolism	
K07072	2	Unclassified; K07072	Metabolism	
K07102	16	Unclassified; K07102	Metabolism	

K07104	17	Unclassified; K07104	Metabolism	
K07106	20	N-acetylmuramic acid 6-phosphate etherase [EC:4.2.-.-]	Metabolism	
K07127	6	5-hydroxyisourate hydrolase [EC:3.5.2.17]	Metabolism	
K07130	24	Unclassified; K07130	Metabolism	
K07173	15	S-ribosylhomocysteine lyase [EC:4.4.1.21]	Metabolism	
K07246	8	tartrate dehydrogenase/decarboxylase / D-malate dehydrogenase	Metabolism	
K07248	4	lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase	Metabolism	
K07250	30	4-aminobutyrate aminotransferase / (S)-3-amino-2-methylpropionate	Metabolism	
K07258	136	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6)	Metabolism	
K07259	26	D-alanyl-D-alanine carboxypeptidase /	Metabolism	
K07260	7	D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4]	Metabolism	
K07281	1	Unclassified; K07281	Metabolism	
K07306	10	anaerobic dimethyl sulfoxide reductase subunit A [EC:1.8.99.-]	Metabolism	
K07307	10	anaerobic dimethyl sulfoxide reductase subunit B (DMSO reductase	Metabolism	
K07308	1	anaerobic dimethyl sulfoxide reductase subunit C (DMSO reductase	Metabolism	
K07309	1	putative dimethyl sulfoxide reductase subunit YnfE [EC:1.8.99.-]	Metabolism	
K07310	1	putative dimethyl sulfoxide reductase subunit YnfF [EC:1.8.99.-]	Metabolism	
K07404	25	6-phosphogluconolactonase [EC:3.1.1.31]	Metabolism	
K07405	7	alpha-amylase [EC:3.2.1.1]	Metabolism	
K07406	10	alpha-galactosidase [EC:3.2.1.22]	Metabolism	
K07407	12	alpha-galactosidase [EC:3.2.1.22]	Metabolism	
K07508	6	acetyl-CoA acyltransferase 2 [EC:2.3.1.16]	Metabolism	
K07516	43	3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]	Metabolism	
K07534	4	cyclohex-1-ene-1-carboxyl-CoA hydratase [EC:4.2.1.-]	Metabolism	
K07535	35	2-hydroxycyclohexanecarboxyl-CoA dehydrogenase [EC:1.1.1.-]	Metabolism	
K07537	4	cyclohexa-1,5-dienecarbonyl-CoA hydratase [EC:4.2.1.100]	Metabolism	
K07538	3	6-hydroxycyclohex-1-ene-1-carboxyl-CoA dehydrogenase [EC:1.1.1.-]	Metabolism	
K07543	23	benzylsuccinate CoA-transferase BbsE subunit [EC:2.8.3.15]	Metabolism	
K07544	22	benzylsuccinate CoA-transferase BbsF subunit [EC:2.8.3.15]	Metabolism	
K07545	1	(R)-benzylsuccinyl-CoA dehydro genase [EC:1.3.99.21]	Metabolism	
K07546	8	E-phenylitaconyl-CoA hydratase [EC:4.2.1.-]	Metabolism	
K07547	16	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsC subunit	Metabolism	
K07548	10	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsD subunit	Metabolism	
K07550	12	benzoylsuccinyl-CoA thiolase BbsB subunit [EC:2.3.1.-]	Metabolism	
K07748	2	sterol-4alpha-carboxylate 3-dehydrogenase (decarboxylating)	Metabolism	
K07758	5	pyridoxal phosphatase [EC:3.1.3.74]	Metabolism	
K07806	20	UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase	Metabolism	
K07823	4	3-oxoadipyl-CoA thiolase [EC:2.3.1.174]	Metabolism	
K07824	6	benzoate 4-monooxygenase [EC:1.14.13.12]	Metabolism	
K08068	1	N-acetylglucosamine-6-phosphate 2-epimerase and phosphatase	Metabolism	
K08093	1	3-hexulose-6-phosphate synthase [EC:4.1.2.43]	Metabolism	
K08097	6	phosphosulfolactate synthase [EC:4.4.1.19]	Metabolism	
K08100	49	bilirubin oxidase [EC:1.3.3.5]	Metabolism	
K08261	13	D-sorbitol dehydrogenase (acceptor) [EC:1.1.99.21]	Metabolism	
K08281	14	nicotinamidase/pyrazinamidase [EC:3.5.1.19 3.5.1.-]	Metabolism	
K08289	4	phosphoribosylglycinamide formyltransferase 2 [EC:2.1.2.2]	Metabolism	
K08295	5	2-aminobenzoate-CoA ligase [EC:6.2.1.32]	Metabolism	
K08302	1	tagatose 1,6-diphosphate aldolase [EC:4.1.2.40]	Metabolism	
K08310	5	dATP pyrophosphohydrolase [EC:3.6.1.-]	Metabolism	
K08318	2	putative dehydrogenase [EC:1.1.-.-]	Metabolism	
K08322	8	starvation sensing protein RspB [EC:1.1.1.-]	Metabolism	
K08323	9	starvation sensing protein RspA	Metabolism	
K08324	3	aldehyde dehydrogenase family protein [EC:1.2.1.-]	Metabolism	
K08351	5	biotin sulfoxide reductase [EC:1.-.-.-]	Metabolism	
K08352	38	thiosulfate reductase [EC:1.-.-.-]	Metabolism	
K08353	5	thiosulfate reductase electron transport protein	Metabolism	
K08354	3	thiosulfate reductase cytochrome b subunit	Metabolism	

K08357	9	tetrathionate reductase subunit A	Metabolism	
K08358	27	tetrathionate reductase subunit B	Metabolism	
K08359	4	tetrathionate reductase subunit C	Metabolism	
K08590	4	carbon-nitrogen hydrolase family protein	Metabolism	
K08591	25	glycerol-3-phosphate acyltransferase PlsY [EC:2.3.1.15]	Metabolism	
K08678	5	UDP-glucuronate decarboxylase [EC:4.1.1.35]	Metabolism	
K08679	5	UDP-glucuronate 4-epimerase [EC:5.1.3.6]	Metabolism	
K08680	8	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	Metabolism	
K08681	4	glutamine amidotransferase [EC:2.6.-.-]	Metabolism	
K08682	2	acyl carrier protein phosphodiesterase [EC:3.1.4.14]	Metabolism	
K08686	15	2-chlorobenzoate 1,2-dioxygenase [EC:1.14.12.13]	Metabolism	
K08687	4	N-carbamoylsarcosine amidase [EC:3.5.1.59]	Metabolism	
K08688	9	creatinase [EC:3.5.3.3]	Metabolism	
K08693	4	3'-nucleotidase [EC:3.1.3.6]	Metabolism	
K08710	5	N-isopropylammelide isopropylaminohydrolase [EC:3.5.99.4]	Metabolism	
K08723	4	5'-nucleotidase [EC:3.1.3.5]	Metabolism	
K08724	5	penicillin-binding protein 2B	Metabolism	
K08738	12	cytochrome c	Metabolism	
K08963	23	methylthioribose-1-phosphate isomerase [EC:5.3.1.23]	Metabolism	
K08964	2	methylthioribulose-1-phosphate dehydratase [EC:4.2.1.109]	Metabolism	
K08965	1	2,3-diketo-5-methylthiopentyl-1-phosphate enolase [EC:3.1.3.77]	Metabolism	
K08966	3	2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase	Metabolism	
K08967	4	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase [EC:1.13.11.53	Metabolism	
K08969	1	aminotransferase [EC:2.6.1.-]	Metabolism	
K09007	8	hypothetical protein	Metabolism	
K09011	7	D-citramalate synthase [EC:2.3.1.182]	Metabolism	
K09018	1	putative monooxygenase RutA [EC:1.14.-.-]	Metabolism	
K09019	4	putative NADH dehydrogenase/NAD(P)H nitroreductase RutE [EC:1.-.-.-]	Metabolism	
K09020	6	putative isochorismatase family protein RutB [EC:3.-.-.-]	Metabolism	
K09023	5	protein RutD	Metabolism	
K09024	2	putative flavin reductase RutF [EC:1.5.1.-]	Metabolism	
K09065	3	N-acetylornithine carbamoyltransferase [EC:2.1.3.9]	Metabolism	
K09251	10	putrescine aminotransferase [EC:2.6.1.82]	Metabolism	
K09457	12	7-cyano-7-deazaguanine reductase [EC:1.7.1.13]	Metabolism	
K09458	82	3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]	Metabolism	
K09459	5	phosphonopyruvate decarboxylase [EC:4.1.1.82]	Metabolism	
K09461	29	anthraniloyl-CoA monooxygenase [EC:1.14.13.40]	Metabolism	
K09471	25	gamma-glutamylputrescine oxidase [EC:1.4.3.-]	Metabolism	
K09472	7	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase [EC:1.2.1.-]	Metabolism	
K09474	2	acid phosphatase (class A) [EC:3.1.3.2]	Metabolism	
K09516	1	all-trans-retinol 13,14-reductase [EC:1.3.99.23]	Metabolism	
K09680	3	type II pantothenate kinase [EC:2.7.1.33]	Metabolism	
K09699	12	2-oxoisovalerate dehydrogenase E2 component (dihydrolipoyl	Metabolism	
K09709	9	hypothetical protein	Metabolism	
K09758	10	aspartate 4-decarboxylase [EC:4.1.1.12]	Metabolism	
K09788	41	hypothetical protein	Metabolism	
K09833	1	homogenitisate phytyltransferase	Metabolism	
K09835	2	carotenoid isomerase [EC:5.-.-.-]	Metabolism	
K09845	3	methoxyneurosporene dehydrogenase [EC:1.14.99.-]	Metabolism	
K09846	18	hydroxyneurosporene methyltransferase [EC:2.1.1.-]	Metabolism	
K09879	1	isorenieratene synthase	Metabolism	
K09882	3	cobaltochelatase CobS [EC:6.6.1.2]	Metabolism	
K09883	6	cobaltochelatase CobT [EC:6.6.1.2]	Metabolism	
K09903	23	uridylate kinase [EC:2.7.4.22]	Metabolism	
K10011	7	UDP-GlcUA decarboxylase/UDP-L-Ara4N formyltransferase	Metabolism	
K10012	8	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	Metabolism	
K10026	15	queuosine biosynthesis protein QueE	Metabolism	

K10027	11	phytoene dehydrogenase [EC:1.14.99.-]	Metabolism	
K10206	25	LL-diaminopimelate aminotransferase [EC:2.6.1.83]	Metabolism	
K10209	1	dehydrosqualene desaturase [EC:1.14.99.-]	Metabolism	
K10210	3	4,4'-diaponeurosporene oxidase [EC:1.-.-.-]	Metabolism	
K10215	11	monooxygenase [EC:1.14.13.-]	Metabolism	
K10217	4	aminomuconate-semialdehyde dehydrogenase [EC:1.2.1.32]	Metabolism	
K10218	5	4-hydroxy-4-methyl-2-oxoglutarate aldolase [EC:4.1.3.17]	Metabolism	
K10219	34	4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase	Metabolism	
K10220	52	4-oxalmesaconate hydratase [EC:4.2.1.83]	Metabolism	
K10221	17	2-pyrone-4,6-dicarboxylate lactonase [EC:3.1.1.57]	Metabolism	
K10353	5	deoxyadenosine kinase [EC:2.7.1.76]	Metabolism	
K10533	3	limonene-1,2-epoxide hydrolase [EC:3.3.2.8]	Metabolism	
K10536	12	agmatine deiminase [EC:3.5.3.12]	Metabolism	
K10616	19	p-cymene monooxygenase [EC:1.14.13.-]	Metabolism	
K10617	7	p-cumic alcohol dehydrogenase	Metabolism	
K10618	7	p-cumic aldehyde dehydrogenase	Metabolism	
K10619	17	p-cumate dioxygenase [EC:1.14.12.-]	Metabolism	
K10620	1	2,3-dihydroxy-2,3-dihydro-p-cumate dehydrogenase [EC:1.3.1.58]	Metabolism	
K10621	5	2,3-dihydroxy-p-cumate-3,4-dioxygenase [EC:1.13.11.-]	Metabolism	
K10622	2	HCOMODA decarboxylase [EC:4.1.1.-]	Metabolism	
K10674	2	ectoine hydroxylase [EC:1.14.11.-]	Metabolism	
K10676	13	2,4-dichlorophenol 6-monooxygenase [EC:1.14.13.20]	Metabolism	
K10678	1	nitroreductase [EC:1.-.-.-]	Metabolism	
K10679	1	nitroreductase / dihydropteridine reductase [EC:1.-.-.- 1.5.1.34]	Metabolism	
K10680	11	N-ethylmaleimide reductase [EC:1.-.-.-]	Metabolism	
K10700	13	ethylbenzene hydroxylase [EC:1.17.99.2]	Metabolism	
K10701	20	acetophenone carboxylase [EC:6.4.1.-]	Metabolism	
K10713	1	formaldehyde-activating enzyme [EC:4.3.-.-]	Metabolism	
K10764	12	O-succinylhomoserine sulfhydrylase [EC:2.5.1.-]	Metabolism	
K10774	6	tyrosine ammonia-lyase [EC:4.3.1.23]	Metabolism	
K10775	1	phenylalanine ammonia-lyase [EC:4.3.1.24]	Metabolism	
K10780	3	enoyl-[acyl carrier protein] reductase III [EC:1.3.1.-]	Metabolism	
K10804	10	acyl-CoA thioesterase I [EC:3.1.2.- 3.1.1.5]	Metabolism	
K10805	10	acyl-CoA thioesterase II [EC:3.1.2.-]	Metabolism	
K10806	4	acyl-CoA thioesterase YciA [EC:3.1.2.-]	Metabolism	
K10807	1	ribonucleoside-diphosphate reductase subunit M1 [EC:1.17.4.1]	Metabolism	
K10810	1	transcriptional regulator TenI	Metabolism	
K10815	1	hydrogen cyanide synthase HcnB [EC:1.4.99.5]	Metabolism	
K10816	2	hydrogen cyanide synthase HcnC [EC:1.4.99.5]	Metabolism	
K10817	32	erythronolide synthase [EC:2.3.1.94]	Metabolism	
K11029	4	anthrax edema toxin adenylate cyclase [EC:4.6.1.1]	Metabolism	
K11175	32	phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]	Metabolism	
K11177	61	xanthine dehydrogenase YagR molybdenum-binding subunit [EC:1.17.1.4]	Metabolism	
K11178	19	xanthine dehydrogenase YagS FAD-binding subunit [EC:1.17.1.4]	Metabolism	
K11180	3	sulfite reductase, dissimilatory-type alpha subunit [EC:1.8.99.3]	Metabolism	
K11181	3	sulfite reductase, dissimilatory-type beta subunit [EC:1.8.99.3]	Metabolism	
K11192	1	PTS system, N-acetylmuramic acid-specific IIC component	Metabolism	
K11212	20	LPPG:FO 2-phospho-L-lactate transferase [EC:2.7.8.-]	Metabolism	
K11258	2	acetolactate synthase II small subunit [EC:2.2.1.6]	Metabolism	
K11261	6	formylmethanofuran dehydrogenase subunit E [EC:1.2.99.5]	Metabolism	
K11263	26	acetyl-/propionyl-CoA carboxylase, biotin carboxylase, biotin	Metabolism	
K11264	2	methylmalonyl-CoA decarboxylase [EC:4.1.1.41]	Metabolism	
K11311	2	anthranilate dioxygenase reductase	Metabolism	
K11333	1	chlorophyllide reductase iron protein subunit X [EC:1.18.6.1]	Metabolism	
K11337	3	3-hydroxyethyl bacteriochlorophyllide a dehydrogenase [EC:1.-.-.-]	Metabolism	
K11358	4	aspartate aminotransferase [EC:2.6.1.1]	Metabolism	
K11381	62	2-oxoisovalerate dehydrogenase E1 component [EC:1.2.4.4]	Metabolism	

K11472	15	glycolate oxidase FAD binding subunit	Metabolism	
K11473	36	glycolate oxidase iron-sulfur subunit	Metabolism	
K11528	4	UDP-N-acetylglucosamine pyrophosphorylase [EC:2.7.7.23]	Metabolism	
K11532	1	fructose-1,6-bisphosphatase II / sedoheptulose-1,7-bisphosphatase	Metabolism	
K11533	1	fatty acid synthase, bacteria type [EC:2.3.1.-]	Metabolism	
K11646	1	dehydroquinate synthase II [EC:1.4.1.-]	Metabolism	
K11693	2	peptidoglycan pentaglycine glycine transferase (the first glycine)	Metabolism	
K11717	72	cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]	Metabolism	
K11731	6	citronellyl-CoA dehydrogenase [EC:1.3.99.-]	Metabolism	
K11751	4	5'-nucleotidase / UDP-sugar diphosphatase [EC:3.1.3.5 3.6.1.45]	Metabolism	
K11752	32	diaminohydroxyphosphoribosylaminopyrimidine deaminase /	Metabolism	
K11753	31	riboflavin kinase / FMN adenylyltransferase [EC:2.7.1.26 2.7.7.2]	Metabolism	
K11754	47	dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12	Metabolism	
K11755	12	phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP	Metabolism	
K11779	20	FO synthase [EC:2.5.1.-]	Metabolism	
K11781	1	FO synthase subunit 2 [EC:2.5.1.-]	Metabolism	
K11782	5	chorismate futalosine-lyase [EC:4.1.99.-]	Metabolism	
K11784	17	de-hypoxanthine futalosine synthase [EC:1.21.-.-]	Metabolism	
K11785	2	1,4-dihydroxy-6-naphthoate synthase [EC:1.14.-.-]	Metabolism	
K11942	14	methylmalonyl-CoA mutase [EC:5.4.99.2]	Metabolism	
K11948	2	1-hydroxy-2-naphthoate dioxygenase [EC:1.13.11.38]	Metabolism	
K11949	1	4-(2-carboxyphenyl)-2-oxobut-3-enoate aldolase [EC:4.1.2.34]	Metabolism	
K11987	1	prostaglandin-endoperoxide synthase 2 [EC:1.14.99.1]	Metabolism	
K12073	3	1,4-dihydroxy-2-naphthoyl-CoA thioesterase [EC:3.1.2.-]	Metabolism	
K12111	2	evolved beta-galactosidase subunit alpha [EC:3.2.1.23]	Metabolism	
K12234	9	F420-0:gamma-glutamyl ligase [EC:6.3.2.-]	Metabolism	
K12238	5	pyochelin biosynthesis protein PchD	Metabolism	
K12240	1	pyochelin synthetase	Metabolism	
K12251	28	N-carbamoylputrescine amidase [EC:3.5.1.53]	Metabolism	
K12252	2	arginine:pyruvate transaminase [EC:2.6.1.84]	Metabolism	
K12253	4	5-guanidino-2-oxopentanoate decarboxylase [EC:4.1.1.75]	Metabolism	
K12254	3	4-guanidinobutyraldehyde dehydrogenase / NAD-dependent aldehyde	Metabolism	
K12255	4	guanidinobutyrase [EC:3.5.3.7]	Metabolism	
K12256	7	putrescine aminotransferase [EC:2.6.1.-]	Metabolism	
K12308	35	beta-galactosidase [EC:3.2.1.23]	Metabolism	
K12339	16	cysteine synthase B [EC:2.5.1.47]	Metabolism	
K12343	4	3-oxo-5-alpha-steroid 4-dehydrogenase 1 [EC:1.3.99.5]	Metabolism	
K12344	4	3-oxo-5-alpha-steroid 4-dehydrogenase 2 [EC:1.3.99.5]	Metabolism	
K12373	31	beta-hexosaminidase [EC:3.2.1.52]	Metabolism	
K12420	16	ketoacyl reductase [EC:1.3.1.-]	Metabolism	
K12452	6	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	Metabolism	
K12454	22	CDP-paratose 2-epimerase [EC:5.1.3.10]	Metabolism	
K12503	5	short-chain Z-isoprenyl diphosphate synthase [EC:2.5.1.68]	Metabolism	
K12506	29	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase /	Metabolism	
K12524	14	bifunctional aspartokinase/homoserine dehydrogenase 1 [EC:2.7.2.4	Metabolism	
K12525	1	bifunctional aspartokinase/homoserine dehydrogenase 2 [EC:2.7.2.4	Metabolism	
K12526	1	bifunctional diaminopimelate decarboxylase/aspartate kinase	Metabolism	
K12527	2	putative selenate reductase [EC:1.97.1.9]	Metabolism	
K12528	2	putative selenate reductase molybdopterin-binding subunit	Metabolism	
K12555	1	penicillin-binding protein 2A [EC:2.4.1.129 2.3.2.-]	Metabolism	
K12645	13	epi-isozizaene 5-monooxygenase [EC:1.14.13.106]	Metabolism	
K12658	5	4-hydroxyproline epimerase [EC:5.1.1.8]	Metabolism	
K12660	5	2-dehydro-3-deoxy-L-rhamnonate aldolase [EC:4.1.2.-]	Metabolism	
K12661	1	L-rhamnonate dehydratase [EC:4.2.1.90]	Metabolism	
K12673	2	N2-(2-carboxyethyl)arginine synthase [EC:2.5.1.66]	Metabolism	
K12960	17	5-methylthioadenosine/S-adenosylhomocysteine deaminase	Metabolism	
K12972	5	gyoxylate/hydroxypyruvate reductase A [EC:1.1.1.79 1.1.1.81]	Metabolism	

K13010	16	perosamine synthetase	Metabolism	
K13014	2	undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]	Metabolism	
K13015	28	UDP-N-acetyl-D-glucosamine dehydrogenase [EC:1.1.1.-]	Metabolism	
K13016	1	UDP-D-GlcNAcA oxidase [EC:1.1.1.-]	Metabolism	
K13017	16	UDP-3-keto-D-GlcNAcA aminotransferase [EC:2.6.1.-]	Metabolism	
K13018	4	UDP-D-GlcNAc3NA acetyltransferase [EC:2.3.1.-]	Metabolism	
K13019	9	UDP-GlcNAc3NAcA epimerase [EC:5.1.3.23]	Metabolism	
K13020	21	UDP-D-GlcNAcA oxidase [EC:1.1.1.-]	Metabolism	
K13038	42	phosphopantothenoylcysteine decarboxylase /	Metabolism	
K13039	5	sulfopyruvate decarboxylase subunit beta [EC:4.1.1.79]	Metabolism	
K13042	2	dimethylglycine N-methyltransferase [EC:2.1.1.161]	Metabolism	
K13057	14	trehalose synthase [EC:2.4.1.245]	Metabolism	
K13317	3	NDP-4-keto-2,6-dideoxyhexose 3-C-methyltransferase	Metabolism	
K13318	6	dTDP-4-keto-6-deoxy-L-hexose 4-reductase	Metabolism	
K13378	29	NADH dehydrogenase I subunit C/D [EC:1.6.5.3]	Metabolism	
K13380	1	NADH dehydrogenase I subunit B/C/D [EC:1.6.5.3]	Metabolism	
K13421	1	uridine monophosphate synthetase [EC:2.4.2.10 4.1.1.23]	Metabolism	
K13479	1	xanthine dehydrogenase FAD-binding subunit [EC:1.17.1.4]	Metabolism	
K13481	2	xanthine dehydrogenase small subunit [EC:1.17.1.4]	Metabolism	
K13482	10	xanthine dehydrogenase large subunit [EC:1.17.1.4]	Metabolism	
K13483	14	xanthine dehydrogenase YagT iron-sulfur-binding subunit	Metabolism	
K13497	7	anthranilate synthase/phosphoribosyltransferase [EC:4.1.3.27	Metabolism	
K13498	7	indole-3-glycerol phosphate synthase / phosphoribosylanthranilate	Metabolism	
K13500	1	chondroitin synthase [EC:2.4.1.175 2.4.1.226]	Metabolism	
K13503	3	anthranilate synthase [EC:4.1.3.27]	Metabolism	
K13522	2	bifunctional NMN adenylyltransferase/nudix hydrolase [EC:2.7.7.1	Metabolism	
K13540	2	precorrin-2 C20-methyltransferase / precorrin-3B	Metabolism	
K13541	3	cobalamin biosynthesis protein CbiG / precorrin-3B	Metabolism	
K13542	25	uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107	Metabolism	
K13543	6	uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107	Metabolism	
K13601	26	bacteriochlorophyll C8 methyltransferase [EC:2.1.1.-]	Metabolism	
K13602	20	bacteriochlorophyll C12 methyltransferase [EC:2.1.1.-]	Metabolism	
K13604	7	bacteriochlorophyll C20 methyltransferase [EC:2.1.1.-]	Metabolism	
K13607	4	cinnamoyl-CoA:phenyllactate CoA-transferase [EC:2.8.3.17]	Metabolism	
K13745	5	L-2,4-diaminobutyrate decarboxylase [EC:4.1.1.86]	Metabolism	
K13746	1	carboxynorspermidine dehydrogenase	Metabolism	
K13747	2	carboxynorspermidine decarboxylase [EC:4.1.1.-]	Metabolism	
K13766	13	methylglutaconyl-CoA hydratase [EC:4.2.1.18]	Metabolism	
K13767	5	enoyl-CoA hydratase [EC:4.2.1.17]	Metabolism	
K13774	3	citronellol/citronellal dehydrogenase	Metabolism	
K13775	5	citronellol/citronellal dehydrogenase	Metabolism	
K13776	1	citronellyl-CoA synthetase [EC:6.2.1.-]	Metabolism	
K13777	1	geranyl-CoA carboxylase alpha subunit [EC:6.4.1.5]	Metabolism	
K13778	4	geranyl-CoA carboxylase beta subunit [EC:6.4.1.5]	Metabolism	
K13787	9	geranylgeranyl diphosphate synthase, type I [EC:2.5.1.1 2.5.1.10	Metabolism	
K13788	5	phosphate acetyltransferase [EC:2.3.1.8]	Metabolism	
K13789	15	geranylgeranyl diphosphate synthase, type II [EC:2.5.1.1 2.5.1.10	Metabolism	
K13797	2	DNA-directed RNA polymerase subunit beta-beta' [EC:2.7.7.6]	Metabolism	
K13799	8	pantoate ligase / cytidylate kinase [EC:6.3.2.1 2.7.4.14]	Metabolism	
K13810	14	transaldolase / glucose-6-phosphate isomerase [EC:2.2.1.2 5.3.1.9]	Metabolism	
K13811	3	3'-phosphoadenosine 5'-phosphosulfate synthase [EC:2.7.7.4 2.7.1.25]	Metabolism	
K13821	28	proline dehydrogenase / delta 1-pyrroline-5-carboxylate	Metabolism	
K13829	16	shikimate kinase / 3-dehydroquinate synthase [EC:2.7.1.71 4.2.3.4]	Metabolism	
K13832	9	3-dehydroquinate dehydratase / shikimate dehydrogenase [EC:4.2.1.10	Metabolism	
K13874	3	L-arabinonolactonase [EC:3.1.1.15]	Metabolism	
K13875	7	L-arabonate dehydrase [EC:4.2.1.25]	Metabolism	
K13876	5	2-keto-3-deoxy-L-arabinonate dehydratase [EC:4.2.1.43]	Metabolism	

K13919	1	propanediol dehydratase medium subunit [EC:4.2.1.28]	Metabolism	
K13922	1	propionaldehyde dehydrogenase	Metabolism	
K13940	13	dihydroneopterin aldolase /	Metabolism	
K13950	9	para-aminobenzoate synthetase [EC:2.6.1.85]	Metabolism	
K13953	52	alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]	Metabolism	
K13954	5	alcohol dehydrogenase [EC:1.1.1.1]	Metabolism	
K13990	19	glutamate formiminotransferase / formiminotetrahydrofolate	Metabolism	
K13995	2	maleamate amidohydrolase [EC:3.5.1.107]	Metabolism	

KEGG ID	Sequences	KEGG pathway	KEGG category	
K00021	14	3-hydroxy-3-methylglutaryl-CoA reductase [EC:1.1.1.34]	Environmental Information Processing	
K00027	40	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]	Environmental Information Processing	
K00066	25	GDP-mannose 6-dehydrogenase [EC:1.1.1.132]	Environmental Information Processing	
K00134	29	glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	Environmental Information Processing	
K00157	22	aldehyde oxidase [EC:1.2.3.1]	Environmental Information Processing	
K00161	65	pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	Environmental Information Processing	
K00162	66	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]	Environmental Information Processing	
K00232	1	acyl-CoA oxidase [EC:1.3.3.6]	Environmental Information Processing	
K00244	39	fumarate reductase flavoprotein subunit [EC:1.3.99.1]	Environmental Information Processing	
K00245	7	fumarate reductase iron-sulfur protein [EC:1.3.99.1]	Environmental Information Processing	
K00246	13	fumarate reductase subunit C [EC:1.3.99.1]	Environmental Information Processing	
K00247	5	fumarate reductase subunit D [EC:1.3.99.1]	Environmental Information Processing	
K00370	34	nitrate reductase 1, alpha subunit [EC:1.7.99.4]	Environmental Information Processing	
K00371	12	nitrate reductase 1, beta subunit [EC:1.7.99.4]	Environmental Information Processing	
K00373	4	nitrate reductase 1, delta subunit [EC:1.7.99.4]	Environmental Information Processing	
K00374	4	nitrate reductase 1, gamma subunit [EC:1.7.99.4]	Environmental Information Processing	
K00404	16	cb-type cytochrome c oxidase subunit I [EC:1.9.3.1]	Environmental Information Processing	
K00405	17	cb-type cytochrome c oxidase subunit II [EC:1.9.3.1]	Environmental Information Processing	
K00406	34	cb-type cytochrome c oxidase subunit III [EC:1.9.3.1]	Environmental Information Processing	
K00407	6	cb-type cytochrome c oxidase subunit IV [EC:1.9.3.1]	Environmental Information Processing	
K00411	10	ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.2]	Environmental Information Processing	
K00412	35	ubiquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.2]	Environmental Information Processing	
K00413	8	ubiquinol-cytochrome c reductase cytochrome c1 subunit [EC:1.10.2.2]	Environmental Information Processing	
K00425	39	cytochrome bd-I oxidase subunit I [EC:1.10.3.-]	Environmental Information Processing	
K00426	23	cytochrome bd-I oxidase subunit II [EC:1.10.3.-]	Environmental Information Processing	
K00494	70	alkanal monooxygenase (FMN-linked) [EC:1.14.14.3]	Environmental Information Processing	
K00507	40	stearoyl-CoA desaturase (delta-9 desaturase) [EC:1.14.19.1]	Environmental Information Processing	
K00575	79	chemotaxis protein methyltransferase CheR [EC:2.1.1.80]	Environmental Information Processing	
K00626	211	acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	Environmental Information Processing	
K00654	7	serine palmitoyltransferase [EC:2.3.1.50]	Environmental Information Processing	
K00693	14	glycogen(starch) synthase [EC:2.4.1.11]	Environmental Information Processing	
K00850	56	6-phosphofructokinase [EC:2.7.1.11]	Environmental Information Processing	
K00901	6	diacylglycerol kinase [EC:2.7.1.107]	Environmental Information Processing	
K00981	27	phosphatidate cytidylyltransferase [EC:2.7.7.41]	Environmental Information Processing	
K00990	45	[protein-PII] uridylyltransferase [EC:2.7.7.59]	Environmental Information Processing	
K00999	4	CDP-diacylglycerol--inositol 3-phosphatidyltransferase [EC:2.7.8.11]	Environmental Information Processing	
K01035	2	acetate CoA-transferase beta subunit [EC:2.8.3.8]	Environmental Information Processing	
K01077	90	alkaline phosphatase [EC:3.1.3.1]	Environmental Information Processing	
K01092	58	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]	Environmental Information Processing	
K01103	1	fructose-2,6-bisphosphatase [EC:3.1.3.46]	Environmental Information Processing	
K01113	42	phosphodiesterase/alkaline phosphatase D [EC:3.1.4.1]	Environmental Information Processing	
K01115	8	phospholipase D [EC:3.1.4.4]	Environmental Information Processing	
K01312	9	trypsin [EC:3.4.21.4]	Environmental Information Processing	
K01467	153	beta-lactamase [EC:3.5.2.6]	Environmental Information Processing	
K01539	6	sodium/potassium-transporting ATPase subunit alpha [EC:3.6.3.9]	Environmental Information Processing	
K01546	18	K+-transporting ATPase ATPase A chain [EC:3.6.3.12]	Environmental Information Processing	
K01547	19	K+-transporting ATPase ATPase B chain [EC:3.6.3.12]	Environmental Information Processing	
K01548	14	K+-transporting ATPase ATPase C chain [EC:3.6.3.12]	Environmental Information Processing	
K01578	19	malonyl-CoA decarboxylase [EC:4.1.1.9]	Environmental Information Processing	
K01596	30	phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]	Environmental Information Processing	
K01634	7	sphinganine-1-phosphate aldolase [EC:4.1.2.27]	Environmental Information Processing	
K01643	11	citrate lyase subunit alpha / citrate CoA-transferase [EC:4.1.3.6	Environmental Information Processing	
K01644	42	citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.6 4.1.3.34]	Environmental Information Processing	
K01689	42	enolase [EC:4.2.1.11]	Environmental Information Processing	
K01915	141	glutamine synthetase [EC:6.3.1.2]	Environmental Information Processing	
K01995	126	branched-chain amino acid transport system ATP-binding protein	Environmental Information Processing	
K01996	125	branched-chain amino acid transport system ATP-binding protein	Environmental Information Processing	
K01997	153	branched-chain amino acid transport system permease protein	Environmental Information Processing	
K01998	326	branched-chain amino acid transport system permease protein	Environmental Information Processing	
K01999	254	branched-chain amino acid transport system substrate-binding protein	Environmental Information Processing	
K02000	5	glycine betaine/proline transport system ATP-binding protein	Environmental Information Processing	
K02001	2	glycine betaine/proline transport system permease protein	Environmental Information Processing	
K02002	2	glycine betaine/proline transport system substrate-binding protein	Environmental Information Processing	
K02006	28	cobalt/nickel transport system ATP-binding protein	Environmental Information Processing	
K02007	5	cobalt/nickel transport system permease protein	Environmental Information Processing	
K02008	17	cobalt/nickel transport system permease protein	Environmental Information Processing	
K02010	19	iron(III) transport system ATP-binding protein [EC:3.6.3.30]	Environmental Information Processing	
K02011	71	iron(III) transport system permease protein	Environmental Information Processing	
K02012	46	iron(III) transport system substrate-binding protein	Environmental Information Processing	

K02013	25	iron complex transport system ATP-binding protein [EC:3.6.3.34]	Environmental Information Processing	
K02015	23	iron complex transport system permease protein	Environmental Information Processing	
K02016	43	iron complex transport system substrate-binding protein	Environmental Information Processing	
K02017	11	molybdate transport system ATP-binding protein [EC:3.6.3.29]	Environmental Information Processing	
K02018	15	molybdate transport system permease protein	Environmental Information Processing	
K02020	55	molybdate transport system substrate-binding protein	Environmental Information Processing	
K02036	24	phosphate transport system ATP-binding protein [EC:3.6.3.27]	Environmental Information Processing	
K02037	43	phosphate transport system permease protein	Environmental Information Processing	
K02038	42	phosphate transport system permease protein	Environmental Information Processing	
K02040	62	phosphate transport system substrate-binding protein	Environmental Information Processing	
K02041	11	phosphonate transport system ATP-binding protein	Environmental Information Processing	
K02042	4	phosphonate transport system permease protein	Environmental Information Processing	
K02044	24	phosphonate transport system substrate-binding protein	Environmental Information Processing	
K02045	11	sulfate transport system ATP-binding protein [EC:3.6.3.25]	Environmental Information Processing	
K02046	14	sulfate transport system permease protein	Environmental Information Processing	
K02047	9	sulfate transport system permease protein	Environmental Information Processing	
K02048	16	sulfate transport system substrate-binding protein	Environmental Information Processing	
K02063	7	thiamine transport system permease protein	Environmental Information Processing	
K02064	3	thiamine transport system substrate-binding protein	Environmental Information Processing	
K02065	37	putative ABC transport system ATP-binding protein	Environmental Information Processing	
K02066	51	putative ABC transport system permease protein	Environmental Information Processing	
K02067	57	putative ABC transport system substrate-binding protein	Environmental Information Processing	
K02071	4	D-methionine transport system ATP-binding protein	Environmental Information Processing	
K02073	2	D-methionine transport system substrate-binding protein	Environmental Information Processing	
K02106	4	short-chain fatty acids transporter	Environmental Information Processing	
K02193	29	heme exporter protein A [EC:3.6.3.41]	Environmental Information Processing	
K02194	15	heme exporter protein B	Environmental Information Processing	
K02195	42	heme exporter protein C	Environmental Information Processing	
K02259	27	cytochrome c oxidase subunit XV assembly protein	Environmental Information Processing	
K02313	51	chromosomal replication initiator protein	Environmental Information Processing	
K02402	1	flagellar transcriptional activator FlhC	Environmental Information Processing	
K02405	21	RNA polymerase sigma factor for flagellar operon FliA	Environmental Information Processing	
K02406	10	flagellin	Environmental Information Processing	
K02424	2	cystine transport system substrate-binding protein	Environmental Information Processing	
K02452	1	general secretion pathway protein C	Environmental Information Processing	
K02453	90	general secretion pathway protein D	Environmental Information Processing	
K02454	48	general secretion pathway protein E	Environmental Information Processing	
K02455	102	general secretion pathway protein F	Environmental Information Processing	
K02456	16	general secretion pathway protein G	Environmental Information Processing	
K02457	2	general secretion pathway protein H	Environmental Information Processing	
K02458	2	general secretion pathway protein I	Environmental Information Processing	
K02459	2	general secretion pathway protein J	Environmental Information Processing	
K02460	10	general secretion pathway protein K	Environmental Information Processing	
K02461	7	general secretion pathway protein L	Environmental Information Processing	
K02464	6	general secretion pathway protein O [EC:3.4.23.43 2.1.1.-]	Environmental Information Processing	
K02471	16	putative ATP-binding cassette transporter	Environmental Information Processing	
K02487	1	type IV pili sensor histidine kinase and response regulator	Environmental Information Processing	
K02488	217	two-component system, cell cycle response regulator	Environmental Information Processing	
K02489	49	two-component system, cell cycle sensor kinase and response	Environmental Information Processing	
K02490	30	two-component system, response regulator, stage 0 sporulation	Environmental Information Processing	
K02491	8	two-component system, sporulation sensor kinase A [EC:2.7.13.3]	Environmental Information Processing	
K02556	5	chemotaxis protein MotA	Environmental Information Processing	
K02584	38	Nif-specific regulatory protein	Environmental Information Processing	
K02650	7	type IV pilus assembly protein PilA	Environmental Information Processing	
K02657	13	twitching motility two-component system response regulator PilG	Environmental Information Processing	
K02658	37	twitching motility two-component system response regulator PilH	Environmental Information Processing	
K02659	5	twitching motility protein PilI	Environmental Information Processing	
K02660	18	twitching motility protein PilJ	Environmental Information Processing	
K02661	2	type IV pilus assembly protein PilK	Environmental Information Processing	
K02667	64	two-component system, NtrC family, response regulator PilR	Environmental Information Processing	
K02668	66	two-component system, NtrC family, sensor histidine kinase PilS	Environmental Information Processing	
K02745	1	PTS system, N-acetylgalactosamine-specific IIB component	Environmental Information Processing	
K02755	1	PTS system, beta-glucosides-specific IIA component [EC:2.7.1.69]	Environmental Information Processing	
K02759	4	PTS system, cellobiose-specific IIA component [EC:2.7.1.69]	Environmental Information Processing	
K02761	9	PTS system, cellobiose-specific IIC component	Environmental Information Processing	
K02765	3	PTS system, D-glucosamine-specific IIC component	Environmental Information Processing	
K02768	6	PTS system, fructose-specific IIA component [EC:2.7.1.69]	Environmental Information Processing	
K02769	1	PTS system, fructose-specific IIB component [EC:2.7.1.69]	Environmental Information Processing	
K02770	12	PTS system, fructose-specific IIC component	Environmental Information Processing	

K02774	5	PTS system, galactitol-specific IIB component [EC:2.7.1.69]	Environmental Information Processing	
K02775	2	PTS system, galactitol-specific IIC component	Environmental Information Processing	
K02777	109	PTS system, glucose-specific IIA component [EC:2.7.1.69]	Environmental Information Processing	
K02779	2	PTS system, glucose-specific IIC component	Environmental Information Processing	
K02784	4	phosphocarrier protein HPr	Environmental Information Processing	
K02793	6	PTS system, mannose-specific IIA component [EC:2.7.1.69]	Environmental Information Processing	
K02794	3	PTS system, mannose-specific IIB component [EC:2.7.1.69]	Environmental Information Processing	
K02795	3	PTS system, mannose-specific IIC component	Environmental Information Processing	
K02796	6	PTS system, mannose-specific IID component	Environmental Information Processing	
K02799	2	PTS system, mannitol-specific IIB component [EC:2.7.1.69]	Environmental Information Processing	
K02800	3	PTS system, mannitol-specific IIC component	Environmental Information Processing	
K02804	1	PTS system, N-acetylglucosamine-specific IIC component	Environmental Information Processing	
K02806	15	PTS system, nitrogen regulatory IIA component [EC:2.7.1.69]	Environmental Information Processing	
K02821	9	PTS system, ascorbate-specific IIA component [EC:2.7.1.69]	Environmental Information Processing	
K03070	74	preprotein translocase subunit SecA	Environmental Information Processing	
K03071	7	preprotein translocase subunit SecB	Environmental Information Processing	
K03072	476	preprotein translocase subunit SecD	Environmental Information Processing	
K03073	2	preprotein translocase subunit SecE	Environmental Information Processing	
K03074	41	preprotein translocase subunit SecF	Environmental Information Processing	
K03075	3	preprotein translocase subunit SecG	Environmental Information Processing	
K03076	36	preprotein translocase subunit SecY	Environmental Information Processing	
K03092	47	RNA polymerase sigma-54 factor	Environmental Information Processing	
K03106	47	signal recognition particle subunit SRP54	Environmental Information Processing	
K03110	23	fused signal recognition particle receptor	Environmental Information Processing	
K03116	10	sec-independent protein translocase protein TatA	Environmental Information Processing	
K03117	4	sec-independent protein translocase protein TatB	Environmental Information Processing	
K03118	57	sec-independent protein translocase protein TatC	Environmental Information Processing	
K03196	1	type IV secretion system protein VirB11	Environmental Information Processing	
K03197	2	type IV secretion system protein VirB2	Environmental Information Processing	
K03198	1	type IV secretion system protein VirB3	Environmental Information Processing	
K03199	8	type IV secretion system protein VirB4	Environmental Information Processing	
K03200	1	type IV secretion system protein VirB5	Environmental Information Processing	
K03201	2	type IV secretion system protein VirB6	Environmental Information Processing	
K03205	7	type IV secretion system protein VirD4	Environmental Information Processing	
K03210	16	preprotein translocase subunit YajC	Environmental Information Processing	
K03217	71	preprotein translocase subunit YidC	Environmental Information Processing	
K03219	1	type III secretion protein SctC	Environmental Information Processing	
K03221	1	type III secretion protein SctF	Environmental Information Processing	
K03222	3	type III secretion protein SctJ	Environmental Information Processing	
K03223	1	type III secretion protein SctL	Environmental Information Processing	
K03224	1	ATP synthase in type III secretion protein SctN [EC:3.6.3.14]	Environmental Information Processing	
K03225	2	type III secretion protein SctQ	Environmental Information Processing	
K03227	2	type III secretion protein SctS	Environmental Information Processing	
K03228	2	type III secretion protein SctT	Environmental Information Processing	
K03229	1	type III secretion protein SctU	Environmental Information Processing	
K03230	2	type III secretion protein SctV	Environmental Information Processing	
K03367	32	D-alanine-poly(phosphoribitol) ligase [EC:6.1.1.13]	Environmental Information Processing	
K03406	186	methyl-accepting chemotaxis protein	Environmental Information Processing	
K03407	82	two-component system, chemotaxis family, sensor kinase CheA	Environmental Information Processing	
K03408	21	purine-binding chemotaxis protein CheW	Environmental Information Processing	
K03412	64	two-component system, chemotaxis family, response regulator CheB	Environmental Information Processing	
K03413	117	two-component system, chemotaxis family, response regulator CheY	Environmental Information Processing	
K03475	1	PTS system, ascorbate-specific IIC component	Environmental Information Processing	
K03523	5	putative biotin biosynthesis protein BioY	Environmental Information Processing	
K03532	3	trimethylamine-N-oxide reductase (cytochrome c) 1, cytochrome c-type	Environmental Information Processing	
K03563	5	carbon storage regulator	Environmental Information Processing	
K03620	12	Ni/Fe-hydrogenase 1 B-type cytochrome subunit	Environmental Information Processing	
K03740	1	D-alanine transfer protein	Environmental Information Processing	
K03776	16	aerotaxis receptor	Environmental Information Processing	
K03781	12	catalase [EC:1.11.1.6]	Environmental Information Processing	
K03841	11	fructose-1,6-bisphosphatase I [EC:3.1.3.11]	Environmental Information Processing	
K04079	17	molecular chaperone HtpG	Environmental Information Processing	
K04496	9	C-terminal binding protein	Environmental Information Processing	
K04564	27	superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	Environmental Information Processing	
K04751	13	nitrogen regulatory protein P-II 1	Environmental Information Processing	
K04771	6	serine protease Do [EC:3.4.21.107]	Environmental Information Processing	
K05338	12	holin-like protein	Environmental Information Processing	
K05339	1	holin-like protein LrgB	Environmental Information Processing	
K05597	1	glutamin-(asparagin-)ase [EC:3.5.1.38]	Environmental Information Processing	

K05685	60	macrolide transport system ATP-binding/permease protein [EC:3.6.3.-]	Environmental Information Processing	
K05692	2	actin beta/gamma 1	Environmental Information Processing	
K05772	8	putative tungstate transport system substrate-binding protein	Environmental Information Processing	
K05773	8	putative tungstate transport system permease protein	Environmental Information Processing	
K05776	4	molybdate transport system ATP-binding protein	Environmental Information Processing	
K05813	23	sn-glycerol 3-phosphate transport system substrate-binding protein	Environmental Information Processing	
K05814	17	sn-glycerol 3-phosphate transport system permease protein	Environmental Information Processing	
K05815	10	sn-glycerol 3-phosphate transport system permease protein	Environmental Information Processing	
K05816	7	sn-glycerol 3-phosphate transport system ATP-binding protein	Environmental Information Processing	
K05845	22	osmoprotectant transport system substrate-binding protein	Environmental Information Processing	
K05846	27	osmoprotectant transport system permease protein	Environmental Information Processing	
K05847	6	osmoprotectant transport system ATP-binding protein	Environmental Information Processing	
K05874	21	methyl-accepting chemotaxis protein I, serine sensor receptor	Environmental Information Processing	
K05875	8	methyl-accepting chemotaxis protein II, aspartate sensor receptor	Environmental Information Processing	
K05876	2	methyl-accepting chemotaxis protein III, ribose and galactose sensor	Environmental Information Processing	
K06596	35	chemosensory pili system protein ChpA (sensor histidine	Environmental Information Processing	
K06726	1	D-ribose pyranase [EC:5.-.-.-]	Environmental Information Processing	
K06857	10	putative tungstate transport system ATP-binding protein	Environmental Information Processing	
K06858	8	vitamin B12 transport system substrate-binding protein	Environmental Information Processing	
K06861	16	lipopolysaccharide export system ATP-binding protein [EC:3.6.3.-]	Environmental Information Processing	
K07091	25	lipopolysaccharide export system permease protein	Environmental Information Processing	
K07122	1	Unclassified; K07122	Environmental Information Processing	
K07260	7	D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4]	Environmental Information Processing	
K07323	15	putative toluene tolerance protein	Environmental Information Processing	
K07636	65	two-component system, OmpR family, phosphate regulon sensor	Environmental Information Processing	
K07637	1	two-component system, OmpR family, sensor histidine kinase PhoQ	Environmental Information Processing	
K07638	12	two-component system, OmpR family, osmolarity sensor histidine	Environmental Information Processing	
K07639	2	two-component system, OmpR family, sensor histidine kinase RstB	Environmental Information Processing	
K07640	6	two-component system, OmpR family, sensor histidine kinase CpxA	Environmental Information Processing	
K07641	4	two-component system, OmpR family, sensor histidine kinase CreC	Environmental Information Processing	
K07642	11	two-component system, OmpR family, sensor histidine kinase BaeS	Environmental Information Processing	
K07643	3	two-component system, OmpR family, sensor histidine kinase BasS	Environmental Information Processing	
K07644	26	two-component system, OmpR family, heavy metal sensor histidine	Environmental Information Processing	
K07645	33	two-component system, OmpR family, sensor histidine kinase QseC	Environmental Information Processing	
K07646	67	two-component system, OmpR family, sensor histidine kinase KdpD	Environmental Information Processing	
K07647	4	two-component system, OmpR family, sensor histidine kinase TorS	Environmental Information Processing	
K07648	1	two-component system, OmpR family, aerobic respiration control	Environmental Information Processing	
K07649	29	two-component system, OmpR family, sensor histidine kinase TctE	Environmental Information Processing	
K07651	11	two-component system, OmpR family, sensor histidine kinase ResE	Environmental Information Processing	
K07652	42	two-component system, OmpR family, sensor histidine kinase VicK	Environmental Information Processing	
K07653	6	two-component system, OmpR family, sensor histidine kinase MprB	Environmental Information Processing	
K07654	5	two-component system, OmpR family, sensor histidine kinase MtrB	Environmental Information Processing	
K07656	1	two-component system, OmpR family, sensor histidine kinase TrcS	Environmental Information Processing	
K07657	68	two-component system, OmpR family, phosphate regulon response	Environmental Information Processing	
K07658	67	two-component system, OmpR family, alkaline phosphatase synthesis	Environmental Information Processing	
K07659	12	two-component system, OmpR family, phosphate regulon response	Environmental Information Processing	
K07660	1	two-component system, OmpR family, response regulator PhoP	Environmental Information Processing	
K07661	1	two-component system, OmpR family, response regulator RstA	Environmental Information Processing	
K07662	5	two-component system, OmpR family, response regulator CpxR	Environmental Information Processing	
K07663	1	two-component system, OmpR family, catabolic regulation response	Environmental Information Processing	
K07664	5	two-component system, OmpR family, response regulator BaeR	Environmental Information Processing	
K07665	23	two-component system, OmpR family, copper resistance phosphate	Environmental Information Processing	
K07666	3	two-component system, OmpR family, response regulator QseB	Environmental Information Processing	
K07667	53	two-component system, OmpR family, KDP operon response regulator	Environmental Information Processing	
K07668	44	two-component system, OmpR family, response regulator VicR	Environmental Information Processing	
K07669	30	two-component system, OmpR family, response regulator MprA	Environmental Information Processing	
K07670	18	two-component system, OmpR family, response regulator MtrA	Environmental Information Processing	
K07671	1	two-component system, OmpR family, response regulator PrrA	Environmental Information Processing	
K07672	1	two-component system, OmpR family, response regulator TrcR	Environmental Information Processing	
K07673	10	two-component system, NarL family, nitrate/nitrite sensor histidine	Environmental Information Processing	
K07674	4	two-component system, NarL family, nitrate/nitrite sensor histidine	Environmental Information Processing	
K07675	49	two-component system, NarL family, sensor histidine kinase UhpB	Environmental Information Processing	
K07677	11	two-component system, NarL family, capsular synthesis sensor	Environmental Information Processing	
K07678	26	two-component system, NarL family, sensor histidine kinase BarA	Environmental Information Processing	
K07679	4	two-component system, NarL family, sensor histidine kinase EvgS	Environmental Information Processing	
K07680	15	two-component system, NarL family, sensor histidine kinase ComP	Environmental Information Processing	
K07681	1	two-component system, NarL family, vancomycin resistance sensor	Environmental Information Processing	
K07682	15	two-component system, NarL family, sensor histidine kinase DevS	Environmental Information Processing	
K07683	4	two-component system, NarL family, sensor histidine kinase NreB	Environmental Information Processing	

K07684	73	two-component system, NarL family, nitrate/nitrite response	Environmental Information Processing	
K07685	6	two-component system, NarL family, nitrate/nitrite response	Environmental Information Processing	
K07686	7	two-component system, NarL family, uhpT operon response regulator	Environmental Information Processing	
K07687	9	two-component system, NarL family, captular synthesis response	Environmental Information Processing	
K07689	20	two-component system, NarL family, invasion response regulator UvrY	Environmental Information Processing	
K07690	5	two-component system, NarL family, response regulator EvgA	Environmental Information Processing	
K07691	24	two-component system, NarL family, competent response regulator ComA	Environmental Information Processing	
K07692	37	two-component system, NarL family, response regulator DegU	Environmental Information Processing	
K07693	3	two-component system, NarL family, response regulator DesR	Environmental Information Processing	
K07694	4	two-component system, NarL family, vancomycin resistance associated	Environmental Information Processing	
K07695	13	two-component system, NarL family, response regulator DevR	Environmental Information Processing	
K07696	4	two-component system, NarL family, response regulator NreC	Environmental Information Processing	
K07697	11	two-component system, sporulation sensor kinase B [EC:2.7.13.3]	Environmental Information Processing	
K07699	1	two-component system, response regulator, stage 0 sporulation	Environmental Information Processing	
K07700	2	two-component system, CitB family, cit operon sensor histidine	Environmental Information Processing	
K07703	1	two-component system, CitB family, response regulator DcuR	Environmental Information Processing	
K07704	7	two-component system, LytT family, sensor histidine kinase LytS	Environmental Information Processing	
K07705	5	two-component system, LytT family, response regulator LytT	Environmental Information Processing	
K07707	4	two-component system, AgrA family, response regulator AgrA	Environmental Information Processing	
K07708	54	two-component system, NtrC family, nitrogen regulation sensor	Environmental Information Processing	
K07709	54	two-component system, NtrC family, sensor histidine kinase HydH	Environmental Information Processing	
K07710	39	two-component system, NtrC family, sensor histidine kinase AtoS	Environmental Information Processing	
K07711	10	two-component system, NtrC family, sensor histidine kinase YfhK	Environmental Information Processing	
K07712	112	two-component system, NtrC family, nitrogen regulation response	Environmental Information Processing	
K07713	64	two-component system, NtrC family, response regulator HydG	Environmental Information Processing	
K07714	48	two-component system, NtrC family, response regulator AtoC	Environmental Information Processing	
K07715	78	two-component system, NtrC family, response regulator YfhA	Environmental Information Processing	
K07716	16	two-component system, cell cycle sensor histidine kinase PleC	Environmental Information Processing	
K07718	1	two-component system, sensor histidine kinase YesM [EC:2.7.13.3]	Environmental Information Processing	
K07720	7	two-component system, response regulator YesN	Environmental Information Processing	
K07768	3	two-component system, OmpR family, sensor histidine kinase SenX3	Environmental Information Processing	
K07769	5	two-component system, OmpR family, sensor histidine kinase NblS	Environmental Information Processing	
K07771	1	two-component system, OmpR family, response regulator BasR	Environmental Information Processing	
K07773	1	two-component system, OmpR family, aerobic respiration control	Environmental Information Processing	
K07774	14	two-component system, OmpR family, response regulator TctD	Environmental Information Processing	
K07775	5	two-component system, OmpR family, response regulator ResD	Environmental Information Processing	
K07776	43	two-component system, OmpR family, response regulator RegX3	Environmental Information Processing	
K07777	14	two-component system, NarL family, sensor histidine kinase DegS	Environmental Information Processing	
K07778	10	two-component system, NarL family, sensor histidine kinase DesK	Environmental Information Processing	
K07782	1	LuxR family transcriptional regulator	Environmental Information Processing	
K07783	2	MFS transporter, OPA family, sugar phosphate sensor protein UhpC	Environmental Information Processing	
K07785	1	MFS transporter, NRE family, putaive nickel resistance protein	Environmental Information Processing	
K07787	112	Cu(I)/Ag(I) efflux system membrane protein CusA	Environmental Information Processing	
K07788	66	RND superfamily, multidrug transport protein MdtB	Environmental Information Processing	
K07789	37	RND superfamily, multidrug transport protein MdtC	Environmental Information Processing	
K07790	1	putative membrane protein PagO	Environmental Information Processing	
K07792	4	anaerobic C4-dicarboxylate transporter DcuB	Environmental Information Processing	
K07793	90	putative tricarboxylic transport membrane protein	Environmental Information Processing	
K07795	87	putative tricarboxylic transport membrane protein	Environmental Information Processing	
K07796	16	Cu(I)/Ag(I) efflux system outer membrane protein CusC	Environmental Information Processing	
K07798	51	Cu(I)/Ag(I) efflux system membrane protein CusB	Environmental Information Processing	
K07799	33	putative multidrug efflux transporter MdtA	Environmental Information Processing	
K07805	1	putative membrane protein PagD	Environmental Information Processing	
K07806	20	UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase	Environmental Information Processing	
K07811	3	trimethylamine-N-oxide reductase (cytochrome c) 1 [EC:1.7.2.3]	Environmental Information Processing	
K08082	4	two-component system, LytT family, sensor histidine kinase AlgZ	Environmental Information Processing	
K08083	11	two-component system, LytT family, response regulator AlgR	Environmental Information Processing	
K08348	39	formate dehydrogenase-N, alpha subunit [EC:1.2.1.2]	Environmental Information Processing	
K08357	9	tetrathionate reductase subunit A	Environmental Information Processing	
K08358	27	tetrathionate reductase subunit B	Environmental Information Processing	
K08359	4	tetrathionate reductase subunit C	Environmental Information Processing	
K08372	45	putative serine protease PepD [EC:3.4.21.-]	Environmental Information Processing	
K08477	2	outer membrane protease E [EC:3.4.21.-]	Environmental Information Processing	
K08478	1	phosphoglycerate transport regulatory protein PgtC	Environmental Information Processing	
K08479	3	two-component system, OmpR family, clock-associated histidine kinase	Environmental Information Processing	
K08483	32	phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]	Environmental Information Processing	
K08484	7	phosphotransferase system, enzyme I, PtsP [EC:2.7.3.9]	Environmental Information Processing	
K08485	1	phosphocarrier protein NPr	Environmental Information Processing	
K08641	17	D-alanyl-D-alanine dipeptidase [EC:3.4.13.-]	Environmental Information Processing	

K08738	12	cytochrome c	Environmental Information Processing	
K09474	2	acid phosphatase (class A) [EC:3.1.3.2]	Environmental Information Processing	
K09477	5	citrate:succinate antiporter	Environmental Information Processing	
K09688	3	capsular polysaccharide transport system permease protein	Environmental Information Processing	
K09689	1	capsular polysaccharide transport system ATP-binding protein	Environmental Information Processing	
K09690	46	lipopolysaccharide transport system permease protein	Environmental Information Processing	
K09691	27	lipopolysaccharide transport system ATP-binding protein	Environmental Information Processing	
K09693	8	teichoic acid transport system ATP-binding protein [EC:3.6.3.40]	Environmental Information Processing	
K09694	20	lipooligosaccharide transport system permease protein	Environmental Information Processing	
K09695	6	lipooligosaccharide transport system ATP-binding protein	Environmental Information Processing	
K09697	5	sodium transport system ATP-binding protein	Environmental Information Processing	
K09808	44	lipoprotein-releasing system permease protein	Environmental Information Processing	
K09810	59	lipoprotein-releasing system ATP-binding protein [EC:3.6.3.-]	Environmental Information Processing	
K09811	32	cell division transport system permease protein	Environmental Information Processing	
K09812	13	cell division transport system ATP-binding protein	Environmental Information Processing	
K09815	10	zinc transport system substrate-binding protein	Environmental Information Processing	
K09816	9	zinc transport system permease protein	Environmental Information Processing	
K09817	8	zinc transport system ATP-binding protein [EC:3.6.3.-]	Environmental Information Processing	
K09969	7	general L-amino acid transport system substrate-binding protein	Environmental Information Processing	
K09970	2	general L-amino acid transport system permease protein	Environmental Information Processing	
K09971	7	general L-amino acid transport system permease protein	Environmental Information Processing	
K09972	2	general L-amino acid transport system ATP-binding protein	Environmental Information Processing	
K09996	9	arginine transport system substrate-binding protein	Environmental Information Processing	
K09999	2	arginine transport system permease protein	Environmental Information Processing	
K10001	14	glutamate/aspartate transport system substrate-binding protein	Environmental Information Processing	
K10002	5	glutamate/aspartate transport system permease protein	Environmental Information Processing	
K10003	8	glutamate/aspartate transport system permease protein	Environmental Information Processing	
K10004	3	glutamate/aspartate transport system ATP-binding protein	Environmental Information Processing	
K10005	1	glutamate transport system substrate-binding protein	Environmental Information Processing	
K10006	2	glutamate transport system permease protein	Environmental Information Processing	
K10007	2	glutamate transport system permease protein	Environmental Information Processing	
K10009	4	cystine transport system permease protein	Environmental Information Processing	
K10010	1	cystine transport system ATP-binding protein [EC:3.6.3.-]	Environmental Information Processing	
K10014	1	histidine transport system substrate-binding protein	Environmental Information Processing	
K10017	1	histidine transport system ATP-binding protein [EC:3.6.3.21]	Environmental Information Processing	
K10036	2	glutamine transport system substrate-binding protein	Environmental Information Processing	
K10037	3	glutamine transport system permease protein	Environmental Information Processing	
K10039	6	putative glutamine transport system substrate-binding protein	Environmental Information Processing	
K10040	3	putative glutamine transport system permease protein	Environmental Information Processing	
K10041	2	putative glutamine transport system ATP-binding protein [EC:3.6.3.-]	Environmental Information Processing	
K10108	11	maltose/maltodextrin transport system substrate-binding protein	Environmental Information Processing	
K10109	5	maltose/maltodextrin transport system permease protein	Environmental Information Processing	
K10110	13	maltose/maltodextrin transport system permease protein	Environmental Information Processing	
K10111	2	maltose/maltodextrin transport system ATP-binding protein	Environmental Information Processing	
K10112	10	maltose/maltodextrin transport system ATP-binding protein	Environmental Information Processing	
K10117	1	multiple sugar transport system substrate-binding protein	Environmental Information Processing	
K10118	3	multiple sugar transport system permease protein	Environmental Information Processing	
K10119	3	multiple sugar transport system permease protein	Environmental Information Processing	
K10125	16	two-component system, NtrC family, C4-dicarboxylate transport sensor	Environmental Information Processing	
K10126	65	two-component system, NtrC family, C4-dicarboxylate transport	Environmental Information Processing	
K10188	9	lactose/L-arabinose transport system substrate-binding protein	Environmental Information Processing	
K10189	8	lactose/L-arabinose transport system permease protein	Environmental Information Processing	
K10190	19	lactose/L-arabinose transport system permease protein	Environmental Information Processing	
K10191	1	lactose/L-arabinose transport system ATP-binding protein	Environmental Information Processing	
K10193	2	oligogalacturonide transport system permease protein	Environmental Information Processing	
K10200	3	N-acetylglucosamine transport system substrate-binding protein	Environmental Information Processing	
K10201	3	N-acetylglucosamine transport system permease protein	Environmental Information Processing	
K10227	10	sorbitol/mannitol transport system substrate-binding protein	Environmental Information Processing	
K10228	1	sorbitol/mannitol transport system permease protein	Environmental Information Processing	
K10229	2	sorbitol/mannitol transport system permease protein	Environmental Information Processing	
K10232	15	alpha-glucoside transport system substrate-binding protein	Environmental Information Processing	
K10233	5	alpha-glucoside transport system permease protein	Environmental Information Processing	
K10234	8	alpha-glucoside transport system permease protein	Environmental Information Processing	
K10236	6	trehalose/maltose transport system substrate-binding protein	Environmental Information Processing	
K10237	4	trehalose/maltose transport system permease protein	Environmental Information Processing	
K10238	3	trehalose/maltose transport system permease protein	Environmental Information Processing	
K10240	2	cellobiose transport system substrate-binding protein	Environmental Information Processing	
K10241	1	cellobiose transport system permease protein	Environmental Information Processing	
K10242	1	cellobiose transport system permease protein	Environmental Information Processing	

K10255	15	omega-6 fatty acid desaturase (delta-12 desaturase) [EC:1.14.19.-]	Environmental Information Processing	
K10439	21	ribose transport system substrate-binding protein	Environmental Information Processing	
K10440	29	ribose transport system permease protein	Environmental Information Processing	
K10441	27	ribose transport system ATP-binding protein [EC:3.6.3.17]	Environmental Information Processing	
K10538	1	L-arabinose transport system permease protein	Environmental Information Processing	
K10541	3	methyl-galactoside transport system permease protein	Environmental Information Processing	
K10542	1	methyl-galactoside transport system ATP-binding protein	Environmental Information Processing	
K10543	5	D-xylose transport system substrate-binding protein	Environmental Information Processing	
K10544	14	D-xylose transport system permease protein	Environmental Information Processing	
K10545	1	D-xylose transport system ATP-binding protein [EC:3.6.3.17]	Environmental Information Processing	
K10547	1	putative multiple sugar transport system permease protein	Environmental Information Processing	
K10549	2	D-allose transport system substrate-binding protein	Environmental Information Processing	
K10552	6	fructose transport system substrate-binding protein	Environmental Information Processing	
K10553	2	fructose transport system permease protein	Environmental Information Processing	
K10554	2	fructose transport system ATP-binding protein	Environmental Information Processing	
K10555	9	AI-2 transport system substrate-binding protein	Environmental Information Processing	
K10556	4	AI-2 transport system permease protein	Environmental Information Processing	
K10557	2	AI-2 transport system permease protein	Environmental Information Processing	
K10559	7	rhamnose transport system substrate-binding protein	Environmental Information Processing	
K10560	3	rhamnose transport system permease protein	Environmental Information Processing	
K10561	1	rhamnose transport system permease protein	Environmental Information Processing	
K10697	6	two-component system, OmpR family, response regulator RpaA	Environmental Information Processing	
K10715	7	two-component system, sensor histidine kinase RpfC [EC:2.7.13.3]	Environmental Information Processing	
K10912	2	two-component system, repressor protein LuxO	Environmental Information Processing	
K10914	3	CRP/FNR family transcriptional regulator, cyclic AMP receptor	Environmental Information Processing	
K10941	18	sigma-54 specific transcriptional regulator, flagellar regulatory	Environmental Information Processing	
K10942	29	two-component system, sensor histidine kinase FlrB [EC:2.7.13.3]	Environmental Information Processing	
K10943	57	two component system, response regulator FlrC	Environmental Information Processing	
K11003	4	hemolysin D	Environmental Information Processing	
K11004	5	ATP-binding cassette, subfamily B, bacterial HlyB/CyaB	Environmental Information Processing	
K11016	4	hemolysin	Environmental Information Processing	
K11017	8	hemolysin activation/secretion protein??	Environmental Information Processing	
K11069	17	spermidine/putrescine transport system substrate-binding protein	Environmental Information Processing	
K11070	19	spermidine/putrescine transport system permease protein	Environmental Information Processing	
K11071	27	spermidine/putrescine transport system permease protein	Environmental Information Processing	
K11072	19	spermidine/putrescine transport system ATP-binding protein	Environmental Information Processing	
K11073	4	putrescine transport system substrate-binding protein	Environmental Information Processing	
K11074	10	putrescine transport system permease protein	Environmental Information Processing	
K11075	10	putrescine transport system permease protein	Environmental Information Processing	
K11076	10	putrescine transport system ATP-binding protein	Environmental Information Processing	
K11079	3	mannopine transport system permease protein	Environmental Information Processing	
K11082	1	2-aminoethylphosphonate transport system permease protein	Environmental Information Processing	
K11085	118	ATP-binding cassette, subfamily B, bacterial MsbA [EC:3.6.3.-]	Environmental Information Processing	
K11103	9	aerobic C4-dicarboxylate transport protein	Environmental Information Processing	
K11183	16	phosphocarrier protein FPr	Environmental Information Processing	
K11192	1	PTS system, N-acetylmuramic acid-specific IIC component	Environmental Information Processing	
K11326	7	cation efflux system protein involved in nickel and cobalt tolerance	Environmental Information Processing	
K11329	27	two-component system, OmpR family, response regulator RpaB	Environmental Information Processing	
K11354	3	two-component system, chemotaxis family, sensor kinase Cph1	Environmental Information Processing	
K11355	3	two-component system, chemotaxis family, response regulator Rcp1	Environmental Information Processing	
K11356	2	two-component system, sensor histidine kinase and response regulator	Environmental Information Processing	
K11357	7	two-component system, cell cycle sensor histidine kinase DivJ	Environmental Information Processing	
K11383	3	two-component system, NtrC family, sensor histidine kinase KinB	Environmental Information Processing	
K11384	7	two-component system, NtrC family, response regulator AlgB	Environmental Information Processing	
K11443	7	two-component system, cell cycle response regulator DivK	Environmental Information Processing	
K11444	8	two-component system, chemotaxis family, response regulator WspR	Environmental Information Processing	
K11523	4	two-component system, chemotaxis family, response regulator PixH	Environmental Information Processing	
K11525	1	methyl-accepting chemotaxis protein PixJ	Environmental Information Processing	
K11526	1	two-component system, chemotaxis family, sensor histidine kinase and	Environmental Information Processing	
K11603	1	manganese transport system ATP-binding protein	Environmental Information Processing	
K11604	1	manganese/iron transport system substrate-binding protein	Environmental Information Processing	
K11606	3	manganese/iron transport system permease protein	Environmental Information Processing	
K11615	3	two-component system, CitB family, response regulator MalR	Environmental Information Processing	
K11616	1	malate:Na+ symporter	Environmental Information Processing	
K11617	3	two-component system, NarL family, sensor histidine kinase LiaS	Environmental Information Processing	
K11618	39	two-component system, NarL family, response regulator LiaR	Environmental Information Processing	
K11619	11	lia operon protein LiaI	Environmental Information Processing	
K11621	1	lia operon protein LiaG	Environmental Information Processing	
K11624	2	two-component system, NarL family, response regulator YdfI	Environmental Information Processing	

K11625	9	membrane protein YdfJ	Environmental Information Processing	
K11634	1	two-component system, OmpR family, response regulator YxdJ	Environmental Information Processing	
K11688	92	C4-dicarboxylate-binding protein DctP	Environmental Information Processing	
K11689	12	C4-dicarboxylate transporter, DctQ subunit	Environmental Information Processing	
K11690	144	C4-dicarboxylate transporter, DctM subunit	Environmental Information Processing	
K11710	3	manganese/zinc/iron transport system ATP- binding protein	Environmental Information Processing	
K11711	16	two-component system, LuxR family, sensor histidine kinase DctS	Environmental Information Processing	
K11712	12	two-component system, LuxR family, response regulator DctR	Environmental Information Processing	
K11720	14	lipopolysaccharide export system permease protein	Environmental Information Processing	
K11891	8	type VI secretion system protein ImpL	Environmental Information Processing	
K11892	8	type VI secretion system protein ImpK	Environmental Information Processing	
K11903	1	type VI secretion system secreted protein Hcp	Environmental Information Processing	
K11904	9	type VI secretion system secreted protein VgrG	Environmental Information Processing	
K11906	7	type VI secretion system protein VasD	Environmental Information Processing	
K11907	13	type VI secretion system protein VasG	Environmental Information Processing	
K11912	28	serine/threonine-protein kinase PpkA [EC:2.7.11.1]	Environmental Information Processing	
K11913	3	type VI secretion system protein	Environmental Information Processing	
K11953	1	bicarbonate transport system ATP-binding protein [EC:3.6.3.-]	Environmental Information Processing	
K11954	2	neutral amino acid transport system substrate-binding protein	Environmental Information Processing	
K11955	1	neutral amino acid transport system permease protein	Environmental Information Processing	
K11956	1	neutral amino acid transport system permease protein	Environmental Information Processing	
K11957	2	neutral amino acid transport system ATP-binding protein	Environmental Information Processing	
K11958	2	neutral amino acid transport system ATP-binding protein	Environmental Information Processing	
K11959	4	urea transport system substrate-binding protein	Environmental Information Processing	
K11960	1	urea transport system permease protein	Environmental Information Processing	
K11961	2	urea transport system permease protein	Environmental Information Processing	
K11963	1	urea transport system ATP-binding protein	Environmental Information Processing	
K11987	1	prostaglandin-endoperoxide synthase 2 [EC:1.14.99.1]	Environmental Information Processing	
K12257	30	SecD/SecF fusion protein	Environmental Information Processing	
K12340	36	outer membrane channel protein TolC	Environmental Information Processing	
K12368	17	dipeptide transport system substrate-binding protein	Environmental Information Processing	
K12369	12	dipeptide transport system permease protein	Environmental Information Processing	
K12370	10	dipeptide transport system permease protein	Environmental Information Processing	
K12371	6	dipeptide transport system ATP-binding protein	Environmental Information Processing	
K12372	1	dipeptide transport system ATP-binding protein	Environmental Information Processing	
K12536	4	ATP-binding cassette, subfamily C, bacterial HasD	Environmental Information Processing	
K12541	3	ATP-binding cassette, subfamily C, bacterial LapB	Environmental Information Processing	
K13041	1	two-component system, LuxR family, response regulator TtrR	Environmental Information Processing	
K13409	1	ATP-binding cassette, subfamily B, bacterial RaxB	Environmental Information Processing	
K13486	2	chemotaxis protein methyltransferase WspC	Environmental Information Processing	
K13490	5	two-component system, chemotaxis family, sensor histidine kinase and	Environmental Information Processing	
K13491	1	two-component system, chemotaxis family, response regulator WspF	Environmental Information Processing	
K13532	2	two-component system, sporulation sensor kinase D [EC:2.7.13.3]	Environmental Information Processing	
K13533	7	two-component system, sporulation sensor kinase E [EC:2.7.13.3]	Environmental Information Processing	
K13584	1	two-component system, cell cycle response regulator CtrA	Environmental Information Processing	
K13587	41	two-component system, cell cycle sensor histidine kinase and	Environmental Information Processing	
K13588	1	histidine phosphotransferase ChpT	Environmental Information Processing	
K13589	2	two-component system, cell cycle response regulator CpdR	Environmental Information Processing	
K13598	35	two-component system, NtrC family, nitrogen regulation sensor	Environmental Information Processing	
K13599	57	two-component system, NtrC family, nitrogen regulation response	Environmental Information Processing	
K13815	21	two-component system, response regulator RpfG	Environmental Information Processing	
K13816	7	DSF synthase	Environmental Information Processing	
K13889	13	glutathione transport system substrate-binding protein	Environmental Information Processing	
K13890	6	glutathione transport system permease protein	Environmental Information Processing	
K13891	2	glutathione transport system permease protein	Environmental Information Processing	
K13892	4	glutathione transport system ATP-binding protein	Environmental Information Processing	
K13893	9	microcin C transport system substrate-binding protein	Environmental Information Processing	
K13894	2	microcin C transport system permease protein	Environmental Information Processing	
K13895	4	microcin C transport system permease protein	Environmental Information Processing	
K13896	3	microcin C transport system ATP-binding protein	Environmental Information Processing	
K13924	124	two-component system, chemotaxis family, CheB/CheR fusion protein	Environmental Information Processing	

KEGG ID	Sequences	KEGG pathway	KEGG category
K00566	48	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Genetic Information Processing
K00604	50	methionyl-tRNA formyltransferase [EC:2.1.2.9]	Genetic Information Processing
K00784	75	ribonuclease Z [EC:3.1.26.11]	Genetic Information Processing
K00850	56	6-phosphofructokinase [EC:2.7.1.11]	Genetic Information Processing
K00937	60	polyphosphate kinase [EC:2.7.4.1]	Genetic Information Processing
K00962	39	polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]	Genetic Information Processing
K00970	57	poly(A) polymerase [EC:2.7.7.19]	Genetic Information Processing
K00974	27	tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.25	Genetic Information Processing
K01011	21	3-mercaptopyruvate sulfurtransferase [EC:2.8.1.2]	Genetic Information Processing
K01042	37	L-seryl-tRNA(Ser) seleniumtransferase [EC:2.9.1.1]	Genetic Information Processing
K01142	29	exodeoxyribonuclease III [EC:3.1.11.2]	Genetic Information Processing
K01151	37	deoxyribonuclease IV [EC:3.1.21.2]	Genetic Information Processing
K01159	34	crossover junction endodeoxyribonuclease RuvC [EC:3.1.22.4]	Genetic Information Processing
K01246	12	DNA-3-methyladenine glycosylase I [EC:3.2.2.20]	Genetic Information Processing
K01247	18	DNA-3-methyladenine glycosylase II [EC:3.2.2.21]	Genetic Information Processing
K01689	42	enolase [EC:4.2.1.11]	Genetic Information Processing
K01866	51	tyrosyl-tRNA synthetase [EC:6.1.1.1]	Genetic Information Processing
K01867	46	tryptophanyl-tRNA synthetase [EC:6.1.1.2]	Genetic Information Processing
K01868	67	threonyl-tRNA synthetase [EC:6.1.1.3]	Genetic Information Processing
K01869	73	leucyl-tRNA synthetase [EC:6.1.1.4]	Genetic Information Processing
K01870	85	isoleucyl-tRNA synthetase [EC:6.1.1.5]	Genetic Information Processing
K01872	71	alanyl-tRNA synthetase [EC:6.1.1.7]	Genetic Information Processing
K01873	99	valyl-tRNA synthetase [EC:6.1.1.9]	Genetic Information Processing
K01874	56	methionyl-tRNA synthetase [EC:6.1.1.10]	Genetic Information Processing
K01875	59	seryl-tRNA synthetase [EC:6.1.1.11]	Genetic Information Processing
K01876	57	aspartyl-tRNA synthetase [EC:6.1.1.12]	Genetic Information Processing
K01878	12	glycyl-tRNA synthetase alpha chain [EC:6.1.1.14]	Genetic Information Processing
K01879	36	glycyl-tRNA synthetase beta chain [EC:6.1.1.14]	Genetic Information Processing
K01880	17	glycyl-tRNA synthetase [EC:6.1.1.14]	Genetic Information Processing
K01881	50	prolyl-tRNA synthetase [EC:6.1.1.15]	Genetic Information Processing
K01883	69	cysteinyl-tRNA synthetase [EC:6.1.1.16]	Genetic Information Processing
K01885	74	glutamyl-tRNA synthetase [EC:6.1.1.17]	Genetic Information Processing
K01886	28	glutaminyl-tRNA synthetase [EC:6.1.1.18]	Genetic Information Processing
K01887	498	arginyl-tRNA synthetase [EC:6.1.1.19]	Genetic Information Processing
K01889	40	phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]	Genetic Information Processing
K01890	515	phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]	Genetic Information Processing
K01892	46	histidyl-tRNA synthetase [EC:6.1.1.21]	Genetic Information Processing
K01893	25	asparaginyl-tRNA synthetase [EC:6.1.1.22]	Genetic Information Processing
K01971	172	DNA ligase (ATP) [EC:6.5.1.1]	Genetic Information Processing
K01972	63	DNA ligase (NAD+) [EC:6.5.1.2]	Genetic Information Processing
K02314	78	replicative DNA helicase [EC:3.6.1.-]	Genetic Information Processing
K02316	65	DNA primase [EC:2.7.7.-]	Genetic Information Processing
K02319	11	DNA polymerase I [EC:2.7.7.7]	Genetic Information Processing
K02330	6	DNA polymerase beta subunit [EC:2.7.7.7 4.2.99.-]	Genetic Information Processing
K02335	90	DNA polymerase I [EC:2.7.7.7]	Genetic Information Processing
K02337	211	DNA polymerase III subunit alpha [EC:2.7.7.7]	Genetic Information Processing
K02338	59	DNA polymerase III subunit beta [EC:2.7.7.7]	Genetic Information Processing
K02339	6	DNA polymerase III subunit chi [EC:2.7.7.7]	Genetic Information Processing
K02340	11	DNA polymerase III subunit delta [EC:2.7.7.7]	Genetic Information Processing
K02341	35	DNA polymerase III subunit delta' [EC:2.7.7.7]	Genetic Information Processing
K02342	60	DNA polymerase III subunit epsilon [EC:2.7.7.7]	Genetic Information Processing
K02343	65	DNA polymerase III subunit gamma/tau [EC:2.7.7.7]	Genetic Information Processing
K02345	1	DNA polymerase III subunit theta [EC:2.7.7.7]	Genetic Information Processing
K02433	141	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit A	Genetic Information Processing
K02434	54	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit B	Genetic Information Processing
K02435	18	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit C	Genetic Information Processing
K02686	4	primosomal replication protein N	Genetic Information Processing
K02863	21	large subunit ribosomal protein L1	Genetic Information Processing
K02864	19	large subunit ribosomal protein L10	Genetic Information Processing
K02867	17	large subunit ribosomal protein L11	Genetic Information Processing
K02871	16	large subunit ribosomal protein L13	Genetic Information Processing

K02874	22	large subunit ribosomal protein L14	Genetic Information Processing
K02876	12	large subunit ribosomal protein L15	Genetic Information Processing
K02878	19	large subunit ribosomal protein L16	Genetic Information Processing
K02879	21	large subunit ribosomal protein L17	Genetic Information Processing
K02881	11	large subunit ribosomal protein L18	Genetic Information Processing
K02884	16	large subunit ribosomal protein L19	Genetic Information Processing
K02886	47	large subunit ribosomal protein L2	Genetic Information Processing
K02887	6	large subunit ribosomal protein L20	Genetic Information Processing
K02888	23	large subunit ribosomal protein L21	Genetic Information Processing
K02890	18	large subunit ribosomal protein L22	Genetic Information Processing
K02892	34	large subunit ribosomal protein L23	Genetic Information Processing
K02895	14	large subunit ribosomal protein L24	Genetic Information Processing
K02897	28	large subunit ribosomal protein L25	Genetic Information Processing
K02899	20	large subunit ribosomal protein L27	Genetic Information Processing
K02902	9	large subunit ribosomal protein L28	Genetic Information Processing
K02904	6	large subunit ribosomal protein L29	Genetic Information Processing
K02906	36	large subunit ribosomal protein L3	Genetic Information Processing
K02907	9	large subunit ribosomal protein L30	Genetic Information Processing
K02909	22	large subunit ribosomal protein L31	Genetic Information Processing
K02911	73	large subunit ribosomal protein L32	Genetic Information Processing
K02913	9	large subunit ribosomal protein L33	Genetic Information Processing
K02914	15	large subunit ribosomal protein L34	Genetic Information Processing
K02916	7	large subunit ribosomal protein L35	Genetic Information Processing
K02919	2	large subunit ribosomal protein L36	Genetic Information Processing
K02926	30	large subunit ribosomal protein L4	Genetic Information Processing
K02931	15	large subunit ribosomal protein L5	Genetic Information Processing
K02933	28	large subunit ribosomal protein L6	Genetic Information Processing
K02935	6	large subunit ribosomal protein L7/L12	Genetic Information Processing
K02939	23	large subunit ribosomal protein L9	Genetic Information Processing
K02945	47	small subunit ribosomal protein S1	Genetic Information Processing
K02946	441	small subunit ribosomal protein S10	Genetic Information Processing
K02948	11	small subunit ribosomal protein S11	Genetic Information Processing
K02950	7	small subunit ribosomal protein S12	Genetic Information Processing
K02952	15	small subunit ribosomal protein S13	Genetic Information Processing
K02954	7	small subunit ribosomal protein S14	Genetic Information Processing
K02956	8	small subunit ribosomal protein S15	Genetic Information Processing
K02959	23	small subunit ribosomal protein S16	Genetic Information Processing
K02961	10	small subunit ribosomal protein S17	Genetic Information Processing
K02963	15	small subunit ribosomal protein S18	Genetic Information Processing
K02965	4	small subunit ribosomal protein S19	Genetic Information Processing
K02967	68	small subunit ribosomal protein S2	Genetic Information Processing
K02968	28	small subunit ribosomal protein S20	Genetic Information Processing
K02970	4	small subunit ribosomal protein S21	Genetic Information Processing
K02982	20	small subunit ribosomal protein S3	Genetic Information Processing
K02986	30	small subunit ribosomal protein S4	Genetic Information Processing
K02988	13	small subunit ribosomal protein S5	Genetic Information Processing
K02990	23	small subunit ribosomal protein S6	Genetic Information Processing
K02992	15	small subunit ribosomal protein S7	Genetic Information Processing
K02994	23	small subunit ribosomal protein S8	Genetic Information Processing
K02996	16	small subunit ribosomal protein S9	Genetic Information Processing
K03040	34	DNA-directed RNA polymerase subunit alpha [EC:2.7.7.6]	Genetic Information Processing
K03043	77	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]	Genetic Information Processing
K03046	516	DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]	Genetic Information Processing
K03060	10	DNA-directed RNA polymerase subunit omega [EC:2.7.7.6]	Genetic Information Processing
K03070	74	preprotein translocase subunit SecA	Genetic Information Processing
K03071	7	preprotein translocase subunit SecB	Genetic Information Processing
K03072	476	preprotein translocase subunit SecD	Genetic Information Processing
K03073	2	preprotein translocase subunit SecE	Genetic Information Processing
K03074	41	preprotein translocase subunit SecF	Genetic Information Processing
K03075	3	preprotein translocase subunit SecG	Genetic Information Processing
K03076	36	preprotein translocase subunit SecY	Genetic Information Processing
K03100	92	signal peptidase I [EC:3.4.21.89]	Genetic Information Processing

K03101	20	signal peptidase II [EC:3.4.23.36]	Genetic Information Processing
K03106	47	signal recognition particle subunit SRP54	Genetic Information Processing
K03110	23	fused signal recognition particle receptor	Genetic Information Processing
K03111	34	single-strand DNA-binding protein	Genetic Information Processing
K03113	2	translation initiation factor SUI1	Genetic Information Processing
K03116	10	sec-independent protein translocase protein TatA	Genetic Information Processing
K03117	4	sec-independent protein translocase protein TatB	Genetic Information Processing
K03118	57	sec-independent protein translocase protein TatC	Genetic Information Processing
K03148	16	adenylyltransferase ThiF [EC:2.7.7.-]	Genetic Information Processing
K03151	4	thiamine biosynthesis protein ThiI	Genetic Information Processing
K03154	5	thiamine biosynthesis ThiS	Genetic Information Processing
K03210	16	preprotein translocase subunit YajC	Genetic Information Processing
K03217	71	preprotein translocase subunit YidC	Genetic Information Processing
K03265	1	peptide chain release factor eRF subunit 1	Genetic Information Processing
K03432	2	proteasome alpha subunit [EC:3.4.25.1]	Genetic Information Processing
K03433	9	proteasome beta subunit [EC:3.4.25.1]	Genetic Information Processing
K03469	41	ribonuclease HI [EC:3.1.26.4]	Genetic Information Processing
K03470	44	ribonuclease HII [EC:3.1.26.4]	Genetic Information Processing
K03471	3	ribonuclease HIII [EC:3.1.26.4]	Genetic Information Processing
K03540	15	ribonuclease P subunit RPR2 [EC:3.1.26.5]	Genetic Information Processing
K03550	21	holliday junction DNA helicase RuvA	Genetic Information Processing
K03551	35	holliday junction DNA helicase RuvB	Genetic Information Processing
K03553	41	recombination protein RecA	Genetic Information Processing
K03555	79	DNA mismatch repair protein MutS	Genetic Information Processing
K03572	44	DNA mismatch repair protein MutL	Genetic Information Processing
K03575	41	A/G-specific adenine glycosylase [EC:3.2.2.-]	Genetic Information Processing
K03581	29	exodeoxyribonuclease V alpha subunit [EC:3.1.11.5]	Genetic Information Processing
K03582	8	exodeoxyribonuclease V beta subunit [EC:3.1.11.5]	Genetic Information Processing
K03583	15	exodeoxyribonuclease V gamma subunit [EC:3.1.11.5]	Genetic Information Processing
K03584	34	DNA repair protein RecO (recombination protein O)	Genetic Information Processing
K03601	45	exodeoxyribonuclease VII large subunit [EC:3.1.11.6]	Genetic Information Processing
K03602	5	exodeoxyribonuclease VII small subunit [EC:3.1.11.6]	Genetic Information Processing
K03628	36	transcription termination factor Rho	Genetic Information Processing
K03629	18	DNA replication and repair protein RecF	Genetic Information Processing
K03635	22	molybdenum cofactor biosynthesis protein E	Genetic Information Processing
K03636	10	molybdenum cofactor biosynthesis protein D	Genetic Information Processing
K03637	16	molybdenum cofactor biosynthesis protein C	Genetic Information Processing
K03639	47	molybdenum cofactor biosynthesis protein A	Genetic Information Processing
K03648	29	uracil-DNA glycosylase [EC:3.2.2.-]	Genetic Information Processing
K03649	18	TDG/mug DNA glycosylase family protein [EC:3.2.2.-]	Genetic Information Processing
K03652	17	DNA-3-methyladenine glycosylase [EC:3.2.2.21]	Genetic Information Processing
K03654	47	ATP-dependent DNA helicase RecQ [EC:3.6.1.-]	Genetic Information Processing
K03655	58	ATP-dependent DNA helicase RecG [EC:3.6.1.-]	Genetic Information Processing
K03657	133	DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.1.-]	Genetic Information Processing
K03666	10	host factor-I protein	Genetic Information Processing
K03685	34	ribonuclease III [EC:3.1.26.3]	Genetic Information Processing
K03701	117	excinuclease ABC subunit A	Genetic Information Processing
K03702	42	excinuclease ABC subunit B	Genetic Information Processing
K03703	61	excinuclease ABC subunit C	Genetic Information Processing
K03723	74	transcription-repair coupling factor (superfamily II helicase)	Genetic Information Processing
K03732	1	ATP-dependent RNA helicase RhlB [EC:3.6.4.13]	Genetic Information Processing
K03763	10	DNA polymerase III subunit alpha, Gram-positive type [EC:2.7.7.7]	Genetic Information Processing
K03831	8	molybdopterin biosynthesis protein Mog	Genetic Information Processing
K04043	64	molecular chaperone DnaK	Genetic Information Processing
K04066	67	primosomal protein N' (replication factor Y) (superfamily II	Genetic Information Processing
K04067	9	primosomal replication protein N"	Genetic Information Processing
K04077	43	chaperonin GroEL	Genetic Information Processing
K04079	17	molecular chaperone HtpG	Genetic Information Processing
K04085	8	tRNA 2-thiouridine synthesizing protein A [EC:2.8.1.-]	Genetic Information Processing
K04487	57	cysteine desulfurase [EC:2.8.1.7]	Genetic Information Processing
K04566	6	lysyl-tRNA synthetase, class I [EC:6.1.1.6]	Genetic Information Processing
K04567	51	lysyl-tRNA synthetase, class II [EC:6.1.1.6]	Genetic Information Processing

K05522	12	endonuclease VIII [EC:3.2.2.- 4.2.99.18]	Genetic Information Processing
K05592	36	ATP-dependent RNA helicase DeaD [EC:3.6.4.13]	Genetic Information Processing
K06187	21	recombination protein RecR	Genetic Information Processing
K06223	4	DNA adenine methylase [EC:2.1.1.72]	Genetic Information Processing
K07178	2	RIO kinase 1 [EC:2.7.11.1]	Genetic Information Processing
K07236	1	tRNA 2-thiouridine synthesizing protein C	Genetic Information Processing
K07237	3	tRNA 2-thiouridine synthesizing protein B	Genetic Information Processing
K07456	34	DNA mismatch repair protein MutS2	Genetic Information Processing
K07462	59	single-stranded-DNA-specific exonuclease [EC:3.1.-.-]	Genetic Information Processing
K08300	19	ribonuclease E [EC:3.1.26.12]	Genetic Information Processing
K08311	4	putative (di)nucleoside polyphosphate hydrolase [EC:3.6.1.-]	Genetic Information Processing
K09698	20	nondiscriminating glutamyl-tRNA synthetase [EC:6.1.1.24]	Genetic Information Processing
K09759	2	nondiscriminating aspartyl-tRNA synthetase [EC:6.1.1.23]	Genetic Information Processing
K10563	62	formamidopyrimidine-DNA glycosylase [EC:3.2.2.23 4.2.99.18]	Genetic Information Processing
K10747	4	DNA ligase 1 [EC:6.5.1.1]	Genetic Information Processing
K10754	4	replication factor C subunit 1	Genetic Information Processing
K10773	24	endonuclease III [EC:4.2.99.18]	Genetic Information Processing
K10843	12	DNA excision repair protein ERCC-3 [EC:3.6.1.-]	Genetic Information Processing
K10844	3	DNA excision repair protein ERCC-2 [EC:3.6.1.-]	Genetic Information Processing
K10857	1	exodeoxyribonuclease X [EC:3.1.11.-]	Genetic Information Processing
K10979	36	DNA end-binding protein Ku	Genetic Information Processing
K11179	14	tRNA 2-thiouridine synthesizing protein E [EC:2.8.1.-]	Genetic Information Processing
K11927	27	ATP-dependent RNA helicase RhlE [EC:3.6.4.13]	Genetic Information Processing
K12257	30	SecD/SecF fusion protein	Genetic Information Processing
K12573	53	ribonuclease R [EC:3.1.-.-]	Genetic Information Processing
K12574	39	ribonuclease J [EC:3.1.-.-]	Genetic Information Processing
K13280	2	signal peptidase, endoplasmic reticulum-type [EC:3.4.-.-]	Genetic Information Processing
K13288	10	oligoribonuclease [EC:3.1.-.-]	Genetic Information Processing
K13525	23	transitional endoplasmic reticulum ATPase	Genetic Information Processing
K13527	10	proteasome-associated ATPase	Genetic Information Processing
K13529	16	AraC family transcriptional regulator, regulatory protein of	Genetic Information Processing
K13797	2	DNA-directed RNA polymerase subunit beta-beta' [EC:2.7.7.6]	Genetic Information Processing
K13993	58	HSP20 family protein	Genetic Information Processing

KEGG I	Sequences	KEGG pathway	KEGG category	
K00036	118	glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49]	Human diseases	
K00079	12	carbonyl reductase (NADPH) [EC:1.1.1.184]	Human diseases	
K00121	49	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	Human diseases	
K00129	2	aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]	Human diseases	
K00134	29	glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	Human diseases	
K00161	65	pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	Human diseases	
K00162	66	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]	Human diseases	
K00239	70	succinate dehydrogenase flavoprotein subunit [EC:1.3.99.1]	Human diseases	
K00274	21	monoamine oxidase [EC:1.4.3.4]	Human diseases	
K00411	10	ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.2]	Human diseases	
K00412	35	ubiquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.2]	Human diseases	
K00413	8	ubiquinol-cytochrome c reductase cytochrome c1 subunit [EC:1.10.2.2]	Human diseases	
K00558	15	DNA (cytosine-5-)-methyltransferase [EC:2.1.1.37]	Human diseases	
K00622	5	arylamine N-acetyltransferase [EC:2.3.1.5]	Human diseases	
K00677	32	UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]	Human diseases	
K00688	90	starch phosphorylase [EC:2.4.1.1]	Human diseases	
K00693	14	glycogen(starch) synthase [EC:2.4.1.11]	Human diseases	
K00758	21	thymidine phosphorylase [EC:2.4.2.4]	Human diseases	
K00799	108	glutathione S-transferase [EC:2.5.1.18]	Human diseases	
K00820	67	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	Human diseases	
K00850	56	6-phosphofructokinase [EC:2.7.1.11]	Human diseases	
K00873	44	pyruvate kinase [EC:2.7.1.40]	Human diseases	
K00901	6	diacylglycerol kinase [EC:2.7.1.107]	Human diseases	
K01000	52	phospho-N-acetylmuramoyl-pentapeptide-transferase [EC:2.7.8.13]	Human diseases	
K01078	17	acid phosphatase [EC:3.1.3.2]	Human diseases	
K01115	8	phospholipase D [EC:3.1.4.4]	Human diseases	
K01207	53	beta-N-acetylhexosaminidase [EC:3.2.1.52]	Human diseases	
K01253	35	microsomal epoxide hydrolase [EC:3.3.2.9]	Human diseases	
K01283	4	peptidyl-dipeptidase A [EC:3.4.15.1]	Human diseases	
K01312	9	trypsin [EC:3.4.21.4]	Human diseases	
K01354	61	oligopeptidase B [EC:3.4.21.83]	Human diseases	
K01389	2	neprilysin [EC:3.4.24.11]	Human diseases	
K01392	9	thimet oligopeptidase [EC:3.4.24.15]	Human diseases	
K01401	1	aureolysin [EC:3.4.24.29]	Human diseases	
K01406	35	serralysin [EC:3.4.24.40]	Human diseases	
K01425	10	glutaminase [EC:3.5.1.2]	Human diseases	
K01428	11	urease alpha subunit [EC:3.5.1.5]	Human diseases	
K01448	611	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]	Human diseases	
K01467	153	beta-lactamase [EC:3.5.2.6]	Human diseases	
K01476	13	arginase [EC:3.5.3.1]	Human diseases	
K01488	35	adenosine deaminase [EC:3.5.4.4]	Human diseases	
K01580	8	glutamate decarboxylase [EC:4.1.1.15]	Human diseases	
K01593	61	aromatic-L-amino-acid decarboxylase [EC:4.1.1.28]	Human diseases	
K01596	30	phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]	Human diseases	
K01679	37	fumarate hydratase, class II [EC:4.2.1.2]	Human diseases	
K01775	45	alanine racemase [EC:5.1.1.1]	Human diseases	
K01834	100	phosphoglycerate mutase [EC:5.4.2.1]	Human diseases	
K01921	88	D-alanine-D-alanine ligase [EC:6.3.2.4]	Human diseases	
K01929	58	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-	Human diseases	
K02040	62	phosphate transport system substrate-binding protein	Human diseases	
K02330	6	DNA polymerase beta subunit [EC:2.7.7.7 4.2.99.-]	Human diseases	
K02405	21	RNA polymerase sigma factor for flagellar operon FliA	Human diseases	
K02406	10	flagellin	Human diseases	
K02545	2	penicillin-binding protein 2 prime	Human diseases	
K02547	1	methicillin resistance protein	Human diseases	
K02563	30	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)	Human diseases	

K03087	22	RNA polymerase nonessential primary-like sigma factor	Human diseases	
K03092	47	RNA polymerase sigma-54 factor	Human diseases	
K03196	1	type IV secretion system protein VirB11	Human diseases	
K03197	2	type IV secretion system protein VirB2	Human diseases	
K03367	32	D-alanine-poly(phosphoribitol) ligase [EC:6.1.1.13]	Human diseases	
K03385	9	formate-dependent nitrite reductase, periplasmic cytochrome c552	Human diseases	
K03585	50	membrane fusion protein	Human diseases	
K03587	74	cell division protein FtsI (penicillin-binding protein 3)	Human diseases	
K03596	50	GTP-binding protein LepA	Human diseases	
K03648	29	uracil-DNA glycosylase [EC:3.2.2.-]	Human diseases	
K03673	13	thiol:disulfide interchange protein DsbA	Human diseases	
K03685	34	ribonuclease III [EC:3.1.26.3]	Human diseases	
K03693	1	penicillin-binding protein	Human diseases	
K03740	1	D-alanine transfer protein	Human diseases	
K03760	1	phosphoethanolamine transferase	Human diseases	
K03767	15	peptidyl-prolyl cis-trans isomerase A (cyclophilin A) [EC:5.2.1.8]	Human diseases	
K03781	12	catalase [EC:1.11.1.6]	Human diseases	
K03943	6	NADH dehydrogenase (ubiquinone) flavoprotein 2 [EC:1.6.5.3 1.6.99.3]	Human diseases	
K04043	64	molecular chaperone DnaK	Human diseases	
K04077	43	chaperonin GroEL	Human diseases	
K04079	17	molecular chaperone HtpG	Human diseases	
K04097	7	glutathione S-transferase [EC:2.5.1.18]	Human diseases	
K04496	9	C-terminal binding protein	Human diseases	
K04564	27	superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	Human diseases	
K04565	6	Cu/Zn superoxide dismutase [EC:1.15.1.1]	Human diseases	
K04771	6	serine protease Do [EC:3.4.21.107]	Human diseases	
K05366	129	penicillin-binding protein 1A [EC:2.4.1.- 3.4.-.-]	Human diseases	
K05515	85	penicillin-binding protein 2	Human diseases	
K05692	2	actin beta/gamma 1	Human diseases	
K05916	3	nitric oxide dioxygenase [EC:1.14.12.17]	Human diseases	
K07173	15	S-ribosylhomocysteine lyase [EC:4.4.1.21]	Human diseases	
K07260	7	D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4]	Human diseases	
K07264	23	4-amino-4-deoxy-L-arabinose transferase [EC:2.-.-.-]	Human diseases	
K07326	7	hemolysin activation/secretion protein	Human diseases	
K07345	1	major type 1 subunit fimbrin (pilin)	Human diseases	
K07347	11	outer membrane usher protein	Human diseases	
K07637	1	two-component system, OmpR family, sensor histidine kinase PhoQ	Human diseases	
K07640	6	two-component system, OmpR family, sensor histidine kinase CpxA	Human diseases	
K07643	3	two-component system, OmpR family, sensor histidine kinase BasS	Human diseases	
K07660	1	two-component system, OmpR family, response regulator PhoP	Human diseases	
K07662	5	two-component system, OmpR family, response regulator CpxR	Human diseases	
K07679	4	two-component system, NarL family, sensor histidine kinase EvgS	Human diseases	
K07690	5	two-component system, NarL family, response regulator EvgA	Human diseases	
K07771	1	two-component system, OmpR family, response regulator BasR	Human diseases	
K07806	20	UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase	Human diseases	
K08218	18	MFS transporter, PAT family, beta-lactamase induction signal	Human diseases	
K08303	23	putative protease [EC:3.4.-.-]	Human diseases	
K08477	2	outer membrane protease E [EC:3.4.21.-]	Human diseases	
K08641	17	D-alanyl-D-alanine dipeptidase [EC:3.4.13.-]	Human diseases	
K08720	3	outer membrane protein OmpU	Human diseases	
K08738	12	cytochrome c	Human diseases	
K10011	7	UDP-GlcUA decarboxylase/UDP-L-Ara4N formyltransferase	Human diseases	
K10012	8	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	Human diseases	
K10912	2	two-component system, repressor protein LuxO	Human diseases	
K10914	3	CRP/FNR family transcriptional regulator, cyclic AMP receptor	Human diseases	
K10915	1	CAI-1 autoinducer synthase [EC:2.3.-.-]	Human diseases	
K10917	8	PadR family transcriptional regulator, regulatory protein AphA	Human diseases	

K10918	14	LysR family transcriptional regulator, transcriptional activator	Human diseases	
K10941	18	sigma-54 specific transcriptional regulator, flagellar regulatory	Human diseases	
K10942	29	two-component system, sensor histidine kinase FlrB [EC:2.7.13.3]	Human diseases	
K10943	57	two component system, response regulator FlrC	Human diseases	
K11003	4	hemolysin D	Human diseases	
K11004	5	ATP-binding cassette, subfamily B, bacterial HlyB/CyaB	Human diseases	
K11029	4	anthrax edema toxin adenylate cyclase [EC:4.6.1.1]	Human diseases	
K11041	2	exfoliative toxin A/B	Human diseases	
K11418	13	histone deacetylase 11 [EC:3.5.1.98]	Human diseases	
K11533	1	fatty acid synthase, bacteria type [EC:2.3.1.-]	Human diseases	
K11987	1	prostaglandin-endoperoxide synthase 2 [EC:1.14.99.1]	Human diseases	
K12264	2	anaerobic nitric oxide reductase flavorubredoxin	Human diseases	
K12265	1	nitric oxide reductase FlRd-NAD(+) reductase [EC:1.18.1.-]	Human diseases	
K12266	6	anaerobic nitric oxide reductase transcription regulator	Human diseases	
K12340	36	outer membrane channel protein TolC	Human diseases	
K12344	4	3-oxo-5-alpha-steroid 4-dehydrogenase 2 [EC:1.3.99.5]	Human diseases	
K12555	1	penicillin-binding protein 2A [EC:2.4.1.129 2.3.2.-]	Human diseases	
K12688	2	autotransporter serine protease [EC:3.4.21.-]	Human diseases	
K13014	2	undecaprenyl phosphate-alpha-L-ara4FN deformylase [EC:3.5.-.-]	Human diseases	
K13285	1	invasin B	Human diseases	
K13525	23	transitional endoplasmic reticulum ATPase	Human diseases	
K13730	107	internalin A	Human diseases	
K13735	100	adhesin/invasin	Human diseases	
K13741	1	guanine nucleotide exchange factor SopE	Human diseases	
K13742	1	protein IpgB1	Human diseases	
K13771	2	Rrf2 family transcriptional regulator, nitric oxide-sensitive	Human diseases	
K13963	11	serpin B	Human diseases	

KEGG ID	Sequences	KEGG pathway	KEGG category
K00031	37	isocitrate dehydrogenase [EC:1.1.1.42]	Cellular Processes
K00232	1	acyl-CoA oxidase [EC:1.3.3.6]	Cellular Processes
K00273	15	D-amino-acid oxidase [EC:1.4.3.3]	Cellular Processes
K00477	2	phytanoyl-CoA hydroxylase [EC:1.14.11.18]	Cellular Processes
K00494	70	alkanal monooxygenase (FMN-linked) [EC:1.14.14.3]	Cellular Processes
K00575	79	chemotaxis protein methyltransferase CheR [EC:2.1.1.80]	Cellular Processes
K00803	23	alkyldihydroxyacetonephosphate synthase [EC:2.5.1.26]	Cellular Processes
K00869	1	mevalonate kinase [EC:2.7.1.36]	Cellular Processes
K01114	33	phospholipase C [EC:3.1.4.3]	Cellular Processes
K01115	8	phospholipase D [EC:3.1.4.4]	Cellular Processes
K01132	17	N-acetylgalactosamine-6-sulfatase [EC:3.1.6.4]	Cellular Processes
K01134	23	arylsulfatase A [EC:3.1.6.8]	Cellular Processes
K01135	17	arylsulfatase B [EC:3.1.6.12]	Cellular Processes
K01136	8	iduronate 2-sulfatase [EC:3.1.6.13]	Cellular Processes
K01137	10	N-acetylglucosamine-6-sulfatase [EC:3.1.6.14]	Cellular Processes
K01173	1	endonuclease [EC:3.1.30.-]	Cellular Processes
K01186	2	sialidase-1 [EC:3.2.1.18]	Cellular Processes
K01192	9	beta-mannosidase [EC:3.2.1.25]	Cellular Processes
K01195	8	beta-glucuronidase [EC:3.2.1.31]	Cellular Processes
K01201	13	glucosylceramidase [EC:3.2.1.45]	Cellular Processes
K01218	6	mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]	Cellular Processes
K01318	1	glutamyl endopeptidase [EC:3.4.21.19]	Cellular Processes
K01338	158	ATP-dependent Lon protease [EC:3.4.21.53]	Cellular Processes
K01342	54	subtilisin [EC:3.4.21.62]	Cellular Processes
K01358	30	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]	Cellular Processes
K01444	9	N4-(beta-N-acetylglucosaminyl)-L-asparaginase [EC:3.5.1.26]	Cellular Processes
K01497	24	GTP cyclohydrolase II [EC:3.5.4.25]	Cellular Processes
K01578	19	malonyl-CoA decarboxylase [EC:4.1.1.9]	Cellular Processes
K01580	8	glutamate decarboxylase [EC:4.1.1.15]	Cellular Processes
K01626	26	3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]	Cellular Processes
K01635	10	tagatose 1,6-diphosphate aldolase [EC:4.1.2.40]	Cellular Processes
K01640	23	hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]	Cellular Processes
K01657	59	anthranilate synthase component I [EC:4.1.3.27]	Cellular Processes
K01658	28	anthranilate synthase component II [EC:4.1.3.27]	Cellular Processes
K01728	1	pectate lyase [EC:4.2.2.2]	Cellular Processes
K01768	403	adenylate cyclase [EC:4.6.1.1]	Cellular Processes
K01796	35	alpha-methylacyl-CoA racemase [EC:5.1.99.4]	Cellular Processes
K01897	294	long-chain acyl-CoA synthetase [EC:6.2.1.3]	Cellular Processes
K01995	126	branched-chain amino acid transport system ATP-binding protein	Cellular Processes
K01996	125	branched-chain amino acid transport system ATP-binding protein	Cellular Processes
K01997	153	branched-chain amino acid transport system permease protein	Cellular Processes
K01998	326	branched-chain amino acid transport system permease protein	Cellular Processes
K01999	254	branched-chain amino acid transport system substrate-binding protein	Cellular Processes
K02031	66	peptide/nickel transport system ATP-binding protein	Cellular Processes
K02032	185	peptide/nickel transport system ATP-binding protein	Cellular Processes
K02033	207	peptide/nickel transport system permease protein	Cellular Processes
K02034	165	peptide/nickel transport system permease protein	Cellular Processes
K02035	407	peptide/nickel transport system substrate-binding protein	Cellular Processes
K02052	32	putative spermidine/putrescine transport system ATP-binding protein	Cellular Processes
K02053	39	putative spermidine/putrescine transport system permease protein	Cellular Processes
K02054	31	putative spermidine/putrescine transport system permease protein	Cellular Processes
K02055	46	putative spermidine/putrescine transport system substrate-binding	Cellular Processes
K02313	51	chromosomal replication initiator protein	Cellular Processes
K02314	78	replicative DNA helicase [EC:3.6.1.-]	Cellular Processes
K02386	1	flagella basal body P-ring formation protein FlgA	Cellular Processes
K02387	12	flagellar basal-body rod protein FlgB	Cellular Processes
K02388	133	flagellar basal-body rod protein FlgC	Cellular Processes
K02389	14	flagellar basal-body rod modification protein FlgD	Cellular Processes
K02390	14	flagellar hook protein FlgE	Cellular Processes

K02391	4	flagellar basal-body rod protein FlgF	Cellular Processes
K02392	15	flagellar basal-body rod protein FlgG	Cellular Processes
K02393	4	flagellar L-ring protein precursor FlgH	Cellular Processes
K02394	6	flagellar P-ring protein precursor FlgI	Cellular Processes
K02396	12	flagellar hook-associated protein 1 FlgK	Cellular Processes
K02397	8	flagellar hook-associated protein 3 FlgL	Cellular Processes
K02400	16	flagellar biosynthesis protein FlhA	Cellular Processes
K02401	8	flagellar biosynthetic protein FlhB	Cellular Processes
K02402	1	flagellar transcriptional activator FlhC	Cellular Processes
K02406	10	flagellin	Cellular Processes
K02407	17	flagellar hook-associated protein 2	Cellular Processes
K02408	2	flagellar hook-basal body complex protein FliE	Cellular Processes
K02409	14	flagellar M-ring protein FliF	Cellular Processes
K02410	16	flagellar motor switch protein FliG	Cellular Processes
K02411	3	flagellar assembly protein FliH	Cellular Processes
K02412	12	flagellum-specific ATP synthase [EC:3.6.3.14]	Cellular Processes
K02413	1	flagellar FliJ protein	Cellular Processes
K02414	1	flagellar hook-length control protein FliK	Cellular Processes
K02416	15	flagellar motor switch protein FliM	Cellular Processes
K02417	6	flagellar motor switch protein FliN/FliY	Cellular Processes
K02418	2	flagellar protein FliO/FliZ	Cellular Processes
K02419	7	flagellar biosynthetic protein FliP	Cellular Processes
K02420	2	flagellar biosynthetic protein FliQ	Cellular Processes
K02421	2	flagellar biosynthetic protein FliR	Cellular Processes
K02422	3	flagellar protein FliS	Cellular Processes
K02488	217	two-component system, cell cycle response regulator	Cellular Processes
K02490	30	two-component system, response regulator, stage 0 sporulation	Cellular Processes
K02556	5	chemotaxis protein MotA	Cellular Processes
K02557	23	chemotaxis protein MotB	Cellular Processes
K02563	30	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)	Cellular Processes
K02651	5	pilus assembly protein Flp/PilA	Cellular Processes
K03070	74	preprotein translocase subunit SecA	Cellular Processes
K03071	7	preprotein translocase subunit SecB	Cellular Processes
K03073	2	preprotein translocase subunit SecE	Cellular Processes
K03075	3	preprotein translocase subunit SecG	Cellular Processes
K03076	36	preprotein translocase subunit SecY	Cellular Processes
K03100	92	signal peptidase I [EC:3.4.21.89]	Cellular Processes
K03106	47	signal recognition particle subunit SRP54	Cellular Processes
K03110	23	fused signal recognition particle receptor	Cellular Processes
K03210	16	preprotein translocase subunit YajC	Cellular Processes
K03217	71	preprotein translocase subunit YidC	Cellular Processes
K03386	31	peroxiredoxin (alkyl hydroperoxide reductase subunit C)	Cellular Processes
K03406	186	methyl-accepting chemotaxis protein	Cellular Processes
K03407	82	two-component system, chemotaxis family, sensor kinase CheA	Cellular Processes
K03408	21	purine-binding chemotaxis protein CheW	Cellular Processes
K03410	4	chemotaxis protein CheC	Cellular Processes
K03411	16	chemotaxis protein CheD [EC:3.5.1.44]	Cellular Processes
K03412	64	two-component system, chemotaxis family, response regulator CheB	Cellular Processes
K03413	117	two-component system, chemotaxis family, response regulator CheY	Cellular Processes
K03414	3	chemotaxis protein CheZ	Cellular Processes
K03426	21	NAD+ diphosphatase [EC:3.6.1.22]	Cellular Processes
K03531	44	cell division protein FtsZ	Cellular Processes
K03544	21	ATP-dependent Clp protease ATP-binding subunit ClpX	Cellular Processes
K03588	46	cell division protein FtsW	Cellular Processes
K03589	17	cell division protein FtsQ	Cellular Processes
K03590	36	cell division protein FtsA	Cellular Processes
K03666	10	host factor-I protein	Cellular Processes
K03776	16	aerotaxis receptor	Cellular Processes
K03781	12	catalase [EC:1.11.1.6]	Cellular Processes
K04562	441	flagellar biosynthesis protein FlhG	Cellular Processes

K04564	27	superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	Cellular Processes
K04565	6	Cu/Zn superoxide dismutase [EC:1.15.1.1]	Cellular Processes
K05692	2	actin beta/gamma 1	Cellular Processes
K05874	21	methyl-accepting chemotaxis protein I, serine sensor receptor	Cellular Processes
K05875	8	methyl-accepting chemotaxis protein II, aspartate sensor receptor	Cellular Processes
K05876	2	methyl-accepting chemotaxis protein III, ribose and galactose sensor	Cellular Processes
K06985	5	aspartyl protease family protein	Cellular Processes
K06998	53	Unclassified; K06998	Cellular Processes
K07173	15	S-ribosylhomocysteine lyase [EC:4.4.1.21]	Cellular Processes
K07177	6	PDZ domain-containing protein	Cellular Processes
K07645	33	two-component system, OmpR family, sensor histidine kinase QseC	Cellular Processes
K07666	3	two-component system, OmpR family, response regulator QseB	Cellular Processes
K07667	53	two-component system, OmpR family, KDP operon response regulator	Cellular Processes
K07680	15	two-component system, NarL family, sensor histidine kinase ComP	Cellular Processes
K07691	24	two-component system, NarL family, competent response regulator Com	Cellular Processes
K07692	37	two-component system, NarL family, response regulator DegU	Cellular Processes
K07699	1	two-component system, response regulator, stage 0 sporulation	Cellular Processes
K07707	4	two-component system, AgrA family, response regulator AgrA	Cellular Processes
K07711	10	two-component system, NtrC family, sensor histidine kinase YfhK	Cellular Processes
K07715	78	two-component system, NtrC family, response regulator YfhA	Cellular Processes
K07716	16	two-component system, cell cycle sensor histidine kinase PleC	Cellular Processes
K07782	1	LuxR family transcriptional regulator	Cellular Processes
K08139	13	MFS transporter, SP family, sugar:H+ symporter	Cellular Processes
K08605	1	coccolysin [EC:3.4.24.30]	Cellular Processes
K08738	12	cytochrome c	Cellular Processes
K08777	1	neutral peptidase B [EC:3.4.24.-]	Cellular Processes
K09936	3	hypothetical protein	Cellular Processes
K10108	11	maltose/maltodextrin transport system substrate-binding protein	Cellular Processes
K10439	21	ribose transport system substrate-binding protein	Cellular Processes
K10715	7	two-component system, sensor histidine kinase RpfC [EC:2.7.13.3]	Cellular Processes
K10912	2	two-component system, repressor protein LuxO	Cellular Processes
K10914	3	CRP/FNR family transcriptional regulator, cyclic AMP receptor	Cellular Processes
K10915	1	CAI-1 autoinducer synthase [EC:2.3.-.-]	Cellular Processes
K10917	8	PadR family transcriptional regulator, regulatory protein AphA	Cellular Processes
K11031	2	thiol-activated cytolysin	Cellular Processes
K11357	7	two-component system, cell cycle sensor histidine kinase DivJ	Cellular Processes
K11443	7	two-component system, cell cycle response regulator DivK	Cellular Processes
K11749	54	regulator of sigma E protease [EC:3.4.24.-]	Cellular Processes
K11752	32	diaminohydroxyphosphoribosylaminopyrimidine deaminase /	Cellular Processes
K12257	30	SecD/SecF fusion protein	Cellular Processes
K12368	17	dipeptide transport system substrate-binding protein	Cellular Processes
K12373	31	beta-hexosaminidase [EC:3.2.1.52]	Cellular Processes
K13063	1	phenazine biosynthesis protein phzE [EC:2.6.1.86]	Cellular Processes
K13075	16	N-acyl homoserine lactone hydrolase [EC:3.1.1.81]	Cellular Processes
K13237	3	peroxisomal 2,4-dienoyl-CoA reductase [EC:1.3.1.34]	Cellular Processes
K13245	7	c-di-GMP-specific phosphodiesterase [EC:3.1.4.52]	Cellular Processes
K13277	3	minor extracellular protease Epr [EC:3.4.21.-]	Cellular Processes
K13581	4	modification methylase [EC:2.1.1.72]	Cellular Processes
K13582	2	localization factor PodJL	Cellular Processes
K13583	3	GcrA cell cycle regulator	Cellular Processes
K13584	1	two-component system, cell cycle response regulator CtrA	Cellular Processes
K13587	41	two-component system, cell cycle sensor histidine kinase and	Cellular Processes
K13588	1	histidine phosphotransferase ChpT	Cellular Processes
K13589	2	two-component system, cell cycle response regulator CpdR	Cellular Processes
K13590	30	diguanylate cyclase	Cellular Processes
K13592	1	regulator of CtrA degradation	Cellular Processes
K13593	1	cyclic-di-GMP phosphodiesterase, flagellum assembly factor TipF	Cellular Processes
K13815	21	two-component system, response regulator RpfG	Cellular Processes
K13816	7	DSF synthase	Cellular Processes
K13820	1	flagellar biosynthetic protein FliR/FlhB	Cellular Processes

K13924	124	two-component system, chemotaxis family, CheB/CheR fusion protein	Cellular Processes	

KEGG ID	Sequences	KEGG pathway	KEGG category
K00016	26	L-lactate dehydrogenase [EC:1.1.1.27]	Organismal system
K00021	14	3-hydroxy-3-methylglutaryl-CoA reductase [EC:1.1.1.34]	Organismal system
K00044	10	estradiol 17beta-dehydrogenase [EC:1.1.1.62]	Organismal system
K00071	3	11beta-hydroxysteroid dehydrogenase [EC:1.1.1.146]	Organismal system
K00161	65	pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	Organismal system
K00162	66	pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]	Organismal system
K00232	1	acyl-CoA oxidase [EC:1.3.3.6]	Organismal system
K00249	223	acyl-CoA dehydrogenase [EC:1.3.99.3]	Organismal system
K00255	14	long-chain-acyl-CoA dehydrogenase [EC:1.3.99.13]	Organismal system
K00261	38	glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]	Organismal system
K00274	21	monoamine oxidase [EC:1.4.3.4]	Organismal system
K00383	19	glutathione reductase (NADPH) [EC:1.8.1.7]	Organismal system
K00411	10	ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.2]	Organismal system
K00412	35	ubiquinol-cytochrome c reductase cytochrome b subunit [EC:1.10.2.2]	Organismal system
K00413	8	ubiquinol-cytochrome c reductase cytochrome c1 subunit [EC:1.10.2.2]	Organismal system
K00432	7	glutathione peroxidase [EC:1.11.1.9]	Organismal system
K00507	40	stearoyl-CoA desaturase (delta-9 desaturase) [EC:1.14.19.1]	Organismal system
K00660	12	chalcone synthase [EC:2.3.1.74]	Organismal system
K00688	90	starch phosphorylase [EC:2.4.1.1]	Organismal system
K00693	14	glycogen(starch) synthase [EC:2.4.1.11]	Organismal system
K00863	8	dihydroxyacetone kinase [EC:2.7.1.29]	Organismal system
K00864	41	glycerol kinase [EC:2.7.1.30]	Organismal system
K00873	44	pyruvate kinase [EC:2.7.1.40]	Organismal system
K00965	24	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]	Organismal system
K01054	3	acylglycerol lipase [EC:3.1.1.23]	Organismal system
K01114	33	phospholipase C [EC:3.1.4.3]	Organismal system
K01115	8	phospholipase D [EC:3.1.4.4]	Organismal system
K01176	36	alpha-amylase [EC:3.2.1.1]	Organismal system
K01253	35	microsomal epoxide hydrolase [EC:3.3.2.9]	Organismal system
K01278	26	dipeptidyl-peptidase 4 [EC:3.4.14.5]	Organismal system
K01283	4	peptidyl-dipeptidase A [EC:3.4.15.1]	Organismal system
K01312	9	trypsin [EC:3.4.21.4]	Organismal system
K01322	103	prolyl oligopeptidase [EC:3.4.21.26]	Organismal system
K01325	2	tissue kallikrein [EC:3.4.21.35]	Organismal system
K01344	1	protein C (activated) [EC:3.4.21.69]	Organismal system
K01358	30	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]	Organismal system
K01389	2	neprilysin [EC:3.4.24.11]	Organismal system
K01392	9	thimet oligopeptidase [EC:3.4.24.15]	Organismal system
K01425	10	glutaminase [EC:3.5.1.2]	Organismal system
K01539	6	sodium/potassium-transporting ATPase subunit alpha [EC:3.6.3.9]	Organismal system
K01580	8	glutamate decarboxylase [EC:4.1.1.15]	Organismal system
K01593	61	aromatic-L-amino-acid decarboxylase [EC:4.1.1.28]	Organismal system
K01596	30	phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]	Organismal system
K01768	403	adenylate cyclase [EC:4.6.1.1]	Organismal system
K01834	100	phosphoglycerate mutase [EC:5.4.2.1]	Organismal system
K01897	294	long-chain acyl-CoA synthetase [EC:6.2.1.3]	Organismal system
K01915	141	glutamine synthetase [EC:6.3.1.2]	Organismal system
K02406	10	flagellin	Organismal system
K03695	75	ATP-dependent Clp protease ATP-binding subunit ClpB	Organismal system
K03781	12	catalase [EC:1.11.1.6]	Organismal system
K03841	11	fructose-1,6-bisphosphatase I [EC:3.1.3.11]	Organismal system
K04043	64	molecular chaperone DnaK	Organismal system
K04077	43	chaperonin GroEL	Organismal system
K04079	17	molecular chaperone HtpG	Organismal system
K04564	27	superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	Organismal system
K04565	6	Cu/Zn superoxide dismutase [EC:1.15.1.1]	Organismal system
K05692	2	actin beta/gamma 1	Organismal system
K06027	29	vesicle-fusing ATPase [EC:3.6.4.6]	Organismal system
K07192	11	flotillin	Organismal system

K07213	6	Unclassified; K07213	Organismal system	
K11031	2	thiol-activated cytolysin	Organismal system	
K11987	1	prostaglandin-endoperoxide synthase 2 [EC:1.14.99.1]	Organismal system	
K12340	36	outer membrane channel protein TolC	Organismal system	
K13408	2	membrane fusion protein RaxA	Organismal system	
K13409	1	ATP-binding cassette, subfamily B, bacterial RaxB	Organismal system	

KEGG category	Counts
Metabolism	41140
Environmetal Information Processing	11379
Genetic Information Processing	9314
Human Diseases	4080
Cellular Processes	7038
Organismal Systems	2542

GO ID	Sequence count	GO terms		
GO:00000	31	phosphopyruvate hydratase complex		
GO:00000	29	mannosyltransferase activity		
GO:00000	7	transition metal ion transport		
GO:00000	82	tRNA binding		
GO:00000	2	fatty-acyl-CoA binding		
GO:00001	15	sulfate assimilation		
GO:00001	133	histidine biosynthetic process		
GO:00001	28	recombinase activity		
GO:00001	173	phosphorelay sensor kinase activity		
GO:00001	63	phosphorelay response regulator activity		
GO:00001	1186	phosphorelay signal transduction system		
GO:00001	1170	nucleotide binding		
GO:00002	9	allantoin catabolic process		
GO:00002	47	polysaccharide biosynthetic process		
GO:00002	2	polysaccharide catabolic process		
GO:00002	137	magnesium ion binding		
GO:00003	3	3-hydroxyanthranilate 3,4-dioxygenase activity		
GO:00004	34	protein peptidyl-prolyl isomerization		
GO:00007	2	telomere maintenance		
GO:00007	21	adenyl-nucleotide exchange factor activity		
GO:00009	36	cell morphogenesis		
GO:00009	6	barrier septum assembly		
GO:00010	2	bacterial-type RNA polymerase core enzyme binding		
GO:00011	1	RNA polymerase II transcription cofactor activity		
GO:00015	125	pseudouridine synthesis		
GO:00018	20	nucleoside binding		
GO:00021	2	tRNA wobble position uridine thiolation		
GO:00021	47	aminoacyl-tRNA editing activity		
GO:00033	240	amino acid transmembrane transport		
GO:00036	429	nucleic acid binding		
GO:00036	2604	DNA binding		
GO:00036	61	DNA helicase activity		
GO:00036	127	damaged DNA binding		
GO:00036	59	single-stranded DNA binding		
GO:00037	821	transcription factor activity, sequence-specific DNA binding		
GO:00037	4	transcription coactivator activity		
GO:00037	541	RNA binding		
GO:00037	77	double-stranded RNA binding		
GO:00037	2	mRNA binding		
GO:00037	487	structural constituent of ribosome		
GO:00037	22	translation initiation factor activity		
GO:00037	34	translation elongation factor activity		
GO:00037	41	translation release factor activity		
GO:00037	34	peptidyl-prolyl cis-trans isomerase activity		
GO:00037	15	motor activity		
GO:00037	5	lysozyme activity		
GO:00038	4368	catalytic activity		
GO:00038	136	gamma-glutamyltransferase activity		
GO:00038	1	1-alkyl-2-acetylglycerophosphocholine esterase activity		
GO:00038	17	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase activity		
GO:00038	13	3-deoxy-7-phosphoheptulonate synthase activity		
GO:00038	9	3-beta-hydroxy-delta5-steroid dehydrogenase activity		
GO:00038	20	3-dehydroquinate dehydratase activity		
GO:00038	2	3-dehydroquinate synthase activity		
GO:00038	98	3-hydroxyacyl-CoA dehydrogenase activity		
GO:00038	26	3-methyl-2-oxobutanoate hydroxymethyltransferase activity		
GO:00038	74	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity		
GO:00038	54	6-phosphofructokinase activity		
GO:00038	26	ATP phosphoribosyltransferase activity		
GO:00038	30	CTP synthase activity		
GO:00038	11	D-arabinono-1,4-lactone oxidase activity		
GO:00038	181	DNA-directed DNA polymerase activity		
GO:00038	69	DNA primase activity		
GO:00038	190	DNA-directed RNA polymerase activity		
GO:00039	14	alkylbase DNA N-glycosylase activity		
GO:00039	64	DNA-(apurinic or apyrimidinic site) lyase activity		
GO:00039	59	DNA ligase (ATP) activity		
GO:00039	63	DNA ligase (NAD+) activity		
GO:00039	28	DNA photolyase activity		
GO:00039	77	DNA topoisomerase activity		
GO:00039	158	DNA topoisomerase type II (ATP-hydrolyzing) activity		
GO:00039	27	FMN adenylyltransferase activity		
GO:00039	23	GMP synthase (glutamine-hydrolyzing) activity		
GO:00039	62	GTPase activity		
GO:00039	8	GTP cyclohydrolase activity		
GO:00039	23	GTP cyclohydrolase II activity		
GO:00039	28	IMP cyclohydrolase activity		
GO:00039	42	N-acetyl-gamma-glutamyl-phosphate reductase activity		
GO:00039	35	NAD+ kinase activity		
GO:00039	19	acetyl-CoA carboxylase activity		
GO:00039	2	acid phosphatase activity		
GO:00039	7	aconitate hydratase activity		
GO:00039	16	acyl-CoA dehydrogenase activity		
GO:00039	1	acyl-CoA oxidase activity		
GO:00040	28	adenosylhomocysteinase activity		
GO:00040	3	adenosylmethionine decarboxylase activity		
GO:00040	43	adenylosuccinate synthase activity		
GO:00040	15	adenylylsulfate kinase activity		
GO:00040	8	allantoicase activity		
GO:00040	2	amidase activity		
GO:00040	27	aminoacyl-tRNA hydrolase activity		
GO:00040	30	argininosuccinate synthase activity		
GO:00040	7	arginyltransferase activity		
GO:00040	24	arylformamidase activity		
GO:00040	152	asparagine synthase (glutamine-hydrolyzing) activity		
GO:00040	6	aspartate 1-decarboxylase activity		
GO:00040	6	aspartate-ammonia ligase activity		
GO:00040	24	carbonate dehydratase activity		
GO:00040	11	catalase activity		
GO:00041	34	chorismate synthase activity		
GO:00041	7	coproporphyrinogen oxidase activity		
GO:00041	2	3',5'-cyclic-AMP phosphodiesterase activity		
GO:00041	2	cytidine deaminase activity		

GO:00041	18	cytidylate kinase activity		
GO:00041	185	cytochrome-c oxidase activity		
GO:00041	68	4-alpha-glucanotransferase activity		
GO:00041	17	amylo-alpha-1,6-glucosidase activity		
GO:00041	19	dephospho-CoA kinase activity		
GO:00041	5	diacylglycerol kinase activity		
GO:00041	59	diacylglycerol O-acyltransferase activity		
GO:00041	12	dihydrofolate reductase activity		
GO:00041	13	dihydroneopterin aldolase activity		
GO:00041	37	electron-transferring-flavoprotein dehydrogenase activity		
GO:00041	107	ATP-dependent peptidase activity		
GO:00041	93	aminopeptidase activity		
GO:00041	78	metallocarboxypeptidase activity		
GO:00041	44	serine-type carboxypeptidase activity		
GO:00041	19	aspartic-type endopeptidase activity		
GO:00041	22	cysteine-type endopeptidase activity		
GO:00042	393	metalloendopeptidase activity		
GO:00042	422	serine-type endopeptidase activity		
GO:00042	25	threonine-type endopeptidase activity		
GO:00043	3	3-oxoacyl-[acyl-carrier-protein] synthase activity		
GO:00043	32	ferrochelatase activity		
GO:00043	22	formate-tetrahydrofolate ligase activity		
GO:00043	16	fructose-bisphosphate aldolase activity		
GO:00043	9	glucokinase activity		
GO:00043	39	glucose-6-phosphate dehydrogenase activity		
GO:00043	52	glucose-6-phosphate isomerase activity		
GO:00043	4	glucosylceramidase activity		
GO:00043	37	glutamate dehydrogenase (NAD+) activity		
GO:00043	115	glutamate-ammonia ligase activity		
GO:00043	48	glutamate-cysteine ligase activity		
GO:00043	31	glutamate N-acetyltransferase activity		
GO:00043	10	glutaminase activity		
GO:00043	21	glutathione synthase activity		
GO:00043	17	glycerol-3-phosphate dehydrogenase [NAD+] activity		
GO:00043	14	glycerone kinase activity		
GO:00043	63	glycine dehydrogenase (decarboxylating) activity		
GO:00043	5	guanylate cyclase activity		
GO:00043	43	histidinol dehydrogenase activity		
GO:00044	27	homogentisate 1,2-dioxygenase activity		
GO:00044	2	hydroxyethylthiazole kinase activity		
GO:00044	28	hydroxymethylbilane synthase activity		
GO:00044	17	hydroxymethylglutaryl-CoA reductase (NADPH) activity		
GO:00044	14	imidazoleglycerol-phosphate dehydratase activity		
GO:00044	19	indole-3-glycerol-phosphate synthase activity		
GO:00044	48	inorganic diphosphatase activity		
GO:00044	10	isocitrate dehydrogenase (NADP+) activity		
GO:00044	12	isocitrate lyase activity		
GO:00044	16	ketol-acid reductoisomerase activity		
GO:00044	47	malate dehydrogenase (decarboxylating) (NAD+) activity		
GO:00044	22	malate synthase activity		
GO:00044	19	mannose-6-phosphate isomerase activity		
GO:00044	19	methionine adenosyltransferase activity		
GO:00044	33	methylenetetrahydrofolate dehydrogenase (NADP+) activity		
GO:00044	53	methylenetetrahydrofolate reductase (NAD(P)H) activity		
GO:00044	1	monooxygenase activity		
GO:00044	6	N,N-dimethylaniline monooxygenase activity		
GO:00045	1	squalene monooxygenase activity		
GO:00045	12	inositol-3-phosphate synthase activity		
GO:00045	35	nicotinate-nucleotide diphosphorylase (carboxylating) activity		
GO:00045	2	nitric-oxide synthase activity		
GO:00045	23	nuclease activity		
GO:00045	101	endonuclease activity		
GO:00045	19	endodeoxyribonuclease activity		
GO:00045	9	endoribonuclease activity		
GO:00045	10	RNA-DNA hybrid ribonuclease activity		
GO:00045	26	ribonuclease III activity		
GO:00045	18	ribonuclease P activity		
GO:00045	15	nucleoside diphosphate kinase activity		
GO:00045	438	hydrolase activity, hydrolyzing O-glycosyl compounds		
GO:00045	5	alpha,alpha-trehalase activity		
GO:00045	22	alpha-galactosidase activity		
GO:00045	7	alpha-mannosidase activity		
GO:00045	18	alpha-L-fucosidase activity		
GO:00045	5	beta-fructofuranosidase activity		
GO:00045	13	beta-galactosidase activity		
GO:00045	1	chitinase activity		
GO:00045	2	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity		
GO:00045	5	sucrose alpha-glucosidase activity		
GO:00045	28	orotidine-5'-phosphate decarboxylase activity		
GO:00045	21	pantoate-beta-alanine ligase activity		
GO:00045	30	pantothenate kinase activity		
GO:00046	34	peroxidase activity		
GO:00046	7	glutathione peroxidase activity		
GO:00046	14	phosphatidylserine decarboxylase activity		
GO:00046	30	phosphoenolpyruvate carboxykinase activity		
GO:00046	20	phosphoenolpyruvate carboxykinase (ATP) activity		
GO:00046	138	phosphogluconate dehydrogenase (decarboxylating) activity		
GO:00046	35	phosphoglycerate kinase activity		
GO:00046	13	phosphoglycerate mutase activity		
GO:00046	8	phospholipase activity		
GO:00046	31	phosphopyruvate hydratase activity		
GO:00046	8	phosphoribosyl-AMP cyclohydrolase activity		
GO:00046	21	phosphoribosylanthranilate isomerase activity		
GO:00046	27	phosphoribosylaminoimidazolecarboxamide formyltransferase activity		
GO:00046	2	polygalacturonase activity		
GO:00046	18	porphobilinogen synthase activity		
GO:00046	92	prenyltransferase activity		
GO:00046	25	prephenate dehydratase activity		
GO:00046	21	prephenate dehydrogenase (NADP+) activity		
GO:00046	12	protein-arginine deiminase activity		
GO:00046	11	protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity		
GO:00046	375	protein kinase activity		
GO:00046	88	protein histidine kinase activity		
GO:00046	1	protein serine/threonine kinase activity		

GO:00047	39	protein-L-isoaspartate (D-aspartate) O-methyltransferase activity		
GO:00047	1	protein tyrosine phosphatase activity		
GO:00047	55	pyridoxamine-phosphate oxidase activity		
GO:00047	42	pyruvate kinase activity		
GO:00047	1	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor		
GO:00047	7	ribose-5-phosphate isomerase activity		
GO:00047	37	shikimate 3-dehydrogenase (NADP+) activity		
GO:00047	16	sulfate adenylyltransferase (ATP) activity		
GO:00047	21	superoxide dismutase activity		
GO:00047	21	thiamine-phosphate diphosphorylase activity		
GO:00047	7	thymidine kinase activity		
GO:00047	9	thymidylate synthase activity		
GO:00048	409	transposase activity		
GO:00048	5	triglyceride lipase activity		
GO:00048	17	triose-phosphate isomerase activity		
GO:00048	8	tRNA adenylyltransferase activity		
GO:00048	696	aminoacyl-tRNA ligase activity		
GO:00048	71	alanine-tRNA ligase activity		
GO:00048	65	arginine-tRNA ligase activity		
GO:00048	46	glycine-tRNA ligase activity		
GO:00048	71	phenylalanine-tRNA ligase activity		
GO:00048	12	proline-tRNA ligase activity		
GO:00048	3	threonine-tRNA ligase activity		
GO:00048	11	tryptophan 2,3-dioxygenase activity		
GO:00048	29	tryptophan synthase activity		
GO:00048	2	ubiquitin-protein transferase activity		
GO:00048	22	uroporphyrinogen-III synthase activity		
GO:00048	40	uroporphyrinogen decarboxylase activity		
GO:00048	10	endopeptidase inhibitor activity		
GO:00048	213	signal transducer activity		
GO:00048	213	receptor activity		
GO:00050	1	GTPase activator activity		
GO:00051	45	structural molecule activity		
GO:00052	1	extracellular matrix structural constituent		
GO:00052	1692	transporter activity		
GO:00052	18	ion channel activity		
GO:00052	4	inward rectifier potassium channel activity		
GO:00052	26	voltage-gated chloride channel activity		
GO:00053	31	inorganic phosphate transmembrane transporter activity		
GO:00053	5	neurotransmitter:sodium symporter activity		
GO:00053	13	iron ion transmembrane transporter activity		
GO:00054	1	monovalent cation:proton antiporter activity		
GO:00054	15	ATP:ADP antiporter activity		
GO:00054	37	binding		
GO:00055	381	iron ion binding		
GO:00055	205	copper ion binding		
GO:00055	83	calcium ion binding		
GO:00055	882	protein binding		
GO:00055	6227	ATP binding		
GO:00055	390	GTP binding		
GO:00055	20	folic acid binding		
GO:00055	48	extracellular region		
GO:00056	11	extracellular space		
GO:00056	7	cell wall		
GO:00056	403	intracellular		
GO:00056	2	nucleus		
GO:00056	1	anaphase-promoting complex		
GO:00056	22	chromosome		
GO:00057	44	extrachromosomal circular DNA		
GO:00057	1	nucleolus		
GO:00057	521	cytoplasm		
GO:00057	1	peroxisome		
GO:00058	25	proteasome core complex		
GO:00058	495	ribosome		
GO:00058	175	plasma membrane		
GO:00058	13	integral component of plasma membrane		
GO:00059	1466	carbohydrate metabolic process		
GO:00059	5	polysaccharide metabolic process		
GO:00059	17	glycogen catabolic process		
GO:00059	5	trehalose metabolic process		
GO:00059	57	trehalose biosynthetic process		
GO:00059	2	monosaccharide metabolic process		
GO:00060	14	fucose metabolic process		
GO:00060	50	glucose metabolic process		
GO:00060	13	glucose catabolic process		
GO:00060	1	UDP-glucose metabolic process		
GO:00060	25	galactose metabolic process		
GO:00060	12	mannose metabolic process		
GO:00060	12	inositol biosynthetic process		
GO:00060	1	chitin catabolic process		
GO:00060	23	amino sugar metabolic process		
GO:00060	42	UDP-N-acetylglucosamine metabolic process		
GO:00060	13	glucuronate catabolic process		
GO:00060	34	glycerol metabolic process		
GO:00060	16	acetyl-CoA metabolic process		
GO:00060	114	gluconeogenesis		
GO:00060	231	glycolytic process		
GO:00060	22	glyoxylate cycle		
GO:00060	12	pentose-phosphate shunt		
GO:00060	56	tricarboxylic acid cycle		
GO:00061	5	fumarate metabolic process		
GO:00061	23	regulation of carbohydrate metabolic process		
GO:00061	92	nucleobase-containing compound metabolic process		
GO:00061	94	purine nucleotide biosynthetic process		
GO:00061	15	nucleoside diphosphate phosphorylation		
GO:00061	23	GMP biosynthetic process		
GO:00061	5	cGMP biosynthetic process		
GO:00061	15	GTP biosynthetic process		
GO:00061	1	IMP biosynthetic process		
GO:00061	34	'de novo' IMP biosynthetic process		
GO:00061	2	cAMP catabolic process		
GO:00062	28	'de novo' pyrimidine nucleobase biosynthetic process		
GO:00062	8	pyrimidine nucleoside metabolic process		
GO:00062	30	pyrimidine nucleotide biosynthetic process		

GO:00062	15	UTP biosynthetic process		
GO:00062	30	dTMP biosynthetic process		
GO:00062	15	CTP biosynthetic process		
GO:00062	7	DNA metabolic process		
GO:00062	486	DNA replication		
GO:00062	234	DNA topological change		
GO:00062	58	DNA replication, synthesis of RNA primer		
GO:00062	1	DNA replication initiation		
GO:00062	1	plasmid maintenance		
GO:00062	371	DNA repair		
GO:00062	9	regulation of DNA repair		
GO:00062	121	base-excision repair		
GO:00062	23	nucleotide-excision repair		
GO:00062	155	mismatch repair		
GO:00063	36	double-strand break repair via nonhomologous end joining		
GO:00063	41	DNA modification		
GO:00063	100	DNA methylation		
GO:00063	11	DNA catabolic process		
GO:00063	360	DNA recombination		
GO:00063	409	transposition, DNA-mediated		
GO:00063	2	DNA packaging		
GO:00063	190	transcription, DNA-templated		
GO:00063	511	DNA-templated transcription, initiation		
GO:00063	6	DNA-templated transcription, termination		
GO:00063	1551	regulation of transcription, DNA-templated		
GO:00063	1	regulation of transcription from RNA polymerase II promoter		
GO:00063	96	rRNA processing		
GO:00063	1	tRNA splicing, via endonucleolytic cleavage and ligation		
GO:00063	284	RNA processing		
GO:00063	1	mRNA processing		
GO:00064	32	tRNA modification		
GO:00064	1	RNA catabolic process		
GO:00064	6	mRNA catabolic process		
GO:00064	488	translation		
GO:00064	40	translational initiation		
GO:00064	34	translational elongation		
GO:00064	48	translational termination		
GO:00064	678	tRNA aminoacylation for protein translation		
GO:00064	71	alanyl-tRNA aminoacylation		
GO:00064	65	arginyl-tRNA aminoacylation		
GO:00064	46	glycyl-tRNA aminoacylation		
GO:00064	1	phenylalanyl-tRNA aminoacylation		
GO:00064	12	prolyl-tRNA aminoacylation		
GO:00064	7	regulation of translational fidelity		
GO:00064	152	protein folding		
GO:00064	2	protein complex assembly		
GO:00064	103	cellular protein modification process		
GO:00064	358	protein phosphorylation		
GO:00064	3	protein dephosphorylation		
GO:00064	11	C-terminal protein methylation		
GO:00064	2	protein glycosylation		
GO:00064	29	protein O-linked glycosylation		
GO:00065	1	GPI anchor metabolic process		
GO:00065	1	GPI anchor biosynthetic process		
GO:00065	1512	proteolysis		
GO:00065	1	ubiquitin-dependent protein catabolic process		
GO:00065	245	cellular amino acid metabolic process		
GO:00065	6	alanine biosynthetic process		
GO:00065	8	arginine metabolic process		
GO:00065	61	arginine biosynthetic process		
GO:00065	8	arginine catabolic process		
GO:00065	158	asparagine biosynthetic process		
GO:00065	3	cysteine biosynthetic process from serine		
GO:00065	56	glutamate biosynthetic process		
GO:00065	25	glutamine metabolic process		
GO:00065	12	glycine biosynthetic process		
GO:00065	63	glycine catabolic process		
GO:00065	53	methionine metabolic process		
GO:00065	19	S-adenosylmethionine biosynthetic process		
GO:00065	27	L-phenylalanine catabolic process		
GO:00065	50	tryptophan metabolic process		
GO:00065	27	tyrosine metabolic process		
GO:00065	21	tyrosine biosynthetic process		
GO:00066	4	protein targeting		
GO:00066	64	SRP-dependent cotranslational protein targeting to membrane		
GO:00066	205	lipid metabolic process		
GO:00066	103	fatty acid metabolic process		
GO:00066	97	fatty acid biosynthetic process		
GO:00066	1	fatty acid beta-oxidation		
GO:00066	4	sphingolipid metabolic process		
GO:00066	9	steroid biosynthetic process		
GO:00067	72	cellular aromatic compound metabolic process		
GO:00067	19	tetrahydrobiopterin biosynthetic process		
GO:00067	40	one-carbon metabolic process		
GO:00067	35	NADP biosynthetic process		
GO:00067	7	NADP catabolic process		
GO:00067	92	ubiquinone biosynthetic process		
GO:00067	136	glutathione metabolic process		
GO:00067	27	glutathione biosynthetic process		
GO:00067	13	folic acid-containing compound metabolic process		
GO:00067	61	Mo-molybdopterin cofactor biosynthetic process		
GO:00067	56	porphyrin-containing compound biosynthetic process		
GO:00067	32	heme biosynthetic process		
GO:00067	27	heme a biosynthetic process		
GO:00067	20	phosphate-containing compound metabolic process		
GO:00068	24	superoxide metabolic process		
GO:00068	328	nitrogen compound metabolic process		
GO:00068	14	regulation of nitrogen utilization		
GO:00068	2	nitric oxide biosynthetic process		
GO:00068	3644	transport		
GO:00068	3	ion transport		
GO:00068	248	cation transport		
GO:00068	112	potassium ion transport		
GO:00068	42	sodium ion transport		

GO:00068	31	phosphate ion transport		
GO:00068	26	chloride transport		
GO:00068	13	high-affinity iron ion transmembrane transport		
GO:00068	31	dicarboxylic acid transport		
GO:00068	5	neurotransmitter transport		
GO:00068	48	drug transmembrane transport		
GO:00068	22	amino acid transport		
GO:00068	5	lipid transport		
GO:00068	1	cellular copper ion homeostasis		
GO:00068	36	cellular iron ion homeostasis		
GO:00068	15	regulation of pH		
GO:00068	4	intracellular protein transport		
GO:00069	18	movement of cell or subcellular component		
GO:00069	141	chemotaxis		
GO:00069	154	response to stress		
GO:00069	78	response to oxidative stress		
GO:00070	1	mitochondrion organization		
GO:00070	64	cell cycle		
GO:00070	60	chromosome segregation		
GO:00071	28	cell communication		
GO:00071	19	cell adhesion		
GO:00071	3	homophilic cell adhesion via plasma membrane adhesion molecules		
GO:00071	199	signal transduction		
GO:00071	1	G-protein coupled receptor signaling pathway		
GO:00072	3	Notch signaling pathway		
GO:00072	1	small GTPase mediated signal transduction		
GO:00076	1	circadian rhythm		
GO:00080	1	beta-catenin binding		
GO:00080	56	ATP-dependent helicase activity		
GO:00080	193	tRNA processing		
GO:00080	14	enzyme activator activity		
GO:00080	285	N-acetyltransferase activity		
GO:00080	36	phosphoric diester hydrolase activity		
GO:00080	10	5S rRNA binding		
GO:00081	1	galactoside 2-alpha-L-fucosyltransferase activity		
GO:00081	25	UDP-glucose:hexose-1-phosphate uridylyltransferase activity		
GO:00081	33	peptide-methionine (S)-S-oxide reductase activity		
GO:00081	2	sarcosine oxidase activity		
GO:00081	19	4-alpha-hydroxytetrahydrobiopterin dehydratase activity		
GO:00081	10	primary amine oxidase activity		
GO:00081	400	transcription factor binding		
GO:00081	62	NADH dehydrogenase (ubiquinone) activity		
GO:00081	2	protein tyrosine/serine/threonine phosphatase activity		
GO:00081	7	sulfotransferase activity		
GO:00081	4852	metabolic process		
GO:00081	660	methyltransferase activity		
GO:00081	100	N-methyltransferase activity		
GO:00081	39	O-methyltransferase activity		
GO:00081	136	RNA methyltransferase activity		
GO:00081	7	tRNA (guanine-N7-)-methyltransferase activity		
GO:00081	42	glycogen phosphorylase activity		
GO:00081	19	ferrous iron binding		
GO:00081	65	ferric iron binding		
GO:00082	117	peptidase activity		
GO:00082	10	cysteine-type peptidase activity		
GO:00082	309	serine-type peptidase activity		
GO:00082	45	metallopeptidase activity		
GO:00082	7	dipeptidyl-peptidase activity		
GO:00082	3	5'-nucleotidase activity		
GO:00082	716	zinc ion binding		
GO:00082	53	sulfate transport		
GO:00082	5	lipid binding		
GO:00082	3	spermidine biosynthetic process		
GO:00082	67	isoprenoid biosynthetic process		
GO:00083	147	cation transmembrane transporter activity		
GO:00083	26	regulation of cell shape		
GO:00084	260	3'-5' exonuclease activity		
GO:00084	66	CoA-transferase activity		
GO:00084	2	fucosyltransferase activity		
GO:00084	11	selenium binding		
GO:00084	48	RNA ligase activity		
GO:00084	25	queuine tRNA-ribosyltransferase activity		
GO:00084	265	transaminase activity		
GO:00084	135	sulfuric ester hydrolase activity		
GO:00084	3	gamma-glutamyl carboxylase activity		
GO:00085	59	ammonium transmembrane transporter activity		
GO:00085	5	acetyl-CoA transporter activity		
GO:00085	1	riboflavin kinase activity		
GO:00085	28	potassium-transporting ATPase activity		
GO:00085	53	protein transporter activity		
GO:00086	121	lipid biosynthetic process		
GO:00086	18	peptidyl-lysine modification to peptidyl-hypusine		
GO:00086	50	pyridoxine biosynthetic process		
GO:00086	70	queuosine biosynthetic process		
GO:00086	42	small protein activating enzyme activity		
GO:00086	3	hexose transport		
GO:00086	25	rRNA methyltransferase activity		
GO:00086	56	cellular amino acid biosynthetic process		
GO:00086	125	phospholipid biosynthetic process		
GO:00086	1	DNA topoisomerase (ATP-hydrolyzing) inhibitor activity		
GO:00086	174	penicillin binding		
GO:00086	40	1-deoxy-D-xylulose-5-phosphate synthase activity		
GO:00086	1	2-dehydro-3-deoxygalactonokinase activity		
GO:00086	30	2-dehydropantoate 2-reductase activity		
GO:00086	18	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase activity		
GO:00086	17	3,4-dihydroxy-2-butanone-4-phosphate synthase activity		
GO:00087	94	5-amino-6-(5-phosphoribosylamino)uracil reductase activity		
GO:00087	25	methionine synthase activity		
GO:00087	64	D-alanine-D-alanine ligase activity		
GO:00087	10	DNA-3-methyladenine glycosylase activity		
GO:00087	3	L-arabinose isomerase activity		
GO:00087	14	L-fucose isomerase activity		
GO:00087	9	L-rhamnose isomerase activity		
GO:00087	56	N-acetylmuramoyl-L-alanine amidase activity		

GO:00087	18	NAD(P)+ transhydrogenase (AB-specific) activity		
GO:00087	6	S-adenosylmethionine-dependent methyltransferase activity		
GO:00087	25	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity		
GO:00087	143	UDP-N-acetylmuramate dehydrogenase activity		
GO:00087	11	UDP-galactopyranose mutase activity		
GO:00087	1	[acyl-carrier-protein] phosphodiesterase activity		
GO:00087	11	[isocitrate dehydrogenase (NADP+)] kinase activity		
GO:00087	19	[protein-PII] uridylyltransferase activity		
GO:00087	3	acetaldehyde dehydrogenase (acetylating) activity		
GO:00087	3	arginine N-succinyltransferase activity		
GO:00087	5	arginine decarboxylase activity		
GO:00088	4	cellulase activity		
GO:00088	3	chloramphenicol O-acetyltransferase activity		
GO:00088	1	citrate CoA-transferase activity		
GO:00088	8	cob(I)yrinic acid a,c-diamide adenosyltransferase activity		
GO:00088	3	cytochrome o ubiquinol oxidase activity		
GO:00088	13	dCTP deaminase activity		
GO:00088	33	dTDP-4-dehydrorhamnose 3,5-epimerase activity		
GO:00088	26	diaminopimelate epimerase activity		
GO:00088	22	4-hydroxy-tetrahydrodipicolinate reductase		
GO:00088	5	ethanolamine ammonia-lyase activity		
GO:00088	49	exodeoxyribonuclease VII activity		
GO:00088	6	glucuronate isomerase activity		
GO:00088	55	[glutamate-ammonia-ligase] adenylyltransferase activity		
GO:00088	42	glutamyl-tRNA reductase activity		
GO:00088	12	glycerate kinase activity		
GO:00088	19	holo-[acyl-carrier-protein] synthase activity		
GO:00088	53	S-adenosylmethionine-homocysteine S-methyltransferase activity		
GO:00088	1	homoserine O-succinyltransferase activity		
GO:00089	12	leucyltransferase activity		
GO:00089	28	lipid-A-disaccharide synthase activity		
GO:00089	7	mannonate dehydratase activity		
GO:00089	5	nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase activity		
GO:00089	8	phosphatidylglycerophosphatase activity		
GO:00089	56	phospho-N-acetylmuramoyl-pentapeptide-transferase activity		
GO:00089	39	phosphoenolpyruvate carboxylase activity		
GO:00089	21	prephenate dehydrogenase activity		
GO:00089	10	protein-N(PI)-phosphohistidine-sugar phosphotransferase activity		
GO:00089	63	protein-glutamate methylesterase activity		
GO:00089	23	quinolinate synthetase A activity		
GO:00090	3	serine O-acetyltransferase activity		
GO:00090	36	serine-type D-Ala-D-Ala carboxypeptidase activity		
GO:00090	5	site-specific DNA-methyltransferase (adenine-specific) activity		
GO:00090	1	N-succinylarginine dihydrolase activity		
GO:00090	11	tetraacyldisaccharide 4'-kinase activity		
GO:00090	3	Type II site-specific deoxyribonuclease activity		
GO:00090	1	xylan 1,4-beta-xylosidase activity		
GO:00090	7	pentose-phosphate shunt, non-oxidative branch		
GO:00090	538	electron carrier activity		
GO:00090	10	catabolic process		
GO:00090	1671	biosynthetic process		
GO:00090	119	aerobic respiration		
GO:00090	49	aromatic amino acid family biosynthetic process		
GO:00090	2	branched-chain amino acid biosynthetic process		
GO:00090	99	methionine biosynthetic process		
GO:00090	48	lysine biosynthetic process via diaminopimelate		
GO:00090	25	L-phenylalanine biosynthetic process		
GO:00091	22	lipopolysaccharide biosynthetic process		
GO:00091	188	nucleoside metabolic process		
GO:00091	3	nucleotide metabolic process		
GO:00091	12	nucleotide biosynthetic process		
GO:00091	41	nucleotide catabolic process		
GO:00091	14	deoxyribonucleoside diphosphate metabolic process		
GO:00091	179	cyclic nucleotide biosynthetic process		
GO:00092	33	thiamine biosynthetic process		
GO:00092	176	riboflavin biosynthetic process		
GO:00092	75	cobalamin biosynthetic process		
GO:00092	64	lipid A biosynthetic process		
GO:00092	9	glycolipid biosynthetic process		
GO:00092	26	protein lipoylation		
GO:00092	5	peptidoglycan biosynthetic process		
GO:00092	61	peptidoglycan catabolic process		
GO:00092	24	peptidoglycan turnover		
GO:00092	25	cellular response to starvation		
GO:00092	7	Gram-negative-bacterium-type cell wall		
GO:00092	19	cell outer membrane		
GO:00092	15	bacterial-type flagellum		
GO:00092	7	pilus		
GO:00092	4	unidirectional conjugation		
GO:00092	37	DNA mediated transformation		
GO:00092	2	nucleoid		
GO:00093	161	protein secretion		
GO:00093	5	DNA restriction-modification system		
GO:00093	10	amine metabolic process		
GO:00093	19	acetyl-CoA carboxylase complex		
GO:00093	5	exodeoxyribonuclease VII complex		
GO:00093	13	beta-galactosidase complex		
GO:00093	1	citrate lyase complex		
GO:00093	15	riboflavin synthase complex		
GO:00093	59	DNA polymerase III complex		
GO:00093	52	four-way junction helicase activity		
GO:00093	13	2'-deoxyribonucleotide metabolic process		
GO:00093	72	folic acid-containing compound biosynthetic process		
GO:00094	36	phosphoenolpyruvate-dependent sugar phosphotransferase system		
GO:00094	2	toxin biosynthetic process		
GO:00094	2	pathogenesis		
GO:00094	1	bacterial-type flagellum hook		
GO:00094	11	bacterial-type flagellum basal body		
GO:00094	2	bacterial-type flagellum basal body, distal rod, L ring		
GO:00094	4	bacterial-type flagellum basal body, distal rod, P ring		
GO:00094	38	SOS response		
GO:00094	58	NAD biosynthetic process		
GO:00094	1	cyanate metabolic process		
GO:00094	12	putrescine biosynthetic process		

GO:00094	140	RNA modification		
GO:00094	6	plastoquinol--plastocyanin reductase activity		
GO:00095	11	detection of visible light		
GO:00096	28	hydrogen-translocating pyrophosphatase activity		
GO:00097	2	photosynthetic electron transport in photosystem II		
GO:00099	2	cytidine deamination		
GO:00099	125	pseudouridine synthase activity		
GO:00100	27	response to organic substance		
GO:00100	10	response to metal ion		
GO:00101	178	FMN binding		
GO:00102	1	chlorophyllide a oxygenase [overall] activity		
GO:00103	1	acireductone dioxygenase [iron(II)-requiring] activity		
GO:00104	8	regulation of gene expression		
GO:00104	17	proteasomal protein catabolic process		
GO:00125	6	vesicle membrane		
GO:00150	37	heme-copper terminal oxidase activity		
GO:00150	2	[heparan sulfate]-glucosamine N-sulfotransferase activity		
GO:00150	172	protein transport		
GO:00150	74	protein disulfide oxidoreductase activity		
GO:00150	384	DNA integration		
GO:00150	1	ion transmembrane transporter activity		
GO:00150	70	hydrogen ion transmembrane transporter activity		
GO:00150	37	potassium ion transmembrane transporter activity		
GO:00150	26	ferrous iron transmembrane transporter activity		
GO:00150	15	nickel cation transmembrane transporter activity		
GO:00151	4	arsenite transmembrane transporter activity		
GO:00151	47	chromate transmembrane transporter activity		
GO:00151	2	phosphate ion transmembrane transporter activity		
GO:00151	53	sulfate transmembrane transporter activity		
GO:00151	5	gluconate transmembrane transporter activity		
GO:00151	13	lactate transmembrane transporter activity		
GO:00151	3	rhamnose transmembrane transporter activity		
GO:00151	37	polysaccharide transmembrane transporter activity		
GO:00151	240	amino acid transmembrane transporter activity		
GO:00152	5	biotin transporter activity		
GO:00152	15	heme transporter activity		
GO:00152	48	drug transmembrane transporter activity		
GO:00152	2	porin activity		
GO:00152	48	antiporter activity		
GO:00152	107	solute:proton antiporter activity		
GO:00153	10	sodium-dependent phosphate transmembrane transporter activity		
GO:00154	2	P-P-bond-hydrolysis-driven protein transmembrane transporter activity		
GO:00154	1	cholesterol binding		
GO:00155	4	glutamate:sodium symporter activity		
GO:00155	4	C4-dicarboxylate transmembrane transporter activity		
GO:00155	2	p-aminobenzoyl-glutamate uptake transmembrane transporter activity		
GO:00156	9	type II protein secretion system complex		
GO:00156	9	protein secretion by the type II secretion system		
GO:00156	1	monovalent inorganic cation transport		
GO:00156	26	ferrous iron transport		
GO:00156	59	ammonium transport		
GO:00157	4	arsenite transport		
GO:00157	47	chromate transport		
GO:00157	13	lactate transport		
GO:00157	4	C4-dicarboxylate transport		
GO:00157	45	polysaccharide transport		
GO:00158	4	L-glutamate transport		
GO:00158	5	biotin transport		
GO:00158	15	heme transport		
GO:00159	12	mannosidase activity		
GO:00159	3	glucosidase activity		
GO:00159	56	glutamate synthase activity		
GO:00159	2	large ribosomal subunit		
GO:00159	17	coenzyme A metabolic process		
GO:00159	19	coenzyme A biosynthetic process		
GO:00159	47	pantothenate biosynthetic process		
GO:00159	35	methanogenesis		
GO:00159	1	guanosine tetraphosphate metabolic process		
GO:00159	39	carbon fixation		
GO:00159	87	photosynthesis		
GO:00159	119	ATP synthesis coupled proton transport		
GO:00159	13	ATP hydrolysis coupled proton transport		
GO:00159	29	proton transport		
GO:00159	87	chlorophyll biosynthetic process		
GO:00160	5394	membrane		
GO:00160	2979	integral component of membrane		
GO:00160	6	lipid catabolic process		
GO:00160	18	carbohydrate biosynthetic process		
GO:00160	1	Wnt signaling pathway		
GO:00161	82	terpenoid biosynthetic process		
GO:00161	13	carotenoid biosynthetic process		
GO:00161	8	translation release factor activity, codon specific		
GO:00161	98	nickel cation binding		
GO:00161	17	urocanate hydratase activity		
GO:00162	113	antioxidant activity		
GO:00162	71	iron-sulfur cluster assembly		
GO:00163	183	kinase activity		
GO:00163	195	phosphorylation		
GO:00163	36	dephosphorylation		
GO:00164	16	acetyltransferase activity		
GO:00164	6	tRNA (adenine-N1-)-methyltransferase activity		
GO:00164	1	tRNA cytidylyltransferase activity		
GO:00164	1	myosin complex		
GO:00164	3	pyrophosphatase activity		
GO:00164	5017	oxidoreductase activity		
GO:00165	1	mediator complex		
GO:00165	49	amino acid binding		
GO:00165	7	protein arginylation		
GO:00166	3	nuclear speck		
GO:00166	176	oxidoreductase activity, acting on CH-OH group of donors		
GO:00166	213	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor		
GO:00166	108	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor		
GO:00166	105	oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor		
GO:00166	69	oxidoreductase activity, acting on the aldehyde or oxo group of donors, iron-sulfur protein as acceptor		

GO:00166	516	oxidoreductase activity, acting on the CH-CH group of donors		
GO:00166	56	oxidoreductase activity, acting on the CH-NH2 group of donors		
GO:00166	3	oxidoreductase activity, acting on the CH-NH group of donors		
GO:00166	94	oxidoreductase activity, acting on NAD(P)H		
GO:00166	2	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor		
GO:00167	407	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen		
GO:00167	6	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into b		
GO:00167	48	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of two atoms of oxygen into one donc		
GO:00167	17	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen		
GO:00167	2	oxidoreductase activity, acting on iron-sulfur proteins as donors		
GO:00167	328	transferase activity		
GO:00167	83	hydroxymethyl-, formyl- and related transferase activity		
GO:00167	78	carboxyl- or carbamoyltransferase activity		
GO:00167	315	transferase activity, transferring acyl groups		
GO:00167	347	transferase activity, transferring acyl groups other than amino-acyl groups		
GO:00167	5	transferase activity, transferring amino-acyl groups		
GO:00167	1	glutathione gamma-glutamylcysteinyltransferase activity		
GO:00167	139	transferase activity, transferring glycosyl groups		
GO:00167	68	transferase activity, transferring hexosyl groups		
GO:00167	16	transferase activity, transferring pentosyl groups		
GO:00167	133	transferase activity, transferring alkyl or aryl (other than methyl) groups		
GO:00167	104	transferase activity, transferring phosphorus-containing groups		
GO:00167	120	phosphotransferase activity, alcohol group as acceptor		
GO:00167	29	phosphotransferase activity, carboxyl group as acceptor		
GO:00167	302	nucleotidyltransferase activity		
GO:00167	73	phosphotransferase activity, for other substituted phosphate groups		
GO:00167	16	sulfurtransferase activity		
GO:00167	1690	hydrolase activity		
GO:00167	101	hydrolase activity, acting on ester bonds		
GO:00167	2	thiolester hydrolase activity		
GO:00167	22	phosphatase activity		
GO:00167	21	hydrolase activity, acting on glycosyl bonds		
GO:00167	64	hydrolase activity, hydrolyzing N-glycosyl compounds		
GO:00168	54	dipeptidase activity		
GO:00168	238	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds		
GO:00168	37	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides		
GO:00168	29	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines		
GO:00168	3	hydrolase activity, acting on acid anhydrides		
GO:00168	146	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides		
GO:00168	5	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances		
GO:00168	185	lyase activity		
GO:00168	172	carboxy-lyase activity		
GO:00168	8	aldehyde-lyase activity		
GO:00168	43	hydro-lyase activity		
GO:00168	1	carbon-nitrogen lyase activity		
GO:00168	32	ammonia-lyase activity		
GO:00168	10	strictosidine synthase activity		
GO:00168	35	carbon-sulfur lyase activity		
GO:00168	179	phosphorus-oxygen lyase activity		
GO:00168	75	magnesium chelatase activity		
GO:00168	6	sirohydrochlorin cobaltochelatase activity		
GO:00168	120	isomerase activity		
GO:00168	20	racemase and epimerase activity, acting on carbohydrates and derivatives		
GO:00168	2	intramolecular oxidoreductase activity, interconverting aldoses and ketoses		
GO:00168	73	intramolecular transferase activity		
GO:00168	121	intramolecular transferase activity, phosphotransferases		
GO:00168	7	intramolecular lyase activity		
GO:00168	53	ligase activity		
GO:00168	111	ligase activity, forming aminoacyl-tRNA and related compounds		
GO:00168	181	carbon-nitrogen ligase activity, with glutamine as amido-N-donor		
GO:00168	1400	ATPase activity		
GO:00168	32	endodeoxyribonuclease activity, producing 5'-phosphomonoesters		
GO:00169	67	oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor		
GO:00169	77	oxidoreductase activity, acting on the aldehyde or oxo group of donors		
GO:00169	489	sigma factor activity		
GO:00169	1	sigma factor antagonist activity		
GO:00169	4	precorrin-8X methylmutase activity		
GO:00169	2	precorrin-6A reductase activity		
GO:00169	6	cell wall macromolecule catabolic process		
GO:00170	78	antibiotic biosynthetic process		
GO:00170	10	protein-heme linkage		
GO:00170	141	cytochrome complex assembly		
GO:00170	3	protein-phycocyanobilin linkage		
GO:00170	32	protein flavinylation		
GO:00170	73	protein import		
GO:00171	37	tRNA dihydrouridine synthase activity		
GO:00171	31	sodium:dicarboxylate symporter activity		
GO:00171	9	cysteine dioxygenase activity		
GO:00171	3	peptidyl-glutamic acid carboxylation		
GO:00180	1	histone-lysine N-methyltransferase activity		
GO:00181	12	proline racemase activity		
GO:00181	4	peptidyl-amino acid modification		
GO:00182	11	protein-chromophore linkage		
GO:00184	7	carbon-monoxide dehydrogenase (acceptor) activity		
GO:00185	67	nitronate monooxygenase activity		
GO:00187	3	methenyltetrahydromethanopterin cyclohydrolase activity		
GO:00188	10	nitrile hydratase activity		
GO:00188	3	alkylmercury lyase activity		
GO:00190	1	guanyl nucleotide binding		
GO:00190	26	molybdopterin synthase complex		
GO:00190	2	viral capsid		
GO:00190	1	viral envelope		
GO:00190	3	viral life cycle		
GO:00190	6	virion assembly		
GO:00190	2	transformation of host cell by virus		
GO:00192	34	deaminase activity		
GO:00192	1	L-methionine biosynthetic process from homoserine via O-succinyl-L-homoserine and cystathionine		
GO:00192	29	isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway		
GO:00192	6	coenzyme M biosynthetic process		
GO:00192	10	rhamnose metabolic process		
GO:00193	9	siroheme biosynthetic process		
GO:00193	7	pyridine nucleotide biosynthetic process		
GO:00193	1	methanogenesis, from acetate		
GO:00194	3	galactitol metabolic process		

GO:00194	51	aromatic compound catabolic process		
GO:00194	35	tryptophan catabolic process to kynurenine		
GO:00194	24	L-lysine catabolic process to acetate		
GO:00194	17	D-amino acid catabolic process		
GO:00194	1	ectoine biosynthetic process		
GO:00195	84	propionate catabolic process		
GO:00195	37	glutamate catabolic process to 2-oxoglutarate		
GO:00196	8	butyrate metabolic process		
GO:00196	2	urea metabolic process		
GO:00196	3	organic phosphonate metabolic process		
GO:00196	1	anaerobic electron transport chain		
GO:00196	4	anaerobic glutamate catabolic process		
GO:00196	2	photosynthesis, light reaction		
GO:00197	1	organic phosphonate catabolic process		
GO:00197	95	carboxylic acid metabolic process		
GO:00198	12	oxygen binding		
GO:00198	61	rRNA binding		
GO:00198	139	outer membrane		
GO:00199	17	modification-dependent protein catabolic process		
GO:00200	692	heme binding		
GO:00228	67	transmembrane transporter activity		
GO:00229	7	electron transport chain		
GO:00229	36	respiratory electron transport chain		
GO:00300	101	metal ion transport		
GO:00301	22	manganese ion binding		
GO:00301	21	molybdenum ion binding		
GO:00301	18	protein catabolic process		
GO:00301	883	pyridoxal phosphate binding		
GO:00302	14	enzyme regulator activity		
GO:00302	1	cellulose biosynthetic process		
GO:00302	4	cellulose catabolic process		
GO:00302	192	carbohydrate binding		
GO:00302	2	protein secretion by the type IV secretion system		
GO:00302	42	lipid glycosylation		
GO:00302	1	chromosome condensation		
GO:00302	1	tetrahydromethanopterin S-methyltransferase activity		
GO:00302	932	outer membrane-bounded periplasmic space		
GO:00304	4	sporulation resulting in formation of a cellular spore		
GO:00304	6	tRNA methylation		
GO:00305	2	pectinesterase activity		
GO:00306	2	bacterial-type flagellum basal body, rod		
GO:00309	1	protein splicing		
GO:00309	42	potassium ion binding		
GO:00309	417	thiamine pyrophosphate binding		
GO:00309	119	mismatched DNA binding		
GO:00310	6	extracellular matrix		
GO:00311	23	rRNA methylation		
GO:00313	12	organic acid phosphorylation		
GO:00314	4	gas vesicle		
GO:00314	6	gas vesicle organization		
GO:00314	145	cobalamin binding		
GO:00315	6	tRNA (m1A) methyltransferase complex		
GO:00315	23	regulation of DNA-templated transcription, termination		
GO:00315	18	transcription antitermination		
GO:00316	1	G-protein beta/gamma-subunit complex binding		
GO:00322	54	methylation		
GO:00323	60	molybdopterin cofactor biosynthetic process		
GO:00327	5	DNA methylation on adenine		
GO:00327	35	regulation of DNA-templated transcription, elongation		
GO:00329	2	regulation of barrier septum assembly		
GO:00330	110	tetrapyrrole biosynthetic process		
GO:00331	8	proton-transporting two-sector ATPase complex, proton-transporting domain		
GO:00331	1	proton-transporting two-sector ATPase complex, catalytic domain		
GO:00331	4	proton-transporting V-type ATPase, V0 domain		
GO:00335	16	fatty acid beta-oxidation using acyl-CoA dehydrogenase		
GO:00335	13	high-affinity iron permease complex		
GO:00337	11	preQ1 synthase activity		
GO:00337	15	peptide-methionine (R)-S-oxide reductase activity		
GO:00338	19	pyridoxine 5'-phosphate synthase activity		
GO:00338	1	ribonuclease T2 activity		
GO:00339	1	ectoine synthase activity		
GO:00341	1	D-galactonate catabolic process		
GO:00342	1	ion transmembrane transport		
GO:00342	2	nicotinamide riboside transmembrane transporter activity		
GO:00342	2	nicotinamide riboside transport		
GO:00344	2	U6 snRNA 3'-end processing		
GO:00349	1	histone lysine methylation		
GO:00354	5	gluconate transmembrane transport		
GO:00354	2	phosphate ion transmembrane transport		
GO:00354	4	cyclic-di-GMP binding		
GO:00354	15	nickel cation transmembrane transport		
GO:00355	179	intracellular signal transduction		
GO:00363	54	racemase activity, acting on amino acids and derivatives		
GO:00364	1	ubiquitinyl hydrolase activity		
GO:00421	73	nitrate assimilation		
GO:00421	31	fructose 1,6-bisphosphate 1-phosphatase activity		
GO:00421	5	lipoprotein metabolic process		
GO:00421	26	lipoprotein biosynthetic process		
GO:00422	1	tissue regeneration		
GO:00422	20	ribosome biogenesis		
GO:00422	9	nitrite reductase (cytochrome, ammonia-forming) activity		
GO:00423	42	cellular modified amino acid biosynthetic process		
GO:00425	2	cell wall modification		
GO:00425	74	pteridine-containing compound metabolic process		
GO:00425	11	phosphoric ester hydrolase activity		
GO:00425	89	periplasmic space		
GO:00426	40	poly-hydroxybutyrate biosynthetic process		
GO:00426	254	ATPase activity, coupled to transmembrane movement of substances		
GO:00426	6	thylakoid membrane		
GO:00427	3	defense response to bacterium		
GO:00427	13	ATP synthesis coupled electron transport		
GO:00428	31	protein homodimerization activity		
GO:00428	12	vitamin B6 biosynthetic process		
GO:00428	12	pyridoxal phosphate biosynthetic process		

GO:00429	1	alkylphosphonate transport		
GO:00429	6	benzoate transport		
GO:00429	6	benzoate transporter activity		
GO:00430	151	tRNA aminoacylation		
GO:00430	17	peptide biosynthetic process		
GO:00431	9	precorrin-2 dehydrogenase activity		
GO:00431	25	ATP-dependent 3'-5' DNA helicase activity		
GO:00431	6	Gram-negative-bacterium-type cell outer membrane assembly		
GO:00431	154	cation binding		
GO:00431	55	ATP-binding cassette (ABC) transporter complex		
GO:00432	10	intracellular membrane-bounded organelle		
GO:00434	4	urea catabolic process		
GO:00435	59	ADP binding		
GO:00435	82	sequence-specific DNA binding		
GO:00437	7	adenosylcobinamide kinase activity		
GO:00437	21	acyl-phosphate glycerol-3-phosphate acyltransferase activity		
GO:00442	27	cellular metabolic process		
GO:00442	17	primary metabolic process		
GO:00442	54	cellular carbohydrate metabolic process		
GO:00443	10	sodium-dependent phosphate transport		
GO:00447	1	bacterial-type flagellum assembly		
GO:00447	3	bacterial-type flagellum organization		
GO:00450	55	glycerolipid biosynthetic process		
GO:00451	2	electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity		
GO:00452	1	capsule polysaccharide biosynthetic process		
GO:00452	42	proton-transporting ATP synthase complex, catalytic core F(1)		
GO:00452	12	proton-transporting ATP synthase complex, coupling factor F(o)		
GO:00453	4	acyl-[acyl-carrier-protein] desaturase activity		
GO:00454	75	cell redox homeostasis		
GO:00454	3	xylan catabolic process		
GO:00455	10	dynein binding		
GO:00458	14	negative regulation of transcription, DNA-templated		
GO:00458	5	positive regulation of transcription, DNA-templated		
GO:00459	3	positive regulation of transcription from RNA polymerase II promoter		
GO:00460	20	dUTP metabolic process		
GO:00461	22	glycerol-3-phosphate catabolic process		
GO:00463	3	aminoglycoside 3-N-acetyltransferase activity		
GO:00463	20	L-arabinose metabolic process		
GO:00464	3	organomercury catabolic process		
GO:00464	3	chorismate metabolic process		
GO:00464	24	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity		
GO:00464	9	L-cysteine metabolic process		
GO:00465	2	2,3-bisphosphoglycerate-independent phosphoglycerate mutase activity		
GO:00465	20	alpha-L-arabinofuranosidase activity		
GO:00465	3	alpha-glucuronidase activity		
GO:00466	2	tetrahydrofolate metabolic process		
GO:00466	14	response to antibiotic		
GO:00466	4	response to copper ion		
GO:00468	60	phosphatidylinositol phosphorylation		
GO:00468	726	metal ion binding		
GO:00468	59	metal ion transmembrane transporter activity		
GO:00469	2	intracellular transport		
GO:00469	54	transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer		
GO:00469	32	transition metal ion binding		
GO:00469	61	proton-transporting ATP synthase activity, rotational mechanism		
GO:00469	1	phytochelatin biosynthetic process		
GO:00469	43	proton-transporting ATPase activity, rotational mechanism		
GO:00469	123	protein dimerization activity		
GO:00472	1	tetrahydrodipicolinate N-acetyltransferase activity		
GO:00473	12	CDP-glycerol glycerophosphotransferase activity		
GO:00475	84	2-methylcitrate dehydratase activity		
GO:00479	8	hydroxybutyrate-dimer hydrolase activity		
GO:00480	1	mRNA 5'-UTR binding		
GO:00480	2	monosaccharide binding		
GO:00480	57	cofactor binding		
GO:00480	157	quinone binding		
GO:00484	8	threonine-phosphate decarboxylase activity		
GO:00485	7	rhythmic process		
GO:00500	19	malonyl-CoA decarboxylase activity		
GO:00500	4	methylaspartate mutase activity		
GO:00501	1	oleate hydratase activity		
GO:00502	4	propanediol dehydratase activity		
GO:00503	36	undecaprenyl-diphosphatase activity		
GO:00503	1	ureidoglycolate lyase activity		
GO:00505	19	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase activity		
GO:00505	11	2-phosphosulfolactate phosphatase activity		
GO:00505	6	protein-glutamine glutaminase activity		
GO:00505	31	4-hydroxythreonine-4-phosphate dehydrogenase activity		
GO:00506	483	flavin adenine dinucleotide binding		
GO:00506	129	NADP binding		
GO:00506	468	coenzyme binding		
GO:00507	21	thymidylate synthase (FAD) activity		
GO:00509	1	regulation of chemotaxis		
GO:00509	29	dimethylallyl diphosphate biosynthetic process		
GO:00510	27	unfolded protein binding		
GO:00510	21	chaperone binding		
GO:00511	9	glucose 6-phosphate metabolic process		
GO:00511	7	cofactor biosynthetic process		
GO:00512	36	protein insertion into membrane		
GO:00512	9	protein oligomerization		
GO:00512	7	protein tetramerization		
GO:00512	545	NAD binding		
GO:00513	147	cell division		
GO:00513	17	chromosome separation		
GO:00515	1045	iron-sulfur cluster binding		
GO:00515	152	2 iron, 2 sulfur cluster binding		
GO:00515	64	4 iron, 4 sulfur cluster binding		
GO:00516	25	proteolysis involved in cellular protein catabolic process		
GO:00517	29	4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity		
GO:00517	7	negative regulation of cell division		
GO:00519	65	peroxiredoxin activity		
GO:00526	4	arabinosyltransferase activity		
GO:00526	2	carboxylic ester hydrolase activity		
GO:00528	24	ADP-dependent NAD(P)H-hydrate dehydratase activity		

GO:00550	6	copper ion homeostasis		
GO:00550	1905	transmembrane transport		
GO:00551	7777	oxidation-reduction process		
GO:00610	27	membrane organization		
GO:00700	71	serine-type exopeptidase activity		
GO:00704	11	NADPH binding		
GO:00704	28	NAD+ binding		
GO:00704	2	rRNA base methylation		
GO:00705	5	uridylyltransferase activity		
GO:00715	13	cell wall organization		
GO:00717	4	Actinobacterium-type cell wall biogenesis		
GO:00717	1	aldehyde decarbonylase activity		
GO:00718	37	potassium ion transmembrane transport		
GO:00719	1	FAD binding		
GO:00719	41	bacterial-type flagellum-dependent cell motility		
GO:19022	2	regulation of bacterial-type flagellum assembly		
GO:19022	1	negative regulation of bacterial-type flagellum assembly		
GO:19026	2	p-aminobenzoyl-glutamate transmembrane transport		