

ERGO Orf Nr.	Ratio der Mediane Voll- zu Minimalmedium (635/532)	Annotation
0003	0,343	Anthranilate synthase, component I
0004	0,353	Anthranilate synthase, component II
0005	0,174	Conserved protein
0006	0,500	Metal-dependent hydrolase
0007	0,538	Ribonuclease
0008	0,411	Hypothetical protein
0009	0,518	Phenylalanyl-tRNA synthetase, beta chain
0012	0,522	Metal-dependent hydrolases
0013	0,564	Conserved protein
0014	0,642	AAA family ATPase
0016	0,565	Glucose-1-phosphate thymidyltransferase
0017	0,542	Phosphoglucomutase/phosphomannomutase
0018	0,509	Glucosamine-fructose-6-phosphate aminotransferase
0019	0,489	Glucose-1-phosphate thymidyltransferase
0020	0,532	Glycine betaine-binding protein
0021	0,450	Glycine betaine transporter, ATP-binding protein
0022	0,400	Glycine betaine transport system, permease protein
0023	0,479	Glycine betaine transport system, permease protein
0033	0,431	Conserved protein
0034	0,435	Amidohydrolase (putative)
0035	0,477	Leucyl-tRNA synthetase
0036	0,434	Threonine synthase
0040	0,459	DNA-cytosine methyltransferase
0041	0,652	T/G-specific DNA glycosylase
0042	0,734	Superfamily II DNA and RNA helicase
0043	0,665	Hypothetical protein
0045	0,681	Hypothetical protein
0046	0,597	Hypothetical protein
0047	0,595	Conserved protein
0048	0,542	Conserved protein
0050	0,372	Conserved protein
0051	0,370	Conserved protein
0052	0,364	Conserved protein

0058	0,372	Dihydroxy-acid dehydratase
0062	0,458	N5-Methyl-H4MPT:coenzyme M methyltransferase, subunit A homolog
0073	0,375	Delta-aminolevulinic acid dehydratase
0074	0,405	Glutamate-1-semialdehyde 2,1-aminomutase
0075	0,346	Porphobilinogen deaminase
0076	0,306	Dihydroorotate dehydrogenase
0077	0,313	Dihydroorotate dehydrogenase electron transfer subunit
0078	0,465	2-Hydroxy-2,4-diene-1,7-dioate isomerase
0079	0,420	Conserved protein
0080	0,401	Glutamyl-tRNA synthetase
0081	0,426	Conserved protein
0085	0,488	D-3-phosphoglycerate dehydrogenase
0086	0,499	Conserved protein
0087	0,504	LSU ribosomal protein L18E
0088	0,456	LSU ribosomal protein L13P
0089	0,439	SSU ribosomal protein S9P
0091	0,336	DNA-directed RNA polymerase subunit K
0092	0,366	SSU ribosomal protein S2P
0093	0,567	Conserved protein
0094	0,332	Mevalonate kinase
0095	0,485	PHOSPHOMEVALONATE KINASE
0097	0,391	Zn-dependent hydrolase
0098	0,572	Geranyltransferase
0099	0,522	Hypothetical protein
0102	0,302	Conserved protein
0103	0,254	Hypothetical protein
0104	0,250	METHYLTRANSFERASE
0111	0,462	Sodium/glutamate symport carrier protein
0125	0,298	10 kDa chaperonin, GroES
0126	0,450	60 kDa chaperonin, GroEL
0126	0,302	60 kDa chaperonin, GroEL
0127	0,324	Conserved protein
0128	0,346	Transporter
0129	0,485	Conserved protein
0130	0,441	Aspartate aminotransferase
0132	0,526	Rubryerythrin

0136	0,509	Translation Initiation Factor 2 subunit alpha IF-2a
0137	0,465	SSU ribosomal protein S27E
0139	0,463	Conserved protein
0140	0,544	DNA primase small subunit
0141	0,585	Conserved protein
0146	1,642	Conserved protein
0148	0,599	Conserved protein
0151	0,704	Replication factor C subunit
0153	0,357	Ferredoxin
0154	0,390	DNA binding protein
0157	0,494	Pyruvate carboxylase, ATP-binding subunit PycA
0158	0,639	Biotin--[Acetyl-CoA-carboxylase] synthase/biotin operon repressor
0159	0,519	Conserved protein
0160	0,504	Transposase
0161	0,685	Phosphoserine phosphatase
0172	0,569	Conserved protein
0174	1,047	Hypothetical protein
0175	1,213	Geranylgeranyl reductase
0177	0,524	Conserved protein
0180	0,820	Dipeptide/oligopeptide ABC transporter, ATP-binding protein
0181	0,587	Dipeptide/ oligopeptide ABC transporter, ATP-binding protein
0186	0,446	Conserved protein
0187	0,364	Transporter
0188	0,302	Transcriptional regulator, MarR family
0193	0,595	Conserved protein
0200	2,649	Conserved protein
0201	0,530	Purine phosphoribosyltransferase
0204	0,509	Putative RNA-binding protein
0205	0,837	DNA-directed RNA polymerase subunit L
0206	0,659	Conserved protein
0208	0,493	Conserved protein
0211	0,506	Hypothetical protein
0212	0,471	Transposase
0213	0,366	Conserved protein
0214	0,504	Conserved protein
0220	0,517	Molybdenum formylmethanofuran dehydrogenase subunit FmdC/D-Fusion (EC 1.2.99.5)

0221	0,600	Molybdenum formylmethanofuran dehydrogenase subunit FmdB (EC 1.2.99.5)
0221	0,413	Molybdenum formylmethanofuran dehydrogenase subunit FmdB (EC 1.2.99.5)
0222	0,606	Conserved protein
0223	0,716	Conserved protein
0224	0,641	Conserved protein
0226	0,875	Conserved protein
0227	0,513	Conserved protein
0228	0,329	Conserved protein
0229	0,606	MOLYBDENUM TRANSPORT SYSTEM PROTEIN MODD HOMOLOG
0230	0,415	Molybdate ABC transporter, ATP-binding protein
0231	0,608	Molybdate ABC transporter, permease protein
0232	0,582	Molybdate-binding protein
0234	0,493	IRON-SULFUR FLAVOPROTEIN
0235	0,268	NADPH-flavin oxidoreductase
0236	0,384	IRON-SULFUR FLAVOPROTEIN
0238	0,416	DNA REPAIR HELICASE
0239	0,375	SURFACE LAYER PROTEIN B
0241	0,474	Conserved protein
0242	0,748	Conserved protein
0243	0,501	Conserved protein
0246	0,265	Conserved protein
0247	0,337	Conserved protein
0248	0,224	Integral membrane protein
0249	0,474	Conserved protein
0250	0,680	Integral membrane protein
0251	0,340	Hypothetical protein
0252	0,302	Cobalamin biosynthesis protein
0254	0,397	Conserved protein
0255	0,546	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENASE, SUBUNIT E
0256	0,545	Conserved protein
0257	0,475	Archaeal protein Translation Initiation Factor 2B subunit 2aIF-2B2
0258	0,679	Acetyltransferase
0259	0,445	ABC transporter, ATP-binding protein
0260	0,275	ABC transporter, permease protein
0261	0,408	HYPOTHETICAL BINDING PROTEIN OF ABC TRANSPORTER
0262	0,370	Uridylate kinase

0263	0,410	Conserved protein
0265	0,525	Transcriptional regulator, TetR family
0266	1,721	OXIDOREDUCTASE, ALDO/KETO REDUCTASE FAMILY
0267	0,566	Phosphoribosylaminoimidazole carboxylase
0269	0,306	Aspartate-semialdehyde dehydrogenase
0270	0,386	Ferredoxin
0273	0,613	Conserved protein
0275	0,825	Conserved protein
0276	0,470	Conserved protein
0277	0,532	Fructose-bisphosphate aldolase
0278	0,754	Deoxycytidine triphosphate deaminase
0279	0,472	Conserved protein
0280	0,981	Conserved protein
0282	0,790	IRON-SULFUR FLAVOPROTEIN
0283	0,503	ABC transporter, ATP-binding protein
0283	0,477	ABC transporter, ATP-binding protein
0284	0,664	Transcriptional regulator
0284	0,601	Transcriptional regulator
0285	0,499	Beta-phosphoglucomutase / Glucose-1-phosphate phosphodismutase
0288	0,270	Putative acetyltransferase
0289	0,558	Putative polysaccharide deacetylase
0290	0,445	GLYCOSYL TRANSFERASE
0291	0,491	OLIGOSACCHARIDE REPEAT UNIT TRANSPORTER
0292	0,526	METHYLTRANSFERASE
0293	0,362	Hypothetical protein
0294	0,590	Methanol:corrinoic methyltransferase MtaB
0295	0,414	Methanol corrinoic protein MtaC
0296	0,474	Conserved protein
0297	0,385	Conserved protein
0299	0,430	Ferredoxin
0300	0,428	Conserved protein
0302	0,687	Conserved protein
0303	0,902	OXIDOREDUCTASE
0304	2,148	POSSIBLE SERINE\THREONINE PROTEIN PHOSPHATASE
0306	0,552	MG2+ TRANSPORTER MGTE
0307	0,611	TYPE I RESTRICTION-MODIFICATION SYSTEM RESTRICTION SUBUNIT

0309	0,640	Conserved protein
0311	0,557	Conserved protein
0315	0,972	ATP-dependent DNA helicase RecG
0316	0,356	TYPE I RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT
0318	0,633	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
0319	0,575	Methyltransferase
0322	0,673	Conserved protein
0324	0,312	Conserved protein
0326	0,461	Pecorin-6Y C5,15-methyltransferase [decarboxylating]
0327	0,379	CbiD protein
0328	0,326	DNA mismatch repair protein
0329	0,693	DNA mismatch repair protein
0330	0,459	O-acetyl transferase
0331	0,604	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
0332	0,660	Iron-sulfur binding protein
0333	0,614	Dimethyl corrinoid protein MtbC
0334	0,535	Trimethylamine:corrinoid methyltransferase MttB
0335	0,812	Trimethylamine:corrinoid methyltransferase MttB (C-terminal domain)
0338	0,636	Conserved protein
0340	0,309	Dimethylamine:Corrinoid Methyltransferase MtbB
0341	1,266	Dimethylamine:corrinoid methyltransferase MtbB (C-terminal domain)
0343	1,163	Lysyl-tRNA synthetase, class I
0343	0,464	Lysyl-tRNA synthetase, class I
0344	0,286	Conserved protein
0345	0,949	Conserved protein
0346	0,389	Protease
0347	0,529	Putative nucleoside-diphosphate-sugar epimerase
0348	0,520	Conserved protein
0349	0,496	Conserved protein
0350	0,741	Histidine biosynthesis protein
0351	0,634	Conserved protein
0352	0,594	Protein-L-isoaspartate O-methyltransferase
0353	0,545	Conserved protein
0354	0,354	Conserved protein
0355	0,615	Conserved protein
0356	0,537	3,4 dihydroxy-2-butanone 4-phosphate synthase

0357	0,370	Cobalt-zinc-cadmium resistance protein
0357	0,344	Cobalt-zinc-cadmium resistance protein
0358	0,409	Chorismate synthase
0359	1,063	Conserved protein
0360	0,679	Conserved protein
0361	0,473	Transcriptional regulator, ArsR family
0363	0,622	Conserved protein
0367	0,703	Conserved protein
0368	0,271	Heme biosynthesis protein
0369	0,560	Heme biosynthesis protein
0378	0,460	Dienelactone hydrolase
0380	0,428	Conserved protein
0381	0,366	Superoxide dismutase
0383	0,472	HYPOTHETICAL PROTEIN
0386	0,545	DNA gyrase, subunit B
0387	0,360	Type II DNA topoisomerase VI, subunit A
0388	0,627	Type II DNA topoisomerase VI, subunit B
0389	0,367	TRANSCRIPTIONAL REGULATORY PROTEIN, ASNC FAMILY
0390	0,597	Hypothetical protein
0392	0,513	Conserved protein
0393	0,641	Conserved protein
0394	0,462	Conserved protein
0395	1,184	Conserved protein
0397	0,479	Cation transporter
0399	0,823	Potassium channel protein
0400	0,537	Hypothetical protein
0401	0,242	Conserved protein
0402	0,591	Hypothetical protein
0403	0,363	Peptide methionine sulfoxide reductase
0404	0,600	ABC transporter, ATP-binding protein
0405	0,533	Heme exporter, protein B
0406	0,740	Heme exporter, protein C
0407	0,399	NADH:flavin oxidoreductases
0408	0,426	Transcriptional regulator, MerR family
0409	0,436	Conserved protein
0410	1,016	Long-chain-fatty-acid--CoA ligase

0410	0,581	Long-chain-fatty-acid--CoA ligase
0412	0,461	Conserved protein
0413	1,067	Cobalt transport protein
0415	1,081	Hypothetical protein
0417	0,461	Conserved protein
0418	0,459	Small nuclear riboprotein (snRNA) homolog
0419	0,373	Conserved protein
0420	0,439	ATP-dependent DNA helicase
0421	0,610	5'-methylthioadenosine phosphorylase
0422	0,532	Conserved transmembrane protein
0423	0,687	Hypothetical protein
0424	0,389	Conserved protein
0425	0,481	Conserved protein
0426	0,430	Conserved protein
0427	0,578	3-isopropylmalate dehydratase
0428	0,449	Phosphoribosyl-ATP pyrophosphatase
0429	0,805	Conserved protein
0430	0,613	GTP-binding protein
0431	0,842	Cytochrome c-type biogenesis protein
0432	0,506	Aspartate aminotransferase
0433	0,654	HEXULOSE-6-PHOSPHATE ISOMERASE
0434	0,479	Conserved protein
0435	0,549	Conserved protein
0436	0,427	GTP-binding protein
0437	0,886	Conserved protein
0438	0,467	Shikimate kinase
0439	0,551	Chorismate mutase / prephenate dehydratase (EC 4.2.1.51)
0440	0,693	Phosphoribosylaminoimidazole carboxylase, catalytic subunit
0441	0,747	Conserved protein
0442	1,025	6-phosphofructokinase (ADP)
0443	0,528	Hypothetical protein
0444	0,454	Conserved protein
0445	0,693	Diphthine synthase
0446	0,365	Thioredoxin
0447	0,603	Thioredoxin reductase
0448	0,744	Conserved protein

0449	0,424	Transcriptional regulator
0450	0,661	O-linked N-acetylglucosamine transferase
0451	0,682	Putative phosphatase
0452	0,931	O-linked N-acetylglucosamine transferase
0453	1,208	Ribosomal protein S6 modification protein
0454	0,995	METHYLTRANSFERASE
0457	0,513	Hypothetical protein
0458	0,649	Oligosaccharyl transferase
0459	0,840	Conserved protein
0460	0,495	Putative sugar kinase
0461	0,500	Conserved protein
0462	0,450	Molybdenum cofactor biosynthesis protein C
0463	0,772	Ribose-phosphate pyrophosphokinase
0464	0,634	Hypothetical protein
0465	0,610	Hypothetical protein
0466	0,503	Hypothetical protein
0467	0,545	Hypothetical protein
0468	0,590	TYPE I RESTRICTION-MODIFICATION SYSTEM SPECIFICITY SUBUNIT
0469	0,551	TYPE I RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT
0470	0,638	Conserved protein
0471	0,713	Conserved protein
0472	0,580	F420-DEPENDENT GLUCOSE-6-PHOSPHATE DEHYDROGENASE
0473	0,517	DNA repair protein RAD50
0474	0,413	DNA REPAIR PROTEIN (MRE11/RAD32 family)
0476	0,685	Hypothetical protein
0477	0,853	Rubrythrin
0478	0,637	Conserved protein
0479	0,494	Conserved protein
0480	0,491	Conserved protein
0481	0,465	Hypothetical protein
0482	0,708	TATA-box binding protein
0482	0,506	TATA-box binding protein
0483	0,626	Hypothetical protein
0484	0,476	Fructose-1,6-bisphosphatase
0484	0,367	Fructose-1,6-bisphosphatase
0485	0,537	GMP synthase [glutamine-hydrolyzing]

0486	0,342	Conserved protein
0487	0,648	Two component system histidine kinase
0488	0,334	F420-NONREDUCING HYDROGENASE III, SUBUNIT CYTOCHROME B
0489	0,241	F420-NONREDUCING HYDROGENASE III, LARGE SUBUNIT
0490	0,570	F420-NONREDUCING HYDROGENASE III PRECURSOR, SMALL SUBUNIT
0491	0,636	Conserved protein
0492	0,467	Conserved protein
0493	0,411	HYDROGENASE EXPRESSION/FORMATION PROTEIN
0494	0,403	F420-NONREDUCING HYDROGENASE II, SUBUNIT CYTOCHROME B
0494	0,295	F420-NONREDUCING HYDROGENASE II, SUBUNIT CYTOCHROME B
0499	0,812	Hydrogenase expression/formation protein
0500	0,498	Hypothetical protein
0500	0,315	Hypothetical protein
0502	0,469	Hypothetical protein
0504	0,394	SSU ribosomal protein S11P
0505	0,356	SSU ribosomal protein S4P
0506	0,325	SSU ribosomal protein S13P
0509	0,188	Hypothetical protein
0511	0,509	Conserved protein
0512	0,656	Phosphoribosylaminoimidazole carboxylase
0513	0,511	Adenylate kinase
0514	0,274	PROTEIN TRANSLOCASE SUBUNIT SECY
0516	0,193	LSU ribosomal protein L30P
0517	0,561	SSU ribosomal protein S5P
0518	0,437	LSU ribosomal protein L18P
0520	0,174	LSU ribosomal protein L32E
0521	0,351	LSU ribosomal protein L6P
0522	0,244	SSU ribosomal protein S8P
0523	0,614	SSU ribosomal protein S14P
0524	0,368	LSU ribosomal protein L5P
0526	0,166	LSU ribosomal protein L14P
0527	0,322	SSU ribosomal protein S17P
0528	0,255	RNaseP subunitP29
0529	0,227	LSU ribosomal protein L29P
0530	0,329	SSU ribosomal protein S3P
0531	0,150	LSU ribosomal protein L22P

0532	0,196	SSU ribosomal protein S19P
0533	0,518	LSU ribosomal protein L2P
0534	0,504	LSU ribosomal protein L23P
0536	0,512	LSU ribosomal protein L3P
0537	0,607	Hypothetical protein
0538	0,382	PUTATIVE SERINE/THREONINE PROTEIN KINASE
0539	0,219	Hypothetical protein
0540	0,221	Hypothetical protein
0541	0,218	Hypothetical protein
0545	0,232	Hypothetical protein
0546	0,666	Hypothetical protein
0547	0,651	Hypothetical protein
0548	0,521	GALACTOSIDE-O-ACETYLTRANSFERASE
0549	0,432	Conserved protein
0550	0,481	Glycosyl transferase
0551	0,448	Glycosyl transferase
0552	0,352	Putative glycosyl transferase
0553	0,170	Putative glycosyl transferase
0554	0,139	Putative Methyltransferase
0555	0,103	Glycosyl Transferase
0557	0,327	Conserved protein
0558	0,420	Conserved protein
0559	0,505	Hypothetical protein
0561	0,664	Hypothetical protein
0562	0,627	Indolepyruvate oxidoreductase, subunit
0563	0,507	Indolepyruvate oxidoreductase, subunit
0564	0,541	CODH nickel-insertion accessory protein (iron-sulfur protein)
0565	0,285	probable transport channel protein
0566	0,282	HTH DNA-binding protein
0567	0,246	CO DEHYDROGENASE/ACETYL-COA SYNTHASE ALPHA SUBUNIT
0568	0,321	CO DEHYDROGENASE/ACETYL-COA SYNTHASE EPSILON SUBUNIT
0573	0,492	Orotidine 5'-phosphate decarboxylase
0574	0,605	DEOXYHYPUSINE SYNTHASE
0575	0,487	ABC transporter, ATP-binding protein
0576	0,428	Galactoside O-acetyltransferase
0577	0,557	Thioredoxin

0578	0,678	Conserved protein
0580	0,890	S-adenosylmethionine synthetase
0581	0,678	4-hydroxybenzoate octaprenyltransferase
0582	0,608	Conserved protein
0586	0,570	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE CARBOXYLATING
0588	0,831	Iron(III) dicitrate transport system permease protein
0589	0,878	Iron(III) dicitrate transport ATP-binding protein
0590	0,929	SSU ribosomal protein S15P
0591	0,871	Conserved protein
0592	1,082	Conserved protein
0593	0,745	Conserved protein
0594	0,615	Conserved protein
0595	0,746	Histidyl-tRNA synthetase
0596	0,754	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE
0597	0,749	CbiB protein
0598	0,691	Hypothetical protein
0599	0,591	Cobalamin [5'-phosphate] synthase
0600	0,638	PUTATIVE NUCLEOTIDYLTRANSFERASE
0601	0,710	ABC transporter, ATP-binding protein
0602	0,797	ABC transporter, ATP-binding protein
0603	0,759	Conserved protein
0604	0,621	Dimethylamine corrinoid protein MtbC
0605	0,564	Dimethylamine:corrinoid methyltransferase MtbB
0607	0,654	Trimethylamine:corrinoid methyltransferase MttB
0608	0,638	Trimethylamine:corrinoid methyltransferase MttB (C-terminal domain)
0609	1,278	Trimethylamine corrinoid protein MttC
0611	0,758	Conserved protein
0613	0,519	Conserved protein
0614	0,711	Hypothetical protein
0615	0,709	Archaeal transcriptional regulator
0617	0,553	TRANSCRIPTIONAL REGULATORY PROTEIN, ASNC FAMILY
0618	0,846	SSU ribosomal protein S8E
0619	0,498	Conserved protein
0620	0,665	Conserved protein
0621	0,694	Conserved protein
0622	0,648	Orotate phosphoribosyltransferase

0623	0,571	Conserved protein
0624	0,518	STOMATIN LIKE-PROTEIN
0627	3,274	Amidotransferase hisH
0630	0,509	Hypothetical protein
0631	0,578	Conserved protein
0632	0,568	Conserved protein
0633	0,528	TRANSPORTER, LysE family
0634	0,522	Conserved protein
0636	0,528	Phosphoribosyl-AMP cyclohydrolase
0637	0,432	Conserved protein
0638	0,490	Conserved protein
0642	1,931	Hypothetical protein
0643	1,553	Hypothetical protein
0644	0,746	Hypothetical protein
0646	0,857	Hypothetical protein
0649	0,584	Sec-independent protein translocase, protein
0650	0,632	Sec-independent protein translocase, protein
0651	0,541	Sec-independent protein translocase protein tata
0652	0,549	Sec-independent protein translocase, protein
0653	0,623	Hypothetical protein
0654	0,526	Pyruvate formate-lyase activating enzyme related protein
0656	9,457	Ferrous iron transport protein A 1
0657	25,995	Ferrous iron transport protein A 2
0658	2,075	Ferrous iron transport protein B
0659	0,725	Hypothetical protein
0660	0,428	Iron dependent transcriptional repressor
0661	0,483	METHYLTRANSFERASE
0662	0,473	ABC transporter, ATP-binding protein
0663	0,569	ABC transporter, ATP-binding protein
0665	0,446	ABC transporter, permease protein
0670	0,909	Hypothetical protein
0671	0,886	Ferredoxin
0673	0,719	Conserved hypothetical protein
0674	0,650	Hypothetical protein
0676	0,620	Hypothetical protein
0677	0,402	Catalase

0678	0,551	ATP-dependent RNA helicase
0679	0,639	Hypothetical protein
0680	0,431	Acetyltransferase
0682	0,621	Hypothetical protein
0683	0,517	Acetyltransferase
0685	0,662	Conserved hypothetical protein
0688	0,638	Conserved hypothetical protein
0689	0,666	Hypothetical protein
0690	0,515	PHOSPHOHYDROLASE (MUTT/NUDIX family protein)
0692	0,825	Conserved hypothetical protein
0693	0,644	Dimethyladenosine transferase
0694	0,651	Conserved hypothetical protein
0695	0,573	Hypothetical protein
0698	0,877	Conserved hypothetical protein
0699	0,745	Hypothetical protein
0701	0,726	Hypothetical protein
0703	0,835	Hypothetical protein
0705	0,758	Hypothetical protein
0706	0,938	Conserved protein
0707	0,456	hypothetical protein
0708	0,445	Phage shock protein A
0709	0,571	Hypothetical protein
0710	0,647	Universal stress protein
0711	0,581	Conserved protein
0712	0,837	GTP-binding protein homolog
0714	0,920	Thiamine biosynthesis protein
0715	0,888	Probable transcriptional regulator
0717	0,665	Archaeal protein Translation Elongation Factor 1, subunit beta
0718	0,822	1-pyrroline-5-carboxylate synthetase
0719	0,462	Hypothetical protein
0720	0,479	Hypothetical protein
0722	0,673	Heat shock protein
0724	0,554	GrpE protein
0725	0,439	Chaperone protein
0726	0,532	Chaperone protein DnaJ
0727	0,830	Trk system potassium uptake protein TrkA

0728	0,564	Trk system potassium uptake protein
0732	0,895	Conserved protein
0733	0,529	Hypothetical protein
0738	0,610	F420H2 dehydrogenase, subunitA
0739	0,411	F420H2 dehydrogenase, subunitB
0740	0,456	F420H2 dehydrogenase, subunitC
0741	0,490	F420H2 dehydrogenase, subunitD
0742	0,506	F420H2 dehydrogenase, subunitH
0743	0,557	F420H2 dehydrogenase, subunitI
0744	0,737	F420H2 dehydrogenase, subunitJ1
0745	0,773	F420H2 dehydrogenase, subunitJ2
0746	0,748	F420H2 dehydrogenase, subunitK
0750	0,450	F420h2 dehydrogenase, subunitO
0752	0,526	Hypothetical protein
0753	0,711	Ribosomal-protein-alanine acetyltransferase
0754	0,597	Hypothetical protein
0755	0,766	Ribosomal-protein-alanine acetyltransferase
0756	0,734	Hypothetical protein
0757	0,883	NUCLEOTIDYLTRANSFERASE
0762	0,761	Metallo cofactor biosynthesis protein (moaA/ nifB /pqqE family)
0763	0,434	Hypothetical protein
0764	0,465	ABC transporter, permease protein
0765	0,590	Hypothetical protein
0766	0,698	Endonuclease III
0767	0,552	Conserved protein
0768	0,481	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
0769	0,483	Metalloendopeptidases (putative)
0770	0,538	Conserved protein
0771	0,520	Hypothetical protein
0772	0,650	Conserved protein
0774	0,586	Response regulator
0775	0,758	TETRATRICOPEPTIDE REPEAT FAMILY PROTEIN
0776	0,541	Hypothetical protein
0777	0,803	Hypothetical protein
0779	0,642	Hypothetical protein
0781	0,641	Putative ribosomal-protein-alanine acetyltransferase

0782	0,919	Conserved protein
0783	0,884	Conserved protein
0784	0,866	Iron-sulfur cluster-binding protein
0785	0,787	O6-methylguanine-DNA methyltransferase
0786	0,809	Conserved protein
0792	0,653	Transcription initiation factor TFIIB
0793	0,689	Transcription initiation factor TFIIB
0868	0,511	F420-dependent methylenetetrahydromethanopterin dehydrogenase
0992	0,757	Pirin
0993	0,814	Conserved protein
0994	0,658	Conserved protein
0999	0,561	Transposase
1003	0,673	Hypothetical protein
1005	0,697	Adenine deaminase
1018	0,564	Ribonuclease BN
1036	0,445	Conserved protein
1038	0,556	Hypothetical protein
1039	0,604	Conserved protein
1040	0,677	Hypothetical protein
1041	0,434	Conserved protein
1044	0,146	Hypothetical sensory transduction histidine kinase
1046	0,442	Conserved protein
1048	0,671	Conserved protein
1049	0,847	Hypothetical protein
1050	0,506	Hypothetical protein
1056	0,951	Conserved protein
1058	0,431	Conserved protein
1060	0,473	Hypothetical protein
1062	0,607	Hypothetical protein
1064	0,148	Hypothetical protein
1066	0,226	Hypothetical protein
1069	0,339	Transposase
1070	0,885	Hypothetical protein
1072	0,271	Coenzyme F420 hydrogenase, beta subunit
1073	0,371	Coenzyme F420 hydrogenase, gamma subunit
1075	0,395	Coenzyme F420 hydrogenase, alpha subunit

1076	0,524	Conserved protein
1081	0,321	OXIDOREDUCTASE
1084	0,574	Hypothetical protein
1087	0,438	Hypothetical protein
1089	0,432	Hypothetical protein
1101	0,480	RNASE P RNA COMPONENT
1102	0,443	Hypothetical protein
1104	0,691	Probable transcriptional regulator
1105	0,729	mRNA 3'-end processing factor
1106	0,568	Hypothetical protein
1114	0,441	Hypothetical protein
1119	0,877	Conserved protein
1123	0,293	Transcriptional regulator, TetR/AcrR family
1127	0,653	Thioredoxin
1128	0,589	Hypothetical protein
1130	0,671	ZINC-FINGER PROTEIN
1132	0,544	Methylenetetrahydrofolate dehydrogenase (NADP+)/ methylenetetrahydrofolate cyclohydrolase
1134	0,606	Phosphoribosylglycinamide formyltransferase
1135	0,632	HTH DNA-binding protein
1137	0,613	NAD+ synthetase
1141	0,636	Conserved protein
1142	0,494	Hypothetical protein
1143	0,595	Hypothetical protein
1144	0,693	Hypothetical protein
1147	0,631	CYTIDYLYLTRANSFERASE
1148	0,611	Conserved protein
1149	0,602	Probable endonuclease IV
1152	0,651	Cobalt transport protein
1153	0,878	Cobalt transport protein
1155	0,840	CbiM protein
1161	1,134	Phosphofructokinase
1161	0,685	Phosphofructokinase
1163	0,615	Putative inosine-5'-monophosphate dehydrogenase
1166	0,680	Hypothetical protein
1167	0,704	Acetyltransferase
1169	0,807	Small heat shock protein

1170	0,781	Hypothetical protein
1173	0,493	Heat shock protein
1174	0,541	Ferredoxin
1175	0,551	Ferredoxin
1179	0,430	Acetyl-CoA synthetase
1180	0,495	Acetate kinase
1181	0,414	Phosphate acetyltransferase
1183	0,410	Putative chloride channel protein
1185	0,801	3-demethylubiquinone-9 3-methyltransferase
1195	0,653	Conserved protein
1201	0,653	Conserved protein
1210	0,545	Hypothetical protein
1214	0,498	Hypothetical protein
1215	0,682	Conserved protein
1217	0,946	Hypothetical protein
1224	0,682	Conserved protein
1226	0,477	Conserved protein
1228	0,447	Hypothetical protein
1231	0,490	Conserved protein
1233	0,729	Nitrogen regulatory protein P-II
1234	0,592	Hypothetical protein
1235	0,710	Hypothetical protein
1236	0,428	Glutathione-regulated potassium-efflux system protein
1239	0,637	Conserved protein
1242	0,497	Putative flagella-related protein H
1244	0,535	Adenylosuccinate lyase
1246	0,535	GERANYLGERANYLGLYCERYL DIPHOSPHATE SYNTHASE
1249	0,582	PUTATIVE NADPH-FLAVIN OXIDOREDUCTASE
1253	0,910	ABC transporter, ATP-binding protein
1263	0,597	Putative small heat shock protein
1264	0,481	Conserved protein
1265	0,497	Integral Membrane protein
1266	1,379	Glutamine synthetase
1267	0,576	Glutamate synthase, large chain
1268	0,364	Glutamate synthase, large chain
1269	0,457	Glutamate synthase, large chain

1270	0,385	Coenzyme F420 hydrogenase beta subunit
1271	0,592	Hypothetical protein
1273	0,514	Conserved protein
1275	0,520	Xaa-Pro aminopeptidase
1276	0,574	Conserved protein
1277	0,469	Protease (putative)
1278	0,529	F420-dependent NADP reductase
1279	0,740	HETERODISULFIDE REDUCTASE, SUBUNIT HDRC
1280	0,649	HETERODISULFIDE REDUCTASE, SUBUNIT HDRB
1281	2,365	Iron-sulfur binding protein
1283	0,528	Conserved protein
1285	0,333	Conserved protein
1286	0,274	Conserved protein
1287	0,419	Conserved protein
1288	0,801	Conserved protein
1289	0,382	HTH DNA-binding protein
1290	0,424	Nucleotide-binding protein
1291	0,404	Thiol-disulfide isomerase/thioredoxin
1293	0,475	Precorrin-8X methylmutase
1294	0,382	Precorrin-3B C17-methyltransferase
1295	0,366	COBALAMIN BIOSYNTHESIS PROTEIN G
1296	0,320	COBALAMIN BIOSYNTHESIS PROTEIN G
1297	0,331	Precorrin-4 C11-methyltransferase
1298	0,378	Precorrin-2 C20-methyltransferase
1299	0,447	Precorrin-6Y C5,15-methyltransferase [decarboxylating]
1300	0,735	2-isopropylmalate synthase
1301	0,557	Isocitrate dehydrogenase [NADP]
1302	0,537	Putative molybdenum cofactor biosynthesis protein
1303	0,669	Zinc finger protein
1304	0,490	26S PROTEASOME REGULATORY SUBUNIT RPT2/S4
1305	0,541	Conserved protein
1306	0,382	Cell division protein
1307	0,423	PROTEIN TRANSLOCASE SUBUNIT SECE
1308	0,599	Putative transcription antitermination protein nusG
1309	0,752	LSU ribosomal protein L11P
1310	0,577	LSU ribosomal protein L1P

1312	0,682	LSU ribosomal protein L12P
1313	0,980	Molybdenum cofactor biosynthesis enzyme (Fe-S oxidoreductase family)
1314	0,885	Conserved protein
1316	0,398	Hypothetical protein
1317	0,586	Hypothetical protein
1318	0,482	Conserved protein
1320	0,562	TRANSLATION INITIATION FACTOR 1A (EIF-1A)
1321	0,365	Serine/threonine protein kinase
1322	0,476	Putative RNA-binding protein
1323	0,543	Dihydroorotase
1324	0,503	Phosphate transport system protein
1325	0,949	Phosphate transporter, ATP-binding protein
1326	1,264	Phosphate transporter, permease protein
1327	0,990	Phosphate transporter, permease protein
1328	1,723	Phosphate transporter, permease protein
1329	0,407	Phosphate-binding protein
1331	0,682	Magnesium-chelatase subunit
1332	0,393	Conserved protein
1333	0,545	Hypothetical protein
1337	0,576	Conserved protein
1338	0,335	Cobalt transport ATP-binding protein
1339	1,099	Cobalt transport protein
1340	1,389	ABC transporter ATP-binding protein
1341	0,627	ABC transporter, permease protein
1342	0,425	Hypothetical protein
1343	0,365	Hypothetical protein
1344	0,583	Hypothetical protein
1348	0,543	Hypothetical Cytosolic protein
1349	0,537	Hypothetical Cytosolic protein
1351	0,537	Alkyl sulfatase
1352	0,472	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENASE, SUBUNIT D
1353	0,522	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENASE, SUBUNIT B
1355	0,916	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENASE, SUBUNIT C
1356	0,831	Conserved protein
1357	0,455	Conserved protein
1358	0,360	Conserved protein

1359	0,445	HISTONE ACETYLTRANSFERASE (ELP3 faminy)
1361	0,506	Conserved protein
1362	0,321	Single-stranded-DNA-specific exonuclease recJ
1363	0,342	Hypothetical protein
1364	0,294	Hypothetical protein
1365	0,323	Hypothetical protein
1366	0,256	Malate dehydrogenase
1367	0,404	Hypothetical protein
1368	0,312	hypothetical protein
1369	0,187	Tyrosyl-tRNA synthetase
1370	0,297	Conserved protein
1371	0,212	Hypothetical protein
1372	0,632	Conserved protein
1373	0,401	Hypothetical protein
1374	0,557	Hit-like protein, involved in cell-cycle regulation
1375	0,525	Hypothetical Transcriptional Regulatory protein
1376	0,571	Hypothetical protein
1377	0,409	Cysteine desulfurase NifS
1378	0,440	NifU protein
1381	0,434	Catalase
1382	0,289	METHYLTRANSFERASE
1384	0,432	Integral membrane protein
1386	0,540	Hypothetical protein
1387	0,371	Transporter
1389	0,653	POLYPRENYLTRANSFERASE
1390	0,657	Glutamine transporter, ATP-binding protein
1391	0,589	Glutamine transporter, permease protein
1393	0,558	Hypothetical protein
1395	0,632	Conserved protein
1396	0,658	Acetyltransferase
1397	0,598	Hypothetical protein
1398	0,615	Integral membrane protein
1400	0,507	Sensory Transduction protein Kinase
1403	0,776	PHOSPHINOTHRICIN ACETYLTRANSFERASE
1406	0,720	hypothetical protein
1407	0,547	Hypothetical protein

1408	0,714	Hypothetical protein
1409	0,788	Hypothetical protein
1410	0,816	NUCLEOTIDYLTRANSFERASE
1414	0,417	Lysyl-tRNA synthetase, class II
1416	0,989	Hypothetical protein
1418	0,526	Hypothetical protein
1419	0,408	Cysteinyl-tRNA synthetase
1420	0,794	Maf protein
1421	0,507	Glutathione-regulated potassium-efflux system protein
1422	0,668	Hypothetical protein
1423	0,542	Isochorismatase
1424	0,542	Conserved protein
1425	0,905	Hypothetical membrane spanning protein
1427	0,491	Hypothetical protein
1428	0,352	Transcriptional regulator, MarR family
1429	0,650	Hypothetical protein
1430	0,543	Hypothetical protein
1431	0,604	Hypothetical protein
1432	0,382	Hypothetical protein
1435	0,683	Phenylacetic acid degradation protein
1447	0,589	Hypothetical protein
1452	0,594	Hypothetical protein
1453	0,895	Hypothetical protein
1454	0,540	26S PROTEASOME REGULATORY SUBUNIT RPT2/S4
1455	0,482	Hypothetical protein
1458	0,400	Conserved protein
1459	0,430	Hypothetical ATP-binding protein
1460	0,386	LSU ribosomal protein L39E
1461	0,383	LSU ribosomal protein L31E
1462	0,397	protein Translation Initiation Factor 6 (IF-6)
1463	0,445	Prefoldin, alpha subunit
1465	0,524	Stress-responsive transcriptional regulator
1468	0,972	Probable peroxiredoxin
1472	0,860	Hypothetical protein
1474	0,537	Hypothetical protein
1475	0,570	Conserved protein

1476	0,451	Hypothetical protein
1480	0,455	Putative 6-aminohexanoate-dimer hydrolase
1483	0,686	Hypothetical protein
1484	0,506	Hypothetical protein
1485	0,614	Hypothetical protein
1486	0,596	Hypothetical protein
1487	0,580	Hypothetical protein
1488	0,604	METHYLTRANSFERASE
1490	0,525	Exodeoxyribonuclease III
1492	0,395	Hypothetical protein
1494	0,524	Hypothetical protein
1495	0,586	TYPE I RESTRICTION-MODIFICATION SYSTEM SPECIFICITY SUBUNIT
1497	0,637	Flavodoxin
1498	0,872	Large-conductance mechanosensitive channel
1499	0,673	Cob(I)alamin adenosyltransferase
1500	0,817	TRANSPORTER, LysE family
1502	0,959	ABC Transporter, ATP-binding protein
1503	0,537	PROTEASE HTPX
1505	0,620	Hypothetical protein
1507	0,796	Hypothetical protein
1508	0,664	Hypothetical protein
1509	0,252	Hypothetical protein
1510	0,561	Hypothetical protein
1511	0,611	Hypothetical protein
1512	0,571	Hypothetical protein
1513	0,580	Hypothetical protein
1514	0,483	Hypothetical protein
1515	0,606	Fe-S OXIDOREDUCTASE
1516	0,710	Hypothetical protein
1517	0,602	Hypothetical protein
1518	0,486	IRON-SULFUR FLAVOPROTEIN
1520	0,543	Transcriptional regulator, MarR family
1521	0,499	Hypothetical protein
1522	0,768	Hypothetical protein
1524	0,586	Hypothetical protein
1525	0,430	Hypothetical protein

1526	0,352	Glycogen phosphorylase
1527	0,630	Hypothetical protein
1528	0,596	Hypothetical protein
1529	0,606	Hypothetical protein
1530	0,356	Probable cytosine deaminase
1531	0,335	Hypothetical protein
1532	0,328	Hypothetical protein
1533	0,349	Conserved protein
1535	0,346	Hypothetical protein
1538	0,338	ABC transporter, permease protein
1539	0,490	Hypothetical protein
1540	0,302	Hypothetical protein
1541	0,308	ABC transporter, ATP-binding protein
1542	0,298	Hypothetical protein
1543	0,321	Transcriptional regulator
1543	0,273	Transcriptional regulator
1544	0,281	Hypothetical protein
1545	0,278	Phycocyanin alpha-subunit phycocyanobilin lyase related protein, CpcE/NbIB family
1547	0,414	Carbonic anhydrase
1548	0,446	Carbonic anhydrase
1550	0,807	Molybdenum formylmethanofuran dehydrogenasel subunit FmdF
1551	0,418	Molybdenum formylmethanofuran dehydrogenasel subunit FmdE
1552	0,414	TUNGSTEN TRANSPORTER, ATP BINDING PROTEIN
1553	0,525	TUNGSTEN TRANSPORTER, PERMEASE PROTEIN
1554	0,459	ABC TRANSPORTER, TUNGSTEN-BINDING PROTEIN
1555	0,364	Hypothetical protein
1557	0,342	Hypothetical protein
1559	0,393	PUTATIVE METAL DEPENDENT HYDROLASE
1560	0,269	Transcriptional regulator
1562	0,462	Hypothetical protein
1563	0,591	Hypothetical protein
1564	0,448	putative molybdenum transport protein ModA
1567	0,295	Tetrahydromethanopterin S-methyltransferase, subunit E
1570	0,263	Tetrahydromethanopterin S-methyltransferase, subunit B
1571	0,354	Tetrahydromethanopterin S-methyltransferase, subunit A
1573	0,325	Tetrahydromethanopterin S-methyltransferase, subunit G

1575	0,367	Hypothetical protein
1576	0,913	Replication factor C subunit
1577	0,705	Conserved protein
1578	0,761	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
1579	0,632	L-fucose phosphate aldolase
1580	0,414	Hypothetical protein
1581	0,372	Molybdopterin biosynthesis MoeB protein/ThiF protein
1584	0,335	Hypothetical protein
1586	0,262	Citrate (si) synthase
1588	0,604	Conserved protein
1589	0,610	Conserved protein
1590	0,657	Zinc metalloprotease
1591	0,394	Putative FeS oxidoreductase
1592	0,369	PHOSPHOGLUCOMUTASE / PHOSPHOMANNOMUTASE
1593	0,491	Conserved protein
1594	0,457	Amino-acid acetyltransferase
1595	0,475	Conserved protein
1596	0,511	Cysteine desulfurase
1597	0,764	Type II secretion system protein
1599	0,615	Hypothetical protein
1600	0,621	Hypothetical protein
1601	0,730	Hypothetical protein
1602	0,877	Hypothetical protein
1603	0,740	Hypothetical protein
1604	0,682	Hypothetical protein
1605	0,652	Hypothetical protein
1606	0,647	Hypothetical protein
1607	0,687	FdhD protein
1608	0,648	Imidazoleglycerol-phosphate dehydratase
1626	0,558	METHYLTRANSFERASE
1627	0,539	Alanyl-tRNA synthetase
1628	0,384	Conserved protein
1629	0,622	Conserved protein
1630	0,170	Hypothetical protein
1631	0,443	Conserved protein
1632	0,402	SWF/SNF FAMILY HELICASE

1633	0,465	Molybdenum cofactor biosynthesis protein B
1634	0,250	Pyruvate formate-lyase activating enzyme
1635	0,522	LSU ribosomal protein L10E
1636	0,133	Probable translation initiation factor 2 beta subunit
1637	0,237	Metallo cofactor biosynthesis protein (moaA/ nifB /pqqE family)
1638	0,188	Conserved protein
1639	0,300	PUTATIVE NUCLEOTIDYLTRANSFERASE
1640	0,292	Tryptophanyl-tRNA synthetase
1641	0,418	Phenylalanyl-tRNA synthetase, alpha chain
1642	0,607	Conserved protein
1643	0,258	Hypothetical protein
1644	0,259	Hypothetical protein
1645	0,241	Hypothetical protein
1646	0,323	Hypothetical membrane spanning protein
1647	1,221	Hypothetical protein
1648	0,599	Copper-exporting ATPase
1649	0,216	Cation-transporting ATPase
1650	0,263	Hypothetical protein
1651	0,560	Conserved protein
1652	0,228	Conserved protein
1653	0,482	Universal stress protein
1654	0,462	Universal stress protein
1655	0,555	Universal stress protein
1656	0,630	Universal stress protein
1657	0,993	Universal stress protein
1658	0,599	Universal stress protein
1659	0,447	Fe-S OXIDOREDUCTASE
1660	1,066	Hypothetical protein
1661	0,598	Hypothetical protein
1662	0,672	Lysly-tRNA synthetase (PylS)
1663	0,605	PylB (Pyrrolysine synthesis)
1664	0,968	PylC (Pyrrolysine synthesis)
1665	0,651	Hypothetical protein
1666	0,489	Inorganic pyrophosphatase
1666	0,344	Inorganic pyrophosphatase
1667	0,633	Conserved protein

1668	0,468	Methylcobalamin:coenzyme M methyltransferase MtbA
1669	1,684	Monomethylamine corrinoid protein MtmC
1669	0,516	Monomethylamine corrinoid protein MtmC
1671	2,248	Monomethylamine:corrinoid methyltransferase MtmB (C-terminal domain)
1672	0,504	Monomethylamine permease MtmP
1673	0,522	Monomethylamine permease MtmP (C-terminal domain)
1676	0,845	Transposase (C-terminus)
1677	0,387	Conserved protein
1678	0,830	REPLICATION FACTOR C SUBUNIT
1679	0,590	PROTEIN TRANSLOCASE, SUBUNIT SECD
1680	1,045	PROTEIN TRANSLOCASE, SUBUNIT SECF
1681	0,657	dCMP DEAMINASE
1682	0,473	Hypothetical protein
1683	0,664	Conserved protein
1684	0,636	Hypothetical protein
1685	0,767	Small heat shock protein
1686	0,349	3-phosphonopyruvate decarboxylase
1687	0,374	Aspartate kinase
1688	0,503	Phosphoribosylformylglycinamide cyclo-ligase
1689	0,474	Conserved protein
1690	0,408	Conserved protein
1691	0,416	Conserved protein
1692	0,392	Hypothetical protein
1693	0,355	Hypothetical protein
1694	0,706	Hypothetical protein
1695	0,419	Hypothetical protein
1696	0,653	archaeosine tRNA-ribosyltransferase
1697	0,533	Conserved protein
1698	0,790	Acetylornithine aminotransferase
1699	1,308	Histidinol-phosphate aminotransferase
1700	0,652	Conserved protein
1701	1,043	CDP-diacylglycerol--serine O-phosphatidyltransferase
1702	0,772	Phosphatidylserine decarboxylase
1703	0,611	Hypothetical protein
1704	0,315	MutT-like protein
1705	0,583	DNA-directed RNA polymerase subunit M

1706	0,443	DNA polymerase sliding clamp
1707	0,503	Conserved protein
1708	0,937	Conserved protein
1709	0,744	Cobyrinic acid a,c-diamide synthase
1710	0,388	Molybdenum cofactor biosynthesis protein A
1712	0,214	Survival protein
1713	0,299	Probable transcriptional regulator
1714	0,433	Conserved protein
1715	0,561	Glycyl-tRNA synthetase
1716	0,516	ATP-DEPENDENT RNA HELICASE, EIF-4A FAMILY
1717	0,539	Hypothetical protein
1718	1,064	Conserved protein
1719	0,693	Superfamily I DNA and RNA helicase
1720	0,512	Phenylalanyl-tRNA synthetase, alpha chain
1721	0,471	Conserved protein
1722	0,568	Chaperone protein
1723	0,579	Chaperone protein
1723	0,373	Chaperone protein
1725	0,618	ORIGIN RECOGNITION COMPLEX SUBUNIT
1726	0,673	Hypothetical protein
1727	0,612	Exopolyphosphatase
1727	0,569	Exopolyphosphatase
1728	0,604	Polyphosphate kinase
1728	0,484	Polyphosphate kinase
1729	0,571	DNA mismatch repair protein
1731	0,596	Hydrolase of the alpha/beta superfamily
1733	0,583	Archaeal protein Translation Initiation Factor 2B subunit 1 (aIF-2B1)
1734	0,303	Myo-inositol-1-phosphate synthase
1735	0,721	DNA repair protein
1736	0,463	Pyruvate:ferredoxin oxidoreductase PorB (EC 1.2.7.1)
1737	0,860	Anaerobic ribonucleoside-triphosphate reductase
1738	0,629	Ribonucleoside-triphosphate reductase activating enzyme
1739	0,492	THIAMIN-MONOPHOSPHATE KINASE
1740	0,636	Hypothetical protein
1741	0,548	Conserved hypothetical protein
1742	0,521	Putative aliphatic sulfonate binding protein precursor

1743	0,770	ABC transporter, permease protein
1744	0,523	ABC transporter, ATP-binding protein
1745	0,525	Hypothetical protein
1746	0,636	PUTATIVE METHYLTRANSFERASE
1750	0,990	Conserved protein
1751	0,294	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1752	0,275	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1753	0,439	Conserved protein
1754	0,861	Arginyl-tRNA synthetase
1754	0,537	Arginyl-tRNA synthetase
1755	1,010	Peptide Chain Release Factor
1756	0,864	Fe-S OXIDOREDUCTASE
1757	0,458	DNA polymerase II small subunit
1758	0,358	SIGNAL SEQUENCE PEPTIDASE
1759	0,440	NifR3-like protein
1760	0,212	Pyruvate synthase, gamma subunit
1761	0,174	Pyruvate synthase, delta subunit
1762	0,526	Pyruvate synthase, alpha subunit
1763	0,897	Pyruvate synthase, beta subunit
1763	0,519	Pyruvate synthase, beta subunit
1764	0,413	Hypothetical protein
1765	0,460	Hypothetical protein
1766	1,039	Hypothetical protein
1767	0,942	Zinc ABC transporter, permease protein
1768	0,908	Zinc ABC transporter, ATP-binding protein
1769	0,846	Zinc ABC transporter, zinc-binding protein
1770	1,212	Iron-dependent repressor
1771	0,493	Gluconate permease
1772	0,562	Chemotaxis protein CheW
1773	0,480	Methyl-accepting chemotaxis protein
1774	0,286	Two-component response regulator
1775	0,325	Chemotaxis protein
1776	0,446	protein-glutamate methylesterase
1777	0,456	Chemotaxis protein
1778	0,900	Chemotaxis protein methyltransferase
1779	0,539	Chemotaxis protein

1780	0,396	Chemotaxis protein
1781	0,462	Formylmethanofuran--tetrahydromethanopterin formyltransferase
1781	0,306	Formylmethanofuran--tetrahydromethanopterin formyltransferase
1782	0,960	Pheromone shutdown protein
1783	0,975	Conserved protein
1784	0,422	Glutamate decarboxylase
1785	0,866	Sodium/proline symporter
1785	0,527	Sodium/proline symporter
1787	0,629	ORIGIN RECOGNITION COMPLEX SUBUNIT
1788	0,440	UMP/CMP kinase related protein
1789	0,718	Conserved protein
1790	0,845	Conserved protein
1791	0,437	Hypothetical protein
1792	0,613	protein Translation Elongation Factor 1A (EF-1A)
1794	0,490	Conserved protein
1795	0,285	HTH DNA-binding protein
1796	0,830	Conserved protein
1797	1,169	Conserved protein
1798	0,980	Conserved protein
1799	0,749	Conserved protein
1800	0,811	Conserved protein
1801	0,218	Transposase
1802	0,323	Replication factor-A protein
1803	0,477	Putative tRNA 2'phosphotransferase
1804	0,711	RNA 3'-terminal phosphate cyclase
1805	0,659	NADH oxidase
1806	0,787	DNA primase
1807	0,578	Conserved protein
1808	0,608	Ribosomal protein S18 alanine acetyltransferase
1809	1,030	Archaeosine tRNA-ribosyltransferase
1810	0,499	(S)-2-hydroxy-acid dehydrogenase
1811	0,423	Fe-S oxidoreductase
1812	0,388	Conserved protein
1815	1,185	Sec-independent transport protein TatD
1816	0,480	2-isopropylmalate synthase
1822	0,610	Conserved protein

1823	0,706	Hypothetical protein
1824	0,198	Hypothetical protein
1826	0,616	Conserved protein
1827	0,550	Hypothetical protein
1828	0,690	Hypothetical protein
1831	0,689	Conserved protein
1832	0,470	Hypothetical protein
1833	0,366	Hypothetical protein
1834	0,670	Hypothetical protein
1835	2,081	Monomethylamine:corrinoïd methyltransferase MtmB (C-terminal domain)
1836	1,395	Monomethylamine:corrinoïd methyltransferase MtmB
1837	1,396	Monomethylamine corrinoïd protein MtmC
1839	0,247	Putative ferredoxin
1840	0,538	Conserved protein
1841	0,560	O-linked N-acetylglucosamine transferase
1842	0,800	Phosphoglycolate phosphatase
1843	0,439	Conserved protein
1844	0,291	Ferredoxin
1845	0,674	ALDEHYDE FERREDOXIN OXIDOREDUCTASE
1846	2,168	permease, Na ⁺ /H ⁺ -dicarboxylate symporter
1846	0,707	permease, Na ⁺ /H ⁺ -dicarboxylate symporter
1847	0,699	Oligopeptide transporter, ATP-binding protein
1848	0,314	Oligopeptide transporter, ATP-binding protein
1850	0,225	Oligopeptide transporter, permease protein
1851	0,345	Oligopeptide transporter, permease protein
1852	0,787	Transport protein
1853	0,475	Conserved protein
1854	0,587	Hypothetical protein
1855	0,443	Hypothetical protein
1856	0,572	N-5'-phosphoribosyl)anthranilate isomerase
1857	0,669	Hypothetical protein
1858	0,659	5-methylcytosine-specific restriction enzyme A
1859	0,548	Acetyltransferase
1860	0,286	Transcriptional regulator, AraC family
1861	0,586	Ferredoxin
1862	0,353	Conserved protein

1863	0,361	Conserved protein
1864	0,694	Conserved protein
1865	1,029	Putative DNA or RNA helicase of superfamily II
1866	0,471	Threonyl-tRNA synthetase
1867	0,701	Hypothetical protein
1868	0,420	Hypothetical protein
1869	0,505	Phosphoadenosine phosphosulfate reductase
1870	0,274	Hypothetical protein
1871	0,724	Glutamate dehydrogenase
1871	0,363	Glutamate dehydrogenase
1873	0,397	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
1874	0,437	Hypothetical protein
1875	0,722	Iron-sulfur cluster-binding protein
1876	0,228	Excinuclease ABC, subunit A
1877	0,590	Excinuclease ABC, subunit C
1878	0,415	Excinuclease ABC, subunit B
1878	0,246	Excinuclease ABC, subunit B
1878	0,225	Excinuclease ABC, subunit B
1879	1,907	Conserved protein
1880	0,576	Hypothetical protein
1881	0,797	Hypothetical protein
1882	0,502	Conserved protein
1883	0,435	Transcriptional regulator
1884	0,570	Putative inorganic pyrophosphatase
1885	0,442	Probable ATP-dependent helicase
1886	0,393	SAM-dependent methyltransferases
1887	0,763	Conserved protein
1888	0,371	Dihydrolipoamide dehydrogenase
1889	0,546	Hypothetical Membrane Spanning protein
1890	0,453	PROTEASE I
1891	0,760	Hypothetical protein
1892	1,034	Conserved protein
1893	0,811	Hypothetical protein
1894	0,324	Putative transport protein
1895	0,602	Glutaredoxin
1896	0,606	Ferredoxin-thioredoxin reductase, catalytic chain

1897	0,465	Serine O-acetyltransferase
1898	0,804	NADPH-flavin oxidoreductase
1899	0,358	Conserved protein
1900	0,292	Hypothetical protein
1902	0,393	Coenzyme F420 hydrogenase beta subunit
1903	0,594	Branched-chain amino acid transport protein
1904	0,460	Branched-chain amino acid transport protein
1905	0,279	Conserved protein
1906	0,577	Hypothetical protein
1907	0,228	Conserved protein
1908	0,463	Hypothetical protein
1909	0,383	Conserved protein
1910	0,625	Hypothetical protein
1911	0,667	Hypothetical protein
1912	0,665	Hypothetical protein
1913	0,277	Hypothetical protein
1914	0,172	Hypothetical protein
1915	0,492	Hypothetical protein
1916	0,582	Hypothetical protein
1917	0,369	Hypothetical protein
1918	0,636	Conserved protein
1920	0,664	Hypothetical protein
1921	0,680	Hypothetical protein
1922	0,570	Hypothetical protein
1923	0,656	Probable transcriptional regulator
1924	0,455	Hypothetical protein
1925	0,401	Conserved protein
1926	0,494	Thiamin-phosphate pyrophosphorylase
1927	0,701	Hydroxyethylthiazole kinase
1928	0,488	HTH DNA-binding protein
1929	0,837	Conserved protein
1930	1,133	Phosphate permease
1930	1,038	Phosphate permease
1932	0,680	Transposase
1933	0,271	Conserved protein
1934	0,416	Conserved protein

1935	0,450	Putative ketoreductase
1936	0,316	ABC Transporter, permease protein)
1937	0,412	ABC transporter, ATP-binding protein
1938	0,665	Conserved protein
1939	0,342	Conserved protein
1940	0,616	Transporter
1941	0,861	Conserved protein
1942	0,268	Conserved protein
1943	0,203	Conserved protein
1944	0,992	Conserved protein
1945	0,417	Conserved protein
1946	0,575	Ferredoxin
1947	0,487	Prismane protein
1948	0,544	Hypothetical protein
1949	0,248	Cation efflux protein
1950	0,304	Transporter
1951	0,593	Transcriptional regulator, ArsR family
1952	0,591	PROTEASE
1953	0,260	Response regulator
1954	0,406	Two component system histidine kinase
1955	0,534	Conserved protein
1956	0,395	Hypothetical protein
1957	0,497	Conserved protein
1958	0,608	Conserved protein
1960	0,549	Transporter
1961	0,816	Hypothetical protein
1962	1,119	Hypothetical protein
1963	0,713	Hypothetical protein
1963	0,372	Hypothetical protein
1964	1,003	Transcriptional regulator, MarR family
1965	0,664	Uncharacterized membrane protein
1966	0,650	Hypothetical membrane spanning protein
1967	0,265	Hypothetical protein
1968	0,639	Hypothetical protein
1969	0,718	Potassium channel protein
1971	0,792	Flavodoxin

1972	0,279	Transporter
1973	0,684	Ornithine decarboxylase
1974	0,563	KETOISOVALERATE OXIDOREDUCTASE SUBUNIT
1975	0,684	KETOISOVALERATE OXIDOREDUCTASE SUBUNIT
1976	0,411	Ketoisovalerate oxidoreductase subunit
1977	0,455	Putative Acetyl-CoA synthetase
1978	0,624	Transcriptional regulator
1979	0,421	Hypothetical protein
1980	0,578	Hypothetical protein
1981	0,508	Hypothetical protein
1982	0,578	Hypothetical protein
1984	0,482	Transcriptional regulator, ArsR family
1985	0,333	PUTATIVE METHYLTRANSFERASE
1986	0,496	Hypothetical protein
1987	0,505	Transcriptional regulator, MerR family
1988	0,481	Hypothetical protein
1991	0,537	Conserved protein
1992	0,218	Putative cation transport regulator
1993	0,785	Conserved protein
1996	0,447	Conserved protein
1997	0,454	Hydrogenase maturation protein
1998	0,455	A1AO H+ ATPASE, SUBUNIT D
1999	0,549	A1AO H+ ATPASE, SUBUNIT B
2000	0,613	A1AO H+ ATPASE, SUBUNIT A
2001	0,464	A1AO H+ ATPASE, SUBUNIT F
2002	0,567	A1AO H+ ATPASE, SUBUNIT C
2003	0,362	A1AO H+ ATPASE, SUBUNIT E
2004	0,762	A1AO H+ ATPASE, SUBUNIT K
2008	0,505	Conserved protein
2009	0,135	Carbon monoxide dehydrogenase
2010	0,468	METAL DEPENDENT HYDROLASE
2011	0,655	Hypothetical protein
2012	0,563	Conserved protein
2013	0,316	Conserved protein
2014	0,417	Conserved protein
2015	0,659	SURFACE LAYER PROTEIN B

2016	0,712	TYPE I RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT
2017	0,681	TYPE I RESTRICTION-MODIFICATION SYSTEM SPECIFICITY SUBUNIT
2018	0,603	TYPE I RESTRICTION-MODIFICATION SYSTEM RESTRICTION SUBUNIT
2019	0,614	Zinc metalloprotease
2020	0,758	Cell surface protein
2021	0,508	Hypothetical protein
2022	0,544	Methyltransferase involved in cell division
2023	0,656	Hypothetical protein
2024	0,460	Conserved protein
2025	0,454	Conserved protein
2026	0,574	DNA/pantothenate metabolism flavoprotein
2027	0,729	Conserved protein
2028	0,465	Hypothetical protein
2029	0,366	Conserved protein
2030	0,865	Chlorohydrolase family protein
2031	0,952	Adenosylhomocysteinase
2032	0,639	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2033	0,576	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2034	0,568	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2035	0,742	DNA-directed RNA polymerase, subunit H
2036	1,035	DNA-directed RNA polymerase, beta chain
2037	0,714	DNA-directed RNA polymerase, beta chain
2038	0,591	DNA-directed RNA polymerase, subunit A'
2039	0,497	DNA-directed RNA polymerase, subunit A''
2040	0,557	LSU ribosomal protein L30E
2041	0,431	NusA protein homolog
2042	0,497	SSU ribosomal protein S12P
2043	0,622	SSU ribosomal protein S7P
2046	0,577	SSU ribosomal protein S10P
2047	0,400	Conserved protein
2048	0,499	Conserved protein
2049	0,643	Conserved protein
2050	0,236	Conserved protein
2051	0,349	Conserved protein
2052	0,330	Conserved protein
2053	0,526	Conserved protein

2054	0,354	Conserved protein
2055	0,448	Dihydropyrimidinase
2056	0,778	Conserved protein
2057	0,065	Tetrahydromethanopterin S-methyltransferase, subunit A
2058	0,417	Conserved protein
2059	0,394	Hypothetical protein
2060	0,388	Conserved protein
2061	0,388	Conserved protein
2063	0,244	Transcriptional regulator, ArsR family
2064	0,825	Conserved protein
2065	0,481	ARSENATE REDUCTASE
2066	0,375	Putative methyltransferase
2067	0,750	Transcriptional regulator, ArsR family
2068	0,653	Cytochrome c-type biogenesis protein CcdA
2069	0,492	Conserved protein
2070	0,578	Conserved protein
2071	0,583	Hypothetical protein
2072	0,454	Transcriptional regulator, ArsR family
2073	0,308	Conserved protein
2074	0,388	Conserved protein
2075	0,416	Conserved protein
2076	0,506	Conserved protein
2077	0,543	Transposase
2078	0,664	Transposase
2079	0,496	Transposase
2080	0,545	Conserved protein
2081	0,189	AMIDOHYDROLASE (putative)
2082	0,211	Acetyltransferase
2083	0,450	Glucoamylase
2084	0,245	Trp repressor binding protein
2085	0,608	Dolichyl-phosphate glucose synthetase
2086	0,521	Galactosyltransferase
2087	0,309	Glycosyltransferase
2088	0,671	Hypothetical protein
2089	0,581	Hypothetical protein
2090	0,899	Transposase

2091	0,812	Conserved protein
2092	0,676	Glucose-1-phosphate thymidyltransferase
2093	0,305	Polysaccharide ABC transporter, ATP-binding protein
2096	0,653	Polysaccharide ABC transporter, ATP-binding protein
2097	0,511	REVERSE TRANSCRIPTASE
2098	0,407	Transposase
2099	0,398	Transposase
2100	0,682	Hypothetical protein
2101	0,426	Hypothetical protein
2102	0,720	TYPE I RESTRICTION-MODIFICATION SYSTEM SPECIFICITY SUBUNIT
2103	0,653	TYPE I RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT
2106	0,494	Conserved protein
2107	0,442	Conserved protein
2108	0,586	Conserved protein
2109	0,807	Conserved protein
2110	0,613	Conserved protein
2111	0,205	Conserved protein
2112	0,618	Conserved protein
2113	0,748	Homoserine dehydrogenase
2114	0,615	ATP-dependent DNA ligase
2115	0,609	Hypothetical protein
2116	0,877	Conserved protein
2117	0,671	Conserved protein
2118	0,516	Hypothetical protein
2119	0,736	Conserved protein
2120	0,504	Hypothetical protein
2121	0,558	Conserved protein
2122	0,742	Hypothetical protein
2123	0,679	Phosphoenolpyruvate synthase
2124	0,579	Conserved protein
2125	0,449	Hypothetical protein
2126	0,384	Conserved protein
2127	0,660	Multiple antibiotic resistance protein
2128	0,615	Conserved protein
2128	0,452	Conserved protein
2129	0,611	Hypothetical protein

2130	0,542	Conserved protein
2131	0,348	Conserved protein
2133	0,429	Conserved protein
2134	0,399	Conserved protein
2135	0,665	TYPE I RESTRICTION-MODIFICATION SYSTEM SPECIFICITY SUBUNIT
2136	0,722	TYPE I RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT
2137	0,367	Hypothetical protein
2138	0,878	Hypothetical protein
2139	1,131	Hypothetical protein
2139	0,281	Hypothetical protein
2140	0,765	Conserved protein
2141	0,542	Conserved protein
2142	2,830	Conserved protein
2143	0,619	Hypothetical protein
2144	0,372	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2145	0,430	Aminoacyl-histidine dipeptidase
2146	0,309	Hypothetical protein
2147	0,470	Conserved protein
2148	0,330	Hypothetical protein
2150	0,571	Hypothetical protein
2151	0,763	Conserved protein
2152	0,504	Hypothetical protein
2153	1,261	Hypothetical protein
2154	1,032	Hypothetical protein
2155	0,543	Hypothetical protein
2156	0,549	Hypothetical protein
2157	0,192	Hypothetical protein
2158	0,278	Hypothetical protein
2159	0,408	Putative DNA recombinase
2160	0,408	Hypothetical protein
2161	0,446	Hypothetical protein
2162	0,282	Hypothetical protein
2163	0,369	Conserved protein
2164	0,510	Iron-containing alcohol dehydrogenase
2165	0,331	Glycogen debranching enzyme
2165	0,249	Glycogen debranching enzyme

2166	0,280	Conserved protein
2167	0,699	Conserved protein
2168	0,607	Two component system histidine kinase
2169	0,430	Conserved protein
2170	0,938	Conserved protein
2171	0,467	Acylphosphatase
2172	0,667	Cobalt-zinc-cadmium resistance protein
2173	0,329	Putative phosphoglycerate mutase
2174	0,278	Hypothetical protein
2176	0,482	Glyceraldehyde 3-phosphate dehydrogenase
2177	0,428	Suppressor protein SuhB homolog
2178	0,309	Hypothetical protein
2181	0,473	Conserved protein
2183	0,451	INDOLEPYRUVATE FERREDOXIN OXIDOREDUCTASE, SUBUNIT ALPHA
2184	0,593	Hypothetical protein
2185	0,385	IRON-SULFUR FLAVOPROTEIN
2186	0,446	DNA repair protein
2187	0,495	Molybdopterin converting factor, subunit 2
2188	0,486	Molybdopterin-guanine dinucleotide biosynthesis protein
2189	0,682	Hypothetical protein
2190	0,599	Conserved protein
2191	0,411	Conserved protein
2192	0,280	Pirin
2193	0,520	Conserved protein
2194	0,379	Conserved protein
2195	0,327	Hypothetical protein
2196	0,454	Hypothetical protein
2197	0,393	Carbon monoxide dehydrogenase accessory protein
2198	0,291	Conserved protein
2199	0,119	Asparagine synthetase [glutamine-hydrolyzing]
2200	0,393	Hypothetical protein
2201	0,589	Phosphoribosylformylglycinamide synthase
2202	2,436	Conserved protein
2203	0,486	Conserved protein
2204	0,500	Conserved protein
2208	0,457	Glutamate 5-kinase

2209	0,677	Gamma-glutamyl phosphate reductase
2210	0,646	Conserved protein
2211	0,523	Conserved protein
2212	0,306	Hypothetical protein
2213	0,781	Conserved protein
2214	0,344	Universal stress protein
2215	0,654	Conserved protein
2216	0,600	Conserved protein
2217	0,691	Conserved protein
2218	0,426	Conserved protein
2219	0,402	Conserved protein
2220	0,657	Molybdopterin biosynthesis MoeA protein
2221	0,465	Molybdopterin converting factor, small subunit
2222	0,418	Conserved protein
2223	0,532	Conserved protein
2224	0,864	Na ⁺ /H ⁺ antiporter
2224	0,365	Na ⁺ /H ⁺ antiporter
2225	0,616	Cation-transporting ATPase
2226	0,488	Conserved protein
2227	0,648	Conserved protein
2228	0,705	Succinate-semialdehyde dehydrogenase [NADP ⁺]
2229	0,406	Conserved protein
2230	0,430	Glycosyltransferases involved in cell wall biogenesis (putative)
2231	0,711	Transcriptional regulator, ArsR family
2232	0,956	Conserved protein
2233	0,473	Coenzyme F390 synthetase/phenylacetyl-CoA ligase
2234	0,315	Hypothetical protein
2235	0,447	Conserved protein
2236	0,760	Conserved protein
2237	0,501	Conserved protein
2238	0,409	Conserved protein
2239	0,208	Bacterioferritin comigratory protein
2240	0,477	Conserved protein
2241	0,541	Conserved protein
2242	0,325	Deoxyribodipyrimidine photolyase
2243	0,421	Conserved protein

2244	0,597	Cell division cycle protein 48 homolog
2245	0,394	Phosphoribosylamidoimidazole-succinocarboxamide synthase
2246	0,882	Conserved protein
2247	0,640	Conserved protein
2248	0,628	protein Translation Initiation Factor 1 (IF-1)
2249	0,685	Conserved protein
2250	0,215	Phosphoribosylformylglycinamide synthase
2251	0,402	Alpha-amylase
2252	0,489	Alpha-amylase
2253	0,656	Conserved protein
2254	0,493	Glucoamylase
2255	0,433	Seryl-tRNA synthetase
2256	0,842	Periplasmic serine protease
2257	0,491	Methionyl-tRNA synthetase
2258	0,442	Adenylate cyclase (EC 4.6.1.1)
2259	0,695	HOLO-[ACYL-CARRIER PROTEIN] SYNTHASE (EC 2.7.8.7)
2260	0,480	Beta-ketoacyl synthase/ thiolase
2261	0,637	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)
2262	0,723	Putative transcriptional regulator
2263	0,692	Conserved protein
2264	0,213	Conserved protein
2265	0,691	Hypothetical protein
2266	0,314	Transposase
2267	0,522	Conserved protein
2269	0,512	Conserved protein
2270	0,495	Conserved protein
2271	0,533	DNA polymerase IV
2272	0,448	Cobalt transporter, ATP-binding protein
2273	1,470	Cobalt transport protein
2274	2,661	Hypothetical protein
2275	0,496	Putative methyltransferase
2276	0,738	Putative methyltransferase
2277	1,192	Hypothetical protein
2278	1,263	Cobalamin biosynthesis protein CbiM
2279	1,011	Cobalamin biosynthesis protein CbiM
2280	0,657	Endonuclease III

2281	0,488	Conserved protein
2282	0,503	Glutathione reductase
2283	0,395	Bifunctional purine biosynthesis protein PurH
2284	0,940	Conserved protein
2285	0,732	Conserved protein
2286	0,380	Cation-transporting ATPase
2287	0,640	Putative methyltransferase
2288	0,427	Transcriptional regulator
2289	0,747	Phosphoglycerate mutase
2290	0,564	Conserved protein
2291	0,440	FLAP ENDONUCLEASE-1 (RAD27/FEN1 family)
2292	0,681	Hypothetical protein
2293	0,466	Conserved protein
2294	0,816	Conserved protein
2295	0,557	POTASSIUM/COPPER-TRANSPORTING ATPASE
2296	0,459	ABC transporter, ATP-binding protein
2297	0,647	Conserved protein
2298	0,620	Conserved protein
2299	0,616	Conserved protein
2300	0,618	Conserved protein
2301	0,670	Conserved protein
2302	0,613	Conserved protein
2303	0,584	4-carboxymuconolactone decarboxylase
2304	0,942	Conserved protein
2305	2,099	MutT related protein
2306	0,819	Aldehyde ferredoxin oxidoreductase
2307	0,387	protein Translation Initiation Factor 5A (IF-5A)
2308	0,871	Agmatinase
2315	0,364	Hypothetical protein
2316	0,617	Hypothetical protein
2317	0,207	Hypothetical protein
2321	1,170	Transposase
2322	0,126	Hypothetical protein
2325	0,473	Hypothetical protein
2326	0,722	INTEGRAL MEMBRANE PROTEIN
2327	0,488	Conserved protein

2328	0,600	Conserved protein
2329	0,559	Conserved protein
2330	0,510	Conserved protein
2331	0,441	Acetolactate synthase small subunit
2332	0,442	Coenzyme F390 synthetase
2333	0,469	Conserved protein
2334	0,710	Prefoldin beta subunit
2335	0,540	Conserved protein
2336	0,466	Hypothetical protein
2337	0,455	2-isopropylmalate synthase
2338	1,006	Acetolactate synthase large subunit
2339	0,415	Acetolactate synthase small subunit
2340	0,905	Ketol-acid reductoisomerase
2341	0,182	Nitroreductase family protein
2342	2,070	Putative nickel-responsive regulator NikR
2343	0,548	Hypothetical protein
2344	0,337	Glutamate synthase [NADPH]
2345	0,642	Probable dihydroorotate dehydrogenase electron transfer subunit
2347	0,345	Transcriptional regulator, ArsR family
2348	0,295	METHYLTRANSFERASE
2349	0,516	MANNOSE-6-PHOSPHATE ISOMERASE/ MANNOSE-1-PHOSPHATE GUANYLYL TRANSFERASE
2350	0,502	GDP-mannose 4,6 dehydratase
2351	0,421	GDP-FUCOSE SYNTHETASE
2352	0,590	Polysaccharide ABC transporter, permease protein
2353	0,502	Polysaccharide ABC transporter, ATP-binding protein
2354	1,047	MANNOSYLTRANSFERASE
2355	1,095	Glycosyltransferase involved in cell wall biogenesis
2356	0,652	Glycosyltransferase involved in cell wall biogenesis
2357	0,675	Glycosyltransferase involved in cell wall biogenesis
2358	0,960	MANNOSYLTRANSFERASE
2359	0,487	GLUCOSYLTRANSFERASE
2360	0,484	GLYCOSYL TRANSFERASE
2362	0,566	Oligosaccharyl transferase
2363	0,433	3-isopropylmalate dehydratase
2364	0,513	Conserved protein
2365	0,367	Conserved protein

2366	0,449	Isocitrate dehydrogenase [NADP]
2367	0,472	Alpha-acetolactate decarboxylase
2368	0,283	PUTATIVE FLAVODOXIN
2369	0,420	Conserved protein
2370	0,618	FLAVOPROTEIN
2371	0,476	IRON-SULFUR FLAVOPROTEIN
2372	0,414	Hypothetical protein
2373	0,331	Desulfoferredoxin
2374	0,464	Hypothetical protein
2375	0,333	Zinc finger protein
2377	0,503	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase
2378	0,468	F420H2 Dehydrogenase Subunit FpoF
2378	0,262	F420H2 Dehydrogenase Subunit FpoF
2379	0,394	Nicotinamide-nucleotide adenyltransferase
2379	0,345	Nicotinamide-nucleotide adenyltransferase
2380	0,447	Conserved protein
2381	0,630	Hypothetical protein
2382	0,390	Transposase
2383	0,150	Transposase
2384	0,525	Hypothetical protein
2385	0,589	Conserved protein
2386	0,592	Conserved protein
2387	0,564	Undecaprenyl pyrophosphate synthetase
2388	0,385	Conserved protein
2389	0,392	Conserved protein
2390	0,479	Long-chain-fatty-acid--CoA ligase
2391	0,905	Conserved protein
2392	0,594	NH3-dependent NAD(+) synthetase
2393	0,508	Iron-sulfur cluster-binding protein
2394	0,921	Acetyltransferases
2395	0,439	Conserved protein
2396	0,522	Probable radical-forming protein
2397	0,305	Hypothetical protein
2398	0,356	Conserved protein
2399	0,254	Conserved protein
2400	0,524	Nucleoside-triphosphatase

2401	0,334	O-sialoglycoprotein endopeptidase
2402	0,346	Conserved protein
2404	0,801	SSU ribosomal protein S24E
2405	0,773	Hypothetical protein
2407	0,425	DNA-directed RNA polymerase subunit E'
2408	0,514	Conserved protein
2409	0,731	protein Translation Initiation Factor 2 subunit gamma (IF-2g)
2410	0,590	Conserved protein
2411	0,712	Integral membrane protein
2412	0,506	Conserved membrane protein
2413	0,660	GLYCEROL 1-PHOSPHATE DEHYDROGENASE (putative)
2414	0,504	Conserved protein
2415	0,771	Conserved protein
2417	0,523	Sulfate adenylyltransferase
2418	0,442	Conserved protein
2418	0,402	Conserved protein
2419	0,652	Conserved protein
2420	0,331	Conserved protein
2422	0,526	GLYCOSYLTRANSFERASE
2423	0,264	Conserved protein
2424	2,134	Hypothetical protein
2425	0,640	Transposase
2426	4,164	Phosphate-binding protein
2426	0,470	Phosphate-binding protein
2427	1,445	Phosphate transport ATP-binding protein
2428	0,210	Phosphate transport system protein
2429	0,961	PUTATIVE PHOSPHATE REGULATORY PROTEIN
2430	0,346	ARSENATE REDUCTASE
2431	0,504	Conserved protein
2432	0,499	Alkaline phosphatase
2433	0,632	Transcriptional regulator, lcc related protein
2434	0,806	ABC transporter, ATP-binding protein
2435	0,243	ABC transporter, ATP-binding protein
2436	0,556	Conserved protein
2437	0,347	Acetyltransferase
2438	0,696	Hypothetical protein

2439	0,468	Transcriptional regulator
2440	1,196	Hypothetical protein
2441	0,982	Hypothetical protein
2442	0,481	Hypothetical protein
2443	0,599	Conserved protein
2444	0,539	Hypothetical protein
2445	0,759	Hypothetical protein
2446	0,306	Hypothetical protein
2447	0,457	Hypothetical protein
2449	0,623	Conserved protein
2450	1,234	Dipeptide ABC transporter, binding protein
2451	0,473	Dipeptide ABC transporter, binding protein
2452	2,093	Dipeptide ABC transporter, permease protein
2453	1,548	Dipeptide ABC transporter, permease protein
2454	0,780	Dipeptide ABC transporter, ATP-binding protein
2455	1,452	Dipeptide ABC transporter, ATP-binding protein
2456	1,003	Conserved protein
2457	0,652	Conserved protein
2458	0,571	Hypothetical protein
2459	0,420	Conserved protein
2460	0,499	RNA SIGNAL RECOGNITION PARTILCE 4.5S RNA
2461	0,480	Conserved protein
2462	0,415	Undecaprenyl pyrophosphate synthetase
2463	0,455	METHYLTRANSFERASE
2466	0,496	Conserved protein
2467	0,408	Conserved protein
2469	0,556	Hypothetical protein
2469	0,464	Hypothetical protein
2470	0,447	Hypothetical protein
2471	0,501	Conserved protein
2472	0,334	Conserved protein
2473	0,911	Superfamily I DNA and RNA helicase
2474	0,323	Conserved protein
2475	1,134	O-linked N-acetylglucosamine transferase
2476	0,281	Hypothetical protein
2477	0,471	Conserved protein

2478	0,470	Conserved protein
2479	0,425	Hypothetical protein
2480	0,565	Argininosuccinate synthase
2481	0,519	Carbamoyl-phosphate synthase large chain
2482	0,489	Carbamoyl-phosphate synthase small chain
2483	1,126	Glycine betaine transporter, ATP-binding protein (OtaA)
2483	0,878	Glycine betaine transporter, ATP-binding protein (OtaA)
2484	0,676	Glycine betaine transporter, permease protein (OtaB)
2484	0,596	Glycine betaine transporter, permease protein (OtaB)
2485	0,567	Glycine betaine transporter, substrate-binding protein (OtaC)
2486	0,682	Conserved protein
2487	0,426	Hypothetical protein
2488	0,554	Hypothetical protein
2489	0,951	Hypothetical protein
2490	0,545	Acetylornithine aminotransferase
2491	0,616	Aldehyde dehydrogenase
2492	0,496	Conserved protein
2492	0,481	Conserved protein
2493	0,811	Glutamyl-tRNA (Gln) amidotransferase
2494	0,289	Hypothetical protein
2496	0,571	Transposase
2497	0,237	Universal stress protein
2500	0,446	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENASE, SUBUNIT F
2501	0,226	Ferredoxin-thioredoxin reductase, catalytic chain
2502	0,489	TUNGSTEN-CONTAINING FORMYLMETHANOFURAN DEHYDROGENASE SUBUNIT B
2502	0,399	TUNGSTEN-CONTAINING FORMYLMETHANOFURAN DEHYDROGENASE SUBUNIT B
2503	0,352	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENASE, SUBUNIT D
2504	0,605	Conserved protein
2505	0,836	SAM-dependent methyltransferases
2506	0,924	SURFACE LAYER PROTEIN B
2507	0,546	SURFACE LAYER PROTEIN B
2508	0,606	CONSERVED PROTEIN
2509	0,660	Hypothetical protein
2510	0,471	N-methylhydantoinase (ATP hydrolyzing)
2511	0,408	Sodium-dependent transporter
2512	0,368	Putative ribosomal RNA methyltransferase

2514	0,470	Thermosome b-subunit
2515	0,639	Ribose 5-phosphate isomerase
2516	0,639	Aspartyl-tRNA synthetase
2517	0,349	Conserved protein
2518	0,239	Hypothetical protein
2519	0,851	Hypothetical protein
2520	0,249	Xanthine-guanine phosphoribosyltransferase
2521	0,478	Conserved protein
2522	0,435	Hypothetical protein
2523	0,897	Hypothetical Cytosolic protein
2524	0,634	Phosphoserine phosphatase
2525	0,229	Shikimate kinase
2526	0,444	Conserved protein
2527	0,592	Hypothetical protein
2528	0,551	Pyrimidine-nucleoside phosphorylase
2529	0,488	Transporter
2530	0,275	Conserved protein
2531	0,520	ABC transporter permease protein
2532	0,381	Conserved protein
2533	0,585	Cobyric acid synthase
2534	0,638	Conserved protein
2535	0,635	Transposase
2536	0,441	Ornithine cyclodeaminase
2537	0,455	Conserved protein
2538	0,372	O-linked N-acetylglucosamine transferase
2539	0,353	Conserved protein
2540	0,374	Conserved protein
2541	0,426	Serine/threonine protein phosphatase
2542	0,434	O-linked N-acetylglucosamine transferase
2544	0,500	FxsA protein
2545	0,765	Hypothetical protein
2546	0,475	Hypothetical protein
2547	0,612	Cysteine desulfhydrase
2548	0,779	NifU protein
2549	0,601	Ribosomal protein S6 modification protein
2550	0,662	Hypothetical protein

2551	0,925	Conserved protein
2553	0,978	Conserved protein
2554	0,275	Putative transmembrane efflux protein
2555	0,517	Transcriptional regulator, MarR family
2556	0,505	Hypothetical protein
2558	0,608	CTP synthase
2559	0,821	Hypothetical protein
2560	0,224	Carbon monoxide dehydrogenase
2561	0,293	Iron-sulfur protein
2562	0,517	Universal stress protein
2563	0,283	Conserved protein
2564	0,666	Universal stress protein
2565	0,651	PmbA protein
2566	0,732	Zinc metalloprotease
2567	0,410	ATP-dependent protease La
2568	0,693	Conserved protein
2569	0,412	Conserved protein
2570	0,719	Conserved protein
2571	0,255	Conserved protein
2572	0,440	Threonine synthase
2573	0,616	Sulfofpyruvate decarboxylase alpha chain
2574	0,419	Ferredoxin oxidoreductase
2575	0,498	Zn-dependent hydrolase
2576	0,704	Conserved protein
2577	0,768	CONSERVED PROTEIN (Archaea)
2578	0,499	Cytochrome c-type biogenesis protein
2579	0,651	Putative Cytochrome c biogenesis factors
2580	0,511	Conserved protein
2581	0,694	Orotate phosphoribosyltransferase
2582	0,509	4-carboxymuconolactone decarboxylase
2584	0,513	Phosphoribosylamine--glycine ligase
2585	0,455	Ornithine carbamoyltransferase
2586	0,634	Transcriptional regulator
2587	0,621	IRON-SULFUR FLAVOPROTEIN
2588	0,398	Conserved protein
2589	0,468	putative nucleoside-diphosphate-sugar epimerase

2590	0,708	Conserved protein
2591	0,739	DNA integration/recombination/inversion protein
2592	0,702	Conserved protein
2593	0,436	Conserved protein
2594	0,704	Conserved protein
2595	0,769	TYPE IIS RESTRICTION ENZYME
2597	0,354	ATP-dependent DNA helicase
2598	0,497	ATP-dependent DNA helicase
2599	0,655	Hypothetical protein
2600	0,995	Conserved protein
2601	0,406	DNA repair protein
2602	0,637	ATP-dependent protease La
2603	0,432	HOMOSPERMIDINE SYNTHASE
2604	0,302	Cobalt-zinc-cadmium resistance protein
2605	0,635	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2606	0,617	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2609	0,462	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2610	0,427	Transporter
2611	0,859	Methanol corrinoid protein MtaC
2612	1,662	Methanol:corrinoic methyltransferase MtaB
2613	0,563	Methylcobalamin:coenzyme M methyltransferase MtaA
2614	0,590	Conserved protein
2615	1,301	Conserved protein
2616	0,622	Conserved protein
2617	0,800	Diamine acetyltransferase
2618	0,633	Conserved protein
2619	0,505	Thiamine biosynthesis protein
2620	0,559	DNA topoisomerase III
2621	1,119	SSU ribosomal protein S3AE
2623	0,548	Short chain dehydrogenase/reductase
2624	1,157	Conserved protein
2625	0,737	NUCLEOTIDYLTRANSFERASE
2626	0,438	Hypothetical nucleotidyltransferase
2627	0,270	Conserved protein
2631	0,460	Transposase
2632	0,219	Hypothetical protein

2633	0,287	TYPE III RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT
2634	0,474	Conserved protein
2635	0,753	Conserved protein
2636	0,467	Conserved protein
2637	0,807	Conserved protein
2638	0,569	ATP-dependent DNA helicase
2640	0,481	Conserved protein
2641	0,284	Conserved protein
2643	0,608	Hypothetical protein
2644	0,617	Hypothetical protein
2646	1,514	Conserved protein
2648	0,378	Hypothetical protein
2649	0,318	Hypothetical protein
2650	0,270	Hypothetical protein
2652	0,411	Cysteine proteinase
2653	0,542	Conserved protein
2654	0,608	Putative single-stranded-DNA-specific exonuclease
2655	0,590	Hypothetical protein
2656	0,243	Hypothetical protein
2657	0,495	Conserved protein
2658	0,484	Conserved protein
2659	0,423	Conserved protein
2660	0,592	Conserved protein
2661	0,347	Fe-S OXIDOREDUCTASE
2662	0,372	THIAZOLE BIOSYNTHETIC ENZYME
2663	0,625	Hypothetical protein
2664	0,274	Molybdenum-pterin-binding-protein
2665	0,558	Conserved protein
2667	0,497	Conserved protein
2668	1,141	SODIUM-CALCIUM EXCHANGER
2669	1,579	Hypothetical protein
2670	0,686	Hypothetical protein
2671	0,422	Alanyl-tRNA synthetase
2672	0,233	Conserved protein
2673	0,319	Conserved protein
2674	0,337	PUTATIVE MECHANOSENSITIVE ION CHANNEL

2675	0,570	Conserved protein
2676	0,437	Hypothetical protein
2677	0,452	Conserved protein
2678	0,569	Ferredoxin
2679	0,748	Hypothetical protein
2680	0,746	Glycerol-3-phosphate cytidyltransferase
2681	0,588	Aspartate aminotransferase
2682	0,457	Riboflavin synthase, subunit beta
2686	0,675	Hypothetical protein
2687	0,376	Conserved protein
2688	0,178	Conserved protein
2690	0,616	Conserved protein
2691	0,426	Serine protease inhibitor
2692	0,338	Conserved protein
2693	0,528	Hypothetical protein
2695	0,334	Hypothetical protein
2696	0,412	Hypothetical protein
2697	0,558	Conserved protein
2698	0,535	Hypothetical protein
2699	0,614	MoxR-like ATPase
2700	0,371	Conserved protein
2701	0,478	ABC transporter, ATP-binding protein
2702	0,460	Conserved protein
2703	0,339	Conserved protein
2704	1,812	(Na ⁺)-linked D-alanine glycine permease
2704	0,511	(Na ⁺)-linked D-alanine glycine permease
2705	0,441	Hypothetical protein
2706	0,418	SODIUM-CALCIUM EXCHANGER PROTEIN
2707	0,580	Acetyltransferase
2708	0,550	Acetyltransferase
2709	0,700	transcriptional regulator
2710	0,175	Peptidyl-prolyl cis-trans isomerase
2711	0,405	Hypothetical protein
2712	0,409	Hypothetical protein
2713	0,518	N ⁵ ,N ¹⁰ -methenyltetrahydromethanopterin cyclohydrolase
2714	0,378	Hypothetical protein

2715	0,382	HYDROLASE
2716	0,486	Aspartate aminotransferase
2717	0,472	Hypothetical protein
2718	0,839	Hypothetical protein
2719	0,532	Sensory Transduction protein Kinase
2720	1,149	Aldehyde ferredoxin oxidoreductase
2720	0,312	Aldehyde ferredoxin oxidoreductase
2721	0,267	Putative molybdopterin converting factor
2722	0,438	Hypothetical protein
2723	0,343	Hypothetical protein
2724	0,688	Conserved protein
2725	0,320	Magnesium and cobalt transport protein CorA
2726	0,696	Conserved protein
2727	0,430	Hypothetical protein
2729	0,658	Coenzyme F390 synthetase
2730	0,522	Putative pyruvate:ferredoxin oxidoreductase
2731	0,801	Indolpyruvate ferredoxin oxidoreductase, alpha subunit
2732	0,249	Hypothetical protein
2735	0,515	NAD-dependent malic enzyme
2736	0,359	Hypothetical protein
2737	0,565	Conserved protein
2738	1,021	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2739	0,482	Conserved protein
2740	0,717	Conserved protein
2740	0,528	Conserved protein
2741	0,510	LSU ribosomal protein L37AE
2742	0,460	Ribonuclease
2743	0,449	Ribonuclease
2744	0,650	Hypothetical protein
2745	0,517	Hypothetical protein
2746	0,344	Proteasome, subunit-alpha
2747	0,525	Hypothetical protein
2748	0,731	Hypothetical protein
2749	0,489	Hypothetical protein
2750	0,467	LSU ribosomal protein L15E
2750	0,437	LSU ribosomal protein L15E

2751	0,366	Hypothetical protein
2752	0,516	Hypothetical protein
2755	0,769	Probable ATP-dependent helicase
2756	0,424	Hypothetical protein
2757	0,489	Type I restriction enzyme
2758	0,569	NUCLEOTIDYLTRANSFERASE
2759	0,389	NUCLEOTIDYLTRANSFERASE
2760	0,223	NUCLEOTIDYLTRANSFERASE
2761	0,447	Hypothetical protein
2763	0,408	Hypothetical protein
2764	0,334	Hypothetical protein
2765	0,520	Zinc metalloprotease
2766	0,383	Conserved protein
2767	0,321	Hypothetical protein
2774	0,209	Transposase
2775	0,494	Conserved protein
2776	0,357	Conserved protein
2777	0,318	Transporter
2778	0,335	Conserved protein
2779	0,230	Hypothetical protein
2780	1,961	Ammonium transporter
2781	2,128	Nitrogen regulatory protein P-II
2782	0,991	SAM-dependent methyltransferases
2783	0,431	Conserved protein
2784	0,627	MOLYBDENUM TRANSPORTER, ATP-BINDING PROTEIN
2785	0,354	Molybdenum transporter, permease protein
2786	0,657	Molybdate-binding protein
2787	0,544	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN
2788	0,432	Nitrogenase iron-molybdenum cofactor biosynthesis protein
2789	1,082	Nitrogenase molybdenum-iron protein beta chain
2790	0,688	Nitrogenase molybdenum-iron protein alpha chain
2791	0,237	Nifl(2), GlnB-like protein
2792	0,276	NITROGEN FIXATION NIFHD REGION GLNB-LIKE PROTEIN
2793	0,933	Nitrogenase iron protein
2794	0,932	Oxidoreductase (flavoprotein)
2795	0,742	Hypothetical protein

2796	0,773	Hypothetical protein
2797	0,505	Pyruvate kinase
2797	0,446	Pyruvate kinase
2798	0,657	Fructose-bisphosphate aldolase
2801	0,341	Fructose-bisphosphate aldolase
2802	0,348	CO DEHYDROGENASE/ACETYL-COA SYNTHASE GAMMA SUBUNIT
2802	0,346	CO DEHYDROGENASE/ACETYL-COA SYNTHASE GAMMA SUBUNIT
2803	0,664	Conserved protein
2804	0,807	Hypothetical protein
2805	0,598	Transcription initiation factor IIE, alpha subunit
2806	0,408	Conserved protein
2807	0,473	Proteasome, beta subunit
2808	0,758	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT
2809	0,950	Beta-phosphoglucomutase
2810	0,625	Cell division protein
2811	0,493	Dihydropteroate synthase
2812	0,466	Conserved protein
2813	2,497	VACUOLAR-TYPE H ⁺ -PYROPHOSPHATASE
2813	0,538	VACUOLAR-TYPE H ⁺ -PYROPHOSPHATASE
2814	1,754	VACUOLAR-TYPE H ⁺ -PYROPHOSPHATASE
2814	0,536	VACUOLAR-TYPE H ⁺ -PYROPHOSPHATASE
2815	0,698	Hypothetical permease
2816	0,993	Hypothetical permease
2820	0,551	Prolyl-tRNA synthetase
2821	0,955	Conserved protein
2824	0,576	Copper-binding protein
2825	0,216	Copper-binding protein
2826	0,546	Hypothetical protein
2827	0,358	Succinate-semialdehyde dehydrogenase [NADP ⁺]
2828	0,413	Acetolactate synthase
2831	0,623	TRANSLATION INITIATION FACTOR 1A (EIF-1A)
2832	0,601	Multidrug efflux pump
2833	0,484	SAM-dependent methyltransferases
2834	0,789	Uncharacterized permease
2835	0,329	Copper-exporting ATPase
2837	0,705	COP associated protein

2838	0,390	Ech Hydrogenase, Subunit EchF
2839	0,413	Ech Hydrogenase, Subunit EchE
2840	0,527	Ech Hydrogenase, Subunit EchD
2840	0,501	Ech Hydrogenase, Subunit EchD
2841	0,360	Ech Hydrogenase, Subunit EchC
2842	0,375	Ech Hydrogenase, Subunit EchB
2843	0,718	Ech Hydrogenase, Subunit EchA
2844	0,709	Hydrogenase expression/formation protein
2845	0,866	HYDROGENASE EXPRESSION/FORMATION PROTEIN
2846	0,888	HYDROGENASE EXPRESSION/FORMATION PROTEIN
2847	0,487	Hydrogenase expression/formation protein
2847	0,401	Hydrogenase expression/formation protein
2848	0,513	Hydrogenase expression/formation protein
2849	0,792	F420-NONREDUCING HYDROGENASE I PRECURSOR
2850	0,310	F420-NONREDUCING HYDROGENASE I, LARGE SUBUNIT
2851	0,490	F420-NONREDUCING HYDROGENASE I, CYTOCHROME B SUBUNIT
2853	0,412	UBIQUINONE BIOSYNTHESIS PROTEIN
2854	0,476	Hypothetical protein
2855	0,318	METHYLTRANSFERASE
2856	0,470	Argininosuccinate lyase
2857	0,616	L-asparaginase
2858	0,201	Sodium/proline symporter
2860	0,389	L-sorbose dehydrogenase
2861	0,700	METHYLTRANSFERASE
2862	0,320	Hypothetical protein
2863	0,493	Hypothetical protein
2864	0,549	Coenzyme F390 Synthetase/Phenylacetate-CoA Ligase
2866	0,492	Conserved protein
2867	0,515	Conserved protein
2868	0,434	Hypothetical protein
2869	0,383	Transcriptional regulator, ArsR family
2870	0,348	Conserved protein
2871	0,437	Hypothetical protein
2872	0,455	Potassium channel protein
2873	0,411	Hypothetical protein
2874	0,417	ABC transporter, ATP-binding protein

2875	0,531	ABC Transporter, permease protein
2876	0,642	Hypothetical protein
2877	0,652	Hypothetical protein
2878	0,937	Membrane protein related to SecD/SecF
2879	0,297	Transcriptional regulator, MarR family
2880	0,291	ABC transporter, permease protein
2881	0,539	Hypothetical permease
2882	0,862	Conserved protein
2883	0,416	Amino acid permease
2884	0,739	Putrescine-ornithine antiporter
2885	0,697	Hypothetical protein
2886	0,350	Hypothetical protein
2887	0,619	Hypothetical protein
2888	0,229	5-NITROIMIDAZOLE ANTIBIOTIC RESISTANCE PROTEIN
2889	0,449	Acetolactate synthase
2890	0,489	Hypothetical protein
2891	0,352	MoxR-like ATPase
2893	0,516	Enolase
2894	0,567	Hypothetical protein
2895	0,385	Hypothetical protein
2896	0,394	ABC transporter, ATP-binding protein
2897	0,484	ABC-Type transporter, permease protein
2898	0,307	ABC-Type transporter, permease protein
2899	0,136	Ribonucleoside-diphosphate
2900	0,610	Peptidyl-prolyl cis-trans isomerase
2901	0,361	Conserved protein
2902	0,339	Hypothetical protein
2903	0,646	Conserved protein
2904	0,480	Hypothetical protein
2905	0,677	GLUCOSE-6-PHOSPHATE DEHYDROGENASE [coenzyme F420 dependent]
2906	0,992	Indole-3-glycerol phosphate synthase
2907	1,279	Tryptophan synthase, beta chain
2908	0,515	Tryptophan synthase, alpha chain
2910	0,757	Anthranilate phosphoribosyltransferase
2911	1,077	N-5'-phosphoribosyl)anthranilate isomerase
2913	0,337	Conserved protein

2914	0,386	Transcriptional regulator, ArsR family
2915	0,572	Conserved protein
2915	0,502	Conserved protein
2916	0,814	Conserved protein
2917	0,426	Transposase
2918	0,524	Transposase
2919	0,705	Conserved protein
2921	0,821	Conserved protein
2921	0,687	Conserved protein
2922	0,829	Conserved protein
2923	0,877	Conserved protein
2924	0,531	ABC transporter, permease protein
2925	1,248	ABC transporter, ATP-binding protein
2926	0,767	Dipeptide/oligopeptide transporter, ATP-binding protein
2927	0,271	Dipeptide/oligopeptide transporter, permease protein
2928	1,024	Dipeptide/oligopeptide transporter, permease protein
2929	1,223	METHYLTRANSFERASE
2930	0,810	Dipeptide/oligopeptide-binding protein
2931	0,631	SSU ribosomal protein S6E
2932	0,367	protein Translation Initiation Factor IF2
2933	0,420	Nucleoside diphosphate kinase
2934	0,513	SSU ribosomal protein S28E
2935	0,538	LSU ribosomal protein L7AE
2936	0,367	REPLICATION FACTOR C SUBUNIT
2937	0,438	CONSERVED PROTEIN (Archaea)
2939	0,259	BRAMP
2940	0,190	Cell division cycle protein (AAA family ATPase)
2941	0,538	Putative inosine monophosphate dehydrogenase
2944	0,431	SUA5 protein
2945	0,541	Ribulose biphosphate carboxylase large chain
2945	0,452	Ribulose biphosphate carboxylase large chain
2946	0,453	Cation transporter
2947	0,387	Cation transporter
2955	0,300	Cation transporter
2956	0,820	Putative heat shock protein
2957	0,917	Putative heat shock protein

2958	1,524	CdcH protein
2959	1,245	Transcriptional regulator, ArsR family
2962	0,413	Conserved protein
2963	0,418	Putative pyridoxine biosynthesis protein
2964	0,347	Imidazoglycerol-phosphate synthase
2965	0,982	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
2969	0,524	Conserved protein
2970	0,312	Phosphohydrolase
2971	0,997	GLYCOSYL TRANSFERASE
2972	0,657	Conserved protein
2973	0,580	Transposase
2974	0,621	Conserved protein
2975	0,637	Conserved protein
2976	0,633	Conserved protein
2977	0,812	Conserved protein
2978	0,730	THIAMIN-MONOPHOSPHATE KINASE
2980	0,524	NifB protein
2981	1,136	NifB protein
2982	2,184	6-pyruvoyltetrahydropterin synthase
2983	2,622	Conserved protein
2984	1,729	Conserved protein
2985	2,151	Conserved protein
2986	0,444	Conserved protein
2987	0,638	Putative serine/threonine protein phosphatase
2988	0,515	Dihydropyrimidinase
2989	0,372	Glutathione-independent formaldehyde dehydrogenase
2990	0,489	Conserved protein
2991	1,204	ATP-dependent RNA helicase
2992	0,312	Conserved protein
2993	0,177	Conserved protein
2994	0,186	Conserved protein
2995	0,255	Conserved protein
2996	0,668	Arsenical-resistance protein
3001	0,472	Conserved protein
3002	0,401	Hypothetical protein
3005	0,508	SIGNAL RECOGNITION PARTICLE, SUBUNIT FFH/SRP54

3006	0,568	GMP synthase [glutamine-hydrolyzing]
3007	1,083	2-dehydro-3-desoxyphosphoheptanote aldolase
3008	0,766	3-dehydroquinase synthase
3009	0,994	3-dehydroquinase dehydratase
3010	1,352	Shikimate 5-dehydrogenase
3011	1,021	Prephenate dehydrogenase
3012	0,911	Hypothetical protein
3013	0,236	METHYLTRANSFERASE
3014	0,851	Triosephosphate isomerase
3015	0,783	Conserved protein involved in sugar metabolism
3016	0,622	Endonuclease III
3017	0,410	Conserved protein
3018	0,450	Conserved protein
3019	0,640	Bacterioferritin
3019	0,593	Bacterioferritin
3021	1,048	Conserved protein
3022	0,756	Hypothetical protein
3023	0,675	Acetyltransferase
3024	1,200	Aspartate aminotransferase
3025	0,610	Myo-inositol 2-dehydrogenase
3026	0,505	NDP-N-acetyl-D-galactosaminuronic acid dehydrogenase
3027	1,001	Conserved protein
3028	0,796	O-antigen translocase
3029	0,681	Conserved protein
3030	0,658	Conserved protein
3031	0,713	Hypothetical protein
3036	0,493	ANTIBIOTIC RESISTANCE PROTEIN
3037	0,524	Putative ferredoxin
3038	0,516	Transcriptional regulator, ArsR family
3040	0,649	Hypothetical protein
3041	0,445	Conserved protein
3042	0,465	Pyruvate formate-lyase activating enzyme
3043	0,239	HYPOTHETICAL SENSORY TRANSDUCTION HISTIDINE KINASE
3044	0,226	Hypothetical protein
3045	0,167	Putative NADH oxidase
3046	1,149	Phosphoglycerate mutase

3047	0,499	Conserved protein
3049	0,814	Hypothetical protein
3050	0,150	Hypothetical protein
3051	0,433	Transposase
3052	0,881	Transposase
3053	0,606	DNA REPAIR HELICASE (RAD25/XPB family)
3054	0,457	Hypothetical protein
3057	0,645	Conserved protein
3058	0,526	Acetyltransferase
3059	0,439	Probable resolvase/ recombinase
3060	0,410	Probable transcriptional regulator
3061	0,603	Probable resolvase/ recombinase
3062	0,668	Membrane metalloprotease
3063	0,285	Periplasmic divalent cation tolerance protein
3064	0,383	Hypothetical protein
3065	1,117	Hypothetical protein
3066	1,947	ABC transporter, permease protein
3067	1,438	Conserved protein
3068	1,390	Hypothetical protein
3069	1,397	Cobalt transport ATP-binding protein
3069	0,411	Cobalt transport ATP-binding protein
3070	0,974	ABC transporter, permease protein
3071	2,786	Conserved protein
3072	0,898	Conserved protein
3073	0,417	Conserved protein
3074	1,218	ABC transporter, ATP-binding protein
3075	2,907	Conserved protein
3076	3,729	Conserved protein
3077	6,132	Conserved protein
3078	1,804	Hypothetical protein
3079	0,179	Hypothetical protein
3080	0,253	Transposase
3081	0,349	Deoxycytidylate deaminase
3082	0,333	Lactoylglutathione lyase
3083	0,424	Conserved protein
3085	0,235	Hypothetical protein

3087	0,728	Transposase
3088	0,838	Transcriptional regulator, ArsR family
3089	0,681	Conserved protein
3092	0,438	Uroporphyrinogen-III synthase
3093	0,582	Metallo cofactor biosynthesis protein (moaA/ nifB /pqqE family
3094	0,405	Hypothetical protein
3095	0,600	Conserved protein
3096	0,920	Hypothetical protein
3097	0,841	Hypothetical protein
3098	0,569	Valyl-tRNA synthetase
3099	0,772	Hypothetical protein
3100	0,326	FLAGELLA RELATED PROTEIN FlaJ
3101	0,477	FLAGELLA RELATED PROTEIN FlaI
3102	0,321	FLAGELLA RELATED PROTEIN FlaH
3103	0,530	Conserved protein
3104	0,531	Hypothetical protein
3105	0,349	Hypothetical protein
3106	0,549	Flagellin B1 precursor
3106	0,431	Flagellin B1 precursor
3107	0,517	Flagellin B1 precursor
3108	0,425	CHEMOTAXIS PROTEIN METHYLTRANSFERASE
3109	0,394	Chemotaxis protein
3110	0,497	Chemotaxis protein
3111	0,498	Chemotaxis protein
3112	0,480	Protein-glutamate methylesterase
3113	0,427	Chemotaxis protein
3114	0,391	Hypothetical Exported protein
3115	0,556	Chemotaxis protein
3115	0,242	Chemotaxis protein
3116	0,654	Methyl-accepting chemotaxis protein
3117	0,401	Hypothetical protein
3118	0,702	3-hydroxy-3-methylglutaryl-coenzyme A reductase
3119	0,435	Conserved protein
3120	0,437	Tryptophan synthase, beta chain
3121	0,424	PUTATIVE PHOSPHOMETHYLPYRIMIDINE KINASE/HYDROXYMETHYLPYRIMIDINE KINASE
3122	0,426	Putative snRNP Sm-like protein

3123	0,797	Amidophosphoribosyltransferase
3123	0,597	Amidophosphoribosyltransferase
3124	0,468	Hypothetical protein
3125	0,570	Probable cation efflux pump
3126	0,543	Transcriptional regulator
3127	0,414	Transcriptional regulator, MarR family
3128	0,567	Hypothetical protein
3129	0,401	Putative cation efflux pump
3130	0,452	Putative molybdopterin biosynthesis protein
3131	8,520	Conserved protein
3132	1,140	Conserved protein
3133	0,160	Hypothetical protein
3134	0,286	Conserved protein
3135	0,598	Glutamate dehydrogenase
3136	0,470	Acetyl-CoA synthetase, alpha subunit
3137	0,559	Hypothetical protein
3138	0,800	Sulfite reductase, assimilatory-type
3139	0,674	Transcriptional regulator, MarR family
3140	0,684	Sulfite reductase, assimilatory-type
3141	0,488	Hypothetical protein
3142	0,429	Hypothetical protein
3143	0,951	Conserved protein
3144	0,713	Ferredoxin
3145	0,514	Hypothetical protein
3146	0,735	Hypothetical protein
3147	0,291	Hypothetical protein
3148	0,491	CHORISMATE MUTASE/ PREPHENATE DEHYDRATASE
3149	0,670	Conserved protein
3150	0,876	MoxR-like ATPase
3151	0,578	Hypothetical Cytosolic protein
3152	0,508	Conserved protein
3153	0,654	Conserved protein
3154	0,447	Conserved protein
3155	0,891	Integral membrane protein
3156	0,969	SUGAR-PHOSPHATE NUCLEOTYDYL TRANSFERASE
3157	0,402	Conserved protein

3158	0,563	Peptidyl-prolyl cis-trans isomerase
3159	0,521	Peptidyl-prolyl cis-trans isomerase
3160	0,642	Peptidyl-prolyl cis-trans isomerase
3161	0,462	Hypothetical protein
3162	0,615	Conserved protein
3163	0,496	Hypothetical protein
3164	0,310	Hypothetical protein
3165	0,605	HETERODISULFIDE REDUCTASE, SUBUNIT HDRA
3166	0,546	HETERODISULFIDE REDUCTASE, SUBUNIT HDRC
3167	0,613	HETERODISULFIDE REDUCTASE, SUBUNIT HDRB
3168	0,484	Surface layer protein (putative)
3169	0,623	Hypothetical protein
3170	0,673	Hypothetical protein similar to C-terminal domain of HdrB
3170	0,328	Hypothetical protein similar to C-terminal domain of HdrB
3171	0,955	Conserved protein
3172	0,835	Conserved protein
3173	1,022	Surface layer protein (putative)
3174	0,432	Transposase
3175	0,552	Conserved protein
3176	0,605	Hypothetical protein similar to C-terminal domain of HdrB
3177	0,416	Conserved protein
3178	0,312	Conserved protein
3179	0,304	Conserved protein
3180	0,444	Hypothetical protein similar to C-terminal domain of HdrB
3181	0,504	Hypothetical protein
3182	0,542	Surface layer protein (putative)
3183	0,595	Conserved protein
3184	0,254	Hypothetical protein similar to C-terminal domain of HdrB
3185	0,633	Hypothetical protein
3186	0,213	3-isopropylmalate dehydratase
3188	0,659	Conserved protein
3189	0,280	FLAGELLA RELATED PROTEIN FlaJ
3190	0,417	FLAGELLA RELATED PROTEIN FlaI
3191	0,543	FLAGELLA RELATED PROTEIN FlaH
3193	0,247	Conserved protein
3194	0,349	Conserved protein

3195	0,164	Flagillin B1
3196	0,371	Pyruvate synthase, subunit beta
3197	0,365	Pyruvate synthase, subunit alpha
3198	0,621	Transposase
3199	0,412	Transposase
3220	0,669	Hypothetical protein
3223	0,393	Conserved protein
3228	5,414	Conserved protein
3231	0,559	Hypothetical protein
3232	0,430	Ferrous iron transport protein B
3234	1,002	Oligopeptide-binding protein OppA
3235	0,807	Putative NADH oxidase
3238	0,183	Hypothetical protein
3240	0,508	Conserved protein
3243	0,433	Conserved protein
3244	0,347	Hypothetical protein
3245	0,309	Transposase
3247	0,225	TRANSCRIPTIONAL REGULATOR, PBSX FAMILY
3249	0,690	Conserved protein
3250	0,332	Hypothetical protein
3251	0,318	Hypothetical protein
3253	0,536	Conserved protein
3254	0,372	Conserved protein
3255	0,319	Conserved protein
3257	0,629	Conserved protein
3258	0,406	Conserved protein
3261	0,144	Hypothetical protein
3262	0,469	Conserved protein
3264	0,548	Hypothetical protein
3265	0,325	Conserved protein
3266	0,400	Hypothetical protein
3267	0,255	Hypothetical protein
3269	0,300	Conserved protein
3270	0,296	Hypothetical protein
3272	0,673	Hypothetical protein
3273	0,280	Hypothetical protein

3275	0,306	Hypothetical protein
3276	0,169	Conserved protein
3277	0,839	Hypothetical protein
3281	0,215	Transposase
3283	0,345	Hypothetical protein
3285	0,929	Hypothetical protein
3286	0,483	Hypothetical protein
3287	0,275	Conserved protein
3288	0,220	Conserved protein
3289	0,645	Transposase
3291	0,385	Iron-dependent repressor
3293	0,644	Hypothetical protein
3295	0,182	Hypothetical protein
3296	0,605	LSU ribosomal protein L24P
3297	0,885	Hypothetical protein
3299	0,312	Hypothetical protein
3304	0,505	Hypothetical protein
3307	0,683	Hypothetical membrane associated protein
3309	0,717	Hypothetical protein
3311	0,373	Hypothetical protein
3313	0,284	Zinc finger protein
3317	0,629	Hypothetical protein
3320	0,393	Conserved protein
3321	0,216	Hypothetical protein
3323	0,603	Conserved protein
3325	0,532	Hypothetical protein
3328	0,572	Hypothetical protein
3330	0,400	Conserved protein
3331	0,303	Conserved protein
3332	0,171	Hypothetical protein
3333	0,469	Chromosomal protein
3334	0,478	Conserved protein
3335	0,528	ABC transporter, permease protein
3336	0,354	Hypothetical protein
3337	0,332	Hypothetical protein
3338	0,400	Conserved protein

3339	0,302	Conserved protein
3342	0,519	Hypothetical protein
3354	0,454	Hypothetical protein
3356	0,508	Hypothetical protein
3357	0,608	Conserved protein
3358	0,234	Conserved protein
3360	0,228	Conserved protein
3362	0,369	Putative Flavodoxin
3371	0,561	Polysaccharide ABC transporter, permease protein
3372	0,877	Transposase
3374	0,358	Conserved protein
3375	0,245	Hypothetical protein
3379	0,526	Conserved protein
3380	0,250	Conserved protein
3381	0,409	Conserved protein
3383	1,345	Hypothetical protein
3386	0,369	Conserved protein
3390	0,839	Conserved protein
3393	0,702	Conserved protein
3394	1,459	Conserved protein
3395	0,407	Conserved protein
3396	27,299	Conserved protein
3397	0,682	Transcriptional regulator, ArsR family
3400	0,824	Conserved protein
3402	0,385	Hypothetical protein
3403	0,619	glutamate dehydrogenase
3404	0,953	Conserved protein
3405	0,605	Hypothetical protein
3408	0,797	Conserved protein
3410	1,788	Conserved protein
3411	0,255	Hypothetical protein
3413	1,159	Conserved protein
3414	0,290	Hypothetical protein
3415	0,523	Conserved protein
3416	0,641	Conserved protein
3417	0,497	Conserved protein

3419	0,351	Conserved protein
3421	1,079	Transposase
3424	0,306	Conserved protein
3425	0,867	Conserved protein
3426	0,463	Conserved protein
3428	0,687	Hypothetical protein
3430	0,392	Conserved protein
3431	0,511	Conserved protein
3434	0,269	Hypothetical protein
3436	0,327	Conserved protein
3442	0,333	Hypothetical protein
3447	0,473	Hypothetical protein
3448	0,457	Transposase
3449	0,489	Conserved transmembrane protein
3454	0,512	Conserved protein
3456	0,587	Hypothetical protein
3458	0,377	Conserved protein
3459	0,371	Conserved protein
3466	0,319	Conserved protein
3475	0,388	Transposase
3477	0,277	Hypothetical protein
3479	0,246	Conserved protein
3481	0,853	Conserved protein
3484	0,475	Conserved transmembrane protein
3486	0,566	Conserved protein
3489	0,200	Conserved protein
3493	0,202	Conserved protein
3496	0,593	Conserved protein
3497	0,244	GLYCOSYL TRANSFERASE
3502	0,365	Endonuclease III
3509	0,471	Conserved protein
3511	0,346	Hypothetical protein
3514	0,451	Hypothetical protein
3515	0,249	Hypothetical protein
3529	0,262	Hypothetical protein
3535	0,440	Conserved protein

3536	0,279	Conserved protein
3545	0,373	Conserved protein
3547	0,591	Conserved protein
3551	0,476	METALLOPROTEINASE
3556	0,453	Conserved protein
3561	0,459	Hypothetical protein
3566	0,572	Hypothetical protein
3576	0,595	Hypothetical protein
3578	0,844	Hypothetical protein
3585	0,369	Hypothetical protein
3594	0,384	Conserved protein
3612	0,349	Hypothetical protein
3614	0,626	Hypothetical protein
3633	0,372	Hypothetical protein
3634	0,527	Conserved protein
3639	0,479	Hypothetical protein
3646	1,304	Conserved protein
3664	0,329	Hypothetical protein
3667	0,283	Hypothetical protein
3671	0,878	Hypothetical protein
3683	0,298	Hypothetical protein
3699	0,480	Conserved protein
3727	0,419	Hypothetical protein
3734	3,106	Hypothetical protein
3737	0,157	Hypothetical protein
3745	0,564	Hypothetical protein
3748	0,373	Hypothetical protein
3753	0,249	Hypothetical protein
3756	0,572	Conserved protein
3762	0,268	Hypothetical protein
3769	0,460	Hypothetical protein
3771	0,603	Hypothetical protein
3785	0,363	Hypothetical protein
3788	0,290	Hypothetical protein
3789	0,525	Hypothetical protein
3800	0,611	Transposase

3802	0,418	Putative ferredoxin
3806	0,450	Hypothetical protein
3809	0,562	LemA PROTEIN
3814	0,866	Hypothetical protein
3817	0,556	Transposase
3819	0,463	TYPE I RESTRICTION-MODIFICATION SYSTEM RESTRICTION SUBUNIT
3829	0,245	2-isopropylmalate synthase
3830	0,361	Conserved protein
3843	0,406	Conserved protein
3847	0,415	Conserved protein
3878	0,664	TYPE I RESTRICTION-MODIFICATION SYSTEM METHYLATION SUBUNIT
3908	0,520	Conserved protein
3911	0,516	Conserved protein
3940	0,476	Heterodisulfate reductase, subunit A
3946	0,254	Hypothetical protein
3956	0,319	DNA helicase II
3960	0,323	Hypothetical protein
3978	1,936	Hypothetical protein
3979	3,216	Hypothetical protein
3986	0,373	Conserved protein
3987	0,778	Conserved protein
3988	0,594	Histidinol dehydrogenase
3992	0,263	Hypothetical protein
3996	0,291	Conserved protein
4000	0,345	Hypothetical protein
4009	0,974	Conserved protein
4015	0,722	Oligosaccharyl transferase
4019	0,290	CO DEHYDROGENASE/ACETYL-COA SYNTHASE ALPHA SUBUNIT
4020	0,341	CO DEHYDROGENASE/ACETYL-COA SYNTHASE EPSILON SUBUNIT
4021	0,391	CO DEHYDROGENASE/ACETYL-COA SYNTHASE BETA SUBUNIT
4023	0,790	Conserved protein
4024	0,726	Conserved protein
4025	0,354	Thioredoxin 2
4028	0,798	Hypothetical protein
4029	0,537	Transposase
4029	0,528	Transposase

4030	0,625	Conserved protein
4032	0,224	Hypothetical protein
4034	0,591	Universal stress protein
4039	0,546	Conserved protein
4041	0,468	A1AO H+ ATPASE, SUBUNIT I
4042	0,587	A1AO H+ ATPASE, SUBUNIT H
4043	0,336	Transposase
4047	0,657	Pyrroline-5-carboxylate reductase
4058	0,205	Hypothetical protein
4063	0,337	Hypothetical protein
4064	0,703	Hypothetical protein
4066	0,446	Hypothetical protein
4070	0,709	Hypothetical protein
4073	0,409	Hypothetical protein
4081	0,241	Hypothetical protein
4086	0,645	Hypothetical protein
4087	0,600	Hypothetical protein
4088	0,544	Hypothetical protein
4090	0,570	Dolichol-phosphate mannosyltransferase
4093	0,590	NUCLEOTIDYLTRANSFERASE
4094	0,488	Conserved protein
4096	0,571	Hypothetical protein
4105	0,354	Conserved protein
4107	0,415	Conserved protein
4110	0,640	Conserved protein, Archaea
4112	0,614	Xanthine-guanine phosphoribosyltransferase
4115	1,141	Hypothetical protein
4116	1,226	Fe-S OXIDOREDUCTASE
4141	0,308	MOLYBDENUM FORMYLMETHANOFURAN DEHYDROGENASE SUBUNIT
4151	0,251	ATPase involved in DNA repair
4182	0,251	Hypothetical protein
4183	0,485	Hypothetical protein
4184	0,717	RNase P
4201	0,272	Hypothetical protein
4214	0,361	Hypothetical protein
4223	0,906	Putative glycosyltransferase

4224	0,420	Glucoamylase
4228	0,416	Conserved protein
4228	0,349	Conserved protein
4230	0,461	Transcriptional regulator
4237	0,467	Hypothetical protein
4244	0,799	Methylthiol:coenzyme M methyltransferase MtsA
4244	0,791	Methylthiol:coenzyme M methyltransferase MtsA
4245	0,342	Methylthiol corrinoid protein MtsB
4251	0,756	Hypothetical protein
4295	0,551	Hypothetical protein
4312	0,568	Hypothetical protein
4313	0,637	Transposase
4317	0,732	Transposase (N-terminal domain)
4359	0,504	Transcriptional regulator, ArsR family
4362	0,938	Transposase (N-terminal domain)
4388	0,509	Transposase
4414	0,638	REVERSE TRANSCRIPTASE
4417	0,627	REVERSE TRANSCRIPTASE
4433	0,714	Hypothetical protein
4434	0,221	Hypothetical protein
4441	0,629	Transposase
4460	0,506	Transposase (N-terminal domain)
4461	0,771	Transposase
4462	0,572	Transposase
4463	0,241	Hypothetical protein
4465	0,307	Hypothetical protein