

Gene id	function
fig 6666666.284511.peg.1	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.2	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.3	hypothetical protein
fig 6666666.284511.peg.4	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.5	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.6	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.7	hypothetical protein
fig 6666666.284511.peg.8	Transcription elongation factor GreA
fig 6666666.284511.peg.9	hypothetical protein
fig 6666666.284511.peg.10	hypothetical protein
fig 6666666.284511.peg.11	hypothetical protein
fig 6666666.284511.peg.12	hypothetical protein
fig 6666666.284511.peg.13	Transcription elongation factor GreA
fig 6666666.284511.peg.14	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.15	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.16	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.17	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.18	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.19	hypothetical protein
fig 6666666.284511.peg.20	Mobile element protein
fig 6666666.284511.peg.21	hypothetical protein
fig 6666666.284511.peg.22	hypothetical protein
fig 6666666.284511.peg.23	hypothetical protein
fig 6666666.284511.peg.24	Mobile element protein
fig 6666666.284511.peg.25	hypothetical protein
fig 6666666.284511.peg.26	Mobile element protein
fig 6666666.284511.peg.27	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.28	Mobile element protein
fig 6666666.284511.peg.29	hypothetical protein
fig 6666666.284511.peg.30	hypothetical protein
fig 6666666.284511.peg.31	hypothetical protein
fig 6666666.284511.peg.32	Mobile element protein
fig 6666666.284511.peg.33	hypothetical protein
fig 6666666.284511.peg.34	hypothetical protein
fig 6666666.284511.peg.35	Probable transmembrane protein
fig 6666666.284511.peg.36	hypothetical protein
fig 6666666.284511.peg.37	Chloride channel protein
fig 6666666.284511.peg.38	hypothetical protein
fig 6666666.284511.peg.39	hypothetical protein
fig 6666666.284511.peg.40	5-nucleotidase SurE (EC 3.1.3.5)
fig 6666666.284511.peg.41	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)
fig 6666666.284511.peg.42	Lipoprotein NlpD

fig 6666666.284511.peg.43	RNA polymerase sigma factor RpoS
fig 6666666.284511.peg.44	Polysaccharide biosynthesis protein WlaX
fig 6666666.284511.peg.45	23S rRNA (Uracil-5-) -methyltransferase RumA (EC 2.1.1.-)
fig 6666666.284511.peg.46	hypothetical protein
fig 6666666.284511.peg.47	Putative TEGT family carrier/transport protein
fig 6666666.284511.peg.48	Ferric siderophore transport system, periplasmic binding protein Tor
fig 6666666.284511.peg.49	hypothetical protein
fig 6666666.284511.peg.50	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)
fig 6666666.284511.peg.51	L-lysine permease
fig 6666666.284511.peg.52	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
fig 6666666.284511.peg.53	Transcription elongation factor GreA
fig 6666666.284511.peg.54	Probable transmembrane protein
fig 6666666.284511.peg.55	FIG004454: RNA binding protein
fig 6666666.284511.peg.56	Heat shock protein FtsJ/RrmJ @ Ribosomal RNA large subunit methy
fig 6666666.284511.peg.57	Cell division protein FtsH (EC 3.4.24.-)
fig 6666666.284511.peg.58	Dihydropteroate synthase (EC 2.5.1.15)
fig 6666666.284511.peg.59	Phosphoglucosamine mutase (EC 5.4.2.10)
fig 6666666.284511.peg.60	Phosphate ABC transporter, periplasmic phosphate-binding protein I
fig 6666666.284511.peg.61	Phosphate transport system permease protein PstC (TC 3.A.1.7.1)
fig 6666666.284511.peg.62	Phosphate transport system permease protein PstA (TC 3.A.1.7.1)
fig 6666666.284511.peg.63	Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1)
fig 6666666.284511.peg.64	Phosphate transport system regulatory protein PhoU
fig 6666666.284511.peg.65	Phosphate regulon transcriptional regulatory protein PhoB (SphR)
fig 6666666.284511.peg.66	Polyphosphate kinase (EC 2.7.4.1)
fig 6666666.284511.peg.67	Exopolyphosphatase (EC 3.6.1.11)
fig 6666666.284511.peg.68	Putative hemolysin
fig 6666666.284511.peg.69	Phosphohistidine phosphatase SixA
fig 6666666.284511.peg.70	hypothetical protein
fig 6666666.284511.peg.71	Spermidine synthase-like protein
fig 6666666.284511.peg.72	Lysyl-tRNA synthetase (class II) (EC 6.1.1.6)
fig 6666666.284511.peg.73	Glucose-6-phosphate isomerase (EC 5.3.1.9)
fig 6666666.284511.peg.74	MgtC family
fig 6666666.284511.peg.75	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)
fig 6666666.284511.peg.76	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)
fig 6666666.284511.peg.77	Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase
fig 6666666.284511.peg.78	Cell division topological specificity factor MinE
fig 6666666.284511.peg.79	Septum site-determining protein MinD
fig 6666666.284511.peg.80	Septum site-determining protein MinC
fig 6666666.284511.peg.81	hypothetical protein
fig 6666666.284511.peg.82	Acyl-CoA dehydrogenase (EC 1.3.8.7)
fig 6666666.284511.peg.83	hypothetical protein
fig 6666666.284511.peg.84	Probable transmembrane protein
fig 6666666.284511.peg.85	Lipoprotein releasing system transmembrane protein LolC

fig 6666666.284511.peg.86	voltage-gated potassium channel beta subunit
fig 6666666.284511.peg.87	Short chain dehydrogenase
fig 6666666.284511.peg.88	Regulatory protein, RpfE type
fig 6666666.284511.peg.89	Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-)
fig 6666666.284511.peg.90	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.91	Lipoprotein releasing system ATP-binding protein LolD
fig 6666666.284511.peg.92	UDP-N-acetylglucosamine 4,6-dehydratase (EC 4.2.1.-)
fig 6666666.284511.peg.93	Lipopolysaccharide biosynthesis protein RffA
fig 6666666.284511.peg.94	transferase hexapeptide repeat
fig 6666666.284511.peg.95	UDP-Bac2Ac4Ac hydrolyzing 2-epimerase NeuC homolog
fig 6666666.284511.peg.96	N-acetylneuraminate synthase (EC 2.5.1.56)
fig 6666666.284511.peg.97	Legionaminic acid cytidyltransferase (EC 2.7.7.43)
fig 6666666.284511.peg.98	hypothetical protein
fig 6666666.284511.peg.99	hypothetical protein
fig 6666666.284511.peg.100	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)
fig 6666666.284511.peg.101	Undecaprenyl-phosphate galactose phosphotransferase (EC 2.7.8.6)
fig 6666666.284511.peg.102	HpcH/HpaI aldolase
fig 6666666.284511.peg.103	virulence factor MVIN family protein
fig 6666666.284511.peg.104	IncP-type DNA relaxase Tral
fig 6666666.284511.peg.105	hypothetical protein
fig 6666666.284511.peg.106	hypothetical protein
fig 6666666.284511.peg.107	hypothetical protein
fig 6666666.284511.peg.108	Hyphothetical protein
fig 6666666.284511.peg.109	DNA primase domain protein
fig 6666666.284511.peg.110	hypothetical protein
fig 6666666.284511.peg.111	hypothetical protein
fig 6666666.284511.peg.112	protein of unknown function DUF132
fig 6666666.284511.peg.113	hypothetical protein
fig 6666666.284511.peg.114	Alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.73)
fig 6666666.284511.peg.115	histidine triad (HIT) protein
fig 6666666.284511.peg.116	conserved protein
fig 6666666.284511.peg.117	Mobile element protein
fig 6666666.284511.peg.118	MoxR-like ATPase in aerotolerance operon
fig 6666666.284511.peg.119	hypothetical protein
fig 6666666.284511.peg.120	hypothetical protein
fig 6666666.284511.peg.121	BatA (Bacteroides aerotolerance operon)
fig 6666666.284511.peg.122	TPR domain protein in aerotolerance operon
fig 6666666.284511.peg.123	hypothetical protein
fig 6666666.284511.peg.124	Integral membrane protein
fig 6666666.284511.peg.125	Mg(2+) transport ATPase protein C
fig 6666666.284511.peg.126	hypothetical protein
fig 6666666.284511.peg.127	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)
fig 6666666.284511.peg.128	hypothetical protein

fig 6666666.284511.peg.129	Enolase (EC 4.2.1.11)
fig 6666666.284511.peg.130	MutS domain protein, family 5
fig 6666666.284511.peg.131	MutS domain protein, family 4
fig 6666666.284511.peg.132	hypothetical protein
fig 6666666.284511.peg.133	Protein crcB homolog
fig 6666666.284511.peg.134	Hydrogenase-4 component B / Formate hydrogenlyase subunit 3
fig 6666666.284511.peg.135	Formate hydrogenlyase subunit 7
fig 6666666.284511.peg.136	Ni,Fe-hydrogenase III large subunit
fig 6666666.284511.peg.137	Hydrogenase-4 component F
fig 6666666.284511.peg.138	Hydrogenase-4 component E
fig 6666666.284511.peg.139	Formate hydrogenlyase subunit 4
fig 6666666.284511.peg.140	GGDEF domain protein
fig 6666666.284511.peg.141	predicted cell surface protein/ lipoprotein
fig 6666666.284511.peg.142	hypothetical protein
fig 6666666.284511.peg.143	Conserved protein
fig 6666666.284511.peg.144	Mobile element protein
fig 6666666.284511.peg.145	hypothetical protein
fig 6666666.284511.peg.146	[NiFe] hydrogenase metallocenter assembly protein HypE
fig 6666666.284511.peg.147	[NiFe] hydrogenase metallocenter assembly protein HypD
fig 6666666.284511.peg.148	Phosphoheptose isomerase (EC 5.3.1.-)
fig 6666666.284511.peg.149	[NiFe] hydrogenase metallocenter assembly protein HypC
fig 6666666.284511.peg.150	[NiFe] hydrogenase metallocenter assembly protein HypF
fig 6666666.284511.peg.151	Uptake hydrogenase large subunit (EC 1.12.99.6)
fig 6666666.284511.peg.152	Uptake hydrogenase small subunit precursor (EC 1.12.99.6)
fig 6666666.284511.peg.153	Signal transduction histidine kinase HoxJ (hydrogenase regulation)
fig 6666666.284511.peg.154	Hydrogenase transcriptional regulatory protein hoxA
fig 6666666.284511.peg.155	[NiFe] hydrogenase nickel incorporation-associated protein HypB
fig 6666666.284511.peg.156	[NiFe] hydrogenase nickel incorporation protein HypA
fig 6666666.284511.peg.157	Hydrogenase maturation factor HoxV/HupK
fig 6666666.284511.peg.158	Hydrogenase maturation factor HoxT/HybE
fig 6666666.284511.peg.159	Rubredoxin
fig 6666666.284511.peg.160	Hydrogenase maturation factor HoxQ
fig 6666666.284511.peg.161	Hydrogenase maturation factor HoxO/HyaE
fig 6666666.284511.peg.162	Hydrogenase maturation protein HupF/HypC/HoxL
fig 6666666.284511.peg.163	Hydrogenase maturation protease (EC 3.4.24.-)
fig 6666666.284511.peg.164	Uptake hydrogenase small subunit precursor (EC 1.12.99.6)
fig 6666666.284511.peg.165	Uptake hydrogenase large subunit (EC 1.12.99.6)
fig 6666666.284511.peg.166	Ni,Fe-hydrogenase I cytochrome b subunit
fig 6666666.284511.peg.167	HoxN/HupN/NixA family nickel/cobalt transporter
fig 6666666.284511.peg.168	Mobile element protein
fig 6666666.284511.peg.169	hypothetical protein
fig 6666666.284511.peg.170	site-specific recombinase, phage integrase family
fig 6666666.284511.peg.171	Leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein

fig 6666666.284511.peg.172	Cytochrome c551/c552
fig 6666666.284511.peg.173	hypothetical protein
fig 6666666.284511.peg.174	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.
fig 6666666.284511.peg.175	Glycine cleavage system H protein
fig 6666666.284511.peg.176	Glycine dehydrogenase [decarboxylating] (glycine cleavage system P
fig 6666666.284511.peg.177	ADA regulatory protein / Methylated-DNA--protein-cysteine methylt
fig 6666666.284511.peg.178	Selenide,water dikinase (EC 2.7.9.3)
fig 6666666.284511.peg.179	LysR family transcriptional regulator YeiE
fig 6666666.284511.peg.180	Iron-sulfur cluster regulator IscR
fig 6666666.284511.peg.181	Cysteine desulfurase (EC 2.8.1.7), IscS subfamily
fig 6666666.284511.peg.182	Iron-sulfur cluster assembly scaffold protein IscU
fig 6666666.284511.peg.183	Iron binding protein IscA for iron-sulfur cluster assembly
fig 6666666.284511.peg.184	Chaperone protein HscB
fig 6666666.284511.peg.185	Chaperone protein HscA
fig 6666666.284511.peg.186	Ferredoxin, 2Fe-2S
fig 6666666.284511.peg.187	hypothetical protein
fig 6666666.284511.peg.188	hypothetical protein
fig 6666666.284511.peg.189	Protein-N(5)-glutamine methyltransferase PrmC, methylates polypep
fig 6666666.284511.peg.190	NAD synthetase (EC 6.3.1.5)
fig 6666666.284511.peg.191	Acyl carrier protein
fig 6666666.284511.peg.192	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
fig 6666666.284511.peg.193	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)
fig 6666666.284511.peg.194	Rhodopsin
fig 6666666.284511.peg.195	Molybdopterin biosynthesis protein MoeA
fig 6666666.284511.peg.196	Molybdopterin-guanine dinucleotide biosynthesis protein MobA
fig 6666666.284511.peg.197	hypothetical protein
fig 6666666.284511.peg.198	Molybdenum cofactor biosynthesis protein MoaA
fig 6666666.284511.peg.199	3-hydroxybutyrate dehydrogenase (EC 1.1.1.30)
fig 6666666.284511.peg.200	thioesterase superfamily
fig 6666666.284511.peg.201	Acetoacetyl-CoA synthetase (EC 6.2.1.16)
fig 6666666.284511.peg.202	Phytoene synthase (EC 2.5.1.32)
fig 6666666.284511.peg.203	Cell division trigger factor (EC 5.2.1.8)
fig 6666666.284511.peg.204	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)
fig 6666666.284511.peg.205	ATP-dependent Clp protease ATP-binding subunit ClpX
fig 6666666.284511.peg.206	ATP-dependent protease La (EC 3.4.21.53) Type I
fig 6666666.284511.peg.207	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.208	Mobile element protein
fig 6666666.284511.peg.209	hypothetical protein
fig 6666666.284511.peg.210	1-phosphofructokinase (EC 2.7.1.56)
fig 6666666.284511.peg.211	hypothetical protein
fig 6666666.284511.peg.212	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)
fig 6666666.284511.peg.213	Porphobilinogen deaminase (EC 2.5.1.61)
fig 6666666.284511.peg.214	Uroporphyrinogen-III synthase (EC 4.2.1.75)

fig 6666666.284511.peg.215	Uroporphyrinogen-III synthase (EC 4.2.1.75) / Homolog of E. coli Hen
fig 6666666.284511.peg.216	Uncharacterized protein EC-HemY, likely associated with heme meta
fig 6666666.284511.peg.217	Anion permease ArsB/NhaD-like
fig 6666666.284511.peg.218	Cysteine synthase B (EC 2.5.1.47)
fig 6666666.284511.peg.219	Molybdopterin biosynthesis MoeB protein
fig 6666666.284511.peg.220	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
fig 6666666.284511.peg.221	Valyl-tRNA synthetase (EC 6.1.1.9)
fig 6666666.284511.peg.222	GMP reductase (EC 1.7.1.7)
fig 6666666.284511.peg.223	ATP-dependent DNA helicase UvrD/PcrA
fig 6666666.284511.peg.224	FIG004694: Hypothetical protein
fig 6666666.284511.peg.225	Beta-propeller domains of methanol dehydrogenase type
fig 6666666.284511.peg.226	LemA family protein
fig 6666666.284511.peg.227	FIGfam005179
fig 6666666.284511.peg.228	Homoserine kinase (EC 2.7.1.39)
fig 6666666.284511.peg.229	hypothetical protein
fig 6666666.284511.peg.230	DNA polymerase I (EC 2.7.7.7)
fig 6666666.284511.peg.231	hypothetical protein
fig 6666666.284511.peg.232	Universal stress protein
fig 6666666.284511.peg.233	Universal stress protein family
fig 6666666.284511.peg.234	Thiosulfate sulfurtransferase, rhodanese (EC 2.8.1.1)
fig 6666666.284511.peg.235	hypothetical protein
fig 6666666.284511.peg.236	Mobile element protein
fig 6666666.284511.peg.237	Phenylpropionate dioxygenase and related ring-hydroxylating dioxyg
fig 6666666.284511.peg.238	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
fig 6666666.284511.peg.239	Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransfer
fig 6666666.284511.peg.240	1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
fig 6666666.284511.peg.241	GTP cyclohydrolase I (EC 3.5.4.16) type 2
fig 6666666.284511.peg.242	Transamidase GatB domain protein
fig 6666666.284511.peg.243	SSU ribosomal protein S21p
fig 6666666.284511.peg.244	TsaD/Kae1/Qri7 protein, required for threonylcarbamoyladenosine t
fig 6666666.284511.peg.245	Ser/Thr protein phosphatase family protein
fig 6666666.284511.peg.246	hypothetical protein
fig 6666666.284511.peg.247	SSU ribosomal protein S15p (S13e)
fig 6666666.284511.peg.248	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)
fig 6666666.284511.peg.249	Quinone oxidoreductase (EC 1.6.5.5)
fig 6666666.284511.peg.250	Triosephosphate isomerase (EC 5.3.1.1)
fig 6666666.284511.peg.251	Preprotein translocase subunit SecG (TC 3.A.5.1.1)
fig 6666666.284511.peg.252	NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)
fig 6666666.284511.peg.253	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)
fig 6666666.284511.peg.254	NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3)
fig 6666666.284511.peg.255	NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3)
fig 6666666.284511.peg.256	NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3)
fig 6666666.284511.peg.257	NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3)

fig 6666666.284511.peg.258	NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3)
fig 6666666.284511.peg.259	NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)
fig 6666666.284511.peg.260	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)
fig 6666666.284511.peg.261	NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3)
fig 6666666.284511.peg.262	NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3)
fig 6666666.284511.peg.263	NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3)
fig 6666666.284511.peg.264	NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3)
fig 6666666.284511.peg.265	NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)
fig 6666666.284511.peg.266	FIG003089: Probable transmembrane protein
fig 6666666.284511.peg.267	ADP-ribose pyrophosphatase (EC 3.6.1.13)
fig 6666666.284511.peg.268	Serine/threonine protein phosphatase (EC 3.1.3.16)
fig 6666666.284511.peg.269	hypothetical protein
fig 6666666.284511.peg.270	protein of unknown function DUF6, transmembrane
fig 6666666.284511.peg.271	FIG00453572: hypothetical protein
fig 6666666.284511.peg.272	Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.17)
fig 6666666.284511.peg.273	conserved hypothetical secreted protein
fig 6666666.284511.peg.274	hypothetical protein
fig 6666666.284511.peg.275	FIG001454: Transglutaminase-like enzymes, putative cysteine protease
fig 6666666.284511.peg.276	FIG002343: hypothetical protein
fig 6666666.284511.peg.277	FIG022979: MoxR-like ATPases
fig 6666666.284511.peg.278	Deacetylases, including yeast histone deacetylase and acetoin utilization
fig 6666666.284511.peg.279	3-methylmercaptopropionyl-CoA ligase (DmdB)
fig 6666666.284511.peg.280	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.281	hypothetical protein
fig 6666666.284511.peg.282	Potassium efflux system KefA protein / Small-conductance mechanosensitive channel
fig 6666666.284511.peg.283	Electron transfer flavoprotein, beta subunit
fig 6666666.284511.peg.284	Electron transfer flavoprotein, alpha subunit
fig 6666666.284511.peg.285	3-methylmercaptopropionyl-CoA dehydrogenase (DmdC)
fig 6666666.284511.peg.286	Dioxygenases related to 2-nitropropane dioxygenase
fig 6666666.284511.peg.287	hypothetical protein
fig 6666666.284511.peg.288	Carbonic anhydrase (EC 4.2.1.1)
fig 6666666.284511.peg.289	RuBisCO operon transcriptional regulator
fig 6666666.284511.peg.290	Ribulose biphosphate carboxylase large chain (EC 4.1.1.39)
fig 6666666.284511.peg.291	Ribulose biphosphate carboxylase small chain (EC 4.1.1.39)
fig 6666666.284511.peg.292	Rubisco activation protein CbbQ
fig 6666666.284511.peg.293	Rubisco activation protein CbbO
fig 6666666.284511.peg.294	hypothetical protein
fig 6666666.284511.peg.295	hypothetical protein
fig 6666666.284511.peg.296	Ribonuclease BN (EC 3.1.-.-)
fig 6666666.284511.peg.297	Flavoprotein WrbA
fig 6666666.284511.peg.298	Probable transmembrane protein
fig 6666666.284511.peg.299	D-2-hydroxyglutarate dehydrogenase
fig 6666666.284511.peg.300	D-2-hydroxyglutarate dehydrogenase

fig 6666666.284511.peg.301	Potassium channel protein
fig 6666666.284511.peg.302	hypothetical protein
fig 6666666.284511.peg.303	Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) @ Fructose-6-ph
fig 6666666.284511.peg.304	Thymidine phosphorylase (EC 2.4.2.4)
fig 6666666.284511.peg.305	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
fig 6666666.284511.peg.306	Metallo-beta-lactamase family protein, RNA-specific
fig 6666666.284511.peg.307	universal stress protein (Usp)
fig 6666666.284511.peg.308	Predicted membrane fusion protein (MFP) component of efflux pum
fig 6666666.284511.peg.309	ABC-type multidrug transport system, ATPase component
fig 6666666.284511.peg.310	ABC transporter multidrug efflux pump, fused ATP-binding domains
fig 6666666.284511.peg.311	ABC transport system, permease component YbhR
fig 6666666.284511.peg.312	ABC-type multidrug transport system, permease component
fig 6666666.284511.peg.313	hypothetical protein
fig 6666666.284511.peg.314	Molecular chaperone (small heat shock protein)
fig 6666666.284511.peg.315	hypothetical protein
fig 6666666.284511.peg.316	granule-associated protein
fig 6666666.284511.peg.317	Acetoacetyl-CoA reductase (EC 1.1.1.36)
fig 6666666.284511.peg.318	hypothetical protein
fig 6666666.284511.peg.319	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase
fig 6666666.284511.peg.320	UDP-galactose-lipid carrier transferase (EC 2.-.-.)
fig 6666666.284511.peg.321	UDP-galactose-lipid carrier transferase (EC 2.-.-.)
fig 6666666.284511.peg.322	blI4412; hypothetical protein
fig 6666666.284511.peg.323	Universal stress protein family
fig 6666666.284511.peg.324	Type I secretion outer membrane protein, TolC precursor
fig 6666666.284511.peg.325	Predicted membrane fusion protein (MFP) component of efflux pum
fig 6666666.284511.peg.326	Mobile element protein
fig 6666666.284511.peg.327	ABC transporter multidrug efflux pump, fused ATP-binding domains
fig 6666666.284511.peg.328	ABC transport system, permease component YbhS
fig 6666666.284511.peg.329	ABC transport system, permease component YbhR
fig 6666666.284511.peg.330	hypothetical protein
fig 6666666.284511.peg.331	hypothetical protein
fig 6666666.284511.peg.332	Polyhydroxyalkanoic acid synthase
fig 6666666.284511.peg.333	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.334	MgtC family
fig 6666666.284511.peg.335	Acetate kinase (EC 2.7.2.1)
fig 6666666.284511.peg.336	Phosphate acetyltransferase (EC 2.3.1.8)
fig 6666666.284511.peg.337	Polyhydroxyalkanoic acid synthase
fig 6666666.284511.peg.338	hypothetical protein
fig 6666666.284511.peg.339	UDP-glucose dehydrogenase (EC 1.1.1.22)
fig 6666666.284511.peg.340	FIG00715019: hypothetical protein
fig 6666666.284511.peg.341	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)
fig 6666666.284511.peg.342	conserved hypothetical membrane protein
fig 6666666.284511.peg.343	FUPA30 P-type ATPase; putative cation-transporting ATPase pacL(EC

fig 6666666.284511.peg.344	FUPA30 P-type ATPase; putative cation-transporting ATPase pacL(EC
fig 6666666.284511.peg.345	hypothetical protein
fig 6666666.284511.peg.346	Mobile element protein
fig 6666666.284511.peg.347	Cobalt-zinc-cadmium resistance protein CzcD
fig 6666666.284511.peg.348	protein of unknown function DUF336
fig 6666666.284511.peg.349	Thiol-disulfide isomerase and thioredoxins
fig 6666666.284511.peg.350	Rhodanese-related sulfurtransferase
fig 6666666.284511.peg.351	Transporter
fig 6666666.284511.peg.352	hypothetical protein
fig 6666666.284511.peg.353	RNA polymerase sigma factor SigZ
fig 6666666.284511.peg.354	hypothetical protein
fig 6666666.284511.peg.355	UPF0235 protein SO_3356
fig 6666666.284511.peg.356	Mobile element protein
fig 6666666.284511.peg.357	Mobile element protein
fig 6666666.284511.peg.358	Cobalt-zinc-cadmium resistance protein
fig 6666666.284511.peg.359	hypothetical protein
fig 6666666.284511.peg.360	transposase, putative
fig 6666666.284511.peg.361	DNA polymerase IV (EC 2.7.7.7)
fig 6666666.284511.peg.362	hypothetical protein
fig 6666666.284511.peg.363	Mobile element protein
fig 6666666.284511.peg.364	hypothetical protein
fig 6666666.284511.peg.365	hypothetical protein
fig 6666666.284511.peg.366	Mobile element protein
fig 6666666.284511.peg.367	Mobile element protein
fig 6666666.284511.peg.368	hypothetical protein
fig 6666666.284511.peg.369	hypothetical protein
fig 6666666.284511.peg.370	hypothetical protein
fig 6666666.284511.peg.371	hypothetical protein
fig 6666666.284511.peg.372	Integrase/recombinase
fig 6666666.284511.peg.373	hypothetical protein
fig 6666666.284511.peg.374	Transposase
fig 6666666.284511.peg.375	Mobile element protein
fig 6666666.284511.peg.376	Mobile element protein
fig 6666666.284511.peg.377	Mobile element protein
fig 6666666.284511.peg.378	Phage integrase
fig 6666666.284511.peg.379	3'-to-5' exoribonuclease RNase R
fig 6666666.284511.peg.380	NAD(P)HX epimerase / NAD(P)HX dehydratase
fig 6666666.284511.peg.381	hypothetical protein
fig 6666666.284511.peg.382	hypothetical protein
fig 6666666.284511.peg.383	Chromate transport protein
fig 6666666.284511.peg.384	Isocitrate lyase (EC 4.1.3.1)
fig 6666666.284511.peg.385	tmRNA-binding protein SmpB
fig 6666666.284511.peg.386	Putative oligoketide cyclase/lipid transport protein, similarity with ye

fig 6666666.284511.peg.387	hypothetical protein
fig 6666666.284511.peg.388	Osmolarity sensory histidine kinase EnvZ
fig 6666666.284511.peg.389	Two-component system response regulator OmpR
fig 6666666.284511.peg.390	ABC transporter ATP-binding protein
fig 6666666.284511.peg.391	Excinuclease ABC subunit A, dimeric form
fig 6666666.284511.peg.392	Excinuclease ABC subunit A, dimeric form
fig 6666666.284511.peg.393	hypothetical protein
fig 6666666.284511.peg.394	FIG022886: Transcriptional regulator, LysR family
fig 6666666.284511.peg.395	Pirin
fig 6666666.284511.peg.396	putative membrane protein
fig 6666666.284511.peg.397	hypothetical protein
fig 6666666.284511.peg.398	tRNA dimethylallyltransferase (EC 2.5.1.75)
fig 6666666.284511.peg.399	DNA mismatch repair protein MutL
fig 6666666.284511.peg.400	DedA protein
fig 6666666.284511.peg.401	Coenzyme PQQ synthesis protein E
fig 6666666.284511.peg.402	Coenzyme PQQ synthesis protein D
fig 6666666.284511.peg.403	Pyrroloquinoline-quinone synthase (EC 1.3.3.11)
fig 6666666.284511.peg.404	Coenzyme PQQ synthesis protein B
fig 6666666.284511.peg.405	Coenzyme PQQ synthesis protein A
fig 6666666.284511.peg.406	Proline iminopeptidase (EC 3.4.11.5)
fig 6666666.284511.peg.407	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)
fig 6666666.284511.peg.408	TsaE protein, required for threonylcarbamoyladenosine t(6)A37 form
fig 6666666.284511.peg.409	Epoxyqueuosine (oQ) reductase QueG
fig 6666666.284511.peg.410	putative membrane protein
fig 6666666.284511.peg.411	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)
fig 6666666.284511.peg.412	Tyrosine recombinase XerD
fig 6666666.284511.peg.413	multiple antibiotic resistance (MarC)-related proteins
fig 6666666.284511.peg.414	cyclic nucleotide-binding domain (cNMP-BD) protein
fig 6666666.284511.peg.415	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.416	COG2833: uncharacterized protein
fig 6666666.284511.peg.417	Putative stomatin/prohibitin-family membrane protease subunit Ybk
fig 6666666.284511.peg.418	Putative activity regulator of membrane protease YbbK
fig 6666666.284511.peg.419	hypothetical protein
fig 6666666.284511.peg.420	hypothetical protein
fig 6666666.284511.peg.421	Arginine decarboxylase (EC 4.1.1.19); Ornithine decarboxylase (EC 4.1.1.17)
fig 6666666.284511.peg.422	hypothetical protein
fig 6666666.284511.peg.423	hypothetical protein
fig 6666666.284511.peg.424	RNA polymerase factor sigma-70
fig 6666666.284511.peg.425	N-succinyl-L,L-diaminopimelate aminotransferase alternative (EC 2.6.1.60)
fig 6666666.284511.peg.426	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (I)
fig 6666666.284511.peg.427	Twitching motility protein PilT
fig 6666666.284511.peg.428	N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18)
fig 6666666.284511.peg.429	Protein-N(5)-glutamine methyltransferase PrmB, methylates LSU ribosomal RNA

fig 6666666.284511.peg.430	Glutathione-regulated potassium-efflux system ATP-binding protein
fig 6666666.284511.peg.431	Multidrug and toxin extrusion (MATE) family efflux pump YdhE/NorM
fig 6666666.284511.peg.432	Probable inner membrane transmembrane protein
fig 6666666.284511.peg.433	LSU ribosomal protein L31p @ LSU ribosomal protein L31p, zinc-inde
fig 6666666.284511.peg.434	Transcription termination factor Rho
fig 6666666.284511.peg.435	Thioredoxin
fig 6666666.284511.peg.436	hypothetical protein
fig 6666666.284511.peg.437	DNA polymerase III subunits gamma and tau (EC 2.7.7.7)
fig 6666666.284511.peg.438	FIG000557: hypothetical protein co-occurring with RecR
fig 6666666.284511.peg.439	Recombination protein RecR
fig 6666666.284511.peg.440	hypothetical protein
fig 6666666.284511.peg.441	NADPH dependent preQ0 reductase (EC 1.7.1.13)
fig 6666666.284511.peg.442	Chromosome partition protein smc
fig 6666666.284511.peg.443	Cell division protein
fig 6666666.284511.peg.444	DNA ligase (EC 6.5.1.2)
fig 6666666.284511.peg.445	ROK family Glucokinase with ambiguous substrate specificity
fig 6666666.284511.peg.446	ADP-L-glycero-D-manno-heptose-6-epimerase (EC 5.1.3.20)
fig 6666666.284511.peg.447	ADP-heptose synthase (EC 2.7.-.-) / D-glycero-beta-D-manno-heptos
fig 6666666.284511.peg.448	Heat shock (predicted periplasmic) protein YciM, precursor
fig 6666666.284511.peg.449	Probable transmembrane protein
fig 6666666.284511.peg.450	Integration host factor beta subunit
fig 6666666.284511.peg.451	hypothetical protein
fig 6666666.284511.peg.452	SSU ribosomal protein S1p
fig 6666666.284511.peg.453	5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)
fig 6666666.284511.peg.454	Cyclohexadienyl dehydrogenase (EC 1.3.1.12)(EC 1.3.1.43)
fig 6666666.284511.peg.455	Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.5)
fig 6666666.284511.peg.456	Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.
fig 6666666.284511.peg.457	Phosphoserine aminotransferase (EC 2.6.1.52)
fig 6666666.284511.peg.458	DNA gyrase subunit A (EC 5.99.1.3)
fig 6666666.284511.peg.459	Outer membrane protein A precursor
fig 6666666.284511.peg.460	hypothetical protein
fig 6666666.284511.peg.461	3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64)
fig 6666666.284511.peg.462	Similar to phosphoglycolate phosphatase, clustered with ubiquinone
fig 6666666.284511.peg.463	hypothetical protein
fig 6666666.284511.peg.464	ABC transporter ATP-binding protein (CycB)
fig 6666666.284511.peg.465	Tungstate ABC transporter, permease protein WtpB
fig 6666666.284511.peg.466	Tungstate ABC transporter, periplasmic substrate-binding protein W
fig 6666666.284511.peg.467	Molybdopterin biosynthesis molybdochelatase MogA
fig 6666666.284511.peg.468	FIG138315: Putative alpha helix protein
fig 6666666.284511.peg.469	TldE protein, part of TldE/TldD proteolytic complex
fig 6666666.284511.peg.470	Dihydrofolate reductase (EC 1.5.1.3)
fig 6666666.284511.peg.471	Thymidylate synthase (EC 2.1.1.45)
fig 6666666.284511.peg.472	probable hydrolase

fig 6666666.284511.peg.473	GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase I
fig 6666666.284511.peg.474	Threonyl-tRNA synthetase (EC 6.1.1.3)
fig 6666666.284511.peg.475	Translation initiation factor 3
fig 6666666.284511.peg.476	LSU ribosomal protein L35p
fig 6666666.284511.peg.477	LSU ribosomal protein L20p
fig 6666666.284511.peg.478	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
fig 6666666.284511.peg.479	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)
fig 6666666.284511.peg.480	Integration host factor alpha subunit
fig 6666666.284511.peg.481	Transcriptional regulator, MerR family
fig 6666666.284511.peg.482	transcriptional regulator, Crp/Fnr family
fig 6666666.284511.peg.483	hypothetical protein
fig 6666666.284511.peg.484	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)
fig 6666666.284511.peg.485	hypothetical protein
fig 6666666.284511.peg.486	Cytochrome c oxidase polypeptide II (EC 1.9.3.1)
fig 6666666.284511.peg.487	Pyruvate decarboxylase (EC 4.1.1.1); Alpha-keto-acid decarboxylase (
fig 6666666.284511.peg.488	hypothetical protein
fig 6666666.284511.peg.489	FIG139928: Putative protease
fig 6666666.284511.peg.490	Putative protease
fig 6666666.284511.peg.491	Ribonucleotide reductase of class III (anaerobic), activating protein (I
fig 6666666.284511.peg.492	Adenosylhomocysteinase (EC 3.3.1.1)
fig 6666666.284511.peg.493	Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.
fig 6666666.284511.peg.494	Mobile element protein
fig 6666666.284511.peg.495	transcriptional regulator SoxR
fig 6666666.284511.peg.496	transcriptional regulator, Crp/Fnr family
fig 6666666.284511.peg.497	hypothetical protein
fig 6666666.284511.peg.498	hypothetical protein
fig 6666666.284511.peg.499	hypothetical protein
fig 6666666.284511.peg.500	ATP-dependent protease La (EC 3.4.21.53) Type II
fig 6666666.284511.peg.501	Coenzyme F390 synthetase
fig 6666666.284511.peg.502	hypothetical protein
fig 6666666.284511.peg.503	Sigma 54 modulation protein YhbH
fig 6666666.284511.peg.504	hypothetical protein
fig 6666666.284511.peg.505	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)
fig 6666666.284511.peg.506	ABC transporter, periplasmic substrate-binding protein
fig 6666666.284511.peg.507	Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1
fig 6666666.284511.peg.508	Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1
fig 6666666.284511.peg.509	Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1
fig 6666666.284511.peg.510	FIG000325: clustered with transcription termination protein NusA
fig 6666666.284511.peg.511	Transcription termination protein NusA
fig 6666666.284511.peg.512	Translation initiation factor 2
fig 6666666.284511.peg.513	Ribosome-binding factor A
fig 6666666.284511.peg.514	tRNA pseudouridine synthase B (EC 4.2.1.70)
fig 6666666.284511.peg.515	GTP-binding protein TypA/BipA

fig 6666666.284511.peg.516	membrane protein, putative
fig 6666666.284511.peg.517	L-fuco-beta-pyranose dehydrogenase (EC 1.1.1.122)
fig 6666666.284511.peg.518	hypothetical protein
fig 6666666.284511.peg.519	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)
fig 6666666.284511.peg.520	hypothetical protein
fig 6666666.284511.peg.521	hypothetical protein
fig 6666666.284511.peg.522	Response regulator
fig 6666666.284511.peg.523	Mobile element protein
fig 6666666.284511.peg.524	Lipid A acylation protein PagP, palmitoyltransferase
fig 6666666.284511.peg.525	Macrolide-specific efflux protein MacA
fig 6666666.284511.peg.526	Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)
fig 6666666.284511.peg.527	RND efflux system, outer membrane lipoprotein, NodT family
fig 6666666.284511.peg.528	Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase) / Delta-1-pyrroline dehydrogenase
fig 6666666.284511.peg.529	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.1.1)
fig 6666666.284511.peg.530	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.1.2)
fig 6666666.284511.peg.531	Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.1.3)
fig 6666666.284511.peg.532	High-affinity branched-chain amino acid transport system permease protein LivN (TC 3.A.1.1.4)
fig 6666666.284511.peg.533	Branched-chain amino acid ABC transporter, amino acid-binding protein LivP (TC 3.A.1.1.5)
fig 6666666.284511.peg.534	Mg(2+) transport ATPase, P-type (EC 3.6.3.2)
fig 6666666.284511.peg.535	hypothetical protein
fig 6666666.284511.peg.536	hypothetical protein
fig 6666666.284511.peg.537	hypothetical protein
fig 6666666.284511.peg.538	NAD(P)H dehydrogenase, quinone family
fig 6666666.284511.peg.539	Biotin synthesis protein BioC
fig 6666666.284511.peg.540	Mobile element protein
fig 6666666.284511.peg.541	putative transposase
fig 6666666.284511.peg.542	hypothetical protein
fig 6666666.284511.peg.543	hypothetical protein
fig 6666666.284511.peg.544	hypothetical protein
fig 6666666.284511.peg.545	hypothetical protein
fig 6666666.284511.peg.546	hypothetical protein
fig 6666666.284511.peg.547	NADPH:quinone oxidoreductase
fig 6666666.284511.peg.548	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.549	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)
fig 6666666.284511.peg.550	multi-sensor hybrid histidine kinase
fig 6666666.284511.peg.551	HEN1 C-terminal domain; double-stranded RNA 3'-methylase
fig 6666666.284511.peg.552	L-serine dehydratase (EC 4.3.1.17)
fig 6666666.284511.peg.553	Low-specificity L-threonine aldolase (EC 4.1.2.48)
fig 6666666.284511.peg.554	Nitrite-sensitive transcriptional repressor NsrR
fig 6666666.284511.peg.555	hypothetical protein
fig 6666666.284511.peg.556	putative inner membrane protein
fig 6666666.284511.peg.557	hypothetical protein
fig 6666666.284511.peg.558	Cytochrome c oxidase (B(O/a)3-type) chain II (EC 1.9.3.1)

fig 6666666.284511.peg.559	Cytochrome c oxidase (B(O/a)3-type) chain I (EC 1.9.3.1)
fig 6666666.284511.peg.560	Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative co
fig 6666666.284511.peg.561	membrane protein
fig 6666666.284511.peg.562	Cell division protein FtsH (EC 3.4.24.-)
fig 6666666.284511.peg.563	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
fig 6666666.284511.peg.564	Cell division protein Bola
fig 6666666.284511.peg.565	Intracellular septation protein IspA
fig 6666666.284511.peg.566	Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12)
fig 6666666.284511.peg.567	Selenoprotein O and cysteine-containing homologs
fig 6666666.284511.peg.568	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.
fig 6666666.284511.peg.569	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.
fig 6666666.284511.peg.570	Leucine-, isoleucine-, valine-, threonine-, and alanine-binding proteir
fig 6666666.284511.peg.571	High-affinity branched-chain amino acid transport system permease
fig 6666666.284511.peg.572	Branched-chain amino acid transport system permease protein LivM
fig 6666666.284511.peg.573	Magnesium and cobalt efflux protein CorC
fig 6666666.284511.peg.574	hypothetical protein
fig 6666666.284511.peg.575	Cystathionine beta-lyase (EC 4.4.1.8)
fig 6666666.284511.peg.576	hypothetical protein
fig 6666666.284511.peg.577	Phosphoserine phosphatase (EC 3.1.3.3)
fig 6666666.284511.peg.578	Transcription-repair coupling factor
fig 6666666.284511.peg.579	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.6)
fig 6666666.284511.peg.580	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)
fig 6666666.284511.peg.581	Acetolactate synthase large subunit (EC 2.2.1.6)
fig 6666666.284511.peg.582	Acetolactate synthase small subunit (EC 2.2.1.6)
fig 6666666.284511.peg.583	Ketol-acid reductoisomerase (EC 1.1.1.86)
fig 6666666.284511.peg.584	Phosphatidylserine decarboxylase (EC 4.1.1.65)
fig 6666666.284511.peg.585	CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)
fig 6666666.284511.peg.586	Choline dehydrogenase (EC 1.1.99.1)
fig 6666666.284511.peg.587	Flavoprotein WrbA
fig 6666666.284511.peg.588	Transcriptional regulator, HxlR family
fig 6666666.284511.peg.589	hypothetical protein
fig 6666666.284511.peg.590	Lysophospholipase L1 and related esterases
fig 6666666.284511.peg.591	CidA-associated membrane protein CidB
fig 6666666.284511.peg.592	Holin-like protein CidA
fig 6666666.284511.peg.593	LysR family regulatory protein CidR
fig 6666666.284511.peg.594	hypothetical protein
fig 6666666.284511.peg.595	hypothetical protein
fig 6666666.284511.peg.596	Histone acetyltransferase HPA2 and related acetyltransferases
fig 6666666.284511.peg.597	transcriptional regulator, Crp/Fnr family
fig 6666666.284511.peg.598	Inner membrane component of tripartite multidrug resistance system
fig 6666666.284511.peg.599	hypothetical protein
fig 6666666.284511.peg.600	hypothetical protein
fig 6666666.284511.peg.601	hypothetical protein

fig 6666666.284511.peg.602	hypothetical protein
fig 6666666.284511.peg.603	Cardiolipin synthetase (EC 2.7.8.-)
fig 6666666.284511.peg.604	Osmotically inducible protein Y precursor
fig 6666666.284511.peg.605	FIG00681120: hypothetical protein
fig 6666666.284511.peg.606	Outer membrane lipoprotein
fig 6666666.284511.peg.607	hypothetical protein
fig 6666666.284511.peg.608	hypothetical protein
fig 6666666.284511.peg.609	transposase, putative
fig 6666666.284511.peg.610	UPF0337 protein yjbJ
fig 6666666.284511.peg.611	membrane protein, putative
fig 6666666.284511.peg.612	hypothetical protein
fig 6666666.284511.peg.613	Mobile element protein
fig 6666666.284511.peg.614	FIG01002808: hypothetical protein
fig 6666666.284511.peg.615	Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16)
fig 6666666.284511.peg.616	Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16)
fig 6666666.284511.peg.617	carbon monoxide dehydrogenase G protein
fig 6666666.284511.peg.618	hypothetical protein
fig 6666666.284511.peg.619	hypothetical protein
fig 6666666.284511.peg.620	NAD(P)H-flavin oxidoreductase
fig 6666666.284511.peg.621	Nitroreductase
fig 6666666.284511.peg.622	Cation transport regulator chaB
fig 6666666.284511.peg.623	hypothetical protein
fig 6666666.284511.peg.624	Cobalt-zinc-cadmium resistance protein CzcD
fig 6666666.284511.peg.625	hypothetical protein
fig 6666666.284511.peg.626	hypothetical protein
fig 6666666.284511.peg.627	hypothetical protein
fig 6666666.284511.peg.628	Acetoin dehydrogenase E1 component alpha-subunit (EC 1.2.4.-)
fig 6666666.284511.peg.629	Acetoin dehydrogenase E1 component beta-subunit (EC 1.2.4.-)
fig 6666666.284511.peg.630	biotin/lipoyl attachment
fig 6666666.284511.peg.631	Lipoate-protein ligase A
fig 6666666.284511.peg.632	Transcriptional activator of acetoin dehydrogenase operon AcoR
fig 6666666.284511.peg.633	Alcohol dehydrogenase (EC 1.1.1.1)
fig 6666666.284511.peg.634	CBS domain protein
fig 6666666.284511.peg.635	hypothetical protein
fig 6666666.284511.peg.636	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)
fig 6666666.284511.peg.637	Phosphoribosyl transferase domain protein
fig 6666666.284511.peg.638	FIG001587: exported protein
fig 6666666.284511.peg.639	ErfK/YbiS/YcfS/YnhG family protein
fig 6666666.284511.peg.640	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
fig 6666666.284511.peg.641	NAD(FAD)-utilizing dehydrogenases
fig 6666666.284511.peg.642	Esterase/lipase
fig 6666666.284511.peg.643	4-hydroxybenzoyl-CoA thioesterase family active site
fig 6666666.284511.peg.644	COG3332

fig 6666666.284511.peg.645	Folate-dependent protein for Fe/S cluster synthesis/repair in oxidati
fig 6666666.284511.peg.646	Folate-dependent protein for Fe/S cluster synthesis/repair in oxidati
fig 6666666.284511.peg.647	FIG004453: protein YceG like
fig 6666666.284511.peg.648	Thymidylate kinase (EC 2.7.4.9)
fig 6666666.284511.peg.649	DNA polymerase III delta prime subunit (EC 2.7.7.7)
fig 6666666.284511.peg.650	Type IV pilus biogenesis protein PilZ
fig 6666666.284511.peg.651	Putative deoxyribonuclease YcfH
fig 6666666.284511.peg.652	FOG: Ankyrin repeat
fig 6666666.284511.peg.653	hypothetical protein
fig 6666666.284511.peg.654	hypothetical protein
fig 6666666.284511.peg.655	hypothetical protein
fig 6666666.284511.peg.656	Phage-related integrase
fig 6666666.284511.peg.657	Mercuric resistance operon regulatory protein
fig 6666666.284511.peg.658	hypothetical protein
fig 6666666.284511.peg.659	hypothetical protein
fig 6666666.284511.peg.660	Mercuric ion reductase (EC 1.16.1.1)
fig 6666666.284511.peg.661	hypothetical protein
fig 6666666.284511.peg.662	hypothetical protein
fig 6666666.284511.peg.663	Transcriptional regulator, ArsR family
fig 6666666.284511.peg.664	Putative ACR protein
fig 6666666.284511.peg.665	Metallo-beta-lactamase family protein
fig 6666666.284511.peg.666	Major facilitator superfamily (MFS) transporter
fig 6666666.284511.peg.667	Lipocalin-related protein and Bos/Can/Equ allergen
fig 6666666.284511.peg.668	hypothetical protein
fig 6666666.284511.peg.669	thioredoxin family protein
fig 6666666.284511.peg.670	Copper tolerance protein
fig 6666666.284511.peg.671	Copper resistance protein B
fig 6666666.284511.peg.672	Multicopper oxidase
fig 6666666.284511.peg.673	Cytochrome c-type biogenesis protein DsbD, protein-disulfide reduct
fig 6666666.284511.peg.674	Thiol:disulfide interchange protein tlpA
fig 6666666.284511.peg.675	hypothetical protein
fig 6666666.284511.peg.676	Potassium voltage-gated channel subfamily KQT; possible potassium
fig 6666666.284511.peg.677	Kef-type K ⁺ transport systems, predicted NAD-binding component
fig 6666666.284511.peg.678	hypothetical protein
fig 6666666.284511.peg.679	multidrug resistance protein, putative
fig 6666666.284511.peg.680	hypothetical protein
fig 6666666.284511.peg.681	hypothetical protein
fig 6666666.284511.peg.682	Multicopper oxidase
fig 6666666.284511.peg.683	Multicopper oxidase
fig 6666666.284511.peg.684	hypothetical protein
fig 6666666.284511.peg.685	hypothetical protein
fig 6666666.284511.peg.686	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.687	hypothetical protein

fig 6666666.284511.peg.688	Periplasmic thiol:disulfide interchange protein DsbA
fig 6666666.284511.peg.689	hypothetical protein
fig 6666666.284511.peg.690	rusticyanin related protein
fig 6666666.284511.peg.691	hypothetical protein
fig 6666666.284511.peg.692	hypothetical protein
fig 6666666.284511.peg.693	hypothetical protein
fig 6666666.284511.peg.694	Mobile element protein
fig 6666666.284511.peg.695	DNA-binding heavy metal response regulator
fig 6666666.284511.peg.696	Heavy metal sensor histidine kinase
fig 6666666.284511.peg.697	INTEGRAL MEMBRANE PROTEIN (Rhomboid family)
fig 6666666.284511.peg.698	periplasmic sensor signal transduction histidine kinase
fig 6666666.284511.peg.699	Sensory histidine kinase QseC
fig 6666666.284511.peg.700	Two-component system response regulator QseB
fig 6666666.284511.peg.701	INTEGRAL MEMBRANE PROTEIN (Rhomboid family)
fig 6666666.284511.peg.702	Propeptide PepSY amd peptidase M4
fig 6666666.284511.peg.703	Bacitracin transport permease protein BCRC
fig 6666666.284511.peg.704	hypothetical protein
fig 6666666.284511.peg.705	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.706	Outer membrane efflux protein
fig 6666666.284511.peg.707	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.708	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.709	Secretion protein HlyD precursor
fig 6666666.284511.peg.710	hypothetical protein
fig 6666666.284511.peg.711	Transcriptional regulator, Mecl family
fig 6666666.284511.peg.712	hypothetical protein
fig 6666666.284511.peg.713	hypothetical protein
fig 6666666.284511.peg.714	Type II secretory pathway, component ExeA (predicted ATPase)
fig 6666666.284511.peg.715	predicted by Framed
fig 6666666.284511.peg.716	hypothetical protein
fig 6666666.284511.peg.717	Phenylacetic acid degradation protein PaaD, thioesterase
fig 6666666.284511.peg.718	hypothetical protein
fig 6666666.284511.peg.719	Putative TEGT family carrier/transport protein
fig 6666666.284511.peg.720	UPF0225 protein YchJ
fig 6666666.284511.peg.721	hypothetical protein
fig 6666666.284511.peg.722	poly-gamma-glutamate synthesis protein (capsule biosynthesis prote
fig 6666666.284511.peg.723	hypothetical protein
fig 6666666.284511.peg.724	hypothetical protein
fig 6666666.284511.peg.725	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.726	hypothetical protein
fig 6666666.284511.peg.727	Outer membrane efflux protein
fig 6666666.284511.peg.728	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.729	hypothetical protein
fig 6666666.284511.peg.730	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p

fig 6666666.284511.peg.731	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion prot
fig 6666666.284511.peg.732	hypothetical protein
fig 6666666.284511.peg.733	Transcriptional regulator, Mecl family
fig 6666666.284511.peg.734	hypothetical protein
fig 6666666.284511.peg.735	hypothetical protein
fig 6666666.284511.peg.736	Mobile element protein
fig 6666666.284511.peg.737	Mobile element protein
fig 6666666.284511.peg.738	hypothetical protein
fig 6666666.284511.peg.739	Rubrerythrin
fig 6666666.284511.peg.740	Rubredoxin
fig 6666666.284511.peg.741	Rubredoxin-NAD(+) reductase (EC 1.18.1.1)
fig 6666666.284511.peg.742	hypothetical protein
fig 6666666.284511.peg.743	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid (
fig 6666666.284511.peg.744	Lysine exporter protein (LYSE/YGGA)
fig 6666666.284511.peg.745	Alkyl hydroperoxide reductase subunit C-like protein
fig 6666666.284511.peg.746	hypothetical protein
fig 6666666.284511.peg.747	hypothetical protein
fig 6666666.284511.peg.748	Branched-chain amino acid ABC transporter, amino acid-binding prot
fig 6666666.284511.peg.749	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.
fig 6666666.284511.peg.750	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.
fig 6666666.284511.peg.751	Branched-chain amino acid transport system permease protein LivM
fig 6666666.284511.peg.752	High-affinity branched-chain amino acid transport system permease
fig 6666666.284511.peg.753	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
fig 6666666.284511.peg.754	Acyl-CoA dehydrogenase (EC 1.3.8.7)
fig 6666666.284511.peg.755	Predicted aminoglycoside phosphotransferase
fig 6666666.284511.peg.756	Putative oxidoreductase YncB
fig 6666666.284511.peg.757	hypothetical protein
fig 6666666.284511.peg.758	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.759	3-methylmercaptopropionyl-CoA dehydrogenase (DmdC)
fig 6666666.284511.peg.760	hypothetical protein
fig 6666666.284511.peg.761	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase
fig 6666666.284511.peg.762	Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-
fig 6666666.284511.peg.763	hypothetical protein
fig 6666666.284511.peg.764	Epoxide hydrolase
fig 6666666.284511.peg.765	Transcriptional regulator, IclR family
fig 6666666.284511.peg.766	hypothetical protein
fig 6666666.284511.peg.767	Acyl-CoA dehydrogenase, long-chain specific, mitochondrial precursor
fig 6666666.284511.peg.768	Acyl-CoA dehydrogenase family protein
fig 6666666.284511.peg.769	Alcohol dehydrogenase (EC 1.1.1.1)
fig 6666666.284511.peg.770	Short-chain dehydrogenase/reductase SDR
fig 6666666.284511.peg.771	Putative Zn-dependent oxidoreductase PA5234
fig 6666666.284511.peg.772	hypothetical protein
fig 6666666.284511.peg.773	hypothetical protein

fig 6666666.284511.peg.774	hypothetical protein
fig 6666666.284511.peg.775	tRNA-specific adenosine-34 deaminase (EC 3.5.4.-)
fig 6666666.284511.peg.776	Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13)
fig 6666666.284511.peg.777	hypothetical protein
fig 6666666.284511.peg.778	hypothetical protein
fig 6666666.284511.peg.779	Nitroreductase family protein
fig 6666666.284511.peg.780	Peptidyl-prolyl cis-trans isomerase PpiD (EC 5.2.1.8)
fig 6666666.284511.peg.781	Respiratory nitrate reductase gamma chain (EC 1.7.99.4)
fig 6666666.284511.peg.782	Respiratory nitrate reductase delta chain (EC 1.7.99.4)
fig 6666666.284511.peg.783	Respiratory nitrate reductase beta chain (EC 1.7.99.4)
fig 6666666.284511.peg.784	Respiratory nitrate reductase alpha chain (EC 1.7.99.4)
fig 6666666.284511.peg.785	Nitrate/nitrite transporter
fig 6666666.284511.peg.786	Nitrate/nitrite transporter
fig 6666666.284511.peg.787	Nitrate/nitrite response regulator protein
fig 6666666.284511.peg.788	Nitrate/nitrite sensor protein (EC 2.7.3.-)
fig 6666666.284511.peg.789	Transcriptional regulator, TetR family
fig 6666666.284511.peg.790	hypothetical protein
fig 6666666.284511.peg.791	hypothetical protein
fig 6666666.284511.peg.792	Mobile element protein
fig 6666666.284511.peg.793	hypothetical protein
fig 6666666.284511.peg.794	Mobile element protein
fig 6666666.284511.peg.795	Mobile element protein
fig 6666666.284511.peg.796	hypothetical protein
fig 6666666.284511.peg.797	ISSoc3, orfA transposase
fig 6666666.284511.peg.798	Lignin beta-ether hydrolase
fig 6666666.284511.peg.799	Glutathione S-transferase (EC 2.5.1.18)
fig 6666666.284511.peg.800	Transcriptional regulator, TetR family
fig 6666666.284511.peg.801	Thioredoxin
fig 6666666.284511.peg.802	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)
fig 6666666.284511.peg.803	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)
fig 6666666.284511.peg.804	hypothetical protein
fig 6666666.284511.peg.805	PROBABLE TRANSMEMBRANE PROTEIN
fig 6666666.284511.peg.806	L-asparaginase (EC 3.5.1.1)
fig 6666666.284511.peg.807	SOS-response repressor and protease LexA (EC 3.4.21.88)
fig 6666666.284511.peg.808	Ribonuclease E inhibitor RraA
fig 6666666.284511.peg.809	Inner membrane protein
fig 6666666.284511.peg.810	Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative co
fig 6666666.284511.peg.811	ClpB protein
fig 6666666.284511.peg.812	Probable transmembrane protein
fig 6666666.284511.peg.813	Probable transmembrane protein
fig 6666666.284511.peg.814	hypothetical protein
fig 6666666.284511.peg.815	Molybdenum cofactor biosynthesis protein MoaE
fig 6666666.284511.peg.816	Molybdenum cofactor biosynthesis protein MoaD

fig 6666666.284511.peg.817	Molybdopterin biosynthesis protein MoeA
fig 6666666.284511.peg.818	Molybdopterin-guanine dinucleotide biosynthesis protein MobB
fig 6666666.284511.peg.819	Threonine synthase (EC 4.2.3.1)
fig 6666666.284511.peg.820	Homoserine dehydrogenase (EC 1.1.1.3)
fig 6666666.284511.peg.821	Aspartate aminotransferase (EC 2.6.1.1)
fig 6666666.284511.peg.822	Membrane protein
fig 6666666.284511.peg.823	Thiol peroxidase, Bcp-type (EC 1.11.1.15)
fig 6666666.284511.peg.824	hypothetical protein
fig 6666666.284511.peg.825	Predicted ATPase related to phosphate starvation-inducible protein I
fig 6666666.284511.peg.826	Replicative DNA helicase (EC 3.6.1.-)
fig 6666666.284511.peg.827	LSU ribosomal protein L9p
fig 6666666.284511.peg.828	SSU ribosomal protein S18p @ SSU ribosomal protein S18p, zinc-induc
fig 6666666.284511.peg.829	hypothetical protein
fig 6666666.284511.peg.830	SSU ribosomal protein S6p
fig 6666666.284511.peg.831	Phosphoenolpyruvate synthase (EC 2.7.9.2)
fig 6666666.284511.peg.832	FIG137360: hypothetical protein
fig 6666666.284511.peg.833	hypothetical protein
fig 6666666.284511.peg.834	23S rRNA (guanosine-2'-O-) -methyltransferase rlmB (EC 2.1.1.-)
fig 6666666.284511.peg.835	Ribonuclease HII (EC 3.1.26.4)
fig 6666666.284511.peg.836	Lipid-A-disaccharide synthase (EC 2.4.1.182)
fig 6666666.284511.peg.837	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransfera
fig 6666666.284511.peg.838	3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form (EC 4.2.1
fig 6666666.284511.peg.839	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3
fig 6666666.284511.peg.840	Outer membrane protein H precursor
fig 6666666.284511.peg.841	Outer membrane protein assembly factor YaeT precursor
fig 6666666.284511.peg.842	Membrane-associated zinc metalloprotease
fig 6666666.284511.peg.843	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)
fig 6666666.284511.peg.844	Phosphatidate cytidylyltransferase (EC 2.7.7.41)
fig 6666666.284511.peg.845	Undecaprenyl diphosphate synthase (EC 2.5.1.31)
fig 6666666.284511.peg.846	Ribosome recycling factor
fig 6666666.284511.peg.847	Uridine monophosphate kinase (EC 2.7.4.22)
fig 6666666.284511.peg.848	Translation elongation factor Ts
fig 6666666.284511.peg.849	SSU ribosomal protein S2p (SAe)
fig 6666666.284511.peg.850	hypothetical protein
fig 6666666.284511.peg.851	Thymidine phosphorylase (EC 2.4.2.4)
fig 6666666.284511.peg.852	23S rRNA (guanosine-2'-O-) -methyltransferase rlmB (EC 2.1.1.-)
fig 6666666.284511.peg.853	Probable ATP-binding ABC transporter protein
fig 6666666.284511.peg.854	Arylesterase precursor (EC 3.1.1.2)
fig 6666666.284511.peg.855	Selenophosphate-dependent tRNA 2-selenouridine synthase
fig 6666666.284511.peg.856	Ni,Fe-hydrogenase III small subunit
fig 6666666.284511.peg.857	Ni,Fe-hydrogenase III large subunit
fig 6666666.284511.peg.858	Formate hydrogenlyase subunit 3/Multisubunit Na ⁺ /H ⁺ antiporter, M
fig 6666666.284511.peg.859	Hydrogenase-4 component E

fig 6666666.284511.peg.860	Formate hydrogenlyase subunit 4
fig 6666666.284511.peg.861	Hydrogenase-4 component B (EC 1.-.-) / Formate hydrogenlyase sul
fig 6666666.284511.peg.862	hypothetical protein
fig 6666666.284511.peg.863	tRNA dihydrouridine synthase A
fig 6666666.284511.peg.864	hypothetical protein
fig 6666666.284511.peg.865	Probable Co/Zn/Cd efflux system membrane fusion protein
fig 6666666.284511.peg.866	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.867	Heavy metal RND efflux outer membrane protein, CzcC family
fig 6666666.284511.peg.868	Permeases of the major facilitator superfamily
fig 6666666.284511.peg.869	Malonyl CoA acyl carrier protein transacylase (EC 2.3.1.39)
fig 6666666.284511.peg.870	Phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.-)
fig 6666666.284511.peg.871	Malonate decarboxylase gamma subunit
fig 6666666.284511.peg.872	Malonate decarboxylase beta subunit
fig 6666666.284511.peg.873	Malonate decarboxylase delta subunit
fig 6666666.284511.peg.874	Triphosphoribosyl-dephospho-CoA synthetase (EC 2.7.8.25)
fig 6666666.284511.peg.875	Malonate decarboxylase alpha subunit
fig 6666666.284511.peg.876	Transcriptional regulator, GntR family
fig 6666666.284511.peg.877	Oxidoreductase, aldo/keto reductase family
fig 6666666.284511.peg.878	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.879	FIG00556689: hypothetical protein
fig 6666666.284511.peg.880	hypothetical protein
fig 6666666.284511.peg.881	Gamma-glutamyltranspeptidase (EC 2.3.2.2)
fig 6666666.284511.peg.882	hypothetical protein
fig 6666666.284511.peg.883	putative oxalate/formate antiporter
fig 6666666.284511.peg.884	hypothetical protein
fig 6666666.284511.peg.885	Transcriptional regulator, GntR family
fig 6666666.284511.peg.886	hypothetical protein
fig 6666666.284511.peg.887	Asp-tRNA ^{Asn} /Glu-tRNA ^{Gln} amidotransferase A subunit and related a
fig 6666666.284511.peg.888	hypothetical protein
fig 6666666.284511.peg.889	hypothetical protein
fig 6666666.284511.peg.890	Nucleoside ABC transporter, ATP-binding protein
fig 6666666.284511.peg.891	Nucleoside ABC transporter, permease protein 1
fig 6666666.284511.peg.892	Nucleoside ABC transporter, permease protein 2
fig 6666666.284511.peg.893	Nucleoside ABC transporter, periplasmic nucleoside-binding protein
fig 6666666.284511.peg.894	Isochorismatase (EC 3.3.2.1)
fig 6666666.284511.peg.895	Isochorismatase (EC 3.3.2.1)
fig 6666666.284511.peg.896	hypothetical protein
fig 6666666.284511.peg.897	hypothetical protein
fig 6666666.284511.peg.898	Molybdate-binding domain of ModE
fig 6666666.284511.peg.899	putative membrane protein
fig 6666666.284511.peg.900	NADP oxidoreductase, coenzyme F420-dependent
fig 6666666.284511.peg.901	Transcriptional regulator, LysR family
fig 6666666.284511.peg.902	Mobile element protein

fig 6666666.284511.peg.903	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.904	Small-conductance mechanosensitive channel
fig 6666666.284511.peg.905	Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)
fig 6666666.284511.peg.906	Hydroxyethylthiazole kinase (EC 2.7.1.50)
fig 6666666.284511.peg.907	4-oxalocrotonate tautomerase (EC 5.3.2.-)
fig 6666666.284511.peg.908	4-oxalocrotonate decarboxylase (EC 4.1.1.77)
fig 6666666.284511.peg.909	4-hydroxy-2-oxovalerate aldolase (EC 4.1.3.39)
fig 6666666.284511.peg.910	Acetaldehyde dehydrogenase, acetylating, (EC 1.2.1.10) in gene clust
fig 6666666.284511.peg.911	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.912	4-oxalocrotonate decarboxylase (EC 4.1.1.77)
fig 6666666.284511.peg.913	2-hydroxymuconic semialdehyde hydrolase (EC 3.7.1.9)
fig 6666666.284511.peg.914	Putative 5-carboxymethyl-2-hydroxymuconate semialdehyde dehydr
fig 6666666.284511.peg.915	Protein GlcG
fig 6666666.284511.peg.916	Catechol 2,3-dioxygenase (EC 1.13.11.2)
fig 6666666.284511.peg.917	Iron-sulfur binding electron transfer protein
fig 6666666.284511.peg.918	Phenol hydroxylase, FAD- and [2Fe-2S]-containing reductase compor
fig 6666666.284511.peg.919	Phenol hydroxylase, P4 oxygenase component DmpO (EC 1.14.13.7)
fig 6666666.284511.peg.920	Phenol hydroxylase, P3 oxygenase component DmpN (EC 1.14.13.7)
fig 6666666.284511.peg.921	Phenol hydroxylase, P2 regulatory component DmpM (EC 1.14.13.7)
fig 6666666.284511.peg.922	Phenol hydroxylase, P1 oxygenase component DmpL (EC 1.14.13.7)
fig 6666666.284511.peg.923	Phenol hydroxylase, assembly protein DmpK
fig 6666666.284511.peg.924	Positive regulator of phenol hydroxylase
fig 6666666.284511.peg.925	Regulatory protein GntR, HTH:GntR, C-terminal
fig 6666666.284511.peg.926	Bacitracin transport permease protein BCRC
fig 6666666.284511.peg.927	Outer membrane efflux protein
fig 6666666.284511.peg.928	Efflux transporter, RND family, MFP subunit, AcrA/E family
fig 6666666.284511.peg.929	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.930	Two-component system response regulator QseB
fig 6666666.284511.peg.931	sensor histidine kinase
fig 6666666.284511.peg.932	Periplasmic aromatic aldehyde oxidoreductase, FAD binding subunit
fig 6666666.284511.peg.933	Periplasmic aromatic aldehyde oxidoreductase, molybdenum binding
fig 6666666.284511.peg.934	Periplasmic aromatic aldehyde oxidoreductase, iron-sulfur subunit Y
fig 6666666.284511.peg.935	hypothetical protein
fig 6666666.284511.peg.936	Transposase
fig 6666666.284511.peg.937	hypothetical protein
fig 6666666.284511.peg.938	ATP-dependent protease La (EC 3.4.21.53) Type I
fig 6666666.284511.peg.939	2-heptaprenyl-1,4-naphthoquinone methyltransferase (EC 2.1.1.163)
fig 6666666.284511.peg.940	hypothetical protein
fig 6666666.284511.peg.941	Glutathione S-transferase (EC 2.5.1.18)
fig 6666666.284511.peg.942	hypothetical protein
fig 6666666.284511.peg.943	Glycine cleavage system transcriptional activator GcvA
fig 6666666.284511.peg.944	Acetyl-CoA hydrolase (EC 3.1.2.1)
fig 6666666.284511.peg.945	Diacylglycerol kinase (EC 2.7.1.107)

fig 6666666.284511.peg.946	Mobile element protein
fig 6666666.284511.peg.947	blr0920; hypothetical protein
fig 6666666.284511.peg.948	Probable transmembrane protein
fig 6666666.284511.peg.949	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.950	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
fig 6666666.284511.peg.951	Citronellol and citronellal dehydrogenase
fig 6666666.284511.peg.952	hypothetical protein
fig 6666666.284511.peg.953	hypothetical protein
fig 6666666.284511.peg.954	hypothetical protein
fig 6666666.284511.peg.955	Copper metallochaperone, bacterial analog of Cox17 protein
fig 6666666.284511.peg.956	macromolecule metabolism; macromolecule synthesis, modification;
fig 6666666.284511.peg.957	hypothetical protein
fig 6666666.284511.peg.958	cytochrome b561
fig 6666666.284511.peg.959	Octaheme tetrathionate reductase
fig 6666666.284511.peg.960	hypothetical protein
fig 6666666.284511.peg.961	NrfJ
fig 6666666.284511.peg.962	FIG00452652: hypothetical protein
fig 6666666.284511.peg.963	Transcriptional regulator, AraC family
fig 6666666.284511.peg.964	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.965	HYPOTHETICAL TRANSMEMBRANE PROTEIN
fig 6666666.284511.peg.966	hypothetical protein
fig 6666666.284511.peg.967	PROBABLE SIGNAL PEPTIDE PROTEIN
fig 6666666.284511.peg.968	FIG01209725: hypothetical protein
fig 6666666.284511.peg.969	Mobile element protein
fig 6666666.284511.peg.970	Mobile element protein
fig 6666666.284511.peg.971	hypothetical protein
fig 6666666.284511.peg.972	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.973	Uncharacterized protein conserved in bacteria
fig 6666666.284511.peg.974	Response regulator of the LytR/AlgR family
fig 6666666.284511.peg.975	Carbon monoxide dehydrogenase medium chain (EC 1.2.99.2)
fig 6666666.284511.peg.976	Carbon monoxide dehydrogenase small chain (EC 1.2.99.2)
fig 6666666.284511.peg.977	Carbon monoxide dehydrogenase form I, large chain (EC 1.2.99.2)
fig 6666666.284511.peg.978	Carbon monoxide oxidation accessory protein CoxG
fig 6666666.284511.peg.979	carbon monoxide dehydrogenase D protein
fig 6666666.284511.peg.980	Carbon monoxide oxidation accessory protein CoxE
fig 6666666.284511.peg.981	Aerobic carbon monoxide dehydrogenase molybdenum cofactor inser
fig 6666666.284511.peg.982	CTP:molybdopterin cytidyltransferase
fig 6666666.284511.peg.983	hypothetical protein
fig 6666666.284511.peg.984	Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF fam
fig 6666666.284511.peg.985	hypothetical protein
fig 6666666.284511.peg.986	Transcriptional regulator, AraC family
fig 6666666.284511.peg.987	diguanylate cyclase
fig 6666666.284511.peg.988	hypothetical protein

fig 6666666.284511.peg.989	CBS-domain-containing protein
fig 6666666.284511.peg.990	2-oxoglutarate oxidoreductase, beta subunit (EC 1.2.7.3)
fig 6666666.284511.peg.991	2-oxoglutarate oxidoreductase, alpha subunit (EC 1.2.7.3)
fig 6666666.284511.peg.992	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)
fig 6666666.284511.peg.993	cAMP-binding proteins - catabolite gene activator and regulatory subunit
fig 6666666.284511.peg.994	Predicted gluconate TRAP family transporter, DctM subunit
fig 6666666.284511.peg.995	TRAP-type C4-dicarboxylate transport system, periplasmic component
fig 6666666.284511.peg.996	Short-chain dehydrogenase/reductase SDR
fig 6666666.284511.peg.997	ATP-dependent DNA helicase RecQ
fig 6666666.284511.peg.998	hypothetical protein
fig 6666666.284511.peg.999	Glutamine ABC transporter, periplasmic glutamine-binding protein (1
fig 6666666.284511.peg.1000	Amino acid ABC transporter permease protein
fig 6666666.284511.peg.1001	Glutamine transport ATP-binding protein GlnQ (TC 3.A.1.3.2)
fig 6666666.284511.peg.1002	ATP-dependent DNA helicase RecQ
fig 6666666.284511.peg.1003	Tetratricopeptide TPR_2 repeat protein
fig 6666666.284511.peg.1004	hypothetical protein
fig 6666666.284511.peg.1005	NADH:flavin oxidoreductase/NADH oxidase
fig 6666666.284511.peg.1006	hypothetical protein
fig 6666666.284511.peg.1007	Acetone carboxylase, beta subunit (EC 6.4.1.6) / N-methylhydantoinase
fig 6666666.284511.peg.1008	Acetone carboxylase, alpha subunit (EC 6.4.1.6)
fig 6666666.284511.peg.1009	Acetone carboxylase, gamma subunit (EC 6.4.1.6)
fig 6666666.284511.peg.1010	Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.1)
fig 6666666.284511.peg.1011	Sigma-54 dependent transcriptional activator
fig 6666666.284511.peg.1012	hypothetical protein
fig 6666666.284511.peg.1013	Transcriptional regulator, MarR family
fig 6666666.284511.peg.1014	hypothetical protein
fig 6666666.284511.peg.1015	Cupin 2, conserved barrel domain protein
fig 6666666.284511.peg.1016	probable short chain oxidoreductase
fig 6666666.284511.peg.1017	Putative metal chaperone, involved in Zn homeostasis, GTPase of CO
fig 6666666.284511.peg.1018	hypothetical protein
fig 6666666.284511.peg.1019	Acetophenone carboxylase subunit Apc4 (EC 6.4.1.8)
fig 6666666.284511.peg.1020	N-methylhydantoinase A (EC 3.5.2.14)
fig 6666666.284511.peg.1021	Acetophenone carboxylase subunit Apc2
fig 6666666.284511.peg.1022	Acetophenone carboxylase subunit Apc1
fig 6666666.284511.peg.1023	Transcriptional regulator, LuxR family
fig 6666666.284511.peg.1024	3-ketoacyl-CoA thiolase (EC 2.3.1.16)
fig 6666666.284511.peg.1025	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
fig 6666666.284511.peg.1026	Transcriptional activator of maltose regulon, MalT
fig 6666666.284511.peg.1027	Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)
fig 6666666.284511.peg.1028	Uncharacterized conserved protein
fig 6666666.284511.peg.1029	Death on curing protein, Doc toxin
fig 6666666.284511.peg.1030	hypothetical protein
fig 6666666.284511.peg.1031	hypothetical protein

fig 6666666.284511.peg.1032	hypothetical protein
fig 6666666.284511.peg.1033	hypothetical protein
fig 6666666.284511.peg.1034	hypothetical protein
fig 6666666.284511.peg.1035	hypothetical protein
fig 6666666.284511.peg.1036	hypothetical protein
fig 6666666.284511.peg.1037	Periplasmic thiol:disulfide interchange protein DsbA
fig 6666666.284511.peg.1038	Transcriptional activator of acetoin dehydrogenase operon AcoR
fig 6666666.284511.peg.1039	Acetoin catabolism protein X
fig 6666666.284511.peg.1040	Acetoin dehydrogenase E1 component alpha-subunit (EC 1.2.4.-)
fig 6666666.284511.peg.1041	Acetoin dehydrogenase E1 component beta-subunit (EC 1.2.4.-)
fig 6666666.284511.peg.1042	Dihydrolipoamide acetyltransferase component (E2) of acetoin dehy
fig 6666666.284511.peg.1043	Lipoate-protein ligase A
fig 6666666.284511.peg.1044	Tryptophanase (EC 4.1.99.1)
fig 6666666.284511.peg.1045	hypothetical protein
fig 6666666.284511.peg.1046	VapC toxin protein
fig 6666666.284511.peg.1047	hypothetical protein
fig 6666666.284511.peg.1048	Growth inhibitor
fig 6666666.284511.peg.1049	hypothetical protein
fig 6666666.284511.peg.1050	hypothetical protein
fig 6666666.284511.peg.1051	hypothetical protein
fig 6666666.284511.peg.1052	FIG016027: protein of unknown function YeaO
fig 6666666.284511.peg.1053	Nitrite-sensitive transcriptional repressor NsrR
fig 6666666.284511.peg.1054	Nitric oxide-dependent regulator DnrN or NorA
fig 6666666.284511.peg.1055	FIG00452930: hypothetical protein
fig 6666666.284511.peg.1056	FIG032766: hypothetical protein
fig 6666666.284511.peg.1057	PaaD-like protein (DUF59) involved in Fe-S cluster assembly
fig 6666666.284511.peg.1058	Putative iron-sulfur cluster assembly scaffold protein for SUF system
fig 6666666.284511.peg.1059	Cysteine desulfurase (EC 2.8.1.7), SufS subfamily
fig 6666666.284511.peg.1060	Iron-sulfur cluster assembly protein SufD
fig 6666666.284511.peg.1061	Iron-sulfur cluster assembly ATPase protein SufC
fig 6666666.284511.peg.1062	Iron-sulfur cluster assembly protein SufB
fig 6666666.284511.peg.1063	hypothetical protein
fig 6666666.284511.peg.1064	hypothetical protein
fig 6666666.284511.peg.1065	Ferredoxin reductase
fig 6666666.284511.peg.1066	hypothetical protein
fig 6666666.284511.peg.1067	FIG022160: hypothetical toxin
fig 6666666.284511.peg.1068	hypothetical protein
fig 6666666.284511.peg.1069	Mobile element protein
fig 6666666.284511.peg.1070	FIG045511: hypothetical antitoxin (to FIG022160: hypothetical toxin)
fig 6666666.284511.peg.1071	hypothetical protein
fig 6666666.284511.peg.1072	Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9)
fig 6666666.284511.peg.1073	Mobile element protein
fig 6666666.284511.peg.1074	hypothetical protein

fig 6666666.284511.peg.1075	putative aldo/keto reductase
fig 6666666.284511.peg.1076	HtaR suppressor protein
fig 6666666.284511.peg.1077	Transposase
fig 6666666.284511.peg.1078	Mobile element protein
fig 6666666.284511.peg.1079	Transposase
fig 6666666.284511.peg.1080	Mobile element protein
fig 6666666.284511.peg.1081	FIG01198409: hypothetical protein
fig 6666666.284511.peg.1082	putative integral membrane transport protein
fig 6666666.284511.peg.1083	hypothetical protein
fig 6666666.284511.peg.1084	Uncharacterized conserved protein
fig 6666666.284511.peg.1085	hypothetical protein
fig 6666666.284511.peg.1086	Sensory transduction histidine kinase
fig 6666666.284511.peg.1087	Pyridine nucleotide-disulfide oxidoreductase; NADH dehydrogenase
fig 6666666.284511.peg.1088	hypothetical protein
fig 6666666.284511.peg.1089	Alcohol dehydrogenase (EC 1.1.1.1); Acetaldehyde dehydrogenase (E
fig 6666666.284511.peg.1090	Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative
fig 6666666.284511.peg.1091	pyridoxal phosphate-dependent deaminase, putative
fig 6666666.284511.peg.1092	Adenylosuccinate lyase (EC 4.3.2.2)
fig 6666666.284511.peg.1093	Argininosuccinate lyase (EC 4.3.2.1)
fig 6666666.284511.peg.1094	Phosphosulfolactate synthase (EC 4.4.1.19)
fig 6666666.284511.peg.1095	hypothetical protein
fig 6666666.284511.peg.1096	3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6); Glutaconate Co
fig 6666666.284511.peg.1097	3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6); Glutaconate Co
fig 6666666.284511.peg.1098	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.1099	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.1100	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)
fig 6666666.284511.peg.1101	hypothetical protein
fig 6666666.284511.peg.1102	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransf
fig 6666666.284511.peg.1103	hypothetical protein
fig 6666666.284511.peg.1104	hypothetical protein
fig 6666666.284511.peg.1105	hypothetical protein
fig 6666666.284511.peg.1106	hypothetical protein
fig 6666666.284511.peg.1107	hypothetical protein
fig 6666666.284511.peg.1108	Rod shape determination protein
fig 6666666.284511.peg.1109	Membrane-associated phospholipid phosphatase
fig 6666666.284511.peg.1110	Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)
fig 6666666.284511.peg.1111	hypothetical protein
fig 6666666.284511.peg.1112	VapC toxin protein
fig 6666666.284511.peg.1113	hypothetical protein
fig 6666666.284511.peg.1114	hypothetical protein
fig 6666666.284511.peg.1115	hypothetical protein
fig 6666666.284511.peg.1116	TonB dependent receptor
fig 6666666.284511.peg.1117	protein of unknown function DUF336

fig 6666666.284511.peg.1118	hypothetical protein
fig 6666666.284511.peg.1119	hypothetical protein
fig 6666666.284511.peg.1120	hypothetical protein
fig 6666666.284511.peg.1121	protein of unknown function DUF336
fig 6666666.284511.peg.1122	hypothetical protein
fig 6666666.284511.peg.1123	hypothetical protein
fig 6666666.284511.peg.1124	ATP synthase beta chain (EC 3.6.3.14)
fig 6666666.284511.peg.1125	ATP synthase epsilon chain (EC 3.6.3.14)
fig 6666666.284511.peg.1126	Sodium-transporting ATPase subunit Q
fig 6666666.284511.peg.1127	hypothetical protein
fig 6666666.284511.peg.1128	ATP synthase F0 sector subunit a
fig 6666666.284511.peg.1129	Mobile element protein
fig 6666666.284511.peg.1130	ATP synthase F0 sector subunit c
fig 6666666.284511.peg.1131	ATP synthase F0 sector subunit b
fig 6666666.284511.peg.1132	ATP synthase alpha chain (EC 3.6.3.14)
fig 6666666.284511.peg.1133	ATP synthase gamma chain (EC 3.6.3.14)
fig 6666666.284511.peg.1134	protein of unknown function DUF336
fig 6666666.284511.peg.1135	Putative membrane protein
fig 6666666.284511.peg.1136	hypothetical protein
fig 6666666.284511.peg.1137	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1138	hypothetical protein
fig 6666666.284511.peg.1139	hypothetical protein
fig 6666666.284511.peg.1140	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1141	isochorismatase hydrolase
fig 6666666.284511.peg.1142	hypothetical protein
fig 6666666.284511.peg.1143	hypothetical protein
fig 6666666.284511.peg.1144	putative membrane protein
fig 6666666.284511.peg.1145	Helix-turn-helix motif
fig 6666666.284511.peg.1146	Transcriptional regulator, AbrB family
fig 6666666.284511.peg.1147	SLI1130 protein
fig 6666666.284511.peg.1148	Non-specific serine/threonine protein kinase(EC:2.7.11.1)
fig 6666666.284511.peg.1149	hypothetical protein
fig 6666666.284511.peg.1150	Helicase, SNF2/RAD54 family
fig 6666666.284511.peg.1151	Short-chain dehydrogenase/reductase SDR
fig 6666666.284511.peg.1152	Acetolactate synthase large subunit (EC 2.2.1.6)
fig 6666666.284511.peg.1153	hypothetical protein
fig 6666666.284511.peg.1154	MII5046 protein
fig 6666666.284511.peg.1155	Uncharacterized protein MJ0754
fig 6666666.284511.peg.1156	hypothetical protein
fig 6666666.284511.peg.1157	hypothetical protein
fig 6666666.284511.peg.1158	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductase
fig 6666666.284511.peg.1159	Universal stress protein UspA and related nucleotide-binding protein
fig 6666666.284511.peg.1160	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)

fig 6666666.284511.peg.1161	Phosphohydrolase (MutT/nudix family protein)
fig 6666666.284511.peg.1162	Ser/Thr protein phosphatase family protein
fig 6666666.284511.peg.1163	Mobile element protein
fig 6666666.284511.peg.1164	Ser/Thr protein phosphatase family protein
fig 6666666.284511.peg.1165	Short-chain dehydrogenase/reductase SDR
fig 6666666.284511.peg.1166	FIG00453399: hypothetical protein
fig 6666666.284511.peg.1167	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)
fig 6666666.284511.peg.1168	UPF0028 protein YchK
fig 6666666.284511.peg.1169	hypothetical protein
fig 6666666.284511.peg.1170	HIT family protein
fig 6666666.284511.peg.1171	hypothetical protein
fig 6666666.284511.peg.1172	putative lipoprotein
fig 6666666.284511.peg.1173	hypothetical protein
fig 6666666.284511.peg.1174	putative transposase
fig 6666666.284511.peg.1175	Mobile element protein
fig 6666666.284511.peg.1176	Mobile element protein
fig 6666666.284511.peg.1177	Mobile element protein
fig 6666666.284511.peg.1178	Mobile element protein
fig 6666666.284511.peg.1179	transposase, putative
fig 6666666.284511.peg.1180	hypothetical protein
fig 6666666.284511.peg.1181	ISSod11, transposase
fig 6666666.284511.peg.1182	hypothetical protein
fig 6666666.284511.peg.1183	hypothetical protein
fig 6666666.284511.peg.1184	hypothetical protein
fig 6666666.284511.peg.1185	Methyl-accepting chemotaxis protein
fig 6666666.284511.peg.1186	protein of unknown function DUF1624
fig 6666666.284511.peg.1187	Phosphoribosylformylglycinamidine synthase, synthetase subunit (EC
fig 6666666.284511.peg.1188	Methionine aminopeptidase (EC 3.4.11.18)
fig 6666666.284511.peg.1189	[Protein-Pil] uridylyltransferase (EC 2.7.7.59)
fig 6666666.284511.peg.1190	Chaperone-modulator protein CbpM
fig 6666666.284511.peg.1191	DnaJ-class molecular chaperone CbpA
fig 6666666.284511.peg.1192	hypothetical protein
fig 6666666.284511.peg.1193	hypothetical protein
fig 6666666.284511.peg.1194	Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative
fig 6666666.284511.peg.1195	diguanylate cyclase
fig 6666666.284511.peg.1196	hypothetical protein
fig 6666666.284511.peg.1197	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1198	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1199	hypothetical protein
fig 6666666.284511.peg.1200	Extracellular Matrix protein PelA
fig 6666666.284511.peg.1201	Extracellular Matrix protein PelB
fig 6666666.284511.peg.1202	Extracellular Matrix protein PelB
fig 6666666.284511.peg.1203	Extracellular Matrix protein PelC

fig 6666666.284511.peg.1204	Extracellular Matrix protein PelD
fig 6666666.284511.peg.1205	Extracellular Matrix protein PelE
fig 6666666.284511.peg.1206	Glycosyltransferase
fig 6666666.284511.peg.1207	Extracellular Matrix protein PelG
fig 6666666.284511.peg.1208	Flagellar motor switch protein FliN
fig 6666666.284511.peg.1209	Flagellar motor switch protein FliM
fig 6666666.284511.peg.1210	Flagellar biosynthesis protein FliL
fig 6666666.284511.peg.1211	Flagellar hook-length control protein FliK
fig 6666666.284511.peg.1212	hypothetical protein
fig 6666666.284511.peg.1213	Flagellum-specific ATP synthase FliI
fig 6666666.284511.peg.1214	Flagellar assembly protein FliH
fig 6666666.284511.peg.1215	Flagellar motor switch protein FliG
fig 6666666.284511.peg.1216	Flagellar M-ring protein FliF
fig 6666666.284511.peg.1217	Flagellar M-ring protein FliF
fig 6666666.284511.peg.1218	Flagellar hook-basal body complex protein FliE
fig 6666666.284511.peg.1219	Flagellar regulatory protein FleQ
fig 6666666.284511.peg.1220	Flagellar regulatory protein FleQ
fig 6666666.284511.peg.1221	DedD protein
fig 6666666.284511.peg.1222	Flagellar motor rotation protein MotB
fig 6666666.284511.peg.1223	hypothetical protein
fig 6666666.284511.peg.1224	Flagellar biosynthesis protein fliS
fig 6666666.284511.peg.1225	Flagellar hook-associated protein FliD
fig 6666666.284511.peg.1226	hypothetical protein
fig 6666666.284511.peg.1227	Flagellin protein FlaB
fig 6666666.284511.peg.1228	hypothetical protein
fig 6666666.284511.peg.1229	hypothetical protein
fig 6666666.284511.peg.1230	hypothetical protein
fig 6666666.284511.peg.1231	hypothetical protein
fig 6666666.284511.peg.1232	FOG: GGDEF domain
fig 6666666.284511.peg.1233	Flagellar basal-body P-ring formation protein flgA
fig 6666666.284511.peg.1234	Flagellar basal-body rod protein FlgB
fig 6666666.284511.peg.1235	Flagellar basal-body rod protein FlgC
fig 6666666.284511.peg.1236	Flagellar basal-body rod modification protein FlgD
fig 6666666.284511.peg.1237	Flagellar hook protein FlgE
fig 6666666.284511.peg.1238	Flagellar basal-body rod protein FlgF
fig 6666666.284511.peg.1239	Flagellar basal-body rod protein FlgG
fig 6666666.284511.peg.1240	Flagellar L-ring protein FlgH
fig 6666666.284511.peg.1241	Flagellar P-ring protein FlgI
fig 6666666.284511.peg.1242	Flagellar protein FlgJ [peptidoglycan hydrolase] (EC 3.2.1.-)
fig 6666666.284511.peg.1243	hypothetical protein
fig 6666666.284511.peg.1244	Flagellar hook-associated protein FlgK
fig 6666666.284511.peg.1245	Flagellar hook-associated protein FlgL
fig 6666666.284511.peg.1246	O-antigen biosynthesis protein

fig 6666666.284511.peg.1247	EAL domain protein
fig 6666666.284511.peg.1248	hypothetical protein
fig 6666666.284511.peg.1249	hypothetical protein
fig 6666666.284511.peg.1250	Carbon storage regulator
fig 6666666.284511.peg.1251	hypothetical protein
fig 6666666.284511.peg.1252	hypothetical protein
fig 6666666.284511.peg.1253	Flagellar motor rotation protein MotB
fig 6666666.284511.peg.1254	Flagellar motor rotation protein MotA
fig 6666666.284511.peg.1255	hypothetical protein
fig 6666666.284511.peg.1256	Chemotaxis regulator - transmits chemoreceptor signals to flagellar
fig 6666666.284511.peg.1257	hypothetical protein
fig 6666666.284511.peg.1258	Signal transduction histidine kinase CheA (EC 2.7.3.-)
fig 6666666.284511.peg.1259	hypothetical protein
fig 6666666.284511.peg.1260	CDP-abequose synthase (Fragment)
fig 6666666.284511.peg.1261	methyl-accepting chemotaxis sensory transducer
fig 6666666.284511.peg.1262	hypothetical protein
fig 6666666.284511.peg.1263	methyl-accepting chemotaxis protein
fig 6666666.284511.peg.1264	Chemotaxis protein CheV (EC 2.7.3.-)
fig 6666666.284511.peg.1265	methyl-accepting chemotaxis sensory transducer
fig 6666666.284511.peg.1266	hypothetical protein
fig 6666666.284511.peg.1267	transposase, putative
fig 6666666.284511.peg.1268	hypothetical protein
fig 6666666.284511.peg.1269	hypothetical protein
fig 6666666.284511.peg.1270	hypothetical protein
fig 6666666.284511.peg.1271	Mobile element protein
fig 6666666.284511.peg.1272	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1273	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1274	GGDEF domain protein
fig 6666666.284511.peg.1275	hypothetical protein
fig 6666666.284511.peg.1276	Flagellar biosynthesis protein FlhB
fig 6666666.284511.peg.1277	hypothetical protein
fig 6666666.284511.peg.1278	hypothetical protein
fig 6666666.284511.peg.1279	hypothetical protein
fig 6666666.284511.peg.1280	hypothetical protein
fig 6666666.284511.peg.1281	Flagellar motor rotation protein MotA
fig 6666666.284511.peg.1282	RNA polymerase sigma factor for flagellar operon
fig 6666666.284511.peg.1283	Flagellar synthesis regulator FleN
fig 6666666.284511.peg.1284	Flagellar biosynthesis protein FlhF
fig 6666666.284511.peg.1285	Flagellar biosynthesis protein FlhA
fig 6666666.284511.peg.1286	Flagellar biosynthesis protein FlhB
fig 6666666.284511.peg.1287	Flagellar biosynthesis protein FliR
fig 6666666.284511.peg.1288	Flagellar biosynthesis protein FliQ
fig 6666666.284511.peg.1289	Flagellar biosynthesis protein FliP

fig 6666666.284511.peg.1290	Mobile element protein
fig 6666666.284511.peg.1291	Extracellular Matrix protein PelG
fig 6666666.284511.peg.1292	antigen
fig 6666666.284511.peg.1293	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1294	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1295	Reverse transcriptase
fig 6666666.284511.peg.1296	Mobile element protein
fig 6666666.284511.peg.1297	Mobile element protein
fig 6666666.284511.peg.1298	hypothetical protein
fig 6666666.284511.peg.1299	Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
fig 6666666.284511.peg.1300	hypothetical protein
fig 6666666.284511.peg.1301	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1302	hypothetical protein
fig 6666666.284511.peg.1303	FIG00976424: hypothetical protein
fig 6666666.284511.peg.1304	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)
fig 6666666.284511.peg.1305	FIG00977943: hypothetical protein
fig 6666666.284511.peg.1306	hypothetical protein
fig 6666666.284511.peg.1307	Cellulose synthase (UDP-forming) (EC 2.4.1.12)
fig 6666666.284511.peg.1308	hypothetical protein
fig 6666666.284511.peg.1309	hypothetical protein
fig 6666666.284511.peg.1310	hypothetical protein
fig 6666666.284511.peg.1311	hypothetical protein
fig 6666666.284511.peg.1312	hypothetical protein
fig 6666666.284511.peg.1313	Aquaporin Z
fig 6666666.284511.peg.1314	hypothetical protein
fig 6666666.284511.peg.1315	hypothetical protein
fig 6666666.284511.peg.1316	hypothetical protein
fig 6666666.284511.peg.1317	C4-type zinc finger protein, DksA/TraR family
fig 6666666.284511.peg.1318	Putative signal peptide protein
fig 6666666.284511.peg.1319	Universal stress protein
fig 6666666.284511.peg.1320	cAMP-binding proteins - catabolite gene activator and regulatory subunit
fig 6666666.284511.peg.1321	cAMP-binding proteins - catabolite gene activator and regulatory subunit
fig 6666666.284511.peg.1322	hypothetical protein
fig 6666666.284511.peg.1323	Circadian clock protein KaiC
fig 6666666.284511.peg.1324	hypothetical protein
fig 6666666.284511.peg.1325	Flagellar hook-length control protein FliK
fig 6666666.284511.peg.1326	hypothetical protein; putative signal peptide
fig 6666666.284511.peg.1327	Osmotically inducible lipoprotein B precursor
fig 6666666.284511.peg.1328	Osmotically inducible protein Y precursor
fig 6666666.284511.peg.1329	hypothetical protein
fig 6666666.284511.peg.1330	Extracellular Matrix protein PelG
fig 6666666.284511.peg.1331	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.1332	hypothetical protein

fig 6666666.284511.peg.1333	Sensory box/GGDEF family protein
fig 6666666.284511.peg.1334	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1335	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1336	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1337	Molecular chaperone (small heat shock protein)
fig 6666666.284511.peg.1338	Heat shock protein, Hsp20 family
fig 6666666.284511.peg.1339	HAD family hydrolase, a
fig 6666666.284511.peg.1340	Thymidylate kinase (EC 2.7.4.9)
fig 6666666.284511.peg.1341	Carbohydrate kinase, FGGY family
fig 6666666.284511.peg.1342	Peptide deformylase (EC 3.5.1.88)
fig 6666666.284511.peg.1343	Xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22)
fig 6666666.284511.peg.1344	Adenylosuccinate synthetase (EC 6.3.4.4)
fig 6666666.284511.peg.1345	ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17)
fig 6666666.284511.peg.1346	hypothetical protein
fig 6666666.284511.peg.1347	HflC protein
fig 6666666.284511.peg.1348	HflK protein
fig 6666666.284511.peg.1349	GTP-binding protein HflX
fig 6666666.284511.peg.1350	RNA-binding protein Hfq
fig 6666666.284511.peg.1351	GTP-binding protein EngA
fig 6666666.284511.peg.1352	Outer membrane protein YfgL, lipoprotein component of the protei
fig 6666666.284511.peg.1353	Mrp7403 protein
fig 6666666.284511.peg.1354	Histidyl-tRNA synthetase (EC 6.1.1.21)
fig 6666666.284511.peg.1355	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.7
fig 6666666.284511.peg.1356	FIG021952: putative membrane protein
fig 6666666.284511.peg.1357	Type IV pilus biogenesis protein PilF
fig 6666666.284511.peg.1358	Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-)
fig 6666666.284511.peg.1359	Nucleoside diphosphate kinase (EC 2.7.4.6)
fig 6666666.284511.peg.1360	Ribosomal large subunit pseudouridine synthase B (EC 4.2.1.70)
fig 6666666.284511.peg.1361	Segregation and condensation protein B
fig 6666666.284511.peg.1362	Oxidoreductase FAD-binding domain protein
fig 6666666.284511.peg.1363	FAD pyrophosphatase (EC 3.6.1.18)
fig 6666666.284511.peg.1364	Heavy-metal-associated domain (N-terminus) and membrane-bound
fig 6666666.284511.peg.1365	transcriptional regulator, Crp/Fnr family
fig 6666666.284511.peg.1366	hypothetical protein
fig 6666666.284511.peg.1367	Putative analog of CcoH, COG3198
fig 6666666.284511.peg.1368	Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in
fig 6666666.284511.peg.1369	Cytochrome c oxidase subunit CcoP (EC 1.9.3.1)
fig 6666666.284511.peg.1370	hypothetical protein
fig 6666666.284511.peg.1371	Cytochrome c oxidase subunit CcoO (EC 1.9.3.1)
fig 6666666.284511.peg.1372	Cytochrome c oxidase subunit CcoN (EC 1.9.3.1)
fig 6666666.284511.peg.1373	Type cbb3 cytochrome oxidase biogenesis protein CcoS, involved in
fig 6666666.284511.peg.1374	Type cbb3 cytochrome oxidase biogenesis protein CcoI; Copper-trans
fig 6666666.284511.peg.1375	Type cbb3 cytochrome oxidase biogenesis protein CcoI; Copper-trans

fig 6666666.284511.peg.1376	hypothetical protein
fig 6666666.284511.peg.1377	hypothetical protein
fig 6666666.284511.peg.1378	hypothetical protein
fig 6666666.284511.peg.1379	hypothetical protein
fig 6666666.284511.peg.1380	Transcriptional regulator, PadR family
fig 6666666.284511.peg.1381	Uncharacterized protein MJ0754
fig 6666666.284511.peg.1382	Mobile element protein
fig 6666666.284511.peg.1383	Transcription accessory protein (S1 RNA-binding domain)
fig 6666666.284511.peg.1384	Response regulator
fig 6666666.284511.peg.1385	FIG146518: Zn-dependent hydrolases, including glyoxylases
fig 6666666.284511.peg.1386	Probable transmembrane protein
fig 6666666.284511.peg.1387	GENE II AND X PROTEINS
fig 6666666.284511.peg.1388	3-methylmercaptopropionyl-CoA ligase (DmdB)
fig 6666666.284511.peg.1389	4Fe-4S ferredoxin, iron-sulfur binding
fig 6666666.284511.peg.1390	Thioredoxin reductase (EC 1.8.1.9)
fig 6666666.284511.peg.1391	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1392	Caffeoyl-CoA O-methyltransferase (EC 2.1.1.104)
fig 6666666.284511.peg.1393	hypothetical protein
fig 6666666.284511.peg.1394	Integral membrane protein
fig 6666666.284511.peg.1395	Flavin reductase-like, FMN-binding domain protein
fig 6666666.284511.peg.1396	Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
fig 6666666.284511.peg.1397	hypothetical protein
fig 6666666.284511.peg.1398	PlcB, ORFX, ORFP, ORFB, ORFA, Idh gene
fig 6666666.284511.peg.1399	hypothetical protein
fig 6666666.284511.peg.1400	Conserved protein
fig 6666666.284511.peg.1401	hypothetical protein
fig 6666666.284511.peg.1402	Copper binding protein, plastocyanin/azurin family
fig 6666666.284511.peg.1403	C4-type zinc finger protein, DksA/TraR family
fig 6666666.284511.peg.1404	hypothetical protein
fig 6666666.284511.peg.1405	hypothetical protein
fig 6666666.284511.peg.1406	hypothetical protein
fig 6666666.284511.peg.1407	hypothetical protein
fig 6666666.284511.peg.1408	probable membrane protein STY1534
fig 6666666.284511.peg.1409	Uncharacterized PE-PGRS family protein PE_PGRS34
fig 6666666.284511.peg.1410	hypothetical protein
fig 6666666.284511.peg.1411	hypothetical protein
fig 6666666.284511.peg.1412	hypothetical protein
fig 6666666.284511.peg.1413	conserved hypothetical protein
fig 6666666.284511.peg.1414	hypothetical protein
fig 6666666.284511.peg.1415	hypothetical protein
fig 6666666.284511.peg.1416	hypothetical protein
fig 6666666.284511.peg.1417	hypothetical protein
fig 6666666.284511.peg.1418	hypothetical protein

fig 6666666.284511.peg.1419	hypothetical protein
fig 6666666.284511.peg.1420	Lysophospholipase (EC 3.1.1.5)
fig 6666666.284511.peg.1421	hypothetical protein
fig 6666666.284511.peg.1422	hypothetical protein
fig 6666666.284511.peg.1423	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases
fig 6666666.284511.peg.1424	hypothetical protein
fig 6666666.284511.peg.1425	hypothetical protein
fig 6666666.284511.peg.1426	2-dehydropantoate 2-reductase (EC 1.1.1.169)
fig 6666666.284511.peg.1427	hypothetical protein
fig 6666666.284511.peg.1428	Mobile element protein
fig 6666666.284511.peg.1429	Permeases of the major facilitator superfamily
fig 6666666.284511.peg.1430	Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminoben:
fig 6666666.284511.peg.1431	Chromosome initiation inhibitor
fig 6666666.284511.peg.1432	protein of unknown function UPF0126
fig 6666666.284511.peg.1433	hypothetical protein
fig 6666666.284511.peg.1434	Gentisate 1,2-dioxygenase (EC 1.13.11.4)
fig 6666666.284511.peg.1435	Putative n-hydroxybenzoate hydroxylase
fig 6666666.284511.peg.1436	Hemerythrin HHE cation binding region
fig 6666666.284511.peg.1437	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.
fig 6666666.284511.peg.1438	ABC transporter ATP-binding protein
fig 6666666.284511.peg.1439	Branched-chain amino acid transport system permease protein LivM
fig 6666666.284511.peg.1440	High-affinity branched-chain amino acid transport system permease
fig 6666666.284511.peg.1441	ABC transporter substrate-binding protein
fig 6666666.284511.peg.1442	Transcriptional regulator, MarR family
fig 6666666.284511.peg.1443	hypothetical protein
fig 6666666.284511.peg.1444	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.
fig 6666666.284511.peg.1445	ABC-type branched-chain amino acid transport systems, ATPase com
fig 6666666.284511.peg.1446	High-affinity branched-chain amino acid transport system permease
fig 6666666.284511.peg.1447	Leucine-, isoleucine-, valine-, threonine-, and alanine-binding proteir
fig 6666666.284511.peg.1448	Acyl-CoA dehydrogenase (EC 1.3.8.7)
fig 6666666.284511.peg.1449	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) @ 17hydroxysteroid
fig 6666666.284511.peg.1450	4-hydroxybenzoyl-CoA thioesterase family active site
fig 6666666.284511.peg.1451	3-ketoacyl-CoA thiolase (EC 2.3.1.16)
fig 6666666.284511.peg.1452	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.1453	Feruloyl-CoA synthetase
fig 6666666.284511.peg.1454	Transcriptional regulator, TetR family
fig 6666666.284511.peg.1455	Maleylacetoacetate isomerase (EC 5.2.1.2) @ Glutathione S-transfer:
fig 6666666.284511.peg.1456	Fumarylacetoacetase (EC 3.7.1.2)
fig 6666666.284511.peg.1457	Putative transcriptional regulator
fig 6666666.284511.peg.1458	Copper resistance protein B
fig 6666666.284511.peg.1459	Multicopper oxidase
fig 6666666.284511.peg.1460	hypothetical protein
fig 6666666.284511.peg.1461	hypothetical protein

fig 6666666.284511.peg.1462	hypothetical protein
fig 6666666.284511.peg.1463	hypothetical protein
fig 6666666.284511.peg.1464	Thiol:disulfide interchange protein DsbG precursor
fig 6666666.284511.peg.1465	Thiol:disulfide interchange protein DsbG precursor
fig 6666666.284511.peg.1466	hypothetical protein
fig 6666666.284511.peg.1467	hypothetical protein
fig 6666666.284511.peg.1468	hypothetical protein
fig 6666666.284511.peg.1469	hypothetical protein
fig 6666666.284511.peg.1470	hypothetical protein
fig 6666666.284511.peg.1471	hypothetical protein
fig 6666666.284511.peg.1472	hypothetical protein
fig 6666666.284511.peg.1473	Programmed cell death antitoxin PemI
fig 6666666.284511.peg.1474	Programmed cell death toxin PemK
fig 6666666.284511.peg.1475	hypothetical protein
fig 6666666.284511.peg.1476	hypothetical protein
fig 6666666.284511.peg.1477	hypothetical protein
fig 6666666.284511.peg.1478	hypothetical protein
fig 6666666.284511.peg.1479	hypothetical protein
fig 6666666.284511.peg.1480	hypothetical protein
fig 6666666.284511.peg.1481	hypothetical protein
fig 6666666.284511.peg.1482	hypothetical protein
fig 6666666.284511.peg.1483	blr4528; hypothetical protein
fig 6666666.284511.peg.1484	hypothetical protein
fig 6666666.284511.peg.1485	DNA primase (EC 2.7.7.-), phage-associated
fig 6666666.284511.peg.1486	hypothetical protein
fig 6666666.284511.peg.1487	hypothetical protein
fig 6666666.284511.peg.1488	hypothetical protein
fig 6666666.284511.peg.1489	hypothetical protein
fig 6666666.284511.peg.1490	hypothetical protein
fig 6666666.284511.peg.1491	Phage integrase
fig 6666666.284511.peg.1492	hypothetical protein
fig 6666666.284511.peg.1493	hypothetical protein
fig 6666666.284511.peg.1494	DNA-directed RNA polymerase specialized sigma subunit, sigma24-lil
fig 6666666.284511.peg.1495	Probable transmembrane protein
fig 6666666.284511.peg.1496	Probable transmembrane protein
fig 6666666.284511.peg.1497	Probable transmembrane protein
fig 6666666.284511.peg.1498	Ser/Thr protein phosphatase family protein, UDP-2,3-diacylglucosam
fig 6666666.284511.peg.1499	Glycosyltransferase
fig 6666666.284511.peg.1500	Diacylglycerol kinase (EC 2.7.1.107)
fig 6666666.284511.peg.1501	Lysine decarboxylase family
fig 6666666.284511.peg.1502	Nitrogen regulatory protein P-II
fig 6666666.284511.peg.1503	NAD synthetase (EC 6.3.1.5) / Glutamine amidotransferase chain of f
fig 6666666.284511.peg.1504	COGs COG3146

fig 6666666.284511.peg.1505	Low molecular weight protein tyrosine phosphatase (EC 3.1.3.48)
fig 6666666.284511.peg.1506	hypothetical protein
fig 6666666.284511.peg.1507	PQQ-dependent oxidoreductase, gdhB family
fig 6666666.284511.peg.1508	Excinuclease ABC subunit B
fig 6666666.284511.peg.1509	hypothetical protein
fig 6666666.284511.peg.1510	Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.5)
fig 6666666.284511.peg.1511	Intracellular PHB depolymerase (EC 3.1.1.-)
fig 6666666.284511.peg.1512	Electron transport complex protein RnfB
fig 6666666.284511.peg.1513	Endonuclease III (EC 4.2.99.18)
fig 6666666.284511.peg.1514	Vitamin B12 ABC transporter, B12-binding component BtuF
fig 6666666.284511.peg.1515	Iron(III) dicitrate transport ATP-binding protein fecE
fig 6666666.284511.peg.1516	Transport system permease protein
fig 6666666.284511.peg.1517	TonB-dependent receptor; Outer membrane receptor for ferrienteroc
fig 6666666.284511.peg.1518	hypothetical protein
fig 6666666.284511.peg.1519	hypothetical protein
fig 6666666.284511.peg.1520	hypothetical protein
fig 6666666.284511.peg.1521	hypothetical protein
fig 6666666.284511.peg.1522	Protein of unknown function DUF81
fig 6666666.284511.peg.1523	Prolipoprotein diacylglycerol transferase (EC 2.4.99.-)
fig 6666666.284511.peg.1524	Dihydroxy-acid dehydratase (EC 4.2.1.9)
fig 6666666.284511.peg.1525	ATP-dependent Clp protease ATP-binding subunit ClpA
fig 6666666.284511.peg.1526	ATP-dependent Clp protease adaptor protein ClpS
fig 6666666.284511.peg.1527	Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)
fig 6666666.284511.peg.1528	Acetyl-CoA acetyltransferase (EC 2.3.1.9) @ Beta-ketoadipyl CoA thic
fig 6666666.284511.peg.1529	Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-
fig 6666666.284511.peg.1530	Alcohol dehydrogenase (EC 1.1.1.1)
fig 6666666.284511.peg.1531	Benzoate anaerobic degradation transcriptional regulator BadR, Mar
fig 6666666.284511.peg.1532	Electron transfer flavoprotein, alpha subunit
fig 6666666.284511.peg.1533	Electron transfer flavoprotein, beta subunit
fig 6666666.284511.peg.1534	Glutaryl-CoA dehydrogenase (EC 1.3.99.7)
fig 6666666.284511.peg.1535	Butyryl-CoA dehydrogenase (EC 1.3.99.2)
fig 6666666.284511.peg.1536	Acetyl-coenzyme A synthetase (EC 6.2.1.1)
fig 6666666.284511.peg.1537	2-ketocyclohexanecarboxyl-CoA hydrolase
fig 6666666.284511.peg.1538	2-ketocyclohexanecarboxyl-CoA hydrolase (EC 4.1.3.36)
fig 6666666.284511.peg.1539	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.1540	hypothetical protein
fig 6666666.284511.peg.1541	ISSoc3, orfA transposase
fig 6666666.284511.peg.1542	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)
fig 6666666.284511.peg.1543	hypothetical protein
fig 6666666.284511.peg.1544	exported protein
fig 6666666.284511.peg.1545	Superoxide dismutase [Fe] (EC 1.15.1.1)
fig 6666666.284511.peg.1546	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
fig 6666666.284511.peg.1547	hypothetical protein

fig 6666666.284511.peg.1548	hypothetical protein
fig 6666666.284511.peg.1549	Ferric siderophore transport system, biopolymer transport protein E
fig 6666666.284511.peg.1550	Biopolymer transport protein ExbD/TolR
fig 6666666.284511.peg.1551	Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130)
fig 6666666.284511.peg.1552	FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster
fig 6666666.284511.peg.1553	3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38)
fig 6666666.284511.peg.1554	Adenylate kinase (EC 2.7.4.3)
fig 6666666.284511.peg.1555	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) @ 17hydroxysteroid
fig 6666666.284511.peg.1556	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1557	hypothetical protein
fig 6666666.284511.peg.1558	RNA polymerase sigma factor RpoD
fig 6666666.284511.peg.1559	hypothetical protein
fig 6666666.284511.peg.1560	Adenylate cyclase (EC 4.6.1.1)
fig 6666666.284511.peg.1561	Ferrochelatase, protoheme ferro-lyase (EC 4.99.1.1)
fig 6666666.284511.peg.1562	Polymyxin resistance protein ArnT, undecaprenyl phosphate-alpha-L
fig 6666666.284511.peg.1563	Heat shock protein GrpE
fig 6666666.284511.peg.1564	Chaperone protein DnaK
fig 6666666.284511.peg.1565	Chaperone protein DnaJ
fig 6666666.284511.peg.1566	hypothetical protein
fig 6666666.284511.peg.1567	Peptide chain release factor 2; programmed frameshift-containing
fig 6666666.284511.peg.1568	Membrane alanine aminopeptidase N (EC 3.4.11.2)
fig 6666666.284511.peg.1569	Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11)
fig 6666666.284511.peg.1570	YihE protein, required for LPS synthesis
fig 6666666.284511.peg.1571	hypothetical protein
fig 6666666.284511.peg.1572	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1573	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1574	hypothetical protein
fig 6666666.284511.peg.1575	Polymyxin resistance protein ArnT, undecaprenyl phosphate-alpha-L
fig 6666666.284511.peg.1576	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.1577	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase (
fig 6666666.284511.peg.1578	Polymyxin resistance protein ArnC, glycosyl transferase (EC 2.4.-.-)
fig 6666666.284511.peg.1579	UDP-4-amino-4-deoxy-L-arabinose formyltransferase (EC 2.1.2.13)
fig 6666666.284511.peg.1580	UDP-glucuronic acid oxidase (UDP-4-keto-hexauronic acid decarboxy
fig 6666666.284511.peg.1581	Polymyxin resistance protein PmrJ, predicted deacetylase
fig 6666666.284511.peg.1582	Acetyl-coenzyme A synthetase (EC 6.2.1.1)
fig 6666666.284511.peg.1583	putative membrane protein
fig 6666666.284511.peg.1584	Fumarate hydratase class I, aerobic (EC 4.2.1.2)
fig 6666666.284511.peg.1585	Exodeoxyribonuclease III (EC 3.1.11.2)
fig 6666666.284511.peg.1586	Nitrogen regulation protein NR(I)
fig 6666666.284511.peg.1587	Nitrogen regulation protein NtrB (EC 2.7.13.3)
fig 6666666.284511.peg.1588	hypothetical protein
fig 6666666.284511.peg.1589	Glutamine synthetase type I (EC 6.3.1.2)
fig 6666666.284511.peg.1590	Molybdopterin-binding protein

fig 6666666.284511.peg.1591	Probable transmembrane protein
fig 6666666.284511.peg.1592	Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)
fig 6666666.284511.peg.1593	putative transmembrane protein
fig 6666666.284511.peg.1594	Short-chain dehydrogenase, associated with 2-hydroxychromene-2-c
fig 6666666.284511.peg.1595	clavaldehyde dehydrogenase
fig 6666666.284511.peg.1596	hypothetical protein
fig 6666666.284511.peg.1597	Cold shock protein CspA
fig 6666666.284511.peg.1598	COG1272: Predicted membrane protein hemolysin III homolog
fig 6666666.284511.peg.1599	Beta-glucosidase (EC 3.2.1.21)
fig 6666666.284511.peg.1600	Beta-glucanase precursor (EC 3.2.1.73)
fig 6666666.284511.peg.1601	Probable glucosyl transferase
fig 6666666.284511.peg.1602	FIG00651212: hypothetical protein
fig 6666666.284511.peg.1603	Laminarinase (EC 3.2.1.39)
fig 6666666.284511.peg.1604	hypothetical protein
fig 6666666.284511.peg.1605	hypothetical protein
fig 6666666.284511.peg.1606	hypothetical protein
fig 6666666.284511.peg.1607	hypothetical protein
fig 6666666.284511.peg.1608	Glycosyl hydrolase
fig 6666666.284511.peg.1609	Various polyols ABC transporter, ATP-binding component
fig 6666666.284511.peg.1610	Beta-glucosidase (EC 3.2.1.21)
fig 6666666.284511.peg.1611	Maltose/maltodextrin ABC transporter, permease protein MalG
fig 6666666.284511.peg.1612	Maltose/maltodextrin ABC transporter, permease protein MalF
fig 6666666.284511.peg.1613	ABC-type sugar transport system, periplasmic component
fig 6666666.284511.peg.1614	Transcriptional regulator, LacI family
fig 6666666.284511.peg.1615	Dienelactone hydrolase and related enzymes
fig 6666666.284511.peg.1616	hypothetical protein
fig 6666666.284511.peg.1617	hypothetical protein
fig 6666666.284511.peg.1618	Uncharacterized conserved protein
fig 6666666.284511.peg.1619	hypothetical protein
fig 6666666.284511.peg.1620	hypothetical protein
fig 6666666.284511.peg.1621	Probable glucosyl transferase
fig 6666666.284511.peg.1622	hypothetical protein
fig 6666666.284511.peg.1623	Methylglyoxal synthase (EC 4.2.3.3)
fig 6666666.284511.peg.1624	4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deo
fig 6666666.284511.peg.1625	Phosphogluconate dehydratase (EC 4.2.1.12)
fig 6666666.284511.peg.1626	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
fig 6666666.284511.peg.1627	6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type
fig 6666666.284511.peg.1628	Glucokinase (EC 2.7.1.2)
fig 6666666.284511.peg.1629	Phosphogluconate repressor HexR, RpiR family
fig 6666666.284511.peg.1630	Glucose-6-phosphate isomerase (EC 5.3.1.9)
fig 6666666.284511.peg.1631	hypothetical protein
fig 6666666.284511.peg.1632	Twitching motility protein PilT
fig 6666666.284511.peg.1633	hypothetical protein

fig 6666666.284511.peg.1634	Type II secretory pathway, ATPase Pule/Tfp pilus assembly pathway,
fig 6666666.284511.peg.1635	SAM-dependent methyltransferases
fig 6666666.284511.peg.1636	hypothetical protein
fig 6666666.284511.peg.1637	hypothetical protein
fig 6666666.284511.peg.1638	hypothetical protein
fig 6666666.284511.peg.1639	hypothetical protein
fig 6666666.284511.peg.1640	Seryl-tRNA synthetase (EC 6.1.1.11)
fig 6666666.284511.peg.1641	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)
fig 6666666.284511.peg.1642	FKBP-type peptidyl-prolyl cis-trans isomerase SlpA (EC 5.2.1.8)
fig 6666666.284511.peg.1643	hypothetical protein
fig 6666666.284511.peg.1644	Uncharacterized protein conserved in bacteria
fig 6666666.284511.peg.1645	Hemoglobin-like protein HbO
fig 6666666.284511.peg.1646	ABC transporter, permease protein, putative
fig 6666666.284511.peg.1647	hypothetical protein
fig 6666666.284511.peg.1648	Peptide chain release factor 3
fig 6666666.284511.peg.1649	Adenylate cyclase (EC 4.6.1.1)
fig 6666666.284511.peg.1650	Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)
fig 6666666.284511.peg.1651	Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)
fig 6666666.284511.peg.1652	site-specific recombinase, phage integrase family
fig 6666666.284511.peg.1653	hypothetical protein
fig 6666666.284511.peg.1654	Superfamily I DNA and RNA helicases
fig 6666666.284511.peg.1655	hypothetical protein
fig 6666666.284511.peg.1656	Mobile element protein
fig 6666666.284511.peg.1657	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.1658	Mobile element protein
fig 6666666.284511.peg.1659	Mobile element protein
fig 6666666.284511.peg.1660	Cell division protein FtsH (EC 3.4.24.-)
fig 6666666.284511.peg.1661	hypothetical protein
fig 6666666.284511.peg.1662	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)
fig 6666666.284511.peg.1663	Mobile element protein
fig 6666666.284511.peg.1664	Modification methylase
fig 6666666.284511.peg.1665	hypothetical protein
fig 6666666.284511.peg.1666	FIG01232333: hypothetical protein
fig 6666666.284511.peg.1667	hypothetical protein
fig 6666666.284511.peg.1668	Endonuclease
fig 6666666.284511.peg.1669	FIG00715517: hypothetical protein
fig 6666666.284511.peg.1670	hypothetical protein
fig 6666666.284511.peg.1671	hypothetical protein
fig 6666666.284511.peg.1672	hypothetical protein
fig 6666666.284511.peg.1673	Rod shape determination protein
fig 6666666.284511.peg.1674	Phage integrase
fig 6666666.284511.peg.1675	hypothetical protein
fig 6666666.284511.peg.1676	hypothetical protein

fig 6666666.284511.peg.1677	hypothetical protein
fig 6666666.284511.peg.1678	hypothetical protein
fig 6666666.284511.peg.1679	Inter-alpha-trypsin inhibitor domain protein
fig 6666666.284511.peg.1680	hypothetical protein
fig 6666666.284511.peg.1681	hypothetical protein
fig 6666666.284511.peg.1682	hypothetical protein
fig 6666666.284511.peg.1683	hypothetical protein
fig 6666666.284511.peg.1684	hypothetical protein
fig 6666666.284511.peg.1685	Replicative DNA helicase, plasmid version
fig 6666666.284511.peg.1686	hypothetical protein
fig 6666666.284511.peg.1687	hypothetical protein
fig 6666666.284511.peg.1688	hypothetical protein
fig 6666666.284511.peg.1689	hypothetical protein
fig 6666666.284511.peg.1690	hypothetical protein
fig 6666666.284511.peg.1691	hypothetical protein
fig 6666666.284511.peg.1692	heavy metal binding protein
fig 6666666.284511.peg.1693	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.1694	Cu(I)-responsive transcriptional regulator
fig 6666666.284511.peg.1695	metallo-beta-lactamase family protein
fig 6666666.284511.peg.1696	hypothetical protein
fig 6666666.284511.peg.1697	hypothetical protein
fig 6666666.284511.peg.1698	Homoserine/homoserine lactone efflux protein
fig 6666666.284511.peg.1699	hypothetical protein
fig 6666666.284511.peg.1700	hypothetical protein
fig 6666666.284511.peg.1701	hypothetical protein
fig 6666666.284511.peg.1702	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.1703	hypothetical protein
fig 6666666.284511.peg.1704	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
fig 6666666.284511.peg.1705	Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)
fig 6666666.284511.peg.1706	2-ketocyclohexanecarboxyl-CoA hydrolase (EC 4.1.3.36)
fig 6666666.284511.peg.1707	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.1708	Mobile element protein
fig 6666666.284511.peg.1709	Mobile element protein
fig 6666666.284511.peg.1710	HigB toxin protein
fig 6666666.284511.peg.1711	HigA protein (antitoxin to HigB)
fig 6666666.284511.peg.1712	hypothetical protein
fig 6666666.284511.peg.1713	hypothetical protein
fig 6666666.284511.peg.1714	FIG00455389: hypothetical protein
fig 6666666.284511.peg.1715	Periplasmic thiol:disulfide oxidoreductase DsbB, required for DsbA re
fig 6666666.284511.peg.1716	hypothetical protein
fig 6666666.284511.peg.1717	Bacterial luciferase family protein
fig 6666666.284511.peg.1718	FIG00461198: hypothetical protein
fig 6666666.284511.peg.1719	granule-associated protein

fig 6666666.284511.peg.1720	Potassium voltage-gated channel subfamily KQT; possible potassium
fig 6666666.284511.peg.1721	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.1722	Mobile element protein
fig 6666666.284511.peg.1723	Mobile element protein
fig 6666666.284511.peg.1724	4-carboxymuconolactone decarboxylase (EC 4.1.1.44)
fig 6666666.284511.peg.1725	hypothetical protein
fig 6666666.284511.peg.1726	Mobile element protein
fig 6666666.284511.peg.1727	hypothetical protein
fig 6666666.284511.peg.1728	hypothetical protein
fig 6666666.284511.peg.1729	DNA-binding protein H-NS
fig 6666666.284511.peg.1730	HoxN/HupN/NixA family nickel/cobalt transporter
fig 6666666.284511.peg.1731	[NiFe] hydrogenase metallocenter assembly protein HypC
fig 6666666.284511.peg.1732	[NiFe] hydrogenase metallocenter assembly protein HypD
fig 6666666.284511.peg.1733	[NiFe] hydrogenase metallocenter assembly protein HypE
fig 6666666.284511.peg.1734	Hydrogenase maturation protease (EC 3.4.24.-)
fig 6666666.284511.peg.1735	Coenzyme F420-reducing hydrogenase, alpha subunit
fig 6666666.284511.peg.1736	hydrogenase/sulfur reductase, delta subunit
fig 6666666.284511.peg.1737	Oxidoreductase FAD/NAD(P)-binding
fig 6666666.284511.peg.1738	cAMP-binding proteins - catabolite gene activator and regulatory sul
fig 6666666.284511.peg.1739	Ferredoxin
fig 6666666.284511.peg.1740	Universal stress protein family COG0589
fig 6666666.284511.peg.1741	Hydrogenase maturation factor HoxV/HupK
fig 6666666.284511.peg.1742	[NiFe] hydrogenase nickel incorporation protein HypA
fig 6666666.284511.peg.1743	[NiFe] hydrogenase nickel incorporation-associated protein HypB
fig 6666666.284511.peg.1744	[NiFe] hydrogenase metallocenter assembly protein HypF
fig 6666666.284511.peg.1745	Hydrogenase maturation protein HupF/HypC/HoxL
fig 6666666.284511.peg.1746	hypothetical protein
fig 6666666.284511.peg.1747	Rubredoxin
fig 6666666.284511.peg.1748	Hydrogenase maturation factor HoxQ
fig 6666666.284511.peg.1749	Hydrogenase maturation factor HoxO/HyaE
fig 6666666.284511.peg.1750	Hydrogenase maturation protease (EC 3.4.24.-)
fig 6666666.284511.peg.1751	Ni,Fe-hydrogenase I cytochrome b subunit
fig 6666666.284511.peg.1752	Uptake hydrogenase large subunit (EC 1.12.99.6)
fig 6666666.284511.peg.1753	Uptake hydrogenase small subunit precursor (EC 1.12.99.6)
fig 6666666.284511.peg.1754	hypothetical protein
fig 6666666.284511.peg.1755	Putative oligoketide cyclase/dehydratase or lipid transport protein Y
fig 6666666.284511.peg.1756	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74)
fig 6666666.284511.peg.1757	Rhodanese-like domain protein
fig 6666666.284511.peg.1758	NrfD protein
fig 6666666.284511.peg.1759	NrfC protein
fig 6666666.284511.peg.1760	Anaerobic dehydrogenases, typically selenocysteine-containing
fig 6666666.284511.peg.1761	Radical SAM domain protein
fig 6666666.284511.peg.1762	Thiosulfate sulfurtransferase, rhodanese (EC 2.8.1.1)

fig 6666666.284511.peg.1763	hypothetical protein
fig 6666666.284511.peg.1764	Radical SAM family enzyme, similar to coproporphyrinogen III oxidase
fig 6666666.284511.peg.1765	Nucleoside 5-triphosphatase RdgB (dHAPTP, dITP, XTP-specific) (EC 3.6.1.15)
fig 6666666.284511.peg.1766	Ribonuclease PH (EC 2.7.7.56)
fig 6666666.284511.peg.1767	Protein phosphatase 2C-like
fig 6666666.284511.peg.1768	Serine/threonine protein kinase (EC 2.7.11.1)
fig 6666666.284511.peg.1769	Protein YicC
fig 6666666.284511.peg.1770	Guanylate kinase (EC 2.7.4.8)
fig 6666666.284511.peg.1771	DNA-directed RNA polymerase omega subunit (EC 2.7.7.6)
fig 6666666.284511.peg.1772	GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase II / Guanine nucleotide exchange factor
fig 6666666.284511.peg.1773	Transcription elongation factor GreB
fig 6666666.284511.peg.1774	Leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein
fig 6666666.284511.peg.1775	hypothetical protein
fig 6666666.284511.peg.1776	DNA polymerase III chi subunit (EC 2.7.7.7)
fig 6666666.284511.peg.1777	Cytosol aminopeptidase PepA (EC 3.4.11.1)
fig 6666666.284511.peg.1778	FIG000988: Predicted permease
fig 6666666.284511.peg.1779	FIG000906: Predicted Permease
fig 6666666.284511.peg.1780	Cys regulon transcriptional activator CysB
fig 6666666.284511.peg.1781	Aspartate aminotransferase (EC 2.6.1.1)
fig 6666666.284511.peg.1782	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.1783	hypothetical protein
fig 6666666.284511.peg.1784	Fumarylacetoacetate hydrolase family protein
fig 6666666.284511.peg.1785	amino acid permease family protein
fig 6666666.284511.peg.1786	ATP-dependent DNA helicase RecQ
fig 6666666.284511.peg.1787	Conserved domain protein
fig 6666666.284511.peg.1788	ABC-type transport system involved in resistance to organic solvents
fig 6666666.284511.peg.1789	ABC transporter ATP-binding protein
fig 6666666.284511.peg.1790	ABC-type transport system involved in resistance to organic solvents
fig 6666666.284511.peg.1791	hypothetical protein
fig 6666666.284511.peg.1792	Type II secretory pathway, ATPase Pule/Tfp pilus assembly pathway,
fig 6666666.284511.peg.1793	G:T/U mismatch-specific uracil/thymine DNA-glycosylase
fig 6666666.284511.peg.1794	tRNA (guanine46-N7-)-methyltransferase (EC 2.1.1.33)
fig 6666666.284511.peg.1795	Undecaprenyl-diphosphatase (EC 3.6.1.27)
fig 6666666.284511.peg.1796	Manganese transport protein MntH
fig 6666666.284511.peg.1797	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)
fig 6666666.284511.peg.1798	Rhodanese-like domain protein
fig 6666666.284511.peg.1799	Lipid IVA 3-deoxy-D-manno-octulosonic acid transferase (EC 2.4.99.1)
fig 6666666.284511.peg.1800	Lipopolysaccharide heptosyltransferase I (EC 2.4.1.-)
fig 6666666.284511.peg.1801	Phosphoglucosamine mutase (EC 5.4.2.10)
fig 6666666.284511.peg.1802	hypothetical protein
fig 6666666.284511.peg.1803	hypothetical protein
fig 6666666.284511.peg.1804	LSU ribosomal protein L28p
fig 6666666.284511.peg.1805	LSU ribosomal protein L33p @ LSU ribosomal protein L33p, zinc-inducible

fig 6666666.284511.peg.1806	hypothetical protein
fig 6666666.284511.peg.1807	hypothetical protein
fig 6666666.284511.peg.1808	FIG074102: hypothetical protein
fig 6666666.284511.peg.1809	hypothetical protein
fig 6666666.284511.peg.1810	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8)
fig 6666666.284511.peg.1811	FIG01199889: hypothetical protein
fig 6666666.284511.peg.1812	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
fig 6666666.284511.peg.1813	Phosphopantothencysteine decarboxylase (EC 4.1.1.36) / Phospho
fig 6666666.284511.peg.1814	Alanyl-tRNA synthetase (EC 6.1.1.7)
fig 6666666.284511.peg.1815	Alanyl-tRNA synthetase (EC 6.1.1.7)
fig 6666666.284511.peg.1816	Aldehyde dehydrogenase B (EC 1.2.1.22)
fig 6666666.284511.peg.1817	Anaerobic dimethyl sulfoxide reductase chain C (EC 1.8.5.3)
fig 6666666.284511.peg.1818	Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.5.3)
fig 6666666.284511.peg.1819	Anaerobic dimethyl sulfoxide reductase chain A (EC 1.8.5.3)
fig 6666666.284511.peg.1820	NADH:flavin oxidoreductases, Old Yellow Enzyme family
fig 6666666.284511.peg.1821	hypothetical protein
fig 6666666.284511.peg.1822	Mobile element protein
fig 6666666.284511.peg.1823	Argininosuccinate synthase (EC 6.3.4.5)
fig 6666666.284511.peg.1824	FIG074102: hypothetical protein
fig 6666666.284511.peg.1825	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
fig 6666666.284511.peg.1826	protein of unknown function DUF395, YeeE/YedE
fig 6666666.284511.peg.1827	membrane protein, putative
fig 6666666.284511.peg.1828	hypothetical protein
fig 6666666.284511.peg.1829	hypothetical protein
fig 6666666.284511.peg.1830	Rhodanese domain protein
fig 6666666.284511.peg.1831	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)
fig 6666666.284511.peg.1832	FIG001943: hypothetical protein YajQ
fig 6666666.284511.peg.1833	Acyl-phosphate:glycerol-3-phosphate O-acyltransferase PlsY
fig 6666666.284511.peg.1834	hypothetical protein
fig 6666666.284511.peg.1835	Transcriptional regulator
fig 6666666.284511.peg.1836	COG0613, Predicted metal-dependent phosphoesterases (PHP family)
fig 6666666.284511.peg.1837	Hypothetical YciO protein, TsaC/YrdC paralog
fig 6666666.284511.peg.1838	FIG004556: membrane metalloprotease
fig 6666666.284511.peg.1839	conserved hypothetical secreted protein
fig 6666666.284511.peg.1840	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)
fig 6666666.284511.peg.1841	DedA family protein
fig 6666666.284511.peg.1842	Cold shock protein CspG
fig 6666666.284511.peg.1843	hypothetical protein
fig 6666666.284511.peg.1844	Riboflavin kinase (EC 2.7.1.26) / FMN adenylyltransferase (EC 2.7.7.2)
fig 6666666.284511.peg.1845	Isoleucyl-tRNA synthetase (EC 6.1.1.5)
fig 6666666.284511.peg.1846	Lipoprotein signal peptidase (EC 3.4.23.36)
fig 6666666.284511.peg.1847	predicted integral membrane protein
fig 6666666.284511.peg.1848	Quinone oxidoreductase (EC 1.6.5.5)

fig 6666666.284511.peg.1849	Permeases of the major facilitator superfamily
fig 6666666.284511.peg.1850	Two-component system response regulator QseB
fig 6666666.284511.peg.1851	Sensory histidine kinase QseC
fig 6666666.284511.peg.1852	hypothetical protein
fig 6666666.284511.peg.1853	tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)
fig 6666666.284511.peg.1854	Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)
fig 6666666.284511.peg.1855	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)
fig 6666666.284511.peg.1856	Cysteinyl-tRNA synthetase (EC 6.1.1.16)
fig 6666666.284511.peg.1857	TPR repeat precursor
fig 6666666.284511.peg.1858	Peptidyl-prolyl cis-trans isomerase PpiA precursor (EC 5.2.1.8)
fig 6666666.284511.peg.1859	Peptidyl-prolyl cis-trans isomerase PpiB (EC 5.2.1.8)
fig 6666666.284511.peg.1860	UDP-2,3-diacetylglucosamine diphosphatase (EC 3.6.1.54)
fig 6666666.284511.peg.1861	Serine acetyltransferase (EC 2.3.1.30)
fig 6666666.284511.peg.1862	tRNA:Cm32/Um32 methyltransferase
fig 6666666.284511.peg.1863	Inositol-1-monophosphatase (EC 3.1.3.25)
fig 6666666.284511.peg.1864	DNA mismatch repair protein MutS
fig 6666666.284511.peg.1865	Predicted hydrolases or acyltransferases (alpha/beta hydrolase supe
fig 6666666.284511.peg.1866	CTP synthase (EC 6.3.4.2)
fig 6666666.284511.peg.1867	2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate synthase (EC 2.
fig 6666666.284511.peg.1868	Enolase (EC 4.2.1.11)
fig 6666666.284511.peg.1869	Cell division protein DivIC (FtsB), stabilizes FtsL against RasP cleavage
fig 6666666.284511.peg.1870	33 kDa chaperonin (Heat shock protein 33) (HSP33)
fig 6666666.284511.peg.1871	carbonic anhydrase, family 3
fig 6666666.284511.peg.1872	Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)
fig 6666666.284511.peg.1873	Arginine-tRNA-protein transferase (EC 2.3.2.8)
fig 6666666.284511.peg.1874	Lipid A acylation protein PagP, palmitoyltransferase
fig 6666666.284511.peg.1875	hypothetical protein
fig 6666666.284511.peg.1876	Predicted Lactate-responsive regulator, IclR family
fig 6666666.284511.peg.1877	Murein-DD-endopeptidase (EC 3.4.99.-)
fig 6666666.284511.peg.1878	hypothetical protein
fig 6666666.284511.peg.1879	DNA polymerase III epsilon subunit (EC 2.7.7.7)
fig 6666666.284511.peg.1880	Ribonuclease HI (EC 3.1.26.4)
fig 6666666.284511.peg.1881	FIG005121: SAM-dependent methyltransferase (EC 2.1.1.-)
fig 6666666.284511.peg.1882	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)
fig 6666666.284511.peg.1883	Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.:
fig 6666666.284511.peg.1884	hypothetical protein
fig 6666666.284511.peg.1885	hypothetical protein
fig 6666666.284511.peg.1886	putative transmembrane protein
fig 6666666.284511.peg.1887	5-oxoprolinase (EC 3.5.2.9)
fig 6666666.284511.peg.1888	Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)
fig 6666666.284511.peg.1889	Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)
fig 6666666.284511.peg.1890	lojap protein
fig 6666666.284511.peg.1891	LSU m3Psi1915 methyltransferase RlmH

fig 6666666.284511.peg.1892	hypothetical protein
fig 6666666.284511.peg.1893	COG0488: ATPase components of ABC transporters with duplicated /
fig 6666666.284511.peg.1894	hypothetical protein
fig 6666666.284511.peg.1895	Septum formation protein Maf
fig 6666666.284511.peg.1896	Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4
fig 6666666.284511.peg.1897	Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4
fig 6666666.284511.peg.1898	Bll3817 protein
fig 6666666.284511.peg.1899	hypothetical protein
fig 6666666.284511.peg.1900	hypothetical protein
fig 6666666.284511.peg.1901	hypothetical protein
fig 6666666.284511.peg.1902	Mobile element protein
fig 6666666.284511.peg.1903	hypothetical protein
fig 6666666.284511.peg.1904	RNA polymerase sigma factor RpoH
fig 6666666.284511.peg.1905	Dihydrofolate reductase (EC 1.5.1.3)
fig 6666666.284511.peg.1906	3-demethylubiquinone-9 3-methyltransferase
fig 6666666.284511.peg.1907	Transcriptional regulator, ArsR family
fig 6666666.284511.peg.1908	hypothetical protein
fig 6666666.284511.peg.1909	Cobalt-zinc-cadmium resistance protein CzcD
fig 6666666.284511.peg.1910	Aldo-keto reductase
fig 6666666.284511.peg.1911	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1912	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.1913	conserved protein of unknown function; putative inner membrane p
fig 6666666.284511.peg.1914	hypothetical protein
fig 6666666.284511.peg.1915	Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.!
fig 6666666.284511.peg.1916	Signal recognition particle receptor protein FtsY (=alpha subunit) (TC
fig 6666666.284511.peg.1917	16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171) ## S
fig 6666666.284511.peg.1918	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)
fig 6666666.284511.peg.1919	4Fe-4S ferredoxin, iron-sulfur binding
fig 6666666.284511.peg.1920	Peptidyl-tRNA hydrolase (EC 3.1.1.29)
fig 6666666.284511.peg.1921	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
fig 6666666.284511.peg.1922	Protein export cytoplasm chaperone protein (SecB, maintains protei
fig 6666666.284511.peg.1923	Glutaredoxin 3 (Grx3)
fig 6666666.284511.peg.1924	FIG136845: Rhodanese-related sulfurtransferase
fig 6666666.284511.peg.1925	hypothetical protein
fig 6666666.284511.peg.1926	Phosphoglycerate mutase (EC 5.4.2.1)
fig 6666666.284511.peg.1927	Carboxyl-terminal protease (EC 3.4.21.102)
fig 6666666.284511.peg.1928	Sulfur carrier protein adenylyltransferase ThiF
fig 6666666.284511.peg.1929	short-chain dehydrogenase/reductase SDR
fig 6666666.284511.peg.1930	hypothetical protein
fig 6666666.284511.peg.1931	hypothetical protein
fig 6666666.284511.peg.1932	Mobile element protein
fig 6666666.284511.peg.1933	hypothetical protein
fig 6666666.284511.peg.1934	hypothetical protein

fig 6666666.284511.peg.1935	hypothetical protein
fig 6666666.284511.peg.1936	transcriptional regulator, MerR family
fig 6666666.284511.peg.1937	Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)
fig 6666666.284511.peg.1938	Choline dehydrogenase (EC 1.1.99.1)
fig 6666666.284511.peg.1939	Aldose 1-epimerase
fig 6666666.284511.peg.1940	putative multidrug-efflux transporter
fig 6666666.284511.peg.1941	RND efflux system, outer membrane lipoprotein, NodT family
fig 6666666.284511.peg.1942	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.1943	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.1944	Probable Co/Zn/Cd efflux system membrane fusion protein
fig 6666666.284511.peg.1945	ATP:Cob(I)alamin adenosyltransferase (EC 2.5.1.17) @ ATP:Cob(I)alai
fig 6666666.284511.peg.1946	D-Lactate dehydrogenase, cytochrome c-dependent (EC 1.1.2.4)
fig 6666666.284511.peg.1947	D-Lactate dehydrogenase, cytochrome c-dependent (EC 1.1.2.4)
fig 6666666.284511.peg.1948	hypothetical protein
fig 6666666.284511.peg.1949	hypothetical protein
fig 6666666.284511.peg.1950	Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD
fig 6666666.284511.peg.1951	Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE
fig 6666666.284511.peg.1952	Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF
fig 6666666.284511.peg.1953	Phenylacetic acid degradation protein PaaN, ring-opening aldehyde c
fig 6666666.284511.peg.1954	Transcriptional regulator, TetR family
fig 6666666.284511.peg.1955	Phenylacetate-CoA oxygenase/reductase, PaaK subunit
fig 6666666.284511.peg.1956	Phenylacetate-CoA oxygenase, PaaJ subunit
fig 6666666.284511.peg.1957	Phenylacetate-CoA oxygenase, PaaI subunit
fig 6666666.284511.peg.1958	Phenylacetate-CoA oxygenase, PaaH subunit
fig 6666666.284511.peg.1959	Phenylacetate-CoA oxygenase, PaaG subunit
fig 6666666.284511.peg.1960	Phenylacetate-coenzyme A ligase (EC 6.2.1.30) PaaF
fig 6666666.284511.peg.1961	Phenylacetic acid degradation protein PaaD, thioesterase
fig 6666666.284511.peg.1962	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.1963	hypothetical protein
fig 6666666.284511.peg.1964	Phenylacetic acid degradation protein PaaY
fig 6666666.284511.peg.1965	Glutathione peroxidase family protein
fig 6666666.284511.peg.1966	PROBABLE TRANSMEMBRANE PROTEIN
fig 6666666.284511.peg.1967	Thioredoxin
fig 6666666.284511.peg.1968	Probable transmembrane protein
fig 6666666.284511.peg.1969	Alanine racemase (EC 5.1.1.1)
fig 6666666.284511.peg.1970	DNA repair protein RadA
fig 6666666.284511.peg.1971	Putative membrane protein
fig 6666666.284511.peg.1972	ABC transporter ATP-binding protein
fig 6666666.284511.peg.1973	hypothetical protein
fig 6666666.284511.peg.1974	hypothetical protein
fig 6666666.284511.peg.1975	hypothetical protein
fig 6666666.284511.peg.1976	Probable lipoprotein
fig 6666666.284511.peg.1977	hypothetical protein

fig 6666666.284511.peg.1978	Branched-chain amino acid aminotransferase (EC 2.6.1.42)
fig 6666666.284511.peg.1979	FIG00453862: hypothetical protein
fig 6666666.284511.peg.1980	ADP-heptose--lipooligosaccharide heptosyltransferase II (EC 2.4.1.-)
fig 6666666.284511.peg.1981	Fructose repressor FruR, LacI family
fig 6666666.284511.peg.1982	Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC
fig 6666666.284511.peg.1983	1-phosphofructokinase (EC 2.7.1.56)
fig 6666666.284511.peg.1984	1-phosphofructokinase (EC 2.7.1.56)
fig 6666666.284511.peg.1985	1-phosphofructokinase (EC 2.7.1.56)
fig 6666666.284511.peg.1986	PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS syste
fig 6666666.284511.peg.1987	RpfN protein
fig 6666666.284511.peg.1988	ATP-dependent RNA helicase RhIE
fig 6666666.284511.peg.1989	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.1990	Putative translation initiation inhibitor, yjgF family
fig 6666666.284511.peg.1991	Topoisomerase IV subunit A (EC 5.99.1.-)
fig 6666666.284511.peg.1992	Topoisomerase IV subunit B (EC 5.99.1.-)
fig 6666666.284511.peg.1993	hypothetical protein
fig 6666666.284511.peg.1994	Putative SAM-dependent methyltransferase Bucepa02006346
fig 6666666.284511.peg.1995	4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7)
fig 6666666.284511.peg.1996	FIG002207: Probable transmembrane protein
fig 6666666.284511.peg.1997	Fatty acid desaturase (EC 1.14.19.1); Delta-9 fatty acid desaturase (E
fig 6666666.284511.peg.1998	Fmu (Sun) /eukaryotic nucleolar NOL1/Nop2p; tRNA and rRNA cytos
fig 6666666.284511.peg.1999	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)
fig 6666666.284511.peg.2000	Mobile element protein
fig 6666666.284511.peg.2001	Ribonucleotide reductase transcriptional regulator NrdR
fig 6666666.284511.peg.2002	Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.
fig 6666666.284511.peg.2003	hypothetical protein
fig 6666666.284511.peg.2004	hypothetical protein
fig 6666666.284511.peg.2005	Aspartate aminotransferase (EC 2.6.1.1)
fig 6666666.284511.peg.2006	Transcription termination protein NusB
fig 6666666.284511.peg.2007	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)
fig 6666666.284511.peg.2008	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTI
fig 6666666.284511.peg.2009	putative exported protein
fig 6666666.284511.peg.2010	Outer membrane protein assembly factor YaeT precursor
fig 6666666.284511.peg.2011	Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)
fig 6666666.284511.peg.2012	4-hydroxybenzoyl-CoA thioesterase family active site
fig 6666666.284511.peg.2013	MotA/TolQ/ExbB proton channel family protein
fig 6666666.284511.peg.2014	Tol biopolymer transport system, TolR protein
fig 6666666.284511.peg.2015	TolA protein
fig 6666666.284511.peg.2016	DNA polymerase III alpha subunit (EC 2.7.7.7)
fig 6666666.284511.peg.2017	hypothetical protein
fig 6666666.284511.peg.2018	Transporter, monovalent cation:proton antiporter-2 (CPA2) family
fig 6666666.284511.peg.2019	FIG074102: hypothetical protein
fig 6666666.284511.peg.2020	Lipid A export ATP-binding/permease protein MsbA

fig 6666666.284511.peg.2021	O-antigen ligase
fig 6666666.284511.peg.2022	Glycosyl transferase, family 2
fig 6666666.284511.peg.2023	Possible glycosyltransferase 2 fused to TPR-repeat domain
fig 6666666.284511.peg.2024	tolB protein precursor, periplasmic protein involved in the tonb-ind
fig 6666666.284511.peg.2025	18K peptidoglycan-associated outer membrane lipoprotein; Peptidog
fig 6666666.284511.peg.2026	TPR repeat containing exported protein; Putative periplasmic protein
fig 6666666.284511.peg.2027	Queuosine Biosynthesis QueC ATPase
fig 6666666.284511.peg.2028	Lipocalin-related protein and Bos/Can/Equ allergen
fig 6666666.284511.peg.2029	Probable HesA/MoeB/ThiF family protein
fig 6666666.284511.peg.2030	FIG00792504: hypothetical protein
fig 6666666.284511.peg.2031	O-antigen export system permease protein RfbD
fig 6666666.284511.peg.2032	hypothetical protein
fig 6666666.284511.peg.2033	FIG01213006: hypothetical protein
fig 6666666.284511.peg.2034	hypothetical protein
fig 6666666.284511.peg.2035	O-antigen export system permease protein RfbD
fig 6666666.284511.peg.2036	Polysaccharide ABC transporter, ATP-binding protein
fig 6666666.284511.peg.2037	hypothetical protein
fig 6666666.284511.peg.2038	Glycosyl transferase, group 2 family protein
fig 6666666.284511.peg.2039	hypothetical protein
fig 6666666.284511.peg.2040	hypothetical protein
fig 6666666.284511.peg.2041	hypothetical protein
fig 6666666.284511.peg.2042	glycosyl transferase, family 2
fig 6666666.284511.peg.2043	hypothetical protein
fig 6666666.284511.peg.2044	ISPg4, transposase
fig 6666666.284511.peg.2045	hypothetical protein
fig 6666666.284511.peg.2046	hypothetical protein
fig 6666666.284511.peg.2047	hypothetical protein
fig 6666666.284511.peg.2048	hypothetical protein
fig 6666666.284511.peg.2049	hypothetical protein
fig 6666666.284511.peg.2050	UDP-glucose 4-epimerase (EC 5.1.3.2)
fig 6666666.284511.peg.2051	hypothetical protein
fig 6666666.284511.peg.2052	Serine hydroxymethyltransferase (EC 2.1.2.1)
fig 6666666.284511.peg.2053	Soluble lytic murein transglycosylase and related regulatory proteins
fig 6666666.284511.peg.2054	3-polyprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.-)
fig 6666666.284511.peg.2055	putative exported protein
fig 6666666.284511.peg.2056	hypothetical protein
fig 6666666.284511.peg.2057	hypothetical protein
fig 6666666.284511.peg.2058	Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11)
fig 6666666.284511.peg.2059	Thiol:disulfide interchange protein DsbG precursor
fig 6666666.284511.peg.2060	Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)
fig 6666666.284511.peg.2061	Cation transport protein chaC
fig 6666666.284511.peg.2062	hypothetical protein
fig 6666666.284511.peg.2063	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)

fig 6666666.284511.peg.2064	Glutamate synthase [NADPH] large chain (EC 1.4.1.13)
fig 6666666.284511.peg.2065	hypothetical protein
fig 6666666.284511.peg.2066	Transposase and inactivated derivatives
fig 6666666.284511.peg.2067	hypothetical protein
fig 6666666.284511.peg.2068	Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)
fig 6666666.284511.peg.2069	hypothetical protein
fig 6666666.284511.peg.2070	Thiazole biosynthesis protein ThiG
fig 6666666.284511.peg.2071	hypothetical protein
fig 6666666.284511.peg.2072	Glycine oxidase ThiO (EC 1.4.3.19)
fig 6666666.284511.peg.2073	Hydroxymethylpyrimidine phosphate synthase ThiC (EC 4.1.99.17)
fig 6666666.284511.peg.2074	FIG027190: Putative transmembrane protein
fig 6666666.284511.peg.2075	Na ⁺ /H ⁺ antiporter NhaA type
fig 6666666.284511.peg.2076	hypothetical protein
fig 6666666.284511.peg.2077	Inorganic pyrophosphatase (EC 3.6.1.1)
fig 6666666.284511.peg.2078	21 kDa hemolysin precursor
fig 6666666.284511.peg.2079	Phosphoheptose isomerase (EC 5.3.1.-)
fig 6666666.284511.peg.2080	rRNA small subunit methyltransferase I
fig 6666666.284511.peg.2081	FOG: GGDEF domain
fig 6666666.284511.peg.2082	NADH:flavin oxidoreductases, Old Yellow Enzyme family
fig 6666666.284511.peg.2083	D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30)
fig 6666666.284511.peg.2084	Ferredoxin reductase
fig 6666666.284511.peg.2085	ATP-dependent DNA helicase Rep
fig 6666666.284511.peg.2086	Glutathione S-transferase (EC 2.5.1.18)
fig 6666666.284511.peg.2087	NAD-dependent epimerase/dehydratase
fig 6666666.284511.peg.2088	Soluble lytic murein transglycosylase precursor (EC 3.2.1.-)
fig 6666666.284511.peg.2089	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)
fig 6666666.284511.peg.2090	Mobile element protein
fig 6666666.284511.peg.2091	hypothetical protein
fig 6666666.284511.peg.2092	Mobile element protein
fig 6666666.284511.peg.2093	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC
fig 6666666.284511.peg.2094	Quinolate synthetase (EC 2.5.1.72)
fig 6666666.284511.peg.2095	Quinolate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.1)
fig 6666666.284511.peg.2096	transcriptional regulator, Crp/Fnr family
fig 6666666.284511.peg.2097	Chromosome partitioning protein ParA
fig 6666666.284511.peg.2098	hypothetical protein
fig 6666666.284511.peg.2099	hypothetical protein
fig 6666666.284511.peg.2100	FIG00433688: hypothetical protein
fig 6666666.284511.peg.2101	Nucleoside ABC transporter, periplasmic nucleoside-binding protein
fig 6666666.284511.peg.2102	Nucleoside ABC transporter, periplasmic nucleoside-binding protein
fig 6666666.284511.peg.2103	Nucleoside ABC transporter, permease protein 2
fig 6666666.284511.peg.2104	Nucleoside ABC transporter, permease protein 1
fig 6666666.284511.peg.2105	ABC transporter ATP-binding protein
fig 6666666.284511.peg.2106	Guanine deaminase (EC 3.5.4.3)

fig 6666666.284511.peg.2107	hypothetical protein
fig 6666666.284511.peg.2108	hypothetical protein
fig 6666666.284511.peg.2109	MFS permease
fig 6666666.284511.peg.2110	hypothetical protein
fig 6666666.284511.peg.2111	hypothetical protein
fig 6666666.284511.peg.2112	hypothetical protein
fig 6666666.284511.peg.2113	Octaprenyl diphosphate synthase (EC 2.5.1.90)
fig 6666666.284511.peg.2114	LSU ribosomal protein L21p
fig 6666666.284511.peg.2115	LSU ribosomal protein L27p
fig 6666666.284511.peg.2116	GTP-binding protein Obg
fig 6666666.284511.peg.2117	Glutamate 5-kinase (EC 2.7.2.11) / RNA-binding C-terminal domain P
fig 6666666.284511.peg.2118	FIG005426: hypothetical protein
fig 6666666.284511.peg.2119	Adenosine (5')-pentaphospho-(5'')-adenosine pyrophosphohydrolase
fig 6666666.284511.peg.2120	Prolyl-tRNA synthetase (EC 6.1.1.15), bacterial type
fig 6666666.284511.peg.2121	FIG016425: Soluble lytic murein transglycosylase and related regulat
fig 6666666.284511.peg.2122	Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)
fig 6666666.284511.peg.2123	CcsA-related protein
fig 6666666.284511.peg.2124	hypothetical protein
fig 6666666.284511.peg.2125	Sensor histidine kinase
fig 6666666.284511.peg.2126	Response regulator of zinc sigma-54-dependent two-component syst
fig 6666666.284511.peg.2127	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) AmpD
fig 6666666.284511.peg.2128	hypothetical protein
fig 6666666.284511.peg.2129	Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17
fig 6666666.284511.peg.2130	Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.
fig 6666666.284511.peg.2131	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
fig 6666666.284511.peg.2132	Deoxycytidine triphosphate deaminase (EC 3.5.4.13)
fig 6666666.284511.peg.2133	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.2134	Argininosuccinate lyase (EC 4.3.2.1)
fig 6666666.284511.peg.2135	Autolysin sensor kinase (EC 2.7.3.-)
fig 6666666.284511.peg.2136	Two-component system regulatory protein
fig 6666666.284511.peg.2137	Undecaprenyl-diphosphatase (EC 3.6.1.27)
fig 6666666.284511.peg.2138	Putative periplasmic cytochrome type-C oxidoreductase signal peptic
fig 6666666.284511.peg.2139	Putative periplasmic cytochrome type-C oxidoreductase signal peptic
fig 6666666.284511.peg.2140	small molecule metabolism; degradation; carbon compounds
fig 6666666.284511.peg.2141	(Y14336) putative extracellular protein containing predicted 35aa sig
fig 6666666.284511.peg.2142	Glyoxylate carboligase (EC 4.1.1.47)
fig 6666666.284511.peg.2143	Hydroxypyruvate isomerase (EC 5.3.1.22)
fig 6666666.284511.peg.2144	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)
fig 6666666.284511.peg.2145	D-glycerate 2-kinase (EC 2.7.1.-)
fig 6666666.284511.peg.2146	Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)
fig 6666666.284511.peg.2147	Mobile element protein
fig 6666666.284511.peg.2148	hypothetical protein
fig 6666666.284511.peg.2149	hypothetical protein

fig 6666666.284511.peg.2150	hypothetical protein
fig 6666666.284511.peg.2151	Type IV fimbrial assembly, ATPase PilB
fig 6666666.284511.peg.2152	Leader peptidase (Prepilin peptidase) (EC 3.4.23.43) / N-methyltrans
fig 6666666.284511.peg.2153	Dephospho-CoA kinase (EC 2.7.1.24)
fig 6666666.284511.peg.2154	FIG002842: hypothetical protein
fig 6666666.284511.peg.2155	hypothetical protein
fig 6666666.284511.peg.2156	Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (E
fig 6666666.284511.peg.2157	putative ATP/GTP-binding protein
fig 6666666.284511.peg.2158	Glutamate N-acetyltransferase (EC 2.3.1.35) / N-acetylglutamate syn
fig 6666666.284511.peg.2159	Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.!
fig 6666666.284511.peg.2160	hypothetical protein
fig 6666666.284511.peg.2161	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC
fig 6666666.284511.peg.2162	Cell division protein FtsZ (EC 3.4.24.-)
fig 6666666.284511.peg.2163	Cell division protein FtsA
fig 6666666.284511.peg.2164	Cell division protein FtsQ
fig 6666666.284511.peg.2165	D-alanine--D-alanine ligase (EC 6.3.2.4)
fig 6666666.284511.peg.2166	UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)
fig 6666666.284511.peg.2167	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyropho
fig 6666666.284511.peg.2168	hypothetical protein
fig 6666666.284511.peg.2169	Cell division protein FtsW
fig 6666666.284511.peg.2170	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)
fig 6666666.284511.peg.2171	Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)
fig 6666666.284511.peg.2172	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-al
fig 6666666.284511.peg.2173	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate lig
fig 6666666.284511.peg.2174	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
fig 6666666.284511.peg.2175	Cell division protein FtsL
fig 6666666.284511.peg.2176	rRNA small subunit methyltransferase H
fig 6666666.284511.peg.2177	Cell division protein MraZ
fig 6666666.284511.peg.2178	hypothetical protein
fig 6666666.284511.peg.2179	Mobile element protein
fig 6666666.284511.peg.2180	Mobile element protein
fig 6666666.284511.peg.2181	hypothetical protein
fig 6666666.284511.peg.2182	Protein crcB homolog
fig 6666666.284511.peg.2183	hypothetical protein
fig 6666666.284511.peg.2184	HIT family hydrolase
fig 6666666.284511.peg.2185	hypothetical protein
fig 6666666.284511.peg.2186	Dihydrooorotase (EC 3.5.2.3)
fig 6666666.284511.peg.2187	Lipid A export ATP-binding/permease protein MsbA
fig 6666666.284511.peg.2188	Acyl-CoA hydrolase (EC 3.1.2.20)
fig 6666666.284511.peg.2189	LSU ribosomal protein L25p
fig 6666666.284511.peg.2190	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
fig 6666666.284511.peg.2191	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)
fig 6666666.284511.peg.2192	Outer membrane lipoprotein LolB

fig 6666666.284511.peg.2193	FIG140336: TPR domain protein
fig 6666666.284511.peg.2194	Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)
fig 6666666.284511.peg.2195	FIG00555615: hypothetical protein
fig 6666666.284511.peg.2196	A/G-specific adenine glycosylase (EC 3.2.2.-)
fig 6666666.284511.peg.2197	Uncharacterized protein, similar to the N-terminal domain of Lon pro
fig 6666666.284511.peg.2198	Hypothetical ATP-binding protein UPF0042, contains P-loop
fig 6666666.284511.peg.2199	DNA repair protein RecN
fig 6666666.284511.peg.2200	NAD kinase (EC 2.7.1.23)
fig 6666666.284511.peg.2201	Heat-inducible transcription repressor HrcA
fig 6666666.284511.peg.2202	Universal stress family protein
fig 6666666.284511.peg.2203	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.2204	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.2205	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)
fig 6666666.284511.peg.2206	hypothetical protein
fig 6666666.284511.peg.2207	Mobile element protein
fig 6666666.284511.peg.2208	hypothetical protein
fig 6666666.284511.peg.2209	hypothetical protein
fig 6666666.284511.peg.2210	hypothetical protein
fig 6666666.284511.peg.2211	Ferredoxin reductase
fig 6666666.284511.peg.2212	Thiol:disulfide interchange protein DsbG precursor
fig 6666666.284511.peg.2213	FIG00792170: hypothetical protein
fig 6666666.284511.peg.2214	Mobile element protein
fig 6666666.284511.peg.2215	hypothetical protein
fig 6666666.284511.peg.2216	hypothetical protein
fig 6666666.284511.peg.2217	hypothetical protein
fig 6666666.284511.peg.2218	sigma factor
fig 6666666.284511.peg.2219	Putative signal peptide protein
fig 6666666.284511.peg.2220	Uncharacterized protein conserved in bacteria, NMA0228-like
fig 6666666.284511.peg.2221	Conserved domain protein
fig 6666666.284511.peg.2222	INTEGRAL MEMBRANE PROTEIN (Rhomboid family)
fig 6666666.284511.peg.2223	Niacin transporter NiaP
fig 6666666.284511.peg.2224	hypothetical protein
fig 6666666.284511.peg.2225	hypothetical protein
fig 6666666.284511.peg.2226	hypothetical protein
fig 6666666.284511.peg.2227	Transcriptional regulator, TetR family
fig 6666666.284511.peg.2228	Mobile element protein
fig 6666666.284511.peg.2229	(S)-2-haloacid dehalogenase (EC 3.8.1.2) (2-haloalkanoic acid dehalo
fig 6666666.284511.peg.2230	hypothetical protein
fig 6666666.284511.peg.2231	hypothetical protein
fig 6666666.284511.peg.2232	ATP-dependent RNA helicase Bcep18194_A5658
fig 6666666.284511.peg.2233	glutamyl-Q-tRNA synthetase
fig 6666666.284511.peg.2234	Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX
fig 6666666.284511.peg.2235	Heme A synthase, cytochrome oxidase biogenesis protein Cox15-Cta

fig 6666666.284511.peg.2236	hypothetical protein in Cytochrome oxidase biogenesis cluster
fig 6666666.284511.peg.2237	Cytochrome oxidase biogenesis protein Surf1, facilitates heme A insertion
fig 6666666.284511.peg.2238	hypothetical protein
fig 6666666.284511.peg.2239	Cytochrome c oxidase polypeptide III (EC 1.9.3.1)
fig 6666666.284511.peg.2240	hypothetical protein
fig 6666666.284511.peg.2241	hypothetical protein
fig 6666666.284511.peg.2242	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)
fig 6666666.284511.peg.2243	Cytochrome c oxidase polypeptide II (EC 1.9.3.1)
fig 6666666.284511.peg.2244	Probable transmembrane protein
fig 6666666.284511.peg.2245	Biotin synthesis protein BioC
fig 6666666.284511.peg.2246	hypothetical protein
fig 6666666.284511.peg.2247	tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207)
fig 6666666.284511.peg.2248	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.2249	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase
fig 6666666.284511.peg.2250	Enoyl-CoA hydratase (EC 4.2.1.17) / 3,2-trans-enoyl-CoA isomerase (I)
fig 6666666.284511.peg.2251	Acyl-CoA dehydrogenase (EC 1.3.8.7)
fig 6666666.284511.peg.2252	Predicted transcriptional regulator for fatty acid degradation FadP, T
fig 6666666.284511.peg.2253	Transcriptional regulator SlmA, TetR family
fig 6666666.284511.peg.2254	Pyridoxal-5'-phosphate phosphatase (EC 3.1.3.74), Alphaproteobacteria
fig 6666666.284511.peg.2255	Acetylglutamate kinase (EC 2.7.2.8)
fig 6666666.284511.peg.2256	hypothetical conserved membrane protein
fig 6666666.284511.peg.2257	Two-component sensor CbrB: intracellular carbon:nitrogen balance
fig 6666666.284511.peg.2258	Aldehyde dehydrogenase (EC 1.2.1.3)
fig 6666666.284511.peg.2259	FIG00450153: hypothetical protein
fig 6666666.284511.peg.2260	Quino(hemo)protein alcohol dehydrogenase, PQQ-dependent (EC 1.1.1.1)
fig 6666666.284511.peg.2261	hypothetical protein
fig 6666666.284511.peg.2262	Probable tonB-dependent receptor yncD precursor
fig 6666666.284511.peg.2263	Probable tonB-dependent receptor yncD precursor
fig 6666666.284511.peg.2264	Probable tonB-dependent receptor yncD precursor
fig 6666666.284511.peg.2265	Probable tonB-dependent receptor yncD precursor
fig 6666666.284511.peg.2266	Outer membrane receptor proteins, mostly Fe transport
fig 6666666.284511.peg.2267	TonB-dependent receptor
fig 6666666.284511.peg.2268	hypothetical protein
fig 6666666.284511.peg.2269	hypothetical protein
fig 6666666.284511.peg.2270	hypothetical protein
fig 6666666.284511.peg.2271	hypothetical protein
fig 6666666.284511.peg.2272	unknown
fig 6666666.284511.peg.2273	hypothetical protein
fig 6666666.284511.peg.2274	Quino(hemo)protein alcohol dehydrogenase, PQQ-dependent (EC 1.1.1.1)
fig 6666666.284511.peg.2275	hypothetical protein
fig 6666666.284511.peg.2276	hypothetical protein
fig 6666666.284511.peg.2277	Acid phosphatase
fig 6666666.284511.peg.2278	hypothetical protein

fig 6666666.284511.peg.2279	hypothetical protein
fig 6666666.284511.peg.2280	Phospholipid-binding protein
fig 6666666.284511.peg.2281	hypothetical protein
fig 6666666.284511.peg.2282	Metal-dependent hydrolases of the beta-lactamase superfamily III
fig 6666666.284511.peg.2283	hypothetical protein
fig 6666666.284511.peg.2284	hypothetical protein
fig 6666666.284511.peg.2285	hypothetical protein
fig 6666666.284511.peg.2286	DNA polymerase III epsilon subunit (EC 2.7.7.7)
fig 6666666.284511.peg.2287	Mobile element protein
fig 6666666.284511.peg.2288	Cytochrome c heme lyase subunit CcmH
fig 6666666.284511.peg.2289	Cytochrome c heme lyase subunit CcmL
fig 6666666.284511.peg.2290	Cytochrome c-type biogenesis protein CcmG/DsbE, thiol:disulfide oxidoreductase
fig 6666666.284511.peg.2291	Cytochrome c heme lyase subunit CcmF
fig 6666666.284511.peg.2292	Cytochrome c-type biogenesis protein CcmE, heme chaperone
fig 6666666.284511.peg.2293	hypothetical protein
fig 6666666.284511.peg.2294	Cytochrome c-type biogenesis protein CcmC, putative heme lyase for CcmH
fig 6666666.284511.peg.2295	ABC transporter involved in cytochrome c biogenesis, CcmB subunit
fig 6666666.284511.peg.2296	ABC transporter involved in cytochrome c biogenesis, ATPase component
fig 6666666.284511.peg.2297	hypothetical protein
fig 6666666.284511.peg.2298	Sensory box histidine kinase
fig 6666666.284511.peg.2299	DNA-binding response regulator, LuxR family
fig 6666666.284511.peg.2300	hypothetical protein
fig 6666666.284511.peg.2301	Cytochrome c551/c552
fig 6666666.284511.peg.2302	periplasmic decaheme cytochrome c, MtrA
fig 6666666.284511.peg.2303	Outer membrane protein
fig 6666666.284511.peg.2304	hypothetical protein
fig 6666666.284511.peg.2305	hypothetical protein
fig 6666666.284511.peg.2306	Transcriptional regulator, LysR family
fig 6666666.284511.peg.2307	FMN-dependent NADH-azoreductase
fig 6666666.284511.peg.2308	Pirin
fig 6666666.284511.peg.2309	ABC-type multidrug transport system, ATPase component
fig 6666666.284511.peg.2310	ABC-type multidrug transport system, permease component
fig 6666666.284511.peg.2311	hypothetical protein
fig 6666666.284511.peg.2312	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E)
fig 6666666.284511.peg.2313	Putative transport protein
fig 6666666.284511.peg.2314	Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative co
fig 6666666.284511.peg.2315	Chloride channel protein
fig 6666666.284511.peg.2316	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.2317	Mobile element protein
fig 6666666.284511.peg.2318	Mobile element protein
fig 6666666.284511.peg.2319	hypothetical protein
fig 6666666.284511.peg.2320	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
fig 6666666.284511.peg.2321	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.1)

fig 6666666.284511.peg.2322	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.1)
fig 6666666.284511.peg.2323	sodium/glucose cotransporter 2
fig 6666666.284511.peg.2324	mechanosensitive ion channel family protein
fig 6666666.284511.peg.2325	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase
fig 6666666.284511.peg.2326	hypothetical protein
fig 6666666.284511.peg.2327	hypothetical protein
fig 6666666.284511.peg.2328	hypothetical protein
fig 6666666.284511.peg.2329	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.2330	hypothetical protein
fig 6666666.284511.peg.2331	hypothetical protein
fig 6666666.284511.peg.2332	Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3.-)
fig 6666666.284511.peg.2333	Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)
fig 6666666.284511.peg.2334	hypothetical protein
fig 6666666.284511.peg.2335	Transport ATP-binding protein CydC
fig 6666666.284511.peg.2336	Transport ATP-binding protein CydD
fig 6666666.284511.peg.2337	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
fig 6666666.284511.peg.2338	hypothetical protein
fig 6666666.284511.peg.2339	hypothetical protein
fig 6666666.284511.peg.2340	SSU ribosomal protein S3p (S3e)
fig 6666666.284511.peg.2341	DNA-binding heavy metal response regulator
fig 6666666.284511.peg.2342	Heavy metal sensor histidine kinase
fig 6666666.284511.peg.2343	hypothetical protein
fig 6666666.284511.peg.2344	Universal stress protein UspA and related nucleotide-binding protein
fig 6666666.284511.peg.2345	hypothetical protein
fig 6666666.284511.peg.2346	NADPH:quinone oxidoreductase
fig 6666666.284511.peg.2347	hypothetical protein
fig 6666666.284511.peg.2348	hypothetical protein
fig 6666666.284511.peg.2349	Membrane carboxypeptidase (penicillin-binding protein)
fig 6666666.284511.peg.2350	hypothetical protein
fig 6666666.284511.peg.2351	Fumarate hydratase class II (EC 4.2.1.2)
fig 6666666.284511.peg.2352	Hydrolases of the alpha/beta superfamily
fig 6666666.284511.peg.2353	Mobile element protein
fig 6666666.284511.peg.2354	Mobile element protein
fig 6666666.284511.peg.2355	hypothetical protein
fig 6666666.284511.peg.2356	MISCELLANEOUS; Unknown
fig 6666666.284511.peg.2357	MISCELLANEOUS; Unknown
fig 6666666.284511.peg.2358	FIG00931248: hypothetical protein
fig 6666666.284511.peg.2359	hypothetical protein
fig 6666666.284511.peg.2360	Transposase IS116/IS110/IS902
fig 6666666.284511.peg.2361	hypothetical protein
fig 6666666.284511.peg.2362	hypothetical protein
fig 6666666.284511.peg.2363	hypothetical protein
fig 6666666.284511.peg.2364	hypothetical protein

fig 6666666.284511.peg.2365	hypothetical protein
fig 6666666.284511.peg.2366	hypothetical protein
fig 6666666.284511.peg.2367	hypothetical protein
fig 6666666.284511.peg.2368	Mobile element protein
fig 6666666.284511.peg.2369	ISSo9, nucleotidyltransferase domain protein
fig 6666666.284511.peg.2370	FIG094328: hypothetical protein
fig 6666666.284511.peg.2371	hypothetical protein
fig 6666666.284511.peg.2372	Mobile element protein
fig 6666666.284511.peg.2373	hypothetical protein
fig 6666666.284511.peg.2374	Response regulator of zinc sigma-54-dependent two-component sys
fig 6666666.284511.peg.2375	hypothetical protein
fig 6666666.284511.peg.2376	hypothetical protein
fig 6666666.284511.peg.2377	Putative kinase protein
fig 6666666.284511.peg.2378	DNA helicase
fig 6666666.284511.peg.2379	hypothetical protein
fig 6666666.284511.peg.2380	5-methylcytosine-specific restriction related enzyme
fig 6666666.284511.peg.2381	hypothetical protein
fig 6666666.284511.peg.2382	hypothetical protein
fig 6666666.284511.peg.2383	hypothetical protein
fig 6666666.284511.peg.2384	hypothetical protein
fig 6666666.284511.peg.2385	Transposition protein, TnsC-related protein
fig 6666666.284511.peg.2386	hypothetical protein
fig 6666666.284511.peg.2387	Transposon Tn7 transposition protein tnsB
fig 6666666.284511.peg.2388	hypothetical protein
fig 6666666.284511.peg.2389	hypothetical protein
fig 6666666.284511.peg.2390	hypothetical protein
fig 6666666.284511.peg.2391	hypothetical protein
fig 6666666.284511.peg.2392	Mobile element protein
fig 6666666.284511.peg.2393	Transcriptional factor Mdch
fig 6666666.284511.peg.2394	hypothetical protein
fig 6666666.284511.peg.2395	hypothetical protein
fig 6666666.284511.peg.2396	hypothetical protein
fig 6666666.284511.peg.2397	ATPase, AAA family
fig 6666666.284511.peg.2398	Cell division protein FtsH (EC 3.4.24.-)
fig 6666666.284511.peg.2399	transcriptional factor
fig 6666666.284511.peg.2400	hypothetical protein
fig 6666666.284511.peg.2401	hypothetical protein
fig 6666666.284511.peg.2402	hypothetical protein
fig 6666666.284511.peg.2403	Tn7-like transposition protein C
fig 6666666.284511.peg.2404	Tn7-like transposition protein B
fig 6666666.284511.peg.2405	Transposon Tn7 transposition protein tnsA
fig 6666666.284511.peg.2406	Mobile element protein
fig 6666666.284511.peg.2407	hypothetical protein

fig 6666666.284511.peg.2408	hypothetical protein
fig 6666666.284511.peg.2409	hypothetical protein
fig 6666666.284511.peg.2410	hypothetical protein
fig 6666666.284511.peg.2411	Tn7-like transposition protein D
fig 6666666.284511.peg.2412	hypothetical protein
fig 6666666.284511.peg.2413	putative recombinase
fig 6666666.284511.peg.2414	Mhp operon transcriptional activator
fig 6666666.284511.peg.2415	putative exported protein
fig 6666666.284511.peg.2416	Monooxygenase, FAD-binding:FAD dependent oxidoreductase(EC:1.
fig 6666666.284511.peg.2417	3-carboxyethylcatechol 2,3-dioxygenase (EC 1.13.11.16)
fig 6666666.284511.peg.2418	2-keto-4-pentenoate hydratase (EC 4.2.1.80)
fig 6666666.284511.peg.2419	Acetaldehyde dehydrogenase, acetylating, (EC 1.2.1.10) in gene clust
fig 6666666.284511.peg.2420	4-hydroxy-2-oxovalerate aldolase (EC 4.1.3.39)
fig 6666666.284511.peg.2421	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-)
fig 6666666.284511.peg.2422	Alcohol dehydrogenase (EC 1.1.1.1)
fig 6666666.284511.peg.2423	BlI6423 protein
fig 6666666.284511.peg.2424	Alcohol dehydrogenase (EC 1.1.1.1)
fig 6666666.284511.peg.2425	Nitrilotriacetate monooxygenase component B (EC 1.14.13.-)
fig 6666666.284511.peg.2426	blr7732; hypothetical protein
fig 6666666.284511.peg.2427	putative exported protein
fig 6666666.284511.peg.2428	Acyl dehydratase
fig 6666666.284511.peg.2429	hypothetical protein
fig 6666666.284511.peg.2430	glycosyl transferase, group 1 family protein
fig 6666666.284511.peg.2431	O-methyltransferase, family 2
fig 6666666.284511.peg.2432	hypothetical protein
fig 6666666.284511.peg.2433	hypothetical protein
fig 6666666.284511.peg.2434	Mobile element protein
fig 6666666.284511.peg.2435	Mobile element protein
fig 6666666.284511.peg.2436	Type I restriction-modification system, DNA-methyltransferase subui
fig 6666666.284511.peg.2437	Type I restriction-modification system, specificity subunit S (EC 3.1.2:
fig 6666666.284511.peg.2438	hypothetical protein
fig 6666666.284511.peg.2439	Type I restriction-modification system, restriction subunit R (EC 3.1.2
fig 6666666.284511.peg.2440	hypothetical protein
fig 6666666.284511.peg.2441	Tn7-like transposition protein D
fig 6666666.284511.peg.2442	Transposon Tn7 transposition protein tnsC
fig 6666666.284511.peg.2443	Transposon Tn7 transposition protein tnsB
fig 6666666.284511.peg.2444	possible transposase
fig 6666666.284511.peg.2445	hypothetical protein
fig 6666666.284511.peg.2446	hypothetical protein
fig 6666666.284511.peg.2447	hypothetical protein
fig 6666666.284511.peg.2448	Arsenite oxidase small subunit precursor (EC 1.20.98.1)
fig 6666666.284511.peg.2449	Assimilatory nitrate reductase large subunit (EC:1.7.99.4)
fig 6666666.284511.peg.2450	probable cytochrome c-552 precursor

fig 6666666.284511.peg.2451	transcriptional regulator
fig 6666666.284511.peg.2452	nitroreductase
fig 6666666.284511.peg.2453	hypothetical protein
fig 6666666.284511.peg.2454	Transcriptional regulator in glycyl-tRNA synthetase containing cluste
fig 6666666.284511.peg.2455	Molybdenum cofactor biosynthesis protein MoaA
fig 6666666.284511.peg.2456	Molybdopterin biosynthesis protein MoeA
fig 6666666.284511.peg.2457	hypothetical protein
fig 6666666.284511.peg.2458	transcriptional regulator, Crp/Fnr family
fig 6666666.284511.peg.2459	Molybdenum cofactor biosynthesis protein MoaD
fig 6666666.284511.peg.2460	Molybdenum cofactor biosynthesis protein MoaE
fig 6666666.284511.peg.2461	CDP-abequose synthase (Fragment)
fig 6666666.284511.peg.2462	hypothetical protein
fig 6666666.284511.peg.2463	Methyl-accepting chemotaxis protein
fig 6666666.284511.peg.2464	hypothetical protein
fig 6666666.284511.peg.2465	Cytochrome c5
fig 6666666.284511.peg.2466	hypothetical protein
fig 6666666.284511.peg.2467	carbon monoxide dehydrogenase G protein
fig 6666666.284511.peg.2468	Thiol-disulfide isomerase and thioredoxins
fig 6666666.284511.peg.2469	Arsenic efflux pump protein
fig 6666666.284511.peg.2470	CBS domain protein
fig 6666666.284511.peg.2471	Pyridine nucleotide-disulfide oxidoreductase; NADH dehydrogenase
fig 6666666.284511.peg.2472	Arsenate reductase (EC 1.20.4.1)
fig 6666666.284511.peg.2473	Arsenical pump-driving ATPase (EC 3.6.3.16)
fig 6666666.284511.peg.2474	Arsenical resistance operon trans-acting repressor ArsD
fig 6666666.284511.peg.2475	Arsenate reductase (EC 1.20.4.1)
fig 6666666.284511.peg.2476	Arsenical resistance operon repressor
fig 6666666.284511.peg.2477	hypothetical protein
fig 6666666.284511.peg.2478	Mobile element protein
fig 6666666.284511.peg.2479	hypothetical protein
fig 6666666.284511.peg.2480	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
fig 6666666.284511.peg.2481	N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23) / G
fig 6666666.284511.peg.2482	Elongation factor-1 alpha
fig 6666666.284511.peg.2483	Chloride channel protein
fig 6666666.284511.peg.2484	Nitrate/nitrite transporter
fig 6666666.284511.peg.2485	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like anti
fig 6666666.284511.peg.2486	hypothetical protein
fig 6666666.284511.peg.2487	4-hydroxybenzoate polyprenyltransferase (EC 2.5.1.39)
fig 6666666.284511.peg.2488	hypothetical protein
fig 6666666.284511.peg.2489	NAD-specific glutamate dehydrogenase (EC 1.4.1.2); NADP-specific g
fig 6666666.284511.peg.2490	Aldo-keto reductase
fig 6666666.284511.peg.2491	hypothetical protein
fig 6666666.284511.peg.2492	hypothetical protein
fig 6666666.284511.peg.2493	MSHA biogenesis protein MshQ

fig 6666666.284511.peg.2494	Type IV fimbrial biogenesis protein PilW
fig 6666666.284511.peg.2495	hypothetical protein
fig 6666666.284511.peg.2496	Type IV fimbrial biogenesis protein FimT
fig 6666666.284511.peg.2497	hypothetical protein
fig 6666666.284511.peg.2498	Type IV fimbrial assembly protein PilC
fig 6666666.284511.peg.2499	Lipid A core - O-antigen ligase and related enzymes
fig 6666666.284511.peg.2500	hypothetical protein
fig 6666666.284511.peg.2501	hypothetical protein
fig 6666666.284511.peg.2502	hypothetical protein
fig 6666666.284511.peg.2503	putative esterase
fig 6666666.284511.peg.2504	Predicted transcriptional regulator LiuR of leucine degradation pathway
fig 6666666.284511.peg.2505	Phenylacetic acid degradation protein PaaD, thioesterase
fig 6666666.284511.peg.2506	Isovaleryl-CoA dehydrogenase (EC 1.3.8.4)
fig 6666666.284511.peg.2507	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase
fig 6666666.284511.peg.2508	hypothetical protein
fig 6666666.284511.peg.2509	Isocitrate dehydrogenase phosphatase (EC 2.7.11.5)/kinase (EC 3.1.3.1)
fig 6666666.284511.peg.2510	3-ketoacyl-CoA thiolase (EC 2.3.1.16)
fig 6666666.284511.peg.2511	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.2512	acetyltransferase
fig 6666666.284511.peg.2513	Butyryl-CoA dehydrogenase (EC 1.3.99.2)
fig 6666666.284511.peg.2514	2-hydroxychromene-2-carboxylate isomerase
fig 6666666.284511.peg.2515	Acetoacetyl-CoA synthetase (EC 6.2.1.16) / Long-chain-fatty-acid--CoA synthetase
fig 6666666.284511.peg.2516	Acetoacetyl-CoA synthetase (EC 6.2.1.16) / Long-chain-fatty-acid--CoA synthetase
fig 6666666.284511.peg.2517	Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.1)
fig 6666666.284511.peg.2518	DinB family protein
fig 6666666.284511.peg.2519	Methylglutaconyl-CoA hydratase (EC 4.2.1.18)
fig 6666666.284511.peg.2520	Biotin synthase (EC 2.8.1.6)
fig 6666666.284511.peg.2521	Mobile element protein
fig 6666666.284511.peg.2522	Mobile element protein
fig 6666666.284511.peg.2523	Probable transmembrane protein
fig 6666666.284511.peg.2524	Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.1)
fig 6666666.284511.peg.2525	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
fig 6666666.284511.peg.2526	hypothetical protein
fig 6666666.284511.peg.2527	Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)
fig 6666666.284511.peg.2528	Uncharacterized protein SCO3165
fig 6666666.284511.peg.2529	hypothetical protein
fig 6666666.284511.peg.2530	tRNA dihydrouridine synthase B (EC 1.-.-.-)
fig 6666666.284511.peg.2531	DNA-binding protein Fis
fig 6666666.284511.peg.2532	IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide
fig 6666666.284511.peg.2533	Crossover junction endodeoxyribonuclease RuvC (EC 3.1.22.4)
fig 6666666.284511.peg.2534	hypothetical protein
fig 6666666.284511.peg.2535	2-isopropylmalate synthase (EC 2.3.3.13)
fig 6666666.284511.peg.2536	hypothetical protein

fig 6666666.284511.peg.2537	Huntingtin interacting protein E-like protein
fig 6666666.284511.peg.2538	3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabA form (EC 4.2.
fig 6666666.284511.peg.2539	Holliday junction DNA helicase RuvA
fig 6666666.284511.peg.2540	hypothetical protein
fig 6666666.284511.peg.2541	Holliday junction DNA helicase RuvB
fig 6666666.284511.peg.2542	Heavy-chain fibroin (Fragment)
fig 6666666.284511.peg.2543	hypothetical protein
fig 6666666.284511.peg.2544	Phosphoglycerate mutase family
fig 6666666.284511.peg.2545	Inner membrane component of tripartite multidrug resistance syster
fig 6666666.284511.peg.2546	Membrane fusion component of tripartite multidrug resistance syste
fig 6666666.284511.peg.2547	Outer membrane component of tripartite multidrug resistance syste
fig 6666666.284511.peg.2548	Transcriptional regulator, MarR family
fig 6666666.284511.peg.2549	Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1)
fig 6666666.284511.peg.2550	3-dehydroquinate synthase (EC 4.2.3.4)
fig 6666666.284511.peg.2551	hypothetical protein
fig 6666666.284511.peg.2552	Shikimate kinase I (EC 2.7.1.71)
fig 6666666.284511.peg.2553	Type IV pilus biogenesis protein PilQ
fig 6666666.284511.peg.2554	Type IV pilus biogenesis protein PilP
fig 6666666.284511.peg.2555	Type IV pilus biogenesis protein PilO
fig 6666666.284511.peg.2556	Type IV pilus biogenesis protein PilN
fig 6666666.284511.peg.2557	Type IV pilus biogenesis protein PilM
fig 6666666.284511.peg.2558	hypothetical protein
fig 6666666.284511.peg.2559	hypothetical protein
fig 6666666.284511.peg.2560	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4
fig 6666666.284511.peg.2561	Frataxin homolog CyaY, facilitates iron supply for heme A synthesis o
fig 6666666.284511.peg.2562	hypothetical protein
fig 6666666.284511.peg.2563	Diaminopimelate decarboxylase (EC 4.1.1.20)
fig 6666666.284511.peg.2564	FIG001196: Membrane protein YedZ
fig 6666666.284511.peg.2565	Putative sulfite oxidase subunit YedY
fig 6666666.284511.peg.2566	Cytochrome c-type biogenesis protein CcsA/ResC
fig 6666666.284511.peg.2567	Cytochrome c-type biogenesis protein Ccs1/ResB
fig 6666666.284511.peg.2568	Cytochrome c4
fig 6666666.284511.peg.2569	GTP-binding protein EngB
fig 6666666.284511.peg.2570	putative patatin-like phospholipase
fig 6666666.284511.peg.2571	hypothetical protein
fig 6666666.284511.peg.2572	hypothetical protein
fig 6666666.284511.peg.2573	Mobile element protein
fig 6666666.284511.peg.2574	hypothetical protein
fig 6666666.284511.peg.2575	Mobile element protein
fig 6666666.284511.peg.2576	Mobile element protein
fig 6666666.284511.peg.2577	Mobile element protein
fig 6666666.284511.peg.2578	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)
fig 6666666.284511.peg.2579	Alcohol dehydrogenase (EC 1.1.1.1)

fig 6666666.284511.peg.2580	hypothetical protein
fig 6666666.284511.peg.2581	cell wall surface anchor family protein
fig 6666666.284511.peg.2582	putative transposase
fig 6666666.284511.peg.2583	Heat shock protein 60 family chaperone GroEL
fig 6666666.284511.peg.2584	Heat shock protein 60 family co-chaperone GroES
fig 6666666.284511.peg.2585	hypothetical protein
fig 6666666.284511.peg.2586	Glycosyltransferase (EC 2.4.1.-)
fig 6666666.284511.peg.2587	Glycosyltransferase (EC 2.4.1.-)
fig 6666666.284511.peg.2588	Aminotransferase, DegT/DnrJ/EryC1/StrS family (EC 4.2.1.-)
fig 6666666.284511.peg.2589	hypothetical protein
fig 6666666.284511.peg.2590	O-acetyltransferase, putative
fig 6666666.284511.peg.2591	putative autotransporter protein
fig 6666666.284511.peg.2592	Mobile element protein
fig 6666666.284511.peg.2593	hypothetical protein
fig 6666666.284511.peg.2594	TPR domain protein, putative component of TonB system
fig 6666666.284511.peg.2595	hypothetical protein
fig 6666666.284511.peg.2596	Hemolysin activation/secretion protein
fig 6666666.284511.peg.2597	PPIC-type PPIASE domain protein
fig 6666666.284511.peg.2598	hypothetical protein
fig 6666666.284511.peg.2599	TPR domain protein
fig 6666666.284511.peg.2600	O-antigen biosynthesis protein rfbC
fig 6666666.284511.peg.2601	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)
fig 6666666.284511.peg.2602	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) / Adenylylsulfate ki
fig 6666666.284511.peg.2603	Mobile element protein
fig 6666666.284511.peg.2604	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.2605	Mobile element protein
fig 6666666.284511.peg.2606	hypothetical protein
fig 6666666.284511.peg.2607	Outer membrane protein (porin)
fig 6666666.284511.peg.2608	hypothetical protein
fig 6666666.284511.peg.2609	Outer membrane protein (porin)
fig 6666666.284511.peg.2610	hypothetical protein
fig 6666666.284511.peg.2611	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase (EC :
fig 6666666.284511.peg.2612	OsmC/Ohr family protein
fig 6666666.284511.peg.2613	Threonine dehydratase biosynthetic (EC 4.3.1.19)
fig 6666666.284511.peg.2614	General secretion pathway protein C
fig 6666666.284511.peg.2615	hypothetical protein
fig 6666666.284511.peg.2616	General secretion pathway protein G
fig 6666666.284511.peg.2617	General secretion pathway protein H
fig 6666666.284511.peg.2618	General secretion pathway protein I
fig 6666666.284511.peg.2619	General secretion pathway protein J
fig 6666666.284511.peg.2620	General secretion pathway protein K
fig 6666666.284511.peg.2621	General secretion pathway protein L
fig 6666666.284511.peg.2622	General secretion pathway protein M

fig 6666666.284511.peg.2623	General secretion pathway protein N
fig 6666666.284511.peg.2624	Mobile element protein
fig 6666666.284511.peg.2625	General secretion pathway protein D
fig 6666666.284511.peg.2626	General secretion pathway protein D
fig 6666666.284511.peg.2627	General secretion pathway protein E
fig 6666666.284511.peg.2628	General secretion pathway protein F
fig 6666666.284511.peg.2629	5'-nucleotidase (EC 3.1.3.5)
fig 6666666.284511.peg.2630	Acyl-CoA-binding protein
fig 6666666.284511.peg.2631	Anthranilate synthase, amidotransferase component (EC 4.1.3.27) @
fig 6666666.284511.peg.2632	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)
fig 6666666.284511.peg.2633	Indole-3-glycerol phosphate synthase (EC 4.1.1.48)
fig 6666666.284511.peg.2634	Translation elongation factor Tu
fig 6666666.284511.peg.2635	Preprotein translocase subunit SecE (TC 3.A.5.1.1)
fig 6666666.284511.peg.2636	Transcription antitermination protein NusG
fig 6666666.284511.peg.2637	LSU ribosomal protein L11p (L12e)
fig 6666666.284511.peg.2638	LSU ribosomal protein L1p (L10Ae)
fig 6666666.284511.peg.2639	LSU ribosomal protein L10p (P0)
fig 6666666.284511.peg.2640	LSU ribosomal protein L7/L12 (P1/P2)
fig 6666666.284511.peg.2641	hypothetical protein
fig 6666666.284511.peg.2642	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)
fig 6666666.284511.peg.2643	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)
fig 6666666.284511.peg.2644	hypothetical protein
fig 6666666.284511.peg.2645	Transcription-repair coupling factor (superfamily II helicase)
fig 6666666.284511.peg.2646	Phage integrase
fig 6666666.284511.peg.2647	Metal-dependent phosphohydrolase, HD region
fig 6666666.284511.peg.2648	hypothetical protein
fig 6666666.284511.peg.2649	hypothetical protein
fig 6666666.284511.peg.2650	hypothetical protein
fig 6666666.284511.peg.2651	Integrase/recombinase
fig 6666666.284511.peg.2652	hypothetical protein
fig 6666666.284511.peg.2653	Acetyltransferase (isoleucine patch superfamily)
fig 6666666.284511.peg.2654	Sulfur oxidation molybdopterin C protein
fig 6666666.284511.peg.2655	Sulfite dehydrogenase cytochrome subunit SoxD
fig 6666666.284511.peg.2656	hypothetical protein
fig 6666666.284511.peg.2657	hypothetical protein
fig 6666666.284511.peg.2658	Phage-related integrase
fig 6666666.284511.peg.2659	Integrase/recombinase
fig 6666666.284511.peg.2660	Phage-related integrase
fig 6666666.284511.peg.2661	sensor histidine kinase
fig 6666666.284511.peg.2662	Osmosensitive K ⁺ channel histidine kinase KdpD (EC 2.7.3.-)
fig 6666666.284511.peg.2663	Potassium-transporting ATPase C chain (EC 3.6.3.12) (TC 3.A.3.7.1)
fig 6666666.284511.peg.2664	Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1)
fig 6666666.284511.peg.2665	Potassium-transporting ATPase A chain (EC 3.6.3.12) (TC 3.A.3.7.1)

fig 6666666.284511.peg.2666	hypothetical protein
fig 6666666.284511.peg.2667	Mobile element protein
fig 6666666.284511.peg.2668	hypothetical protein
fig 6666666.284511.peg.2669	hypothetical protein
fig 6666666.284511.peg.2670	hypothetical protein
fig 6666666.284511.peg.2671	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.2672	Cysteine desulfurase (EC 2.8.1.7)
fig 6666666.284511.peg.2673	hypothetical protein
fig 6666666.284511.peg.2674	hypothetical protein
fig 6666666.284511.peg.2675	Adenylate cyclase (EC 4.6.1.1)
fig 6666666.284511.peg.2676	hypothetical protein
fig 6666666.284511.peg.2677	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.2678	hypothetical protein
fig 6666666.284511.peg.2679	Sensory box/GGDEF family protein
fig 6666666.284511.peg.2680	hypothetical protein
fig 6666666.284511.peg.2681	Aldehyde dehydrogenase (EC 1.2.1.3)
fig 6666666.284511.peg.2682	hypothetical protein
fig 6666666.284511.peg.2683	Mobile element protein
fig 6666666.284511.peg.2684	Transcriptional activator MetR
fig 6666666.284511.peg.2685	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransf
fig 6666666.284511.peg.2686	hypothetical protein
fig 6666666.284511.peg.2687	hypothetical protein
fig 6666666.284511.peg.2688	D-amino acid dehydrogenase small subunit (EC 1.4.99.1)
fig 6666666.284511.peg.2689	Thiazole biosynthesis protein ThiG
fig 6666666.284511.peg.2690	hypothetical protein
fig 6666666.284511.peg.2691	Mobile element protein
fig 6666666.284511.peg.2692	Putative protease
fig 6666666.284511.peg.2693	Ribonucleotide reductase of class III (anaerobic), activating protein (f
fig 6666666.284511.peg.2694	Adenosylhomocysteinase (EC 3.3.1.1)
fig 6666666.284511.peg.2695	Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.
fig 6666666.284511.peg.2696	Glutamine amidotransferase class-I (EC 6.3.5.2)
fig 6666666.284511.peg.2697	hypothetical protein
fig 6666666.284511.peg.2698	Protein
fig 6666666.284511.peg.2699	hypothetical protein
fig 6666666.284511.peg.2700	PaaD-like protein (DUF59) involved in Fe-S cluster assembly
fig 6666666.284511.peg.2701	hypothetical protein
fig 6666666.284511.peg.2702	hypothetical protein
fig 6666666.284511.peg.2703	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
fig 6666666.284511.peg.2704	hypothetical protein
fig 6666666.284511.peg.2705	hypothetical protein
fig 6666666.284511.peg.2706	transcriptional regulator, Crp/Fnr family
fig 6666666.284511.peg.2707	Thiol:disulfide interchange protein DsbG precursor
fig 6666666.284511.peg.2708	ISXo7 transposase

fig 6666666.284511.peg.2709	Mobile element protein
fig 6666666.284511.peg.2710	carboxymuconolactone decarboxylase
fig 6666666.284511.peg.2711	probable uroporphyrin-III c-methyltransferase (EC 2.1.1.107)
fig 6666666.284511.peg.2712	282aa long conserved hypothetical protein
fig 6666666.284511.peg.2713	hypothetical protein
fig 6666666.284511.peg.2714	hypothetical protein
fig 6666666.284511.peg.2715	Glutathione S-transferase (EC 2.5.1.18)
fig 6666666.284511.peg.2716	Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX
fig 6666666.284511.peg.2717	Putative periplasmic cytochrome type-C oxidoreductase signal peptid
fig 6666666.284511.peg.2718	Putative periplasmic cytochrome type-C oxidoreductase signal peptid
fig 6666666.284511.peg.2719	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)
fig 6666666.284511.peg.2720	Mobile element protein
fig 6666666.284511.peg.2721	Mobile element protein
fig 6666666.284511.peg.2722	Mobile element protein
fig 6666666.284511.peg.2723	Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)
fig 6666666.284511.peg.2724	hypothetical protein
fig 6666666.284511.peg.2725	hypothetical protein
fig 6666666.284511.peg.2726	hypothetical protein
fig 6666666.284511.peg.2727	hypothetical protein
fig 6666666.284511.peg.2728	Mobile element protein
fig 6666666.284511.peg.2729	Mobile element protein
fig 6666666.284511.peg.2730	Cytochrome c oxidase (B(O/a)3-type) chain II (EC 1.9.3.1)
fig 6666666.284511.peg.2731	Cytochrome c oxidase (B(O/a)3-type) chain I (EC 1.9.3.1)
fig 6666666.284511.peg.2732	Nitric-oxide reductase subunit C (EC 1.7.99.7)
fig 6666666.284511.peg.2733	Nitric-oxide reductase subunit B (EC 1.7.99.7)
fig 6666666.284511.peg.2734	hypothetical protein
fig 6666666.284511.peg.2735	hypothetical protein
fig 6666666.284511.peg.2736	Mobile element protein
fig 6666666.284511.peg.2737	Mobile element protein
fig 6666666.284511.peg.2738	Mobile element protein
fig 6666666.284511.peg.2739	4Fe-4S ferredoxin, iron-sulfur binding
fig 6666666.284511.peg.2740	hypothetical protein
fig 6666666.284511.peg.2741	Mobile element protein
fig 6666666.284511.peg.2742	hypothetical protein
fig 6666666.284511.peg.2743	hypothetical protein
fig 6666666.284511.peg.2744	hypothetical protein
fig 6666666.284511.peg.2745	hypothetical protein
fig 6666666.284511.peg.2746	Chorismate--pyruvate lyase (EC 4.1.3.40)
fig 6666666.284511.peg.2747	Mobile element protein
fig 6666666.284511.peg.2748	Mobile element protein
fig 6666666.284511.peg.2749	hypothetical protein
fig 6666666.284511.peg.2750	hypothetical protein
fig 6666666.284511.peg.2751	hypothetical protein

fig 6666666.284511.peg.2752	MloA
fig 6666666.284511.peg.2753	hypothetical protein
fig 6666666.284511.peg.2754	Transcription-repair coupling factor (superfamily II helicase)
fig 6666666.284511.peg.2755	Phage integrase
fig 6666666.284511.peg.2756	Metal-dependent phosphohydrolase, HD region
fig 6666666.284511.peg.2757	hypothetical protein
fig 6666666.284511.peg.2758	hypothetical protein
fig 6666666.284511.peg.2759	hypothetical protein
fig 6666666.284511.peg.2760	hypothetical protein
fig 6666666.284511.peg.2761	hypothetical protein
fig 6666666.284511.peg.2762	hypothetical protein
fig 6666666.284511.peg.2763	hypothetical protein
fig 6666666.284511.peg.2764	hypothetical protein
fig 6666666.284511.peg.2765	hypothetical protein
fig 6666666.284511.peg.2766	hypothetical protein
fig 6666666.284511.peg.2767	hypothetical protein
fig 6666666.284511.peg.2768	CRISPR-associated protein Cas1
fig 6666666.284511.peg.2769	hypothetical protein
fig 6666666.284511.peg.2770	CRISPR-associated protein, Csy3 family
fig 6666666.284511.peg.2771	hypothetical protein
fig 6666666.284511.peg.2772	hypothetical protein
fig 6666666.284511.peg.2773	hypothetical protein
fig 6666666.284511.peg.2774	CRISPR-associated helicase Cas3, Yersinia-type
fig 6666666.284511.peg.2775	hypothetical protein
fig 6666666.284511.peg.2776	hypothetical protein
fig 6666666.284511.peg.2777	hypothetical protein
fig 6666666.284511.peg.2778	Mobile element protein
fig 6666666.284511.peg.2779	Mobile element protein
fig 6666666.284511.peg.2780	Mobile element protein
fig 6666666.284511.peg.2781	FIG022160: hypothetical toxin
fig 6666666.284511.peg.2782	FIG045511: hypothetical antitoxin (to FIG022160: hypothetical toxin)
fig 6666666.284511.peg.2783	hypothetical protein
fig 6666666.284511.peg.2784	hypothetical protein
fig 6666666.284511.peg.2785	hypothetical protein
fig 6666666.284511.peg.2786	hypothetical protein
fig 6666666.284511.peg.2787	Mobile element protein
fig 6666666.284511.peg.2788	Mobile element protein
fig 6666666.284511.peg.2789	Mobile element protein
fig 6666666.284511.peg.2790	Type I restriction-modification system, restriction subunit R (EC 3.1.2)
fig 6666666.284511.peg.2791	hypothetical protein
fig 6666666.284511.peg.2792	hypothetical protein
fig 6666666.284511.peg.2793	Type I restriction-modification system, specificity subunit S (EC 3.1.2)
fig 6666666.284511.peg.2794	Putative DNA-binding protein in cluster with Type I restriction-modif

fig 6666666.284511.peg.2795	Type I restriction-modification system, DNA-methyltransferase subu
fig 6666666.284511.peg.2796	hypothetical protein
fig 6666666.284511.peg.2797	hypothetical protein
fig 6666666.284511.peg.2798	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.2799	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.2800	Cysteine desulfurase (EC 2.8.1.7)
fig 6666666.284511.peg.2801	hypothetical protein
fig 6666666.284511.peg.2802	hypothetical protein
fig 6666666.284511.peg.2803	Adenylate cyclase (EC 4.6.1.1)
fig 6666666.284511.peg.2804	hypothetical protein
fig 6666666.284511.peg.2805	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.2806	hypothetical protein
fig 6666666.284511.peg.2807	Sensory box/GGDEF family protein
fig 6666666.284511.peg.2808	Aldehyde dehydrogenase (EC 1.2.1.3)
fig 6666666.284511.peg.2809	hypothetical protein
fig 6666666.284511.peg.2810	hypothetical protein
fig 6666666.284511.peg.2811	hypothetical protein
fig 6666666.284511.peg.2812	D-amino acid dehydrogenase small subunit (EC 1.4.99.1)
fig 6666666.284511.peg.2813	Thiazole biosynthesis protein ThiG
fig 6666666.284511.peg.2814	hypothetical protein
fig 6666666.284511.peg.2815	Aspartate 1-decarboxylase (EC 4.1.1.11)
fig 6666666.284511.peg.2816	Metal-dependent phosphohydrolase, HD region
fig 6666666.284511.peg.2817	hypothetical protein
fig 6666666.284511.peg.2818	hypothetical protein
fig 6666666.284511.peg.2819	Helix-turn-helix motif
fig 6666666.284511.peg.2820	Phage-related protein
fig 6666666.284511.peg.2821	hypothetical protein
fig 6666666.284511.peg.2822	hypothetical protein
fig 6666666.284511.peg.2823	hypothetical protein
fig 6666666.284511.peg.2824	Mobile element protein
fig 6666666.284511.peg.2825	hypothetical protein
fig 6666666.284511.peg.2826	hypothetical protein
fig 6666666.284511.peg.2827	hypothetical protein
fig 6666666.284511.peg.2828	Heavy metal sensor histidine kinase
fig 6666666.284511.peg.2829	DNA-binding heavy metal response regulator
fig 6666666.284511.peg.2830	Heavy metal RND efflux outer membrane protein, CzcC family
fig 6666666.284511.peg.2831	RND-type multidrug efflux pump, membrane permease
fig 6666666.284511.peg.2832	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.2833	hypothetical protein
fig 6666666.284511.peg.2834	Thiol:disulfide interchange protein tlpA
fig 6666666.284511.peg.2835	Cytochrome c-type biogenesis protein DsbD, protein-disulfide reduct
fig 6666666.284511.peg.2836	Thymidylate kinase (EC 2.7.4.9)
fig 6666666.284511.peg.2837	hypothetical protein

fig 6666666.284511.peg.2838	hypothetical protein
fig 6666666.284511.peg.2839	hypothetical protein
fig 6666666.284511.peg.2840	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.2841	hypothetical protein
fig 6666666.284511.peg.2842	Transcriptional regulator, MerR family
fig 6666666.284511.peg.2843	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.2844	Mobile element protein
fig 6666666.284511.peg.2845	hypothetical protein
fig 6666666.284511.peg.2846	Heavy metal RND efflux outer membrane protein, CzcC family
fig 6666666.284511.peg.2847	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion prot
fig 6666666.284511.peg.2848	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p
fig 6666666.284511.peg.2849	hypothetical protein
fig 6666666.284511.peg.2850	hypothetical protein
fig 6666666.284511.peg.2851	hypothetical protein
fig 6666666.284511.peg.2852	hypothetical protein
fig 6666666.284511.peg.2853	Cytochrome c-type biogenesis protein ResA
fig 6666666.284511.peg.2854	hypothetical protein
fig 6666666.284511.peg.2855	Mobile element protein
fig 6666666.284511.peg.2856	Chorismate--pyruvate lyase (EC 4.1.3.40)
fig 6666666.284511.peg.2857	Mobile element protein
fig 6666666.284511.peg.2858	Mobile element protein
fig 6666666.284511.peg.2859	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.2860	Mobile element protein
fig 6666666.284511.peg.2861	hypothetical protein
fig 6666666.284511.peg.2862	hypothetical protein
fig 6666666.284511.peg.2863	hypothetical protein
fig 6666666.284511.peg.2864	hypothetical protein
fig 6666666.284511.peg.2865	hypothetical protein
fig 6666666.284511.peg.2866	MloA
fig 6666666.284511.peg.2867	MloA
fig 6666666.284511.peg.2868	Chromosome partition protein smc
fig 6666666.284511.peg.2869	Chromosome partition protein smc
fig 6666666.284511.peg.2870	Chromosome partition protein smc
fig 6666666.284511.peg.2871	Chromosome partition protein smc
fig 6666666.284511.peg.2872	Chromosome partition protein smc
fig 6666666.284511.peg.2873	Chromosome partition protein smc
fig 6666666.284511.peg.2874	hypothetical protein
fig 6666666.284511.peg.2875	Chromosome partition protein smc
fig 6666666.284511.peg.2876	Chromosome partition protein smc
fig 6666666.284511.peg.2877	LemA PROTEIN
fig 6666666.284511.peg.2878	LemA PROTEIN
fig 6666666.284511.peg.2879	hypothetical protein
fig 6666666.284511.peg.2880	Uracil permease

fig 6666666.284511.peg.2881	Uracil permease
fig 6666666.284511.peg.2882	Uracil permease
fig 6666666.284511.peg.2883	Uracil permease
fig 6666666.284511.peg.2884	Uracil permease
fig 6666666.284511.peg.2885	hypothetical protein
fig 6666666.284511.peg.2886	Uracil phosphoribosyltransferase (EC 2.4.2.9)
fig 6666666.284511.peg.2887	Uracil phosphoribosyltransferase (EC 2.4.2.9)
fig 6666666.284511.peg.2888	Uracil phosphoribosyltransferase (EC 2.4.2.9)
fig 6666666.284511.peg.2889	Uracil phosphoribosyltransferase (EC 2.4.2.9)
fig 6666666.284511.peg.2890	Uracil permease
fig 6666666.284511.peg.2891	Uracil permease
fig 6666666.284511.peg.2892	Uracil permease
fig 6666666.284511.peg.2893	Uracil permease
fig 6666666.284511.peg.2894	hypothetical protein
fig 6666666.284511.peg.2895	LemA PROTEIN
fig 6666666.284511.peg.2896	Ser/Thr protein phosphatase family protein
fig 6666666.284511.peg.2897	hypothetical protein
fig 6666666.284511.peg.2898	hypothetical protein
fig 6666666.284511.peg.2899	hypothetical protein
fig 6666666.284511.peg.2900	hypothetical protein
fig 6666666.284511.peg.2901	hypothetical protein
fig 6666666.284511.peg.2902	hypothetical protein
fig 6666666.284511.peg.2903	TOPRIM domain protein
fig 6666666.284511.peg.2904	Replication protein C
fig 6666666.284511.peg.2905	DNA repair exonuclease family protein YhaO
fig 6666666.284511.peg.2906	DNA double-strand break repair Rad50 ATPase
fig 6666666.284511.peg.2907	hypothetical protein
fig 6666666.284511.peg.2908	hypothetical protein
fig 6666666.284511.peg.2909	hypothetical protein
fig 6666666.284511.peg.2910	hypothetical protein
fig 6666666.284511.peg.2911	Propeptide PepSY amd peptidase M4
fig 6666666.284511.peg.2912	Type I restriction-modification system, DNA-methyltransferase subu
fig 6666666.284511.peg.2913	Type I restriction-modification system, specificity subunit S (EC 3.1.2:
fig 6666666.284511.peg.2914	putative type II restriction endonuclease
fig 6666666.284511.peg.2915	hypothetical protein
fig 6666666.284511.peg.2916	Type I restriction-modification system, restriction subunit R (EC 3.1.2
fig 6666666.284511.peg.2917	hypothetical protein
fig 6666666.284511.peg.2918	hypothetical protein
fig 6666666.284511.peg.2919	hypothetical protein
fig 6666666.284511.peg.2920	DNA primase (EC 2.7.7.-), phage related
fig 6666666.284511.peg.2921	Integrase
fig 6666666.284511.peg.2922	Peptidyl-prolyl cis-trans isomerase PpiD (EC 5.2.1.8)
fig 6666666.284511.peg.2923	DNA-binding protein HU-beta

fig 6666666.284511.peg.2924	Tartrate dehydrogenase (EC 1.1.1.93) / Tartrate decarboxylase (EC 4.
fig 6666666.284511.peg.2925	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
fig 6666666.284511.peg.2926	Excinuclease ABC subunit C
fig 6666666.284511.peg.2927	Uracil-DNA glycosylase, family 5
fig 6666666.284511.peg.2928	hypothetical protein
fig 6666666.284511.peg.2929	hypothetical protein
fig 6666666.284511.peg.2930	Translation elongation factor P
fig 6666666.284511.peg.2931	hypothetical protein
fig 6666666.284511.peg.2932	hypothetical protein
fig 6666666.284511.peg.2933	Type IV fimbrial biogenesis protein PilW
fig 6666666.284511.peg.2934	hypothetical protein
fig 6666666.284511.peg.2935	Mobile element protein
fig 6666666.284511.peg.2936	Type IV fimbrial biogenesis protein PilY1
fig 6666666.284511.peg.2937	hypothetical protein
fig 6666666.284511.peg.2938	Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC :
fig 6666666.284511.peg.2939	DNA recombination protein RmuC
fig 6666666.284511.peg.2940	Glyoxylate reductase (EC 1.1.1.79) / Glyoxylate reductase (EC 1.1.1.2
fig 6666666.284511.peg.2941	hypothetical protein
fig 6666666.284511.peg.2942	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)
fig 6666666.284511.peg.2943	Oxygen-insensitive NADPH nitroreductase (EC 1.-.-.-)
fig 6666666.284511.peg.2944	Deacetylases, including yeast histone deacetylase and acetoin utiliza
fig 6666666.284511.peg.2945	granule-associated protein
fig 6666666.284511.peg.2946	2-dehydropantoate 2-reductase (EC 1.1.1.169)
fig 6666666.284511.peg.2947	putative membrane protein
fig 6666666.284511.peg.2948	MFS permease protein
fig 6666666.284511.peg.2949	hypothetical protein
fig 6666666.284511.peg.2950	Mobile element protein
fig 6666666.284511.peg.2951	Probable hydrolase protein (EC 3.-.-.-)
fig 6666666.284511.peg.2952	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)
fig 6666666.284511.peg.2953	Putative esterase, FIGfam005057
fig 6666666.284511.peg.2954	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.2955	Exoribonuclease II (EC 3.1.13.1)
fig 6666666.284511.peg.2956	TonB protein
fig 6666666.284511.peg.2957	Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)
fig 6666666.284511.peg.2958	Monofunctional biosynthetic peptidoglycan transglycosylase (EC 2.4.
fig 6666666.284511.peg.2959	Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)
fig 6666666.284511.peg.2960	Hydroxymethylpyrimidine phosphate kinase ThiD (EC 2.7.4.7)
fig 6666666.284511.peg.2961	Rubredoxin
fig 6666666.284511.peg.2962	twitching motility protein PilG
fig 6666666.284511.peg.2963	twitching motility protein PilH
fig 6666666.284511.peg.2964	type IV pili signal transduction protein Pill
fig 6666666.284511.peg.2965	twitching motility protein PilJ
fig 6666666.284511.peg.2966	Signal transduction histidine kinase CheA (EC 2.7.3.-)

fig 6666666.284511.peg.2967	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)
fig 6666666.284511.peg.2968	UPF0301 protein YqgE
fig 6666666.284511.peg.2969	Putative Holliday junction resolvase YggF
fig 6666666.284511.peg.2970	Uracil phosphoribosyltransferase (EC 2.4.2.9) / Pyrimidine operon re
fig 6666666.284511.peg.2971	Aspartate carbamoyltransferase (EC 2.1.3.2)
fig 6666666.284511.peg.2972	Dihydroorotase (EC 3.5.2.3)
fig 6666666.284511.peg.2973	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
fig 6666666.284511.peg.2974	Chorismate synthase (EC 4.2.3.5)
fig 6666666.284511.peg.2975	Ferrous iron transport protein B
fig 6666666.284511.peg.2976	hypothetical protein
fig 6666666.284511.peg.2977	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminop
fig 6666666.284511.peg.2978	Predicted nucleotidyltransferase
fig 6666666.284511.peg.2979	Cytochrome c-type biogenesis protein ResA
fig 6666666.284511.peg.2980	3-dehydroquinate dehydratase II (EC 4.2.1.10)
fig 6666666.284511.peg.2981	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
fig 6666666.284511.peg.2982	Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)
fig 6666666.284511.peg.2983	Ribosomal protein L11 methyltransferase (EC 2.1.1.-)
fig 6666666.284511.peg.2984	possible membrane protein
fig 6666666.284511.peg.2985	Probable transmembrane protein
fig 6666666.284511.peg.2986	Beta N-acetyl-glucosaminidase (EC 3.2.1.52)
fig 6666666.284511.peg.2987	Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)
fig 6666666.284511.peg.2988	Pyridoxine 5'-phosphate synthase (EC 2.6.99.2)
fig 6666666.284511.peg.2989	DNA recombination and repair protein RecO
fig 6666666.284511.peg.2990	GTP-binding protein Era
fig 6666666.284511.peg.2991	Ribonuclease III (EC 3.1.26.3)
fig 6666666.284511.peg.2992	PROBABLE TRANSMEMBRANE PROTEIN
fig 6666666.284511.peg.2993	Signal peptidase I (EC 3.4.21.89)
fig 6666666.284511.peg.2994	Translation elongation factor LepA
fig 6666666.284511.peg.2995	HtrA protease/chaperone protein
fig 6666666.284511.peg.2996	hypothetical protein
fig 6666666.284511.peg.2997	Sigma factor RpoE negative regulatory protein RseB precursor
fig 6666666.284511.peg.2998	hypothetical protein
fig 6666666.284511.peg.2999	RNA polymerase sigma factor RpoE
fig 6666666.284511.peg.3000	hypothetical protein
fig 6666666.284511.peg.3001	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)
fig 6666666.284511.peg.3002	Acyl carrier protein
fig 6666666.284511.peg.3003	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.3004	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)
fig 6666666.284511.peg.3005	3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.180)
fig 6666666.284511.peg.3006	Phosphate:acyl-ACP acyltransferase PlsX
fig 6666666.284511.peg.3007	LSU ribosomal protein L32p
fig 6666666.284511.peg.3008	COG1399 protein, clustered with ribosomal protein L32p
fig 6666666.284511.peg.3009	protein of unknown function DUF395, YeeE/YedE

fig 6666666.284511.peg.3010	protein of unknown function DUF395, YeeE/YedE
fig 6666666.284511.peg.3011	Septum formation protein Maf
fig 6666666.284511.peg.3012	Tetrapyrrole methylase family protein
fig 6666666.284511.peg.3013	Periplasmic serine proteases (ClpP class)
fig 6666666.284511.peg.3014	Similar to phosphoglycolate phosphatase, clustered with ribosomal L
fig 6666666.284511.peg.3015	Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)
fig 6666666.284511.peg.3016	Ribonuclease E (EC 3.1.26.12)
fig 6666666.284511.peg.3017	Nucleoside-diphosphate-sugar epimerases
fig 6666666.284511.peg.3018	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductase
fig 6666666.284511.peg.3019	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.1.1.1)
fig 6666666.284511.peg.3020	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.1.1.1)
fig 6666666.284511.peg.3021	Branched-chain amino acid transport system permease protein LivM
fig 6666666.284511.peg.3022	High-affinity branched-chain amino acid transport system permease
fig 6666666.284511.peg.3023	FIG065221: Holliday junction DNA helicase
fig 6666666.284511.peg.3024	Outer membrane lipoprotein carrier protein LolA
fig 6666666.284511.peg.3025	Cell division protein FtsK
fig 6666666.284511.peg.3026	cAMP-binding proteins - catabolite gene activator and regulatory subunit
fig 6666666.284511.peg.3027	Thioredoxin reductase (EC 1.8.1.9)
fig 6666666.284511.peg.3028	hypothetical protein
fig 6666666.284511.peg.3029	Acetyl-coenzyme A synthetase (EC 6.2.1.1)
fig 6666666.284511.peg.3030	3'-to-5' oligoribonuclease (orn)
fig 6666666.284511.peg.3031	macromolecule metabolism; macromolecule degradation; degradation
fig 6666666.284511.peg.3032	Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96)
fig 6666666.284511.peg.3033	Ribosome small subunit-stimulated GTPase EngC
fig 6666666.284511.peg.3034	hypothetical protein
fig 6666666.284511.peg.3035	hypothetical protein
fig 6666666.284511.peg.3036	Ornithine carbamoyltransferase (EC 2.1.3.3)
fig 6666666.284511.peg.3037	Acetylornithine aminotransferase (EC 2.6.1.11)
fig 6666666.284511.peg.3038	PhnO protein
fig 6666666.284511.peg.3039	SSU ribosomal protein S20p
fig 6666666.284511.peg.3040	Proposed peptidoglycan lipid II flippase MurJ
fig 6666666.284511.peg.3041	DnaK suppressor protein
fig 6666666.284511.peg.3042	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)
fig 6666666.284511.peg.3043	Putative permease often clustered with de novo purine synthesis
fig 6666666.284511.peg.3044	DnaA regulatory inactivator Hda (Homologous to DnaA)
fig 6666666.284511.peg.3045	Phosphoserine phosphatase (EC 3.1.3.3)
fig 6666666.284511.peg.3046	Poly(A) polymerase (EC 2.7.7.19)
fig 6666666.284511.peg.3047	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase
fig 6666666.284511.peg.3048	Probable transmembrane protein
fig 6666666.284511.peg.3049	GCN5-related N-acetyltransferase
fig 6666666.284511.peg.3050	SSU ribosomal protein S16p
fig 6666666.284511.peg.3051	16S rRNA processing protein RimM
fig 6666666.284511.peg.3052	tRNA (Guanine37-N1) -methyltransferase (EC 2.1.1.31)

fig 6666666.284511.peg.3053	LSU ribosomal protein L19p
fig 6666666.284511.peg.3054	Hypothetical nudix hydrolase YeaB
fig 6666666.284511.peg.3055	Adenosylcobinamide-phosphate synthase (EC 6.3.1.10)
fig 6666666.284511.peg.3056	Phospholipid N-methyltransferase
fig 6666666.284511.peg.3057	hypothetical protein
fig 6666666.284511.peg.3058	Chaperone protein HtpG
fig 6666666.284511.peg.3059	Putative deoxyribonuclease YjjV
fig 6666666.284511.peg.3060	hypothetical protein
fig 6666666.284511.peg.3061	hypothetical protein
fig 6666666.284511.peg.3062	COGs COG1397
fig 6666666.284511.peg.3063	Glutamate synthase [NADPH] large chain (EC 1.4.1.13)
fig 6666666.284511.peg.3064	hypothetical protein
fig 6666666.284511.peg.3065	hypothetical protein
fig 6666666.284511.peg.3066	hypothetical protein
fig 6666666.284511.peg.3067	FIG074102: hypothetical protein
fig 6666666.284511.peg.3068	Phospholipase/carboxylesterase family protein (EC 3.1.-.-)
fig 6666666.284511.peg.3069	Trp repressor binding protein
fig 6666666.284511.peg.3070	putative membrane protein
fig 6666666.284511.peg.3071	hypothetical protein
fig 6666666.284511.peg.3072	hypothetical protein
fig 6666666.284511.peg.3073	HlyD family secretion protein
fig 6666666.284511.peg.3074	ABC-type multidrug transport system, permease component
fig 6666666.284511.peg.3075	ABC-type multidrug transport system, permease component
fig 6666666.284511.peg.3076	hypothetical protein
fig 6666666.284511.peg.3077	RecA/RadA recombinase
fig 6666666.284511.peg.3078	DNA polymerase-like protein PA0670
fig 6666666.284511.peg.3079	DNA polymerase III alpha subunit (EC 2.7.7.7)
fig 6666666.284511.peg.3080	ATP-dependent DNA helicase UvrD/PcrA, proteobacterial paralog
fig 6666666.284511.peg.3081	P-hydroxybenzoate hydroxylase (EC 1.14.13.2)
fig 6666666.284511.peg.3082	Transcriptional regulator, IclR family
fig 6666666.284511.peg.3083	hypothetical protein
fig 6666666.284511.peg.3084	Trans-feruloyl-CoA synthase (EC 6.2.1.34)
fig 6666666.284511.peg.3085	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.3086	hypothetical protein
fig 6666666.284511.peg.3087	FIG01024444: hypothetical protein
fig 6666666.284511.peg.3088	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1; Vani
fig 6666666.284511.peg.3089	Transcriptional regulator for ferulate or vanillate catabolism
fig 6666666.284511.peg.3090	Probable vanillate O-demethylase oxygenase subunit oxidoreductase
fig 6666666.284511.peg.3091	hypothetical protein
fig 6666666.284511.peg.3092	Transcriptional regulator, MarR family
fig 6666666.284511.peg.3093	2,3-dihydroxy-2,3-dihydro-phenylpropionate dehydrogenase (EC 1.3
fig 6666666.284511.peg.3094	Probable VANILLIN dehydrogenase oxidoreductase protein (EC 1.-.-.-
fig 6666666.284511.peg.3095	putative permease component of ABC transporter

fig 6666666.284511.peg.3096	High-affinity branched-chain amino acid transport system permease
fig 6666666.284511.peg.3097	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.
fig 6666666.284511.peg.3098	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.
fig 6666666.284511.peg.3099	ABC transporter, substrate binding protein
fig 6666666.284511.peg.3100	Outer membrane protein (porin)
fig 6666666.284511.peg.3101	Transcriptional regulator, LysR family
fig 6666666.284511.peg.3102	Transcriptional regulator, LysR family
fig 6666666.284511.peg.3103	Protocatechuate 4,5-dioxygenase alpha chain (EC 1.13.11.8)
fig 6666666.284511.peg.3104	similar to protocatechuate 4,5-dioxygenase beta chain
fig 6666666.284511.peg.3105	Aldo-keto reductase
fig 6666666.284511.peg.3106	4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase
fig 6666666.284511.peg.3107	Protocatechuate 4,5-dioxygenase beta chain (EC 1.13.11.8)
fig 6666666.284511.peg.3108	Protocatechuate 4,5-dioxygenase alpha chain (EC 1.13.11.8)
fig 6666666.284511.peg.3109	2-pyrone-4,6-dicarboxylic acid hydrolase
fig 6666666.284511.peg.3110	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid (
fig 6666666.284511.peg.3111	4-carboxy-4-hydroxy-2-oxoadipate aldolase (EC 4.1.3.17)
fig 6666666.284511.peg.3112	4-oxalomesaconate hydratase (EC 4.2.1.83)
fig 6666666.284511.peg.3113	FldA protein
fig 6666666.284511.peg.3114	Transcriptional regulator ligR, LysR family
fig 6666666.284511.peg.3115	Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)
fig 6666666.284511.peg.3116	Exodeoxyribonuclease V beta chain (EC 3.1.11.5)
fig 6666666.284511.peg.3117	Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)
fig 6666666.284511.peg.3118	hypothetical protein
fig 6666666.284511.peg.3119	Arsenate reductase (EC 1.20.4.1)
fig 6666666.284511.peg.3120	Arsenic efflux pump protein
fig 6666666.284511.peg.3121	Arsenate reductase (EC 1.20.4.1)
fig 6666666.284511.peg.3122	glyoxalase family protein
fig 6666666.284511.peg.3123	Arsenical resistance operon repressor
fig 6666666.284511.peg.3124	putative membrane protein
fig 6666666.284511.peg.3125	D-serine deaminase
fig 6666666.284511.peg.3126	FAD/FMN-containing dehydrogenases
fig 6666666.284511.peg.3127	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)
fig 6666666.284511.peg.3128	hypothetical protein
fig 6666666.284511.peg.3129	Response regulatory protein
fig 6666666.284511.peg.3130	Sensor histidine kinase
fig 6666666.284511.peg.3131	Phosphonate ABC transporter phosphate-binding periplasmic compc
fig 6666666.284511.peg.3132	hypothetical protein
fig 6666666.284511.peg.3133	Arsenite oxidase small subunit precursor (EC 1.20.98.1)
fig 6666666.284511.peg.3134	Assimilatory nitrate reductase large subunit (EC:1.7.99.4)
fig 6666666.284511.peg.3135	hypothetical protein
fig 6666666.284511.peg.3136	Mobile element protein
fig 6666666.284511.peg.3137	nitroreductase
fig 6666666.284511.peg.3138	hypothetical protein

fig 6666666.284511.peg.3139	Tetrathionate reductase subunit A
fig 6666666.284511.peg.3140	Tetrathionate reductase subunit C
fig 6666666.284511.peg.3141	Tetrathionate reductase subunit B
fig 6666666.284511.peg.3142	hypothetical protein
fig 6666666.284511.peg.3143	Transporter
fig 6666666.284511.peg.3144	hypothetical protein
fig 6666666.284511.peg.3145	Rhodanese-related sulfurtransferase
fig 6666666.284511.peg.3146	hypothetical protein
fig 6666666.284511.peg.3147	redox-active disulfide protein 2
fig 6666666.284511.peg.3148	hypothetical protein
fig 6666666.284511.peg.3149	Cobalt-zinc-cadmium resistance protein CzcD
fig 6666666.284511.peg.3150	hypothetical protein
fig 6666666.284511.peg.3151	hypothetical protein
fig 6666666.284511.peg.3152	FUPA30 P-type ATPase; putative cation-transporting ATPase pacL(EC
fig 6666666.284511.peg.3153	hypothetical protein
fig 6666666.284511.peg.3154	hypothetical protein
fig 6666666.284511.peg.3155	outer membrane efflux protein
fig 6666666.284511.peg.3156	RND efflux system, membrane fusion protein CmeA
fig 6666666.284511.peg.3157	RND multidrug efflux transporter; Acriflavin resistance protein
fig 6666666.284511.peg.3158	Aspartate 1-decarboxylase (EC 4.1.1.11)
fig 6666666.284511.peg.3159	hypothetical protein
fig 6666666.284511.peg.3160	hypothetical protein
fig 6666666.284511.peg.3161	hypothetical protein
fig 6666666.284511.peg.3162	hypothetical protein
fig 6666666.284511.peg.3163	hypothetical protein
fig 6666666.284511.peg.3164	hypothetical protein
fig 6666666.284511.peg.3165	Cytochrome c, class I
fig 6666666.284511.peg.3166	hypothetical protein
fig 6666666.284511.peg.3167	Hydrolase, alpha/beta fold family functionally coupled to Phosphorik
fig 6666666.284511.peg.3168	Alternative dihydrofolate reductase 3
fig 6666666.284511.peg.3169	Formyltetrahydrofolate deformylase (EC 3.5.1.10)
fig 6666666.284511.peg.3170	hypothetical protein
fig 6666666.284511.peg.3171	Putative signal peptide protein
fig 6666666.284511.peg.3172	Isocitrate dehydrogenase [NAD] (EC 1.1.1.41)
fig 6666666.284511.peg.3173	hypothetical protein
fig 6666666.284511.peg.3174	Glutaminyl-tRNA synthetase (EC 6.1.1.18)
fig 6666666.284511.peg.3175	hypothetical protein
fig 6666666.284511.peg.3176	phosphoesterase, PA-phosphatase related
fig 6666666.284511.peg.3177	Virulence protein
fig 6666666.284511.peg.3178	Acyl carrier protein (ACP1)
fig 6666666.284511.peg.3179	FIG017861: hypothetical protein
fig 6666666.284511.peg.3180	FIGfam138462: Acyl-CoA synthetase, AMP-(fatty) acid ligase
fig 6666666.284511.peg.3181	hypothetical protein

fig 6666666.284511.peg.3182	Lysophospholipid acyltransferase
fig 6666666.284511.peg.3183	FIG027190: Putative transmembrane protein
fig 6666666.284511.peg.3184	FIG021862: membrane protein, exporter
fig 6666666.284511.peg.3185	Polysaccharide deacetylase
fig 6666666.284511.peg.3186	hypothetical protein
fig 6666666.284511.peg.3187	3-oxoacyl-[ACP] synthase (EC 2.3.1.41) FabV like
fig 6666666.284511.peg.3188	hypothetical protein
fig 6666666.284511.peg.3189	3-oxoacyl-[ACP] synthase
fig 6666666.284511.peg.3190	3-hydroxydecanoyl-[ACP] dehydratase (EC 4.2.1.60)
fig 6666666.284511.peg.3191	3-oxoacyl-[ACP] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.3192	FIG143263: Glycosyl transferase
fig 6666666.284511.peg.3193	FIG018329: 1-acyl-sn-glycerol-3-phosphate acyltransferase
fig 6666666.284511.peg.3194	putative outer membrane protein
fig 6666666.284511.peg.3195	Mobile element protein
fig 6666666.284511.peg.3196	FIG022199: FAD-binding protein
fig 6666666.284511.peg.3197	ATPase component BioM of energizing module of biotin ECF transpo
fig 6666666.284511.peg.3198	FIG000859: hypothetical protein YebC
fig 6666666.284511.peg.3199	Phosphoribosylamine--glycine ligase (EC 6.3.4.13)
fig 6666666.284511.peg.3200	L-carnitine dehydratase/bile acid-inducible protein F (EC 2.8.3.16)
fig 6666666.284511.peg.3201	probable membrane protein NMA1176
fig 6666666.284511.peg.3202	Acetate permease ActP (cation/acetate symporter)
fig 6666666.284511.peg.3203	hypothetical protein
fig 6666666.284511.peg.3204	macromolecule metabolism; macromolecule synthesis, modification;
fig 6666666.284511.peg.3205	N-acetylglutamate synthase (EC 2.3.1.1)
fig 6666666.284511.peg.3206	FIG001341: Probable Fe(2+)-trafficking protein YggX
fig 6666666.284511.peg.3207	putative facilitator of salicylate uptake
fig 6666666.284511.peg.3208	Transcriptional regulator
fig 6666666.284511.peg.3209	membrane protein, putative
fig 6666666.284511.peg.3210	Ribosomal protein S12p Asp88 (E. coli) methylthiotransferase
fig 6666666.284511.peg.3211	PhbF
fig 6666666.284511.peg.3212	Acetoacetyl-CoA reductase (EC 1.1.1.36)
fig 6666666.284511.peg.3213	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase
fig 6666666.284511.peg.3214	Polyhydroxyalkanoic acid synthase
fig 6666666.284511.peg.3215	hypothetical protein
fig 6666666.284511.peg.3216	COG1496: Uncharacterized conserved protein
fig 6666666.284511.peg.3217	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)
fig 6666666.284511.peg.3218	Probable component of the lipoprotein assembly complex (forms a c
fig 6666666.284511.peg.3219	DinG family ATP-dependent helicase YoaA
fig 6666666.284511.peg.3220	hypothetical protein
fig 6666666.284511.peg.3221	Protein phosphatase 2C-like
fig 6666666.284511.peg.3222	Translation initiation factor 2 (IF-2; GTPase)
fig 6666666.284511.peg.3223	hypothetical protein
fig 6666666.284511.peg.3224	ATPase component BioM of energizing module of biotin ECF transpo

fig 6666666.284511.peg.3225	Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase
fig 6666666.284511.peg.3226	Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase
fig 6666666.284511.peg.3227	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)
fig 6666666.284511.peg.3228	hypothetical protein
fig 6666666.284511.peg.3229	Sulfur oxidation protein SoxB
fig 6666666.284511.peg.3230	Sulfur oxidation protein SoxX
fig 6666666.284511.peg.3231	sulfur oxidation protein SoxA
fig 6666666.284511.peg.3232	Sulfur oxidation protein SoxZ
fig 6666666.284511.peg.3233	Sulfur oxidation protein SoxY
fig 6666666.284511.peg.3234	Sulfite dehydrogenase cytochrome subunit SoxD
fig 6666666.284511.peg.3235	Sulfur oxidation molybdopterin C protein
fig 6666666.284511.peg.3236	transcriptional regulator SoxR
fig 6666666.284511.peg.3237	Propionate--CoA ligase (EC 6.2.1.17)
fig 6666666.284511.peg.3238	Alcohol dehydrogenase (EC 1.1.1.1)
fig 6666666.284511.peg.3239	NLP/P60
fig 6666666.284511.peg.3240	Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex
fig 6666666.284511.peg.3241	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex
fig 6666666.284511.peg.3242	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)
fig 6666666.284511.peg.3243	Probable two-component transmembrane sensor histidine kinase transducer
fig 6666666.284511.peg.3244	Nitrogen regulation protein NR(I)
fig 6666666.284511.peg.3245	Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / MTHFD
fig 6666666.284511.peg.3246	Oligopeptidase A (EC 3.4.24.70)
fig 6666666.284511.peg.3247	hypothetical protein
fig 6666666.284511.peg.3248	Ribose 5-phosphate isomerase A (EC 5.3.1.6)
fig 6666666.284511.peg.3249	Dihydroorotate dehydrogenase (EC 1.3.3.1)
fig 6666666.284511.peg.3250	hypothetical protein
fig 6666666.284511.peg.3251	Glutamyl-tRNA synthetase (EC 6.1.1.17)
fig 6666666.284511.peg.3252	O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) / O-succinylhomoserine sulfhydrylase
fig 6666666.284511.peg.3253	Amidophosphoribosyltransferase (EC 2.4.2.14)
fig 6666666.284511.peg.3254	Colicin V production protein
fig 6666666.284511.peg.3255	DedD protein
fig 6666666.284511.peg.3256	Dihydrofolate synthase (EC 6.3.2.12) @ Folylpolyglutamate synthase
fig 6666666.284511.peg.3257	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)
fig 6666666.284511.peg.3258	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)
fig 6666666.284511.peg.3259	Tryptophan synthase alpha chain (EC 4.2.1.20)
fig 6666666.284511.peg.3260	Tryptophan synthase beta chain (EC 4.2.1.20)
fig 6666666.284511.peg.3261	Phosphoribosylanthranilate isomerase (EC 5.3.1.24)
fig 6666666.284511.peg.3262	tRNA pseudouridine synthase A (EC 4.2.1.70)
fig 6666666.284511.peg.3263	Probable type iv pilus assembly fimv-related transmembrane protein
fig 6666666.284511.peg.3264	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)
fig 6666666.284511.peg.3265	3-isopropylmalate dehydrogenase (EC 1.1.1.85)
fig 6666666.284511.peg.3266	3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)
fig 6666666.284511.peg.3267	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)

fig 6666666.284511.peg.3268	Citrate synthase (si) (EC 2.3.3.1)
fig 6666666.284511.peg.3269	YgfY COG2938
fig 6666666.284511.peg.3270	Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)
fig 6666666.284511.peg.3271	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)
fig 6666666.284511.peg.3272	Succinate dehydrogenase hydrophobic membrane anchor protein
fig 6666666.284511.peg.3273	Succinate dehydrogenase cytochrome b-556 subunit
fig 6666666.284511.peg.3274	Putative alkanesulfonate metabolism utilization regulator
fig 6666666.284511.peg.3275	Malate dehydrogenase (EC 1.1.1.37)
fig 6666666.284511.peg.3276	Methylisocitrate lyase (EC 4.1.3.30)
fig 6666666.284511.peg.3277	2-methylcitrate synthase (EC 2.3.3.5)
fig 6666666.284511.peg.3278	conserved hypothetical protein
fig 6666666.284511.peg.3279	2-methylcitrate dehydratase (EC 4.2.1.79)
fig 6666666.284511.peg.3280	Aconitate hydratase (EC 4.2.1.3) @ 2-methylisocitrate dehydratase (I
fig 6666666.284511.peg.3281	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)
fig 6666666.284511.peg.3282	Rubrerythrin
fig 6666666.284511.peg.3283	Fe-S oxidoreductase-like protein in Rubrerythrin cluster
fig 6666666.284511.peg.3284	Hypothetical protein i Rubrerythrin cluster
fig 6666666.284511.peg.3285	UPF0246 protein YaaA
fig 6666666.284511.peg.3286	hypothetical protein
fig 6666666.284511.peg.3287	Mobile element protein
fig 6666666.284511.peg.3288	Mobile element protein
fig 6666666.284511.peg.3289	hypothetical protein
fig 6666666.284511.peg.3290	hypothetical protein
fig 6666666.284511.peg.3291	hypothetical protein
fig 6666666.284511.peg.3292	hypothetical protein
fig 6666666.284511.peg.3293	hypothetical protein
fig 6666666.284511.peg.3294	YafQ toxin protein
fig 6666666.284511.peg.3295	hypothetical protein
fig 6666666.284511.peg.3296	hypothetical protein
fig 6666666.284511.peg.3297	Mobile element protein
fig 6666666.284511.peg.3298	Mobile element protein
fig 6666666.284511.peg.3299	hypothetical protein
fig 6666666.284511.peg.3300	Mobile element protein
fig 6666666.284511.peg.3301	hypothetical protein
fig 6666666.284511.peg.3302	hypothetical protein
fig 6666666.284511.peg.3303	Mobile element protein
fig 6666666.284511.peg.3304	Mobile element protein
fig 6666666.284511.peg.3305	hypothetical protein
fig 6666666.284511.peg.3306	hypothetical protein
fig 6666666.284511.peg.3307	COGs COG2378
fig 6666666.284511.peg.3308	GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase I
fig 6666666.284511.peg.3309	hypothetical protein
fig 6666666.284511.peg.3310	Mobile element protein

fig 6666666.284511.peg.3311	hypothetical protein
fig 6666666.284511.peg.3312	GII2284 protein
fig 6666666.284511.peg.3313	hypothetical protein
fig 6666666.284511.peg.3314	hypothetical protein
fig 6666666.284511.peg.3315	Death on curing protein, Doc toxin
fig 6666666.284511.peg.3316	hypothetical protein
fig 6666666.284511.peg.3317	hypothetical protein
fig 6666666.284511.peg.3318	Putative DNA-binding protein in cluster with Type I restriction-modif
fig 6666666.284511.peg.3319	hypothetical protein
fig 6666666.284511.peg.3320	putative helicase
fig 6666666.284511.peg.3321	hypothetical protein
fig 6666666.284511.peg.3322	Mobile element protein
fig 6666666.284511.peg.3323	FIG032766: hypothetical protein
fig 6666666.284511.peg.3324	FIG001353: Acetyltransferase
fig 6666666.284511.peg.3325	hypothetical protein
fig 6666666.284511.peg.3326	hypothetical protein
fig 6666666.284511.peg.3327	Biotin synthesis protein BioC
fig 6666666.284511.peg.3328	hypothetical protein
fig 6666666.284511.peg.3329	Mobile element protein
fig 6666666.284511.peg.3330	Mobile element protein
fig 6666666.284511.peg.3331	hypothetical protein
fig 6666666.284511.peg.3332	Transcriptional regulator
fig 6666666.284511.peg.3333	Propeptide PepSY amd peptidase M4
fig 6666666.284511.peg.3334	Membrane-flanked domain
fig 6666666.284511.peg.3335	hypothetical protein
fig 6666666.284511.peg.3336	hypothetical protein
fig 6666666.284511.peg.3337	hypothetical protein
fig 6666666.284511.peg.3338	Thiol peroxidase, Tpx-type (EC 1.11.1.15)
fig 6666666.284511.peg.3339	Glycerol kinase (EC 2.7.1.30)
fig 6666666.284511.peg.3340	Sugar kinases, ribokinase family
fig 6666666.284511.peg.3341	Fosmidomycin resistance protein
fig 6666666.284511.peg.3342	Sarcosine oxidase beta subunit (EC 1.5.3.1)
fig 6666666.284511.peg.3343	Lipoprotein releasing system ATP-binding protein LolD
fig 6666666.284511.peg.3344	Lipoprotein releasing system transmembrane protein LolC
fig 6666666.284511.peg.3345	Macrolide-specific efflux protein MacA
fig 6666666.284511.peg.3346	Glutamine amidotransferase, class-II
fig 6666666.284511.peg.3347	putative exported protein
fig 6666666.284511.peg.3348	HtrA protease/chaperone protein
fig 6666666.284511.peg.3349	hypothetical protein
fig 6666666.284511.peg.3350	hypothetical protein
fig 6666666.284511.peg.3351	Fibronectin type III domain protein
fig 6666666.284511.peg.3352	hypothetical protein
fig 6666666.284511.peg.3353	Virulence protein

fig 6666666.284511.peg.3354	hypothetical protein
fig 6666666.284511.peg.3355	ABC transporter, ATP-binding protein
fig 6666666.284511.peg.3356	Thiol-disulfide isomerase and thioredoxins
fig 6666666.284511.peg.3357	Acylphosphate phosphohydrolase (EC 3.6.1.7), putative
fig 6666666.284511.peg.3358	hypothetical protein
fig 6666666.284511.peg.3359	Hypothetical protein YggS, proline synthase co-transcribed bacterial
fig 6666666.284511.peg.3360	hypothetical protein
fig 6666666.284511.peg.3361	Twitching motility protein PilT
fig 6666666.284511.peg.3362	cAMP-binding proteins - catabolite gene activator and regulatory subunit
fig 6666666.284511.peg.3363	Twitching motility protein PilT
fig 6666666.284511.peg.3364	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein
fig 6666666.284511.peg.3365	hypothetical protein
fig 6666666.284511.peg.3366	Mobile element protein
fig 6666666.284511.peg.3367	hypothetical protein
fig 6666666.284511.peg.3368	hypothetical protein
fig 6666666.284511.peg.3369	Fused spore maturation proteins A and B
fig 6666666.284511.peg.3370	DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)
fig 6666666.284511.peg.3371	NADH dehydrogenase (EC 1.6.99.3)
fig 6666666.284511.peg.3372	hypothetical protein
fig 6666666.284511.peg.3373	Putative sensory histidine kinase YfhA
fig 6666666.284511.peg.3374	hypothetical protein
fig 6666666.284511.peg.3375	Putative sensor-like histidine kinase YfhK
fig 6666666.284511.peg.3376	Protein involved in catabolism of external DNA
fig 6666666.284511.peg.3377	hypothetical protein
fig 6666666.284511.peg.3378	hypothetical protein
fig 6666666.284511.peg.3379	FIG00581344: hypothetical protein
fig 6666666.284511.peg.3380	Rhodanese domain protein
fig 6666666.284511.peg.3381	hypothetical protein
fig 6666666.284511.peg.3382	Mobile element protein
fig 6666666.284511.peg.3383	Cardiolipin synthetase (EC 2.7.8.-)
fig 6666666.284511.peg.3384	Endonuclease/exonuclease/phosphatase
fig 6666666.284511.peg.3385	Dihydroneopterin triphosphate pyrophosphohydrolase type 2
fig 6666666.284511.peg.3386	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I al
fig 6666666.284511.peg.3387	hypothetical protein
fig 6666666.284511.peg.3388	hypothetical protein
fig 6666666.284511.peg.3389	Aspartyl-tRNA synthetase (EC 6.1.1.12) @ Aspartyl-tRNA(Asn) synthetase
fig 6666666.284511.peg.3390	Transporter
fig 6666666.284511.peg.3391	Type I antifreeze protein
fig 6666666.284511.peg.3392	hypothetical protein
fig 6666666.284511.peg.3393	tRNA(Cytosine32)-2-thiocytidine synthetase
fig 6666666.284511.peg.3394	Dihydroneopterin aldolase (EC 4.1.2.25)
fig 6666666.284511.peg.3395	FolM Alternative dihydrofolate reductase 1
fig 6666666.284511.peg.3396	COG1565: Uncharacterized conserved protein

fig 6666666.284511.peg.3397	hypothetical protein
fig 6666666.284511.peg.3398	major facilitator superfamily (MFS) transporter
fig 6666666.284511.peg.3399	LysR family transcriptional regulator YnfL
fig 6666666.284511.peg.3400	tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25)
fig 6666666.284511.peg.3401	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.3402	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
fig 6666666.284511.peg.3403	Scaffold protein for [4Fe-4S] cluster assembly ApbC, MRP-like
fig 6666666.284511.peg.3404	Methionyl-tRNA synthetase (EC 6.1.1.10)
fig 6666666.284511.peg.3405	hypothetical protein
fig 6666666.284511.peg.3406	Lipopolysaccharide heptosyltransferase I
fig 6666666.284511.peg.3407	hypothetical protein
fig 6666666.284511.peg.3408	Segregation and condensation protein A
fig 6666666.284511.peg.3409	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
fig 6666666.284511.peg.3410	Pantoate--beta-alanine ligase (EC 6.3.2.1)
fig 6666666.284511.peg.3411	Ribulose-5-phosphate 4-epimerase and related epimerases and aldo
fig 6666666.284511.peg.3412	hypothetical protein
fig 6666666.284511.peg.3413	hypothetical protein
fig 6666666.284511.peg.3414	L-aspartate oxidase (EC 1.4.3.16)
fig 6666666.284511.peg.3415	Inositol-1-monophosphatase (EC 3.1.3.25)
fig 6666666.284511.peg.3416	AMP nucleosidase (EC 3.2.2.4)
fig 6666666.284511.peg.3417	LysR family regulatory protein
fig 6666666.284511.peg.3418	hypothetical protein
fig 6666666.284511.peg.3419	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)
fig 6666666.284511.peg.3420	Adenosylhomocysteinase (EC 3.3.1.1)
fig 6666666.284511.peg.3421	L-lysine permease
fig 6666666.284511.peg.3422	S-adenosylmethionine synthetase (EC 2.5.1.6)
fig 6666666.284511.peg.3423	Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-)
fig 6666666.284511.peg.3424	Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-)
fig 6666666.284511.peg.3425	Diaminopimelate epimerase (EC 5.1.1.7)
fig 6666666.284511.peg.3426	Protein of unknown function DUF484
fig 6666666.284511.peg.3427	Tyrosine recombinase XerC
fig 6666666.284511.peg.3428	LSU m5C1962 methyltransferase Rlml
fig 6666666.284511.peg.3429	Putative metal chaperone, involved in Zn homeostasis, GTPase of CO
fig 6666666.284511.peg.3430	hypothetical protein
fig 6666666.284511.peg.3431	C4-type zinc finger protein, DksA/TraR family
fig 6666666.284511.peg.3432	hypothetical protein
fig 6666666.284511.peg.3433	ATP-dependent protease HslV (EC 3.4.25.-)
fig 6666666.284511.peg.3434	ATP-dependent hsl protease ATP-binding subunit HslU
fig 6666666.284511.peg.3435	hypothetical protein
fig 6666666.284511.peg.3436	Pantothenate kinase type III, CoaX-like (EC 2.7.1.33)
fig 6666666.284511.peg.3437	FIG028220: hypothetical protein co-occurring with HEAT repeat prot
fig 6666666.284511.peg.3438	Ubiquinone/menaquinone biosynthesis methyltransferase UbiE (EC :
fig 6666666.284511.peg.3439	putative membrane protein

fig 6666666.284511.peg.3440	Protein YigP (COG3165) clustered with ubiquinone biosynthetic gene
fig 6666666.284511.peg.3441	Ubiquinone biosynthesis monooxygenase UbiB
fig 6666666.284511.peg.3442	Oxidoreductase, aldo/keto reductase family
fig 6666666.284511.peg.3443	B12 binding domain / kinase domain / Methylmalonyl-CoA mutase (f
fig 6666666.284511.peg.3444	FIG01199223: hypothetical protein
fig 6666666.284511.peg.3445	Cytochrome c4
fig 6666666.284511.peg.3446	FIG002261: Cytochrome c family protein
fig 6666666.284511.peg.3447	putative integral membrane protein
fig 6666666.284511.peg.3448	hypothetical protein
fig 6666666.284511.peg.3449	hypothetical protein
fig 6666666.284511.peg.3450	Flavoprotein WrbA
fig 6666666.284511.peg.3451	YaeQ protein
fig 6666666.284511.peg.3452	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.3453	hypothetical protein
fig 6666666.284511.peg.3454	ClpXP protease specificity-enhancing factor / Stringent starvation pro
fig 6666666.284511.peg.3455	Stringent starvation protein A
fig 6666666.284511.peg.3456	ubiquinol cytochrome C oxidoreductase, cytochrome C1 subunit
fig 6666666.284511.peg.3457	Ubiquinol--cytochrome c reductase, cytochrome B subunit (EC 1.10.2
fig 6666666.284511.peg.3458	Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)
fig 6666666.284511.peg.3459	hypothetical protein
fig 6666666.284511.peg.3460	hypothetical protein
fig 6666666.284511.peg.3461	Large-conductance mechanosensitive channel
fig 6666666.284511.peg.3462	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)
fig 6666666.284511.peg.3463	FIG137478: Hypothetical protein Ybgl
fig 6666666.284511.peg.3464	Outer membrane stress sensor protease DegS
fig 6666666.284511.peg.3465	Twin-arginine translocation protein TatC
fig 6666666.284511.peg.3466	Twin-arginine translocation protein TatB
fig 6666666.284511.peg.3467	Twin-arginine translocation protein TatA
fig 6666666.284511.peg.3468	FIG146285: Diadenosine tetraphosphate (Ap4A) hydrolase and other
fig 6666666.284511.peg.3469	Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)
fig 6666666.284511.peg.3470	Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19)
fig 6666666.284511.peg.3471	Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-)
fig 6666666.284511.peg.3472	Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide is
fig 6666666.284511.peg.3473	Imidazole glycerol phosphate synthase amidotransferase subunit (EC
fig 6666666.284511.peg.3474	Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)
fig 6666666.284511.peg.3475	Histidinol-phosphate aminotransferase (EC 2.6.1.9)
fig 6666666.284511.peg.3476	Histidinol dehydrogenase (EC 1.1.1.23)
fig 6666666.284511.peg.3477	ATP phosphoribosyltransferase (EC 2.4.2.17)
fig 6666666.284511.peg.3478	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)
fig 6666666.284511.peg.3479	YrbA protein
fig 6666666.284511.peg.3480	ABC-type multidrug transport system, permease component
fig 6666666.284511.peg.3481	ABC-type multidrug transport system, ATPase component
fig 6666666.284511.peg.3482	hypothetical protein

fig 6666666.284511.peg.3483	ABC-type transport system involved in resistance to organic solvents
fig 6666666.284511.peg.3484	Nucleoside ABC transporter, periplasmic nucleoside-binding protein
fig 6666666.284511.peg.3485	Uncharacterized ABC transporter, periplasmic component YrbD
fig 6666666.284511.peg.3486	Uncharacterized ABC transporter, permease component YrbE
fig 6666666.284511.peg.3487	Methionine ABC transporter ATP-binding protein
fig 6666666.284511.peg.3488	thiol methyltransferase
fig 6666666.284511.peg.3489	transcriptional regulator, Crp/Fnr family
fig 6666666.284511.peg.3490	DNA-binding protein H-NS
fig 6666666.284511.peg.3491	NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)
fig 6666666.284511.peg.3492	NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)
fig 6666666.284511.peg.3493	NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)
fig 6666666.284511.peg.3494	hypothetical protein
fig 6666666.284511.peg.3495	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.3496	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.3497	NTP pyrophosphohydrolases including oxidative damage repair enzyme
fig 6666666.284511.peg.3498	tRNA-specific 2-thiouridylase MnmA
fig 6666666.284511.peg.3499	FIG00771185: hypothetical protein
fig 6666666.284511.peg.3500	Rhodanese-related sulfurtransferase
fig 6666666.284511.peg.3501	Acriflavin resistance protein
fig 6666666.284511.peg.3502	Efflux transporter, RND family, MFP subunit, AcrA/E family
fig 6666666.284511.peg.3503	outer membrane efflux protein
fig 6666666.284511.peg.3504	hypothetical protein
fig 6666666.284511.peg.3505	hypothetical protein
fig 6666666.284511.peg.3506	Sugar transport PTS system Ila component
fig 6666666.284511.peg.3507	Phosphocarrier protein of PTS system
fig 6666666.284511.peg.3508	hypothetical protein
fig 6666666.284511.peg.3509	Response regulator receiver:Transcriptional regulatory protein, C ter
fig 6666666.284511.peg.3510	probable two-component sensor
fig 6666666.284511.peg.3511	Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC
fig 6666666.284511.peg.3512	Exported zinc metalloprotease YfgC precursor
fig 6666666.284511.peg.3513	Lipid A core - O-antigen ligase and related enzymes
fig 6666666.284511.peg.3514	Branched-chain amino acid transport protein AzlC
fig 6666666.284511.peg.3515	Probable transmembrane protein
fig 6666666.284511.peg.3516	Pyruvate kinase (EC 2.7.1.40)
fig 6666666.284511.peg.3517	hypothetical protein
fig 6666666.284511.peg.3518	Protein serine/threonine phosphatase PrpC, regulation of stationary
fig 6666666.284511.peg.3519	Membrane protein TerC, possibly involved in tellurium resistance
fig 6666666.284511.peg.3520	Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5)
fig 6666666.284511.peg.3521	hypothetical protein
fig 6666666.284511.peg.3522	Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)
fig 6666666.284511.peg.3523	hypothetical protein
fig 6666666.284511.peg.3524	Regulatory protein RecX
fig 6666666.284511.peg.3525	RecA protein

fig 6666666.284511.peg.3526	hypothetical protein
fig 6666666.284511.peg.3527	Phospholipase/lecithinase/hemolysin
fig 6666666.284511.peg.3528	hypothetical protein
fig 6666666.284511.peg.3529	Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1
fig 6666666.284511.peg.3530	Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.
fig 6666666.284511.peg.3531	FIG000875: Thioredoxin domain-containing protein EC-YbbN
fig 6666666.284511.peg.3532	ThiJ/Pfpl family protein
fig 6666666.284511.peg.3533	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.:
fig 6666666.284511.peg.3534	hypothetical protein
fig 6666666.284511.peg.3535	Rhodanese domain protein
fig 6666666.284511.peg.3536	hypothetical protein
fig 6666666.284511.peg.3537	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alp
fig 6666666.284511.peg.3538	UDP-galactose-lipid carrier transferase (EC 2.-.-.)
fig 6666666.284511.peg.3539	Probable ALANIN-rich signal peptide protein
fig 6666666.284511.peg.3540	Cytochrome B561
fig 6666666.284511.peg.3541	TldD protein, part of TldE/TldD proteolytic complex
fig 6666666.284511.peg.3542	Molybdenum cofactor biosynthesis protein MoaC
fig 6666666.284511.peg.3543	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)
fig 6666666.284511.peg.3544	Uracil-DNA glycosylase, family 4
fig 6666666.284511.peg.3545	Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-)
fig 6666666.284511.peg.3546	Mobile element protein
fig 6666666.284511.peg.3547	TsaB protein, required for threonylcarbamoyladenosine (t(6)A) form:
fig 6666666.284511.peg.3548	hypothetical protein
fig 6666666.284511.peg.3549	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)
fig 6666666.284511.peg.3550	Potassium efflux system KefA protein / Small-conductance mechano:
fig 6666666.284511.peg.3551	DNA-binding response regulator
fig 6666666.284511.peg.3552	periplasmic sensor signal transduction histidine kinase
fig 6666666.284511.peg.3553	DNA topoisomerase III, Burkholderia type (EC 5.99.1.2)
fig 6666666.284511.peg.3554	DNA topoisomerase III, Burkholderia type (EC 5.99.1.2)
fig 6666666.284511.peg.3555	Thioredoxin-like protein
fig 6666666.284511.peg.3556	Proteins containing SET domain
fig 6666666.284511.peg.3557	Biotin-protein ligase (EC 6.3.4.15)
fig 6666666.284511.peg.3558	hypothetical protein
fig 6666666.284511.peg.3559	hypothetical protein
fig 6666666.284511.peg.3560	hypothetical protein
fig 6666666.284511.peg.3561	COGs COG2002
fig 6666666.284511.peg.3562	Catalyzes the cleavage of p-aminobenzoyl-glutamate to p-aminoben:
fig 6666666.284511.peg.3563	N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)
fig 6666666.284511.peg.3564	hypothetical protein
fig 6666666.284511.peg.3565	Anaerobic dehydrogenases, typically selenocysteine-containing
fig 6666666.284511.peg.3566	Cytochrome c-type biogenesis protein DsbD, protein-disulfide reduct
fig 6666666.284511.peg.3567	ABC-type multidrug transport system, permease component
fig 6666666.284511.peg.3568	ABC, transporter, ATP-binding protein

fig 6666666.284511.peg.3569	LSU ribosomal protein L17p
fig 6666666.284511.peg.3570	DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)
fig 6666666.284511.peg.3571	SSU ribosomal protein S4p (S9e)
fig 6666666.284511.peg.3572	SSU ribosomal protein S11p (S14e)
fig 6666666.284511.peg.3573	SSU ribosomal protein S13p (S18e)
fig 6666666.284511.peg.3574	LSU ribosomal protein L36p
fig 6666666.284511.peg.3575	Translation initiation factor 1
fig 6666666.284511.peg.3576	Preprotein translocase secY subunit (TC 3.A.5.1.1)
fig 6666666.284511.peg.3577	LSU ribosomal protein L15p (L27Ae)
fig 6666666.284511.peg.3578	LSU ribosomal protein L30p (L7e)
fig 6666666.284511.peg.3579	SSU ribosomal protein S5p (S2e)
fig 6666666.284511.peg.3580	LSU ribosomal protein L18p (L5e)
fig 6666666.284511.peg.3581	LSU ribosomal protein L6p (L9e)
fig 6666666.284511.peg.3582	SSU ribosomal protein S8p (S15Ae)
fig 6666666.284511.peg.3583	SSU ribosomal protein S14p (S29e) @ SSU ribosomal protein S14p (S
fig 6666666.284511.peg.3584	LSU ribosomal protein L5p (L11e)
fig 6666666.284511.peg.3585	LSU ribosomal protein L24p (L26e)
fig 6666666.284511.peg.3586	LSU ribosomal protein L14p (L23e)
fig 6666666.284511.peg.3587	SSU ribosomal protein S17p (S11e)
fig 6666666.284511.peg.3588	LSU ribosomal protein L29p (L35e)
fig 6666666.284511.peg.3589	LSU ribosomal protein L16p (L10e)
fig 6666666.284511.peg.3590	SSU ribosomal protein S3p (S3e)
fig 6666666.284511.peg.3591	LSU ribosomal protein L22p (L17e)
fig 6666666.284511.peg.3592	SSU ribosomal protein S19p (S15e)
fig 6666666.284511.peg.3593	LSU ribosomal protein L2p (L8e)
fig 6666666.284511.peg.3594	LSU ribosomal protein L23p (L23Ae)
fig 6666666.284511.peg.3595	LSU ribosomal protein L4p (L1e)
fig 6666666.284511.peg.3596	LSU ribosomal protein L3p (L3e)
fig 6666666.284511.peg.3597	SSU ribosomal protein S10p (S20e)
fig 6666666.284511.peg.3598	Translation elongation factor Tu
fig 6666666.284511.peg.3599	Translation elongation factor G
fig 6666666.284511.peg.3600	SSU ribosomal protein S7p (S5e)
fig 6666666.284511.peg.3601	SSU ribosomal protein S12p (S23e)
fig 6666666.284511.peg.3602	hypothetical protein
fig 6666666.284511.peg.3603	BatA (Bacteroides aerotolerance operon)
fig 6666666.284511.peg.3604	BatA (Bacteroides aerotolerance operon)
fig 6666666.284511.peg.3605	hypothetical protein
fig 6666666.284511.peg.3606	hypothetical protein
fig 6666666.284511.peg.3607	MoxR-like ATPase in aerotolerance operon
fig 6666666.284511.peg.3608	Chromate transport protein ChrA
fig 6666666.284511.peg.3609	Mobile element protein
fig 6666666.284511.peg.3610	Proposed lipoate regulatory protein YbeD
fig 6666666.284511.peg.3611	D-alanine aminotransferase (EC 2.6.1.21)

fig 6666666.284511.peg.3612	response regulator
fig 6666666.284511.peg.3613	Phosphate starvation-inducible protein PhoH, predicted ATPase
fig 6666666.284511.peg.3614	Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome
fig 6666666.284511.peg.3615	Apolipoprotein N-acyltransferase (EC 2.3.1.-) / Copper homeostasis p
fig 6666666.284511.peg.3616	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)
fig 6666666.284511.peg.3617	hypothetical protein
fig 6666666.284511.peg.3618	Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)
fig 6666666.284511.peg.3619	Histidinol-phosphatase (EC 3.1.3.15)
fig 6666666.284511.peg.3620	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
fig 6666666.284511.peg.3621	Putative predicted metal-dependent hydrolase
fig 6666666.284511.peg.3622	Lactoylglutathione lyase (EC 4.4.1.5)
fig 6666666.284511.peg.3623	hypothetical protein
fig 6666666.284511.peg.3624	Ribosome-associated heat shock protein implicated in the recycling c
fig 6666666.284511.peg.3625	Far-related protein
fig 6666666.284511.peg.3626	hypothetical protein
fig 6666666.284511.peg.3627	Preprotein translocase subunit YajC (TC 3.A.5.1.1)
fig 6666666.284511.peg.3628	hypothetical protein
fig 6666666.284511.peg.3629	Protein-export membrane protein SecD (TC 3.A.5.1.1)
fig 6666666.284511.peg.3630	Protein-export membrane protein SecF (TC 3.A.5.1.1)
fig 6666666.284511.peg.3631	hypothetical protein
fig 6666666.284511.peg.3632	hypothetical protein
fig 6666666.284511.peg.3633	Protein of unknown function Smg
fig 6666666.284511.peg.3634	hypothetical protein
fig 6666666.284511.peg.3635	Mobile element protein
fig 6666666.284511.peg.3636	hypothetical protein
fig 6666666.284511.peg.3637	Uncharacterized protein with LysM domain, COG1652
fig 6666666.284511.peg.3638	Peptide deformylase (EC 3.5.1.88)
fig 6666666.284511.peg.3639	Methionyl-tRNA formyltransferase (EC 2.1.2.9)
fig 6666666.284511.peg.3640	Peptidase M48, Ste24p precursor
fig 6666666.284511.peg.3641	Mobile element protein
fig 6666666.284511.peg.3642	putative membrane protein
fig 6666666.284511.peg.3643	Adenylosuccinate lyase (EC 4.3.2.2)
fig 6666666.284511.peg.3644	Glutathione S-transferase family protein
fig 6666666.284511.peg.3645	hypothetical protein
fig 6666666.284511.peg.3646	C-terminal domain of CinA type S; Protein Implicated in DNA repair f
fig 6666666.284511.peg.3647	Phosphatidylglycerophosphatase A (EC 3.1.3.27)
fig 6666666.284511.peg.3648	Thiamine-monophosphate kinase (EC 2.7.4.16)
fig 6666666.284511.peg.3649	NADP-dependent malic enzyme (EC 1.1.1.40)
fig 6666666.284511.peg.3650	hypothetical protein
fig 6666666.284511.peg.3651	hypothetical protein
fig 6666666.284511.peg.3652	Guanyl-specific ribonuclease Sa
fig 6666666.284511.peg.3653	Histone acetyltransferase HPA2 and related acetyltransferases
fig 6666666.284511.peg.3654	SSU rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransfe

fig 6666666.284511.peg.3655	Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase S
fig 6666666.284511.peg.3656	Outer membrane protein Imp, required for envelope biogenesis / Or
fig 6666666.284511.peg.3657	COG3178: Predicted phosphotransferase related to Ser/Thr protein I
fig 6666666.284511.peg.3658	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)
fig 6666666.284511.peg.3659	Xaa-Pro aminopeptidase (EC 3.4.11.9)
fig 6666666.284511.peg.3660	2-octaprenyl-6-methoxyphenol hydroxylase (EC 1.14.13.-)
fig 6666666.284511.peg.3661	FIG00457332: hypothetical protein
fig 6666666.284511.peg.3662	Carbohydrate-selective porin
fig 6666666.284511.peg.3663	3-polyprenyl-4-hydroxybenzoate carboxy-lyase UbiX (EC 4.1.1.-)
fig 6666666.284511.peg.3664	Glutaredoxin-related protein
fig 6666666.284511.peg.3665	Protein-N(5)-glutamine methyltransferase PrmC, methylates polypep
fig 6666666.284511.peg.3666	Peptide chain release factor 1
fig 6666666.284511.peg.3667	Glutamyl-tRNA reductase (EC 1.2.1.70)
fig 6666666.284511.peg.3668	hypothetical protein
fig 6666666.284511.peg.3669	Protein rarD
fig 6666666.284511.peg.3670	GTP-binding and nucleic acid-binding protein YchF
fig 6666666.284511.peg.3671	hypothetical protein
fig 6666666.284511.peg.3672	hypothetical protein
fig 6666666.284511.peg.3673	LemA PROTEIN
fig 6666666.284511.peg.3674	hypothetical protein
fig 6666666.284511.peg.3675	Uracil permease
fig 6666666.284511.peg.3676	hypothetical protein
fig 6666666.284511.peg.3677	Uracil phosphoribosyltransferase (EC 2.4.2.9)
fig 6666666.284511.peg.3678	hypothetical protein
fig 6666666.284511.peg.3679	Leucine-, isoleucine-, valine-, threonine-, and alanine-binding protei
fig 6666666.284511.peg.3680	High-affinity branched-chain amino acid transport system permease
fig 6666666.284511.peg.3681	Branched-chain amino acid transport system permease protein LivM
fig 6666666.284511.peg.3682	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.
fig 6666666.284511.peg.3683	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.
fig 6666666.284511.peg.3684	AsmA protein
fig 6666666.284511.peg.3685	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase (EC :
fig 6666666.284511.peg.3686	Thiol:disulfide interchange protein DsbC
fig 6666666.284511.peg.3687	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.3688	Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Gluta
fig 6666666.284511.peg.3689	Putative heme iron utilization protein
fig 6666666.284511.peg.3690	hypothetical protein
fig 6666666.284511.peg.3691	Queuosine biosynthesis QueD, PTPS-I
fig 6666666.284511.peg.3692	Queuosine Biosynthesis QueE Radical SAM
fig 6666666.284511.peg.3693	4-hydroxybenzoate transporter
fig 6666666.284511.peg.3694	Transcriptional regulator
fig 6666666.284511.peg.3695	lipoprotein, putative
fig 6666666.284511.peg.3696	hypothetical protein
fig 6666666.284511.peg.3697	hypothetical protein

fig 6666666.284511.peg.3698	hypothetical protein
fig 6666666.284511.peg.3699	hypothetical protein
fig 6666666.284511.peg.3700	hypothetical protein
fig 6666666.284511.peg.3701	hypothetical protein
fig 6666666.284511.peg.3702	hypothetical protein
fig 6666666.284511.peg.3703	Mobile element protein
fig 6666666.284511.peg.3704	hypothetical protein
fig 6666666.284511.peg.3705	hypothetical protein
fig 6666666.284511.peg.3706	hypothetical protein
fig 6666666.284511.peg.3707	HtaR suppressor protein
fig 6666666.284511.peg.3708	hypothetical protein
fig 6666666.284511.peg.3709	hypothetical protein
fig 6666666.284511.peg.3710	hypothetical protein
fig 6666666.284511.peg.3711	hypothetical protein
fig 6666666.284511.peg.3712	hypothetical protein
fig 6666666.284511.peg.3713	Transcriptional regulator, XRE family
fig 6666666.284511.peg.3714	hypothetical protein
fig 6666666.284511.peg.3715	hypothetical protein
fig 6666666.284511.peg.3716	Response regulator containing CheY-like receiver, AAA-type ATPase,
fig 6666666.284511.peg.3717	Nitrogen regulation protein NtrY (EC 2.7.3.-)
fig 6666666.284511.peg.3718	Probable proline rich signal peptide protein
fig 6666666.284511.peg.3719	Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)
fig 6666666.284511.peg.3720	Blr3520 protein homolog, hypothetical protein
fig 6666666.284511.peg.3721	hypothetical protein
fig 6666666.284511.peg.3722	Blr3520 protein homolog, hypothetical protein
fig 6666666.284511.peg.3723	hypothetical protein
fig 6666666.284511.peg.3724	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)
fig 6666666.284511.peg.3725	hypothetical protein
fig 6666666.284511.peg.3726	Alanine dehydrogenase (EC 1.4.1.1)
fig 6666666.284511.peg.3727	Transcriptional regulator, AsnC family
fig 6666666.284511.peg.3728	hypothetical protein
fig 6666666.284511.peg.3729	Ammonium transporter
fig 6666666.284511.peg.3730	hypothetical protein
fig 6666666.284511.peg.3731	hypothetical protein
fig 6666666.284511.peg.3732	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.3733	Arginase (EC 3.5.3.1)
fig 6666666.284511.peg.3734	Decarboxylase family protein
fig 6666666.284511.peg.3735	Cytochrome c family protein
fig 6666666.284511.peg.3736	hypothetical protein
fig 6666666.284511.peg.3737	hypothetical protein
fig 6666666.284511.peg.3738	hypothetical protein
fig 6666666.284511.peg.3739	hypothetical protein
fig 6666666.284511.peg.3740	Surface antigen

fig 6666666.284511.peg.3741	Probable transmembrane protein
fig 6666666.284511.peg.3742	GTP cyclohydrolase I (EC 3.5.4.16) type 1
fig 6666666.284511.peg.3743	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.3744	Methionine biosynthesis protein MetW
fig 6666666.284511.peg.3745	Homoserine O-acetyltransferase (EC 2.3.1.31)
fig 6666666.284511.peg.3746	hypothetical protein
fig 6666666.284511.peg.3747	hypothetical protein
fig 6666666.284511.peg.3748	hypothetical protein
fig 6666666.284511.peg.3749	hypothetical protein
fig 6666666.284511.peg.3750	Proline-rich region
fig 6666666.284511.peg.3751	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4
fig 6666666.284511.peg.3752	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4
fig 6666666.284511.peg.3753	Thiol:disulfide oxidoreductase TlpA
fig 6666666.284511.peg.3754	major facilitator superfamily MFS_1
fig 6666666.284511.peg.3755	hypothetical protein
fig 6666666.284511.peg.3756	Glutathione-regulated potassium-efflux system protein KefB
fig 6666666.284511.peg.3757	hypothetical protein
fig 6666666.284511.peg.3758	Acid phosphatase
fig 6666666.284511.peg.3759	Methylamine utilization protein mauG precursor
fig 6666666.284511.peg.3760	Transcriptional regulator
fig 6666666.284511.peg.3761	Transcriptional regulator, AraC family
fig 6666666.284511.peg.3762	FIG006238: AzlC family protein
fig 6666666.284511.peg.3763	FIG028593: membrane protein
fig 6666666.284511.peg.3764	Shufflon-specific DNA recombinase
fig 6666666.284511.peg.3765	Replication protein A
fig 6666666.284511.peg.3766	Type III restriction-modification enzyme, helicase subunit
fig 6666666.284511.peg.3767	hypothetical protein
fig 6666666.284511.peg.3768	Possible DNA methylase
fig 6666666.284511.peg.3769	LtrC-like protein
fig 6666666.284511.peg.3770	hypothetical protein
fig 6666666.284511.peg.3771	hypothetical protein
fig 6666666.284511.peg.3772	hypothetical protein
fig 6666666.284511.peg.3773	Possible transmembrane protein
fig 6666666.284511.peg.3774	Adenine phosphoribosyltransferase (EC 2.4.2.7)
fig 6666666.284511.peg.3775	hypothetical protein
fig 6666666.284511.peg.3776	hypothetical protein
fig 6666666.284511.peg.3777	conserved hypothetical protein
fig 6666666.284511.peg.3778	UDP-glucose 4-epimerase (EC 5.1.3.2)
fig 6666666.284511.peg.3779	UDP-glucose dehydrogenase (EC 1.1.1.22)
fig 6666666.284511.peg.3780	FIG071646: Sugar transferase
fig 6666666.284511.peg.3781	FIG123464: Polysaccharide export protein
fig 6666666.284511.peg.3782	Glycine-rich cell wall structural protein precursor
fig 6666666.284511.peg.3783	FIG022606: AAA ATPase

fig 6666666.284511.peg.3784	Lipopolysaccharide biosynthesis chain length determinant protein
fig 6666666.284511.peg.3785	Protein-tyrosine kinase (EC 2.7.1.112)
fig 6666666.284511.peg.3786	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)
fig 6666666.284511.peg.3787	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)
fig 6666666.284511.peg.3788	4'-phosphopantetheinyl transferase (EC 2.7.8.-)
fig 6666666.284511.peg.3789	Hydrolases of the alpha/beta superfamily
fig 6666666.284511.peg.3790	hypothetical protein
fig 6666666.284511.peg.3791	Glycosyl transferase, group 2 family protein
fig 6666666.284511.peg.3792	Polysaccharide deacetylase
fig 6666666.284511.peg.3793	possible bicarbonate transporter, ICT family
fig 6666666.284511.peg.3794	Glycosyl transferase, group 1 family protein
fig 6666666.284511.peg.3795	polysaccharide deacetylase
fig 6666666.284511.peg.3796	Glycosyltransferase (EC 2.4.1.-)
fig 6666666.284511.peg.3797	Putative membrane protein
fig 6666666.284511.peg.3798	hypothetical protein
fig 6666666.284511.peg.3799	transposase, putative
fig 6666666.284511.peg.3800	serine O-acetyltransferase
fig 6666666.284511.peg.3801	glycosyl transferase, group 1
fig 6666666.284511.peg.3802	polysaccharide biosynthesis protein
fig 6666666.284511.peg.3803	putative glycosyltransferase
fig 6666666.284511.peg.3804	cellulose biosynthesis protein
fig 6666666.284511.peg.3805	polysaccharide deacetylase
fig 6666666.284511.peg.3806	hypothetical protein
fig 6666666.284511.peg.3807	2'-5' RNA ligase
fig 6666666.284511.peg.3808	Mobile element protein
fig 6666666.284511.peg.3809	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.3810	hypothetical protein
fig 6666666.284511.peg.3811	Rhodanese domain protein UPF0176, Betaproteobacterial subgroup
fig 6666666.284511.peg.3812	Lysophospholipid transporter LpIT / 2-acylglycerophosphoethanolam
fig 6666666.284511.peg.3813	tRNA-guanine transglycosylase (EC 2.4.2.29)
fig 6666666.284511.peg.3814	hypothetical protein
fig 6666666.284511.peg.3815	hypothetical protein
fig 6666666.284511.peg.3816	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-)
fig 6666666.284511.peg.3817	Fatty-acid-CoA ligase FadD7
fig 6666666.284511.peg.3818	hypothetical protein
fig 6666666.284511.peg.3819	Non-ribosomal peptide synthetase
fig 6666666.284511.peg.3820	Catalase (EC 1.11.1.6) / Peroxidase (EC 1.11.1.7)
fig 6666666.284511.peg.3821	FOG: GGDEF domain
fig 6666666.284511.peg.3822	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.3823	Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.
fig 6666666.284511.peg.3824	Aldehyde dehydrogenase (EC 1.2.1.3)
fig 6666666.284511.peg.3825	Predicted enzyme of the cupin superfamily
fig 6666666.284511.peg.3826	Uncharacterized protein in putrescine utilization cluster

fig 6666666.284511.peg.3827	Putrescine transport system permease protein PotI (TC 3.A.1.11.2)
fig 6666666.284511.peg.3828	Putrescine transport system permease protein PotH (TC 3.A.1.11.2)
fig 6666666.284511.peg.3829	Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2)
fig 6666666.284511.peg.3830	Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)
fig 6666666.284511.peg.3831	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.60)
fig 6666666.284511.peg.3832	glutamine synthetase family protein
fig 6666666.284511.peg.3833	Gamma-glutamyl-GABA hydrolase (EC 3.5.1.94)
fig 6666666.284511.peg.3834	hypothetical protein
fig 6666666.284511.peg.3835	Transcriptional regulator, GntR family domain / Aspartate aminotransferase
fig 6666666.284511.peg.3836	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.11.2)
fig 6666666.284511.peg.3837	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.11.2)
fig 6666666.284511.peg.3838	Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.11.2)
fig 6666666.284511.peg.3839	High-affinity branched-chain amino acid transport system permease protein LivN (TC 3.A.1.11.2)
fig 6666666.284511.peg.3840	Branched-chain amino acid ABC transporter, amino acid-binding protein LivP (TC 3.A.1.11.2)
fig 6666666.284511.peg.3841	Putative oxidoreductase in putrescine utilization cluster
fig 6666666.284511.peg.3842	Agmatinase (EC 3.5.3.11)
fig 6666666.284511.peg.3843	Aminotransferase class-III
fig 6666666.284511.peg.3844	Blr3520 protein homolog, hypothetical protein
fig 6666666.284511.peg.3845	Rhodanese domain protein
fig 6666666.284511.peg.3846	hypothetical protein
fig 6666666.284511.peg.3847	Rod shape-determining protein RodA
fig 6666666.284511.peg.3848	Penicillin-binding protein 2 (PBP-2)
fig 6666666.284511.peg.3849	Rod shape-determining protein MreD
fig 6666666.284511.peg.3850	Rod shape-determining protein MreC
fig 6666666.284511.peg.3851	Rod shape-determining protein MreB
fig 6666666.284511.peg.3852	Aspartyl-tRNA(Asn) amidotransferase subunit C (EC 6.3.5.6) @ Glutathione
fig 6666666.284511.peg.3853	Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutathione
fig 6666666.284511.peg.3854	Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.6) @ Glutathione
fig 6666666.284511.peg.3855	hypothetical protein
fig 6666666.284511.peg.3856	Exodeoxyribonuclease III (EC 3.1.11.2)
fig 6666666.284511.peg.3857	hypothetical protein
fig 6666666.284511.peg.3858	hypothetical protein
fig 6666666.284511.peg.3859	Probable type IV pilus assembly FimV-related transmembrane protein
fig 6666666.284511.peg.3860	Glutathione S-transferase (EC 2.5.1.18)
fig 6666666.284511.peg.3861	Glutathione S-transferase (EC 2.5.1.18)
fig 6666666.284511.peg.3862	hypothetical protein
fig 6666666.284511.peg.3863	L-Proline/Glycine betaine transporter ProP
fig 6666666.284511.peg.3864	Transposase
fig 6666666.284511.peg.3865	ISSoc3, orfA transposase
fig 6666666.284511.peg.3866	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with
fig 6666666.284511.peg.3867	hypothetical protein
fig 6666666.284511.peg.3868	hypothetical protein
fig 6666666.284511.peg.3869	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with

fig 6666666.284511.peg.3870	Hypothetical protein YaeJ with similarity to translation release factor
fig 6666666.284511.peg.3871	Hydrogen peroxide-inducible genes activator
fig 6666666.284511.peg.3872	Hydrogen peroxide-inducible genes activator
fig 6666666.284511.peg.3873	NADH dehydrogenase, subunit 5
fig 6666666.284511.peg.3874	Hypothetical transmembrane protein coupled to NADH-ubiquinone c
fig 6666666.284511.peg.3875	Alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.73)
fig 6666666.284511.peg.3876	hypothetical protein
fig 6666666.284511.peg.3877	Methyltransferase type 11
fig 6666666.284511.peg.3878	Methyltransferase type 11
fig 6666666.284511.peg.3879	thioredoxin family protein
fig 6666666.284511.peg.3880	hypothetical protein
fig 6666666.284511.peg.3881	Lipocalin-related protein and Bos/Can/Equ allergen
fig 6666666.284511.peg.3882	Major facilitator superfamily (MFS) transporter
fig 6666666.284511.peg.3883	Metallo-beta-lactamase family protein
fig 6666666.284511.peg.3884	Putative ACR protein
fig 6666666.284511.peg.3885	Transcriptional regulator, ArsR family
fig 6666666.284511.peg.3886	Aromatic-amino-acid aminotransferase (EC 2.6.1.57)
fig 6666666.284511.peg.3887	Permease of the drug/metabolite transporter (DMT) superfamily
fig 6666666.284511.peg.3888	Transcriptional regulator, GntR family domain / Aspartate aminotran
fig 6666666.284511.peg.3889	transporter, putative
fig 6666666.284511.peg.3890	multidrug resistance protein B
fig 6666666.284511.peg.3891	Nicotinamidase/isochorismatase family protein
fig 6666666.284511.peg.3892	Transcriptional regulator, AraC family
fig 6666666.284511.peg.3893	hypothetical protein
fig 6666666.284511.peg.3894	Methyltransferase type 11
fig 6666666.284511.peg.3895	hypothetical protein
fig 6666666.284511.peg.3896	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.3897	hypothetical protein
fig 6666666.284511.peg.3898	hypothetical protein
fig 6666666.284511.peg.3899	hypothetical protein
fig 6666666.284511.peg.3900	Death on curing protein, Doc toxin
fig 6666666.284511.peg.3901	hypothetical protein
fig 6666666.284511.peg.3902	PUTATIVE HEMAGGLUTININ-RELATED PROTEIN
fig 6666666.284511.peg.3903	Mobile element protein
fig 6666666.284511.peg.3904	Hypothetical metal-binding enzyme, YcbL homolog
fig 6666666.284511.peg.3905	hypothetical protein
fig 6666666.284511.peg.3906	Orotate phosphoribosyltransferase (EC 2.4.2.10)
fig 6666666.284511.peg.3907	AmpG permease
fig 6666666.284511.peg.3908	Arabinose 5-phosphate isomerase (EC 5.3.1.13)
fig 6666666.284511.peg.3909	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.
fig 6666666.284511.peg.3910	Probable transmembrane protein
fig 6666666.284511.peg.3911	Oxidoreductase, short-chain dehydrogenase/reductase family (EC 1.:
fig 6666666.284511.peg.3912	ABC-type Fe ³⁺ -hydroxamate transport system, periplasmic compone

fig 6666666.284511.peg.3913	Formate hydrogenlyase subunit 3/Multisubunit Na ⁺ /H ⁺ antiporter, N
fig 6666666.284511.peg.3914	putative membrane protein
fig 6666666.284511.peg.3915	Thioredoxin
fig 6666666.284511.peg.3916	hypothetical protein
fig 6666666.284511.peg.3917	cytochrome C
fig 6666666.284511.peg.3918	hypothetical protein
fig 6666666.284511.peg.3919	hypothetical protein
fig 6666666.284511.peg.3920	hypothetical protein
fig 6666666.284511.peg.3921	Phenazine biosynthesis protein PhzF like
fig 6666666.284511.peg.3922	DNA topoisomerase III (EC 5.99.1.2)
fig 6666666.284511.peg.3923	hypothetical protein
fig 6666666.284511.peg.3924	hypothetical protein
fig 6666666.284511.peg.3925	hypothetical protein
fig 6666666.284511.peg.3926	Cytochrome c-type biogenesis protein ResA
fig 6666666.284511.peg.3927	Octanoate-[acyl-carrier-protein]-protein-N-octanoyltransferase
fig 6666666.284511.peg.3928	Lipoate synthase
fig 6666666.284511.peg.3929	hypothetical protein
fig 6666666.284511.peg.3930	hypothetical protein
fig 6666666.284511.peg.3931	hypothetical protein
fig 6666666.284511.peg.3932	ISXo7 transposase
fig 6666666.284511.peg.3933	hypothetical protein
fig 6666666.284511.peg.3934	hypothetical protein
fig 6666666.284511.peg.3935	Mobile element protein
fig 6666666.284511.peg.3936	Mobile element protein
fig 6666666.284511.peg.3937	Mobile element protein
fig 6666666.284511.peg.3938	Putative oxidoreductase in 4-hydroxyproline catabolic gene cluster
fig 6666666.284511.peg.3939	Putative oxidoreductase in 4-hydroxyproline catabolic gene cluster
fig 6666666.284511.peg.3940	Hypothetical, similar to sarcosine oxidase alpha subunit, 2Fe-2S dom
fig 6666666.284511.peg.3941	D-amino-acid oxidase (EC 1.4.3.3)
fig 6666666.284511.peg.3942	4-hydroxyproline epimerase (EC 5.1.1.8)
fig 6666666.284511.peg.3943	Amino acid ABC transporter, ATP-binding protein
fig 6666666.284511.peg.3944	polar amino acid ABC transporter, inner membrane subunit
fig 6666666.284511.peg.3945	Amino acid ABC transporter, periplasmic amino acid-binding protein
fig 6666666.284511.peg.3946	1-pyrroline-4-hydroxy-2-carboxylate deaminase (EC 3.5.4.22)
fig 6666666.284511.peg.3947	Ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26)
fig 6666666.284511.peg.3948	L-alanine-DL-glutamate epimerase and related enzymes of enolase s
fig 6666666.284511.peg.3949	Predicted regulator PutR for proline utilization, GntR family
fig 6666666.284511.peg.3950	Ornithine cyclodeaminase (EC 4.3.1.12)
fig 6666666.284511.peg.3951	2-methylaconitate racemase
fig 6666666.284511.peg.3952	Mobile element protein
fig 6666666.284511.peg.3953	Mobile element protein
fig 6666666.284511.peg.3954	hypothetical protein
fig 6666666.284511.peg.3955	Sulfate permease

fig 6666666.284511.peg.3956	hypothetical protein
fig 6666666.284511.peg.3957	1-pyrroline-4-hydroxy-2-carboxylate deaminase (EC 3.5.4.22)
fig 6666666.284511.peg.3958	Branched-chain amino acid ABC transporter, amino acid-binding protein
fig 6666666.284511.peg.3959	High-affinity branched-chain amino acid transport system permease
fig 6666666.284511.peg.3960	Branched-chain amino acid transport system permease protein LivM
fig 6666666.284511.peg.3961	Branched-chain amino acid transport ATP-binding protein LivG (TC 3.5.4.22)
fig 6666666.284511.peg.3962	Branched-chain amino acid transport ATP-binding protein LivF (TC 3.5.4.22)
fig 6666666.284511.peg.3963	4-hydroxyproline epimerase (EC 5.1.1.8)
fig 6666666.284511.peg.3964	D-amino-acid oxidase (EC 1.4.3.3)
fig 6666666.284511.peg.3965	Hypothetical, similar to sarcosine oxidase alpha subunit, 2Fe-2S domain
fig 6666666.284511.peg.3966	Putative oxidoreductase in 4-hydroxyproline catabolic gene cluster
fig 6666666.284511.peg.3967	Mobile element protein
fig 6666666.284511.peg.3968	Ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26) # hydroxy-
fig 6666666.284511.peg.3969	Transcriptional regulator, AraC family
fig 6666666.284511.peg.3970	Outer membrane protein (porin)
fig 6666666.284511.peg.3971	hypothetical protein
fig 6666666.284511.peg.3972	type I restriction-modification system, M subunit, putative
fig 6666666.284511.peg.3973	hypothetical protein
fig 6666666.284511.peg.3974	Mobile element protein
fig 6666666.284511.peg.3975	Mobile element protein
fig 6666666.284511.peg.3976	hypothetical protein
fig 6666666.284511.peg.3977	putative ATPase
fig 6666666.284511.peg.3978	Subtilisin-like serine proteases
fig 6666666.284511.peg.3979	MII9366 protein
fig 6666666.284511.peg.3980	TniB NTP-binding protein
fig 6666666.284511.peg.3981	TniA putative transposase
fig 6666666.284511.peg.3982	FIGfam050825
fig 6666666.284511.peg.3983	hypothetical protein
fig 6666666.284511.peg.3984	hypothetical protein
fig 6666666.284511.peg.3985	hypothetical protein
fig 6666666.284511.peg.3986	hypothetical protein
fig 6666666.284511.peg.3987	hypothetical protein
fig 6666666.284511.peg.3988	Predicted methyltransferase, DUF43 family
fig 6666666.284511.peg.3989	Mobile element protein
fig 6666666.284511.peg.3990	hypothetical protein
fig 6666666.284511.peg.3991	hypothetical protein
fig 6666666.284511.peg.3992	hypothetical protein
fig 6666666.284511.peg.3993	Mobile element protein
fig 6666666.284511.peg.3994	Two-component system regulatory protein
fig 6666666.284511.peg.3995	Two-component system sensor protein
fig 6666666.284511.peg.3996	Heavy metal RND efflux outer membrane protein, CzcC family
fig 6666666.284511.peg.3997	RND-type multidrug efflux pump, membrane permease
fig 6666666.284511.peg.3998	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system p

fig 6666666.284511.peg.3999	hypothetical protein
fig 6666666.284511.peg.4000	Heavy metal sensor histidine kinase
fig 6666666.284511.peg.4001	DNA-binding heavy metal response regulator
fig 6666666.284511.peg.4002	hypothetical protein
fig 6666666.284511.peg.4003	blr6985; hypothetical protein
fig 6666666.284511.peg.4004	hypothetical protein
fig 6666666.284511.peg.4005	hypothetical protein
fig 6666666.284511.peg.4006	Probable low-affinity inorganic phosphate transporter
fig 6666666.284511.peg.4007	transposase, putative
fig 6666666.284511.peg.4008	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
fig 6666666.284511.peg.4009	hypothetical protein
fig 6666666.284511.peg.4010	Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)
fig 6666666.284511.peg.4011	hypothetical protein
fig 6666666.284511.peg.4012	hypothetical protein
fig 6666666.284511.peg.4013	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)
fig 6666666.284511.peg.4014	hypothetical protein
fig 6666666.284511.peg.4015	hypothetical protein
fig 6666666.284511.peg.4016	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (E
fig 6666666.284511.peg.4017	hypothetical protein
fig 6666666.284511.peg.4018	Outer membrane efflux protein
fig 6666666.284511.peg.4019	ABC transporter ATP-binding protein YvcR
fig 6666666.284511.peg.4020	ABC transporter, permease protein
fig 6666666.284511.peg.4021	Probable RND efflux membrane fusion protein
fig 6666666.284511.peg.4022	hypothetical protein
fig 6666666.284511.peg.4023	hypothetical secreted protein
fig 6666666.284511.peg.4024	hypothetical protein
fig 6666666.284511.peg.4025	hypothetical protein
fig 6666666.284511.peg.4026	Manganese transport protein MntH
fig 6666666.284511.peg.4027	hypothetical protein
fig 6666666.284511.peg.4028	MaoC-related protein
fig 6666666.284511.peg.4029	hypothetical protein
fig 6666666.284511.peg.4030	Carboxylate/Amino Acid/Amine Transporter, membrane protein
fig 6666666.284511.peg.4031	Glutathione S-transferase (EC 2.5.1.18)
fig 6666666.284511.peg.4032	Glutathione S-transferase (EC 2.5.1.18)
fig 6666666.284511.peg.4033	Anthranilate synthase, aminase component (EC 4.1.3.27)
fig 6666666.284511.peg.4034	FIG026291: Hypothetical periplasmic protein
fig 6666666.284511.peg.4035	FIG026291: Hypothetical periplasmic protein
fig 6666666.284511.peg.4036	Phosphoglycolate phosphatase (EC 3.1.3.18)
fig 6666666.284511.peg.4037	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)
fig 6666666.284511.peg.4038	ApaG protein
fig 6666666.284511.peg.4039	Site-specific recombinase
fig 6666666.284511.peg.4040	Membrane-bound lytic murein transglycosylase A precursor (EC 3.2.1.17)
fig 6666666.284511.peg.4041	Outer membrane protein, OmpA/MotB family

fig 6666666.284511.peg.4042	hypothetical protein
fig 6666666.284511.peg.4043	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits
fig 6666666.284511.peg.4044	Benzoate transport protein
fig 6666666.284511.peg.4045	Transcriptional regulator yidN, Cro/Ci family
fig 6666666.284511.peg.4046	Helicase PriA essential for oriC/DnaA-independent DNA replication
fig 6666666.284511.peg.4047	Uroporphyrinogen III decarboxylase (EC 4.1.1.37)
fig 6666666.284511.peg.4048	hypothetical protein
fig 6666666.284511.peg.4049	Zinc ABC transporter, periplasmic-binding protein ZnuA
fig 6666666.284511.peg.4050	Zinc ABC transporter, ATP-binding protein ZnuC
fig 6666666.284511.peg.4051	Zinc ABC transporter, inner membrane permease protein ZnuB
fig 6666666.284511.peg.4052	Zinc uptake regulation protein ZUR
fig 6666666.284511.peg.4053	hypothetical protein
fig 6666666.284511.peg.4054	Transcriptional regulator, LysR family
fig 6666666.284511.peg.4055	Malate synthase (EC 2.3.3.9)
fig 6666666.284511.peg.4056	hypothetical protein
fig 6666666.284511.peg.4057	hypothetical protein
fig 6666666.284511.peg.4058	hypothetical protein
fig 6666666.284511.peg.4059	Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) @ Fructose-6-ph
fig 6666666.284511.peg.4060	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.4061	Mercuric ion reductase (EC 1.16.1.1)
fig 6666666.284511.peg.4062	FIG00984050: hypothetical protein
fig 6666666.284511.peg.4063	Phosphoglucomutase (EC 5.4.2.2)
fig 6666666.284511.peg.4064	Transketolase (EC 2.2.1.1)
fig 6666666.284511.peg.4065	5-keto-2-deoxygluconokinase (EC 2.7.1.92) / uncharacterized domain
fig 6666666.284511.peg.4066	Glucose-6-phosphate isomerase (EC 5.3.1.9)
fig 6666666.284511.peg.4067	Transaldolase (EC 2.2.1.2)
fig 6666666.284511.peg.4068	hypothetical protein
fig 6666666.284511.peg.4069	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
fig 6666666.284511.peg.4070	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
fig 6666666.284511.peg.4071	Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
fig 6666666.284511.peg.4072	hypothetical protein
fig 6666666.284511.peg.4073	hypothetical protein
fig 6666666.284511.peg.4074	hypothetical protein
fig 6666666.284511.peg.4075	PUTATIVE ARYLESTERASE PROTEIN
fig 6666666.284511.peg.4076	GTP-binding protein related to HflX
fig 6666666.284511.peg.4077	hypothetical protein
fig 6666666.284511.peg.4078	Mobile element protein
fig 6666666.284511.peg.4079	Transcriptional regulator, TetR family
fig 6666666.284511.peg.4080	hypothetical protein
fig 6666666.284511.peg.4081	Mobile element protein
fig 6666666.284511.peg.4082	hypothetical protein
fig 6666666.284511.peg.4083	FIG01060185: hypothetical protein
fig 6666666.284511.peg.4084	hypothetical protein

fig 6666666.284511.peg.4085	Mobile element protein
fig 6666666.284511.peg.4086	hypothetical protein
fig 6666666.284511.peg.4087	DNA gyrase subunit B (EC 5.99.1.3)
fig 6666666.284511.peg.4088	DNA polymerase III beta subunit (EC 2.7.7.7)
fig 6666666.284511.peg.4089	hypothetical protein
fig 6666666.284511.peg.4090	Chromosomal replication initiator protein DnaA
fig 6666666.284511.peg.4091	hypothetical protein
fig 6666666.284511.peg.4092	LSU ribosomal protein L34p
fig 6666666.284511.peg.4093	hypothetical protein
fig 6666666.284511.peg.4094	Protein YidD
fig 6666666.284511.peg.4095	Inner membrane protein translocase component YidC, long form
fig 6666666.284511.peg.4096	GTPase and tRNA-U34 5-formylation enzyme TrmE
fig 6666666.284511.peg.4097	Twin-arginine translocation protein TatA
fig 6666666.284511.peg.4098	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
fig 6666666.284511.peg.4099	carbon monoxide dehydrogenase G protein
fig 6666666.284511.peg.4100	Glutathione-regulated potassium-efflux system protein KefB
fig 6666666.284511.peg.4101	transcriptional regulator, ArsR family protein
fig 6666666.284511.peg.4102	major facilitator superfamily MFS_1
fig 6666666.284511.peg.4103	hypothetical protein
fig 6666666.284511.peg.4104	Putative PROLIN-rich signal peptide protein
fig 6666666.284511.peg.4105	hypothetical protein
fig 6666666.284511.peg.4106	Alginate regulatory protein AlgP
fig 6666666.284511.peg.4107	hypothetical protein
fig 6666666.284511.peg.4108	FIG00932717: hypothetical protein
fig 6666666.284511.peg.4109	Chromosome (plasmid) partitioning protein ParB
fig 6666666.284511.peg.4110	hypothetical protein
fig 6666666.284511.peg.4111	Chromosome (plasmid) partitioning protein ParA
fig 6666666.284511.peg.4112	rRNA small subunit 7-methylguanosine (m7G) methyltransferase Gid
fig 6666666.284511.peg.4113	tRNA uridine 5-carboxymethylaminomethyl modification enzyme Gic
fig 6666666.284511.peg.4114	hypothetical protein
fig 6666666.284511.peg.4115	Permeases of the major facilitator superfamily
fig 6666666.284511.peg.4116	FIG011065: hypothetical protein
fig 6666666.284511.peg.4117	Multiple antibiotic resistance protein marC
fig 6666666.284511.peg.4118	ATP-dependent protease domain protein (EC 3.4.21.-)
fig 6666666.284511.peg.4119	hypothetical protein
fig 6666666.284511.peg.4120	DNA primase (EC 2.7.7.-)
fig 6666666.284511.peg.4121	Kup system potassium uptake protein
fig 6666666.284511.peg.4122	hypothetical protein
fig 6666666.284511.peg.4123	Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22)
fig 6666666.284511.peg.4124	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family 1
fig 6666666.284511.peg.4125	hypothetical protein
fig 6666666.284511.peg.4126	FIG111991: hypothetical protein
fig 6666666.284511.peg.4127	RNA polymerase sigma factor

fig 6666666.284511.peg.4128	putative exported protein
fig 6666666.284511.peg.4129	hypothetical protein
fig 6666666.284511.peg.4130	FAD/FMN-containing dehydrogenases
fig 6666666.284511.peg.4131	FAD/FMN-containing dehydrogenases
fig 6666666.284511.peg.4132	5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)
fig 6666666.284511.peg.4133	3-dehydroquinate synthase (EC 4.2.3.4)
fig 6666666.284511.peg.4134	transcriptional regulator SoxR
fig 6666666.284511.peg.4135	cAMP-binding proteins - catabolite gene activator and regulatory subunit
fig 6666666.284511.peg.4136	5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)
fig 6666666.284511.peg.4137	RND multidrug efflux transporter; Acriflavin resistance protein
fig 6666666.284511.peg.4138	Probable Co/Zn/Cd efflux system membrane fusion protein
fig 6666666.284511.peg.4139	Outer membrane protein assembly factor YaeT precursor
fig 6666666.284511.peg.4140	Transcriptional regulator, AraC family
fig 6666666.284511.peg.4141	O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) / O-succinylhomoserine sulfhydrylase
fig 6666666.284511.peg.4142	Outer membrane lipoprotein
fig 6666666.284511.peg.4143	Putative cytoplasmic protein
fig 6666666.284511.peg.4144	hypothetical protein
fig 6666666.284511.peg.4145	hypothetical protein
fig 6666666.284511.peg.4146	hypothetical protein
fig 6666666.284511.peg.4147	Nitrogen regulatory protein P-II
fig 6666666.284511.peg.4148	Ammonium transporter
fig 6666666.284511.peg.4149	Glutamate--cysteine ligase (EC 6.3.2.2), divergent, of Alpha- and Beta-classes
fig 6666666.284511.peg.4150	Glutathione synthetase (EC 6.3.2.3)
fig 6666666.284511.peg.4151	hypothetical protein
fig 6666666.284511.peg.4152	hypothetical protein
fig 6666666.284511.peg.4153	Methyltransferase (EC 2.1.1.-)
fig 6666666.284511.peg.4154	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
fig 6666666.284511.peg.4155	Twin-arginine translocation pathway signal
fig 6666666.284511.peg.4156	Cytochrome c551/c552
fig 6666666.284511.peg.4157	hypothetical protein
fig 6666666.284511.peg.4158	Phospholipid-binding protein
fig 6666666.284511.peg.4159	Cobalt-zinc-cadmium resistance protein
fig 6666666.284511.peg.4160	ABC-type anion transport system, duplicated permease component
fig 6666666.284511.peg.4161	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component
fig 6666666.284511.peg.4162	1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157); diglucosyldiacylglycerol transferase
fig 6666666.284511.peg.4163	hypothetical protein
fig 6666666.284511.peg.4164	Molybdenum cofactor biosynthesis protein MoaD
fig 6666666.284511.peg.4165	Nitrite reductase probable [NAD(P)H] subunit (EC 1.7.1.4)
fig 6666666.284511.peg.4166	Tungsten-containing aldehyde:ferredoxin oxidoreductase (EC 1.2.7.5)
fig 6666666.284511.peg.4167	Iron-sulfur cluster-binding protein
fig 6666666.284511.peg.4168	Outer membrane lipoprotein omp16 precursor
fig 6666666.284511.peg.4169	FIG003879: Predicted amidohydrolase
fig 6666666.284511.peg.4170	FIG005080: Possible exported protein

fig 6666666.284511.peg.4171	Glutamate-ammonia-ligase adenylyltransferase (EC 2.7.7.42)
fig 6666666.284511.peg.4172	Transaldolase (EC 2.2.1.2)
fig 6666666.284511.peg.4173	RuBisCO operon transcriptional regulator CbbR
fig 6666666.284511.peg.4174	Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11)
fig 6666666.284511.peg.4175	Phosphoribulokinase (EC 2.7.1.19)
fig 6666666.284511.peg.4176	Transketolase (EC 2.2.1.1)
fig 6666666.284511.peg.4177	Phosphoglycolate phosphatase (EC 3.1.3.18)
fig 6666666.284511.peg.4178	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2
fig 6666666.284511.peg.4179	Phosphoglycerate kinase (EC 2.7.2.3)
fig 6666666.284511.peg.4180	Fructose-bisphosphate aldolase class II (EC 4.1.2.13)
fig 6666666.284511.peg.4181	PPO candidate 1
fig 6666666.284511.peg.4182	Hypothetical protein CbbY
fig 6666666.284511.peg.4183	DNA polymerase III delta subunit (EC 2.7.7.7)
fig 6666666.284511.peg.4184	LPS-assembly lipoprotein RlpB precursor (Rare lipoprotein B)
fig 6666666.284511.peg.4185	Leucyl-tRNA synthetase (EC 6.1.1.4)
fig 6666666.284511.peg.4186	Mobile element protein
fig 6666666.284511.peg.4187	hypothetical protein
fig 6666666.284511.peg.4188	Biopolymer transport protein ExbD/TolR
fig 6666666.284511.peg.4189	MotA/TolQ/ExbB proton channel family protein
fig 6666666.284511.peg.4190	4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)
fig 6666666.284511.peg.4191	Outer membrane lipoprotein SmpA, a component of the essential Ya
fig 6666666.284511.peg.4192	Ferric uptake regulation protein FUR
fig 6666666.284511.peg.4193	HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-)
fig 6666666.284511.peg.4194	PTS system nitrogen-specific IIA component, PtsN
fig 6666666.284511.peg.4195	Ribosome hibernation protein YhbH
fig 6666666.284511.peg.4196	hypothetical protein
fig 6666666.284511.peg.4197	Magnesium and cobalt transport protein CorA
fig 6666666.284511.peg.4198	FIG002994: Putative transcriptional regulator
fig 6666666.284511.peg.4199	Oxidoreductase, short-chain dehydrogenase/reductase family (EC 1.:
fig 6666666.284511.peg.4200	FIG002577: Putative lipoprotein precursor
fig 6666666.284511.peg.4201	FIG097052: Sugar transporter
fig 6666666.284511.peg.4202	FIG026291: Hypothetical periplasmic protein
fig 6666666.284511.peg.4203	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)
fig 6666666.284511.peg.4204	Hypothetical protein COG3496
fig 6666666.284511.peg.4205	COG2907: Amine oxidase, flavin-containing
fig 6666666.284511.peg.4206	GTP cyclohydrolase I (EC 3.5.4.16) type 2
fig 6666666.284511.peg.4207	Glutathione peroxidase family protein
fig 6666666.284511.peg.4208	Transcriptional regulator, MerR family, associated with photolyase
fig 6666666.284511.peg.4209	Chloride channel protein
fig 6666666.284511.peg.4210	ADP-heptose synthase (EC 2.7.-.-) / D-glycero-beta-D-manno-heptos
fig 6666666.284511.peg.4211	RNA polymerase sigma-54 factor RpoN
fig 6666666.284511.peg.4212	Lipopolysaccharide ABC transporter, ATP-binding protein LptB
fig 6666666.284511.peg.4213	Protein yhbN precursor

fig 6666666.284511.peg.4214	Periplasmic thiol:disulfide interchange protein DsbA
fig 6666666.284511.peg.4215	Probable cell division ftsn transmembrane protein
fig 6666666.284511.peg.4216	Arginyl-tRNA synthetase (EC 6.1.1.19)
fig 6666666.284511.peg.4217	Phosphate starvation-inducible protein PsiF
fig 6666666.284511.peg.4218	Rare lipoprotein A precursor
fig 6666666.284511.peg.4219	hypothetical protein
fig 6666666.284511.peg.4220	hypothetical protein
fig 6666666.284511.peg.4221	tRNA-i(6)A37 methylthiotransferase
fig 6666666.284511.peg.4222	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)
fig 6666666.284511.peg.4223	Alpha/beta hydrolase
fig 6666666.284511.peg.4224	Probable transmembrane protein
fig 6666666.284511.peg.4225	Protoporphyrinogen IX oxidase, novel form, HemJ (EC 1.3.-.-)
fig 6666666.284511.peg.4226	Porphobilinogen synthase (EC 4.2.1.24)
fig 6666666.284511.peg.4227	putative exported protein
fig 6666666.284511.peg.4228	ATP synthase protein I
fig 6666666.284511.peg.4229	ATP synthase F0 sector subunit a
fig 6666666.284511.peg.4230	ATP synthase F0 sector subunit c
fig 6666666.284511.peg.4231	ATP synthase F0 sector subunit b
fig 6666666.284511.peg.4232	ATP synthase delta chain (EC 3.6.3.14)
fig 6666666.284511.peg.4233	ATP synthase alpha chain (EC 3.6.3.14)
fig 6666666.284511.peg.4234	ATP synthase gamma chain (EC 3.6.3.14)
fig 6666666.284511.peg.4235	ATP synthase beta chain (EC 3.6.3.14)
fig 6666666.284511.peg.4236	ATP synthase epsilon chain (EC 3.6.3.14)
fig 6666666.284511.peg.4237	hypothetical protein
fig 6666666.284511.peg.4238	hypothetical protein
fig 6666666.284511.peg.4239	ISSoc3, orfA transposase
fig 6666666.284511.peg.4240	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)
fig 6666666.284511.peg.4241	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)
fig 6666666.284511.peg.4242	Enoyl-CoA hydratase (EC 4.2.1.17)
fig 6666666.284511.peg.4243	protease, putative
fig 6666666.284511.peg.4244	diguanylate cyclase/phosphodiesterase
fig 6666666.284511.peg.4245	Molybdenum ABC transporter ATP-binding protein
fig 6666666.284511.peg.4246	Inner membrane protein
fig 6666666.284511.peg.4247	Putative 2-component regulator
fig 6666666.284511.peg.4248	Dienelactone hydrolase family
fig 6666666.284511.peg.4249	Dienelactone hydrolase family
fig 6666666.284511.peg.4250	Ribulosamine/erythrulosamine 3-kinase potentially involved in prote
fig 6666666.284511.peg.4251	Excinuclease ABC subunit A
fig 6666666.284511.peg.4252	hypothetical protein
fig 6666666.284511.peg.4253	hypothetical protein
fig 6666666.284511.peg.4254	Putative transport protein
fig 6666666.284511.peg.4255	Single-stranded DNA-binding protein
fig 6666666.284511.peg.4256	Flp pilus assembly protein TadD, contains TPR repeat

fig 6666666.284511.peg.4257	Type II/IV secretion system protein TadC, associated with Flp pilus as
fig 6666666.284511.peg.4258	Flp pilus assembly protein TadB
fig 6666666.284511.peg.4259	Type II/IV secretion system ATP hydrolase TadA/VirB11/CpaF, TadA s
fig 6666666.284511.peg.4260	Type II/IV secretion system ATPase TadZ/CpaE, associated with Flp p
fig 6666666.284511.peg.4261	Similar to TadZ/CpaE, associated with Flp pilus assembly
fig 6666666.284511.peg.4262	Similar to TadZ/CpaE, associated with Flp pilus assembly
fig 6666666.284511.peg.4263	Von Willebrand factor type A domain protein, associated with Flp pil
fig 6666666.284511.peg.4264	hypothetical protein
fig 6666666.284511.peg.4265	Type II/IV secretion system secretin RcpA/CpaC, associated with Flp p
fig 6666666.284511.peg.4266	Flp pilus assembly protein RcpC/CpaB
fig 6666666.284511.peg.4267	Predicted ATPase with chaperone activity, associated with Flp pilus a
fig 6666666.284511.peg.4268	Type IV prepilin peptidase TadV/CpaA
fig 6666666.284511.peg.4269	hypothetical protein
fig 6666666.284511.peg.4270	hypothetical protein
fig 6666666.284511.peg.4271	Putative two-component system response regulator
fig 6666666.284511.peg.4272	Putative two-component system response regulator
fig 6666666.284511.peg.4273	Sensor histidine kinase (EC 2.7.3.-)
fig 6666666.284511.peg.4274	hypothetical protein
fig 6666666.284511.peg.4275	OsmC family protein
fig 6666666.284511.peg.4276	hypothetical protein
fig 6666666.284511.peg.4277	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)
fig 6666666.284511.peg.4278	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)
fig 6666666.284511.peg.4279	hypothetical protein
fig 6666666.284511.peg.4280	putative sugar transport protein
fig 6666666.284511.peg.4281	hypothetical protein
fig 6666666.284511.peg.4282	Formate dehydrogenase-O, major subunit (EC 1.2.1.2)
fig 6666666.284511.peg.4283	Formate dehydrogenase-O, iron-sulfur subunit (EC 1.2.1.2); Putative
fig 6666666.284511.peg.4284	hypothetical protein
fig 6666666.284511.peg.4285	Formate dehydrogenase -O, gamma subunit (EC 1.2.1.2)
fig 6666666.284511.peg.4286	putative exported protein
fig 6666666.284511.peg.4287	Formate dehydrogenase chain D (EC 1.2.1.2)
fig 6666666.284511.peg.4288	FIG00431662: hypothetical protein
fig 6666666.284511.peg.4289	FIG00433900: hypothetical protein
fig 6666666.284511.peg.4290	Iron-sulfur cluster-binding protein
fig 6666666.284511.peg.4291	Putative formate dehydrogenase-specific chaperone
fig 6666666.284511.peg.4292	C4-dicarboxylate transporter/malic acid transport protein
fig 6666666.284511.peg.4293	Hydrogen peroxide-inducible genes activator
fig 6666666.284511.peg.4294	MFS permease
fig 6666666.284511.peg.4295	tungsten-containing formate dehydrogenase beta subunit
fig 6666666.284511.peg.4296	tungsten-containing formate dehydrogenase alpha subunit
fig 6666666.284511.peg.4297	UPF0028 protein YchK
fig 6666666.284511.peg.4298	DNA-binding domain of ModE
fig 6666666.284511.peg.4299	hypothetical protein

fig 6666666.284511.peg.4300	UPF0100 protein PH0151
fig 6666666.284511.peg.4301	Molybdenum transport system permease protein ModB (TC 3.A.1.8.1)
fig 6666666.284511.peg.4302	Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1)
fig 6666666.284511.peg.4303	8-amino-7-oxononanoate synthase (EC 2.3.1.47)
fig 6666666.284511.peg.4304	hypothetical protein
fig 6666666.284511.peg.4305	Dethiobiotin synthetase (EC 6.3.3.3)
fig 6666666.284511.peg.4306	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.10)
fig 6666666.284511.peg.4307	hypothetical protein
fig 6666666.284511.peg.4308	N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)
fig 6666666.284511.peg.4309	Transglycosylase-associated protein
fig 6666666.284511.peg.4310	Tyrosyl-tRNA synthetase (EC 6.1.1.1)
fig 6666666.284511.peg.4311	hypothetical protein
fig 6666666.284511.peg.4312	Peptidase, M23/M37 family
fig 6666666.284511.peg.4313	Membrane proteins related to metalloendopeptidases
fig 6666666.284511.peg.4314	Anhydro-N-acetylmuramic acid kinase (EC 2.7.1.-)
fig 6666666.284511.peg.4315	probable iron binding protein from the HesB_IscA_SufA family
fig 6666666.284511.peg.4316	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)
fig 6666666.284511.peg.4317	SSU ribosomal protein S9p (S16e)
fig 6666666.284511.peg.4318	LSU ribosomal protein L13p (L13Ae)
fig 6666666.284511.peg.4319	Histone acetyltransferase HPA2 and related acetyltransferases
fig 6666666.284511.peg.4320	hypothetical protein
fig 6666666.284511.peg.4321	PUTATIVE LIPASE TRANSMEMBRANE PROTEIN
fig 6666666.284511.peg.4322	Aldehyde dehydrogenase (EC 1.2.1.3); Probable coniferyl aldehyde d
fig 6666666.284511.peg.4323	Beta-lactamase-like
fig 6666666.284511.peg.4324	hypothetical protein
fig 6666666.284511.peg.4325	Hydrogen peroxide-inducible genes activator
fig 6666666.284511.peg.4326	ATP-dependent DNA helicase RecG (EC 3.6.1.-)
fig 6666666.284511.peg.4327	Leucine-responsive regulatory protein, regulator for leucine (or Irp) r
fig 6666666.284511.peg.4328	Acetoacetate decarboxylase (EC 4.1.1.4)
fig 6666666.284511.peg.4329	hypothetical protein
fig 6666666.284511.peg.4330	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)
fig 6666666.284511.peg.4331	hypothetical protein
fig 6666666.284511.peg.4332	hypothetical protein
fig 6666666.284511.peg.4333	Type I restriction-modification system, DNA-methyltransferase subu
fig 6666666.284511.peg.4334	hypothetical protein
fig 6666666.284511.peg.4335	Type I restriction-modification system, specificity subunit S (EC 3.1.2.1)
fig 6666666.284511.peg.4336	Type I restriction-modification system, restriction subunit R (EC 3.1.2.1)
fig 6666666.284511.peg.4337	hypothetical protein
fig 6666666.284511.peg.4338	hypothetical protein
fig 6666666.284511.peg.4339	hypothetical protein
fig 6666666.284511.peg.4340	hypothetical protein
fig 6666666.284511.peg.4341	hypothetical protein
fig 6666666.284511.peg.4342	Addiction module antidote protein

fig 6666666.284511.peg.4343	hypothetical protein
fig 6666666.284511.peg.4344	FIG00965493: hypothetical protein
fig 6666666.284511.peg.4345	Protein gp47, recombination-related [Bacteriophage A118]
fig 6666666.284511.peg.4346	Mycobacteriophage Barnyard protein gp56
fig 6666666.284511.peg.4347	conserved hypothetical protein
fig 6666666.284511.peg.4348	hypothetical protein
fig 6666666.284511.peg.4349	hypothetical protein
fig 6666666.284511.peg.4350	hypothetical protein
fig 6666666.284511.peg.4351	Hyphothetical protein
fig 6666666.284511.peg.4352	hypothetical protein
fig 6666666.284511.peg.4353	hypothetical protein
fig 6666666.284511.peg.4354	hypothetical protein
fig 6666666.284511.peg.4355	hypothetical protein
fig 6666666.284511.peg.4356	hypothetical protein
fig 6666666.284511.peg.4357	Probable transmembrane protein
fig 6666666.284511.peg.4358	hypothetical protein
fig 6666666.284511.peg.4359	TnpR protein
fig 6666666.284511.peg.4360	hypothetical protein
fig 6666666.284511.peg.4361	Chromosome (plasmid) partitioning protein ParA / Sporulation initial
fig 6666666.284511.peg.4362	hypothetical protein
fig 6666666.284511.peg.4363	Integrase
fig 6666666.284511.peg.4364	Mobile element protein
fig 6666666.284511.peg.4365	Mobile element protein
fig 6666666.284511.peg.4366	Mobile element protein
fig 6666666.284511.peg.4367	Mobile element protein
fig 6666666.284511.peg.4368	Mobile element protein
fig 6666666.284511.peg.4369	hypothetical protein
fig 6666666.284511.peg.4370	Alkyl hydroperoxide reductase subunit C-like protein
fig 6666666.284511.peg.4371	hypothetical protein
fig 6666666.284511.peg.4372	Mobile element protein
fig 6666666.284511.peg.4373	Mobile element protein
fig 6666666.284511.peg.4374	Gamma-glutamyltranspeptidase (EC 2.3.2.2)
fig 6666666.284511.peg.4375	hypothetical protein
fig 6666666.284511.peg.4376	Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2)
fig 6666666.284511.peg.4377	Oxidoreductase probably involved in sulfite reduction
fig 6666666.284511.peg.4378	Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8) / Adeny
fig 6666666.284511.peg.4379	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)
fig 6666666.284511.peg.4380	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)
fig 6666666.284511.peg.4381	Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)
fig 6666666.284511.peg.4382	Thioredoxin reductase (EC 1.8.1.9)
fig 6666666.284511.peg.4383	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.4384	L-lactate dehydrogenase (EC 1.1.2.3)
fig 6666666.284511.peg.4385	L-lactate permease

fig 6666666.284511.peg.4386	Lactate-responsive regulator LldR in Enterobacteria, GntR family
fig 6666666.284511.peg.4387	Transcriptional regulator, MarR family
fig 6666666.284511.peg.4388	Transcriptional regulator, AsnC family
fig 6666666.284511.peg.4389	D-amino acid dehydrogenase small subunit (EC 1.4.99.1)
fig 6666666.284511.peg.4390	Large protein containing transglutaminase-like domain
fig 6666666.284511.peg.4391	Protein containing domains DUF404, DUF407
fig 6666666.284511.peg.4392	Protein containing domains DUF403
fig 6666666.284511.peg.4393	hypothetical protein
fig 6666666.284511.peg.4394	Cyanate hydratase (EC 4.2.1.104)
fig 6666666.284511.peg.4395	Sirohydrochlorin cobaltochelataase (EC 4.99.1.3)
fig 6666666.284511.peg.4396	Urease accessory protein UreG
fig 6666666.284511.peg.4397	Urease accessory protein UreF
fig 6666666.284511.peg.4398	Urease accessory protein UreE
fig 6666666.284511.peg.4399	Urease alpha subunit (EC 3.5.1.5)
fig 6666666.284511.peg.4400	Urease beta subunit (EC 3.5.1.5)
fig 6666666.284511.peg.4401	Urease gamma subunit (EC 3.5.1.5)
fig 6666666.284511.peg.4402	Urea ABC transporter, urea binding protein
fig 6666666.284511.peg.4403	Urea ABC transporter, permease protein UrtB
fig 6666666.284511.peg.4404	Urea ABC transporter, permease protein UrtC
fig 6666666.284511.peg.4405	Urea ABC transporter, ATPase protein UrtD
fig 6666666.284511.peg.4406	Urea ABC transporter, ATPase protein UrtE
fig 6666666.284511.peg.4407	Urease accessory protein UreD
fig 6666666.284511.peg.4408	Antibiotic biosynthesis monooxygenase
fig 6666666.284511.peg.4409	Haloacetate dehalogenase H-1 (EC 3.8.1.3)
fig 6666666.284511.peg.4410	hypothetical protein
fig 6666666.284511.peg.4411	Methylglutaconyl-CoA hydratase (EC 4.2.1.18)
fig 6666666.284511.peg.4412	Benzoyl-CoA oxygenase component A
fig 6666666.284511.peg.4413	Benzoyl-CoA oxygenase component B
fig 6666666.284511.peg.4414	Benzoyl-CoA-dihydrodiol lyase (EC 4.1.2.44)
fig 6666666.284511.peg.4415	Regulatory protein of benzoate catabolism
fig 6666666.284511.peg.4416	P-hydroxylaminobenzoate lyase
fig 6666666.284511.peg.4417	Benzoate-CoA ligase (EC 6.2.1.25)
fig 6666666.284511.peg.4418	benzoate degradation ring-cleavage hydrolase
fig 6666666.284511.peg.4419	Alpha/beta hydrolase fold (EC 3.8.1.5)
fig 6666666.284511.peg.4420	hypothetical protein
fig 6666666.284511.peg.4421	Urea carboxylase-related ABC transporter, periplasmic substrate-bin
fig 6666666.284511.peg.4422	Urea carboxylase-related ABC transporter, permease protein
fig 6666666.284511.peg.4423	Urea carboxylase-related ABC transporter, ATPase protein
fig 6666666.284511.peg.4424	Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10)
fig 6666666.284511.peg.4425	Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10)
fig 6666666.284511.peg.4426	Urea carboxylase (EC 6.3.4.6)
fig 6666666.284511.peg.4427	Allophanate hydrolase (EC 3.5.1.54)
fig 6666666.284511.peg.4428	hypothetical protein

fig 6666666.284511.peg.4429	N-acyl homoserine lactone hydrolase
fig 6666666.284511.peg.4430	Isochorismatase (EC 3.3.2.1)
fig 6666666.284511.peg.4431	Creatinine amidohydrolase (EC 3.5.2.10)
fig 6666666.284511.peg.4432	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
fig 6666666.284511.peg.4433	Dehydrogenases with different specificities (related to short-chain al
fig 6666666.284511.peg.4434	Fatty acid desaturase
fig 6666666.284511.peg.4435	Urea carboxylase-related ABC transporter, periplasmic substrate-bin
fig 6666666.284511.peg.4436	hypothetical protein
fig 6666666.284511.peg.4437	probable dioxygenase
fig 6666666.284511.peg.4438	putative phage integrase
fig 6666666.284511.peg.4439	HigB toxin protein
fig 6666666.284511.peg.4440	HigA protein (antitoxin to HigB)
fig 6666666.284511.peg.4441	MloA
fig 6666666.284511.peg.4442	hypothetical protein
fig 6666666.284511.peg.4443	hypothetical protein
fig 6666666.284511.peg.4444	hypothetical protein
fig 6666666.284511.peg.4445	hypothetical protein
fig 6666666.284511.peg.4446	hypothetical protein
fig 6666666.284511.peg.4447	hypothetical protein
fig 6666666.284511.peg.4448	hypothetical protein
fig 6666666.284511.peg.4449	KfrA protein
fig 6666666.284511.peg.4450	Mobile element protein
fig 6666666.284511.peg.4451	Mobile element protein
fig 6666666.284511.peg.4452	putative DNA-invertase
fig 6666666.284511.peg.4453	Prevent host death protein, Phd antitoxin
fig 6666666.284511.peg.4454	Death on curing protein, Doc toxin
fig 6666666.284511.peg.4455	hypothetical protein
fig 6666666.284511.peg.4456	hypothetical protein
fig 6666666.284511.peg.4457	Phage DNA-binding protein
fig 6666666.284511.peg.4458	YPPCP.09C homologue
fig 6666666.284511.peg.4459	hypothetical protein
fig 6666666.284511.peg.4460	Chromosome (plasmid) partitioning protein ParA
fig 6666666.284511.peg.4461	hypothetical protein
fig 6666666.284511.peg.4462	hypothetical protein
fig 6666666.284511.peg.4463	hypothetical protein
fig 6666666.284511.peg.4464	DNA cytosine methyltransferase M.NgoMIII
fig 6666666.284511.peg.4465	hypothetical protein
fig 6666666.284511.peg.4466	Site-specific recombinase XerC
fig 6666666.284511.peg.4467	hypothetical protein
fig 6666666.284511.peg.4468	hypothetical protein
fig 6666666.284511.peg.4469	hypothetical protein
fig 6666666.284511.peg.4470	hypothetical protein
fig 6666666.284511.peg.4471	hypothetical protein

fig 6666666.284511.peg.4472	KfrA protein
fig 6666666.284511.peg.4473	Mobile element protein
fig 6666666.284511.peg.4474	putative DNA-invertase
fig 6666666.284511.peg.4475	Prevent host death protein, Phd antitoxin
fig 6666666.284511.peg.4476	Death on curing protein, Doc toxin

bolism based on gene clustering with hemC, hemD in Proteobacteria (unrelated to HemY-type PI

ase (EC 2.5.1.1) / Geranyltranstransferase (farnesyldiphosphate synthase) (EC 2.5.1.10) / Geranyl

-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl

C 6.3.5.3) / Phosphoribosylformylglycinamidine synthase, glutamine amidotransferase subunit (E

led cytochrome biogenesis cycZ-like domain, possible membrane copper tolerance protein

57) @ Aromatic-amino-acid aminotransferase (EC 2.6.1.57) @ Aspartate aminotransferase (EC 2.6.1.1)

3-hydroxyacyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.36)

glycan-associated lipoprotein precursor; Outer membrane protein P6; OmpA/MotB precursor

6) / Hydroxypyruvate reductase (EC 1.1.1.81); 2-ketoaldonate reductase, broad specificity (EC 1.1

ine acyltransferase (EC 2.3.1.40) / Acyl-[acyl-carrier-protein] synthetase (EC 6.2.1.20)

geranyl pyrophosphate synthetase (EC 2.5.1.29)