

ERGO Orf	Ratio der Mediane Acetat- zu Methanolmedium (635/532)	Name
0003	6,76	Anthranilate synthase_ component I
0004	3,34	Anthranilate synthase_ component II
0005	3,50	Conserved protein
0006	1,19	Metal-dependent hydrolase
0007	1,00	Ribonuclease
0008	1,00	Hypothetical protein
0009	0,81	Phenylalanyl-tRNA synthetase_ beta chain
0012	0,79	Metal-dependent hydrolases
0013	1,03	Conserved protein
0014	0,81	AAA family ATPase
0016	0,82	Glucose-1-phosphate thymidyltransferase
0017	0,76	Phosphoglucomutase/phosphomannomutase
0018	0,96	Glucosamine--fructose-6-phosphate aminotransferase
0019	0,06	Glucose-1-phosphate thymidyltransferase
0020	0,87	Glycine betaine-binding protein
0021	0,89	Glycine betaine transporter_ ATP-binding
0022	1,00	Glycine betaine transport system_ permease
0023	1,00	Glycine betaine transport system_ permease
0025	3,38	Conserved protein
0028	0,97	Hypothetical protein
0030	1,10	Transcriptional regulator_ ArsR family
0031	0,90	Deoxyhypusine synthase
0032	0,30	Hypothetical protein
0033	0,70	Conserved protein
0034	0,88	Amidohydrolase (putative)
0035	1,06	Leucyl-tRNA synthetase
0036	0,94	Threonine synthase
0037	0,95	Hypothetical protein
0038	0,96	Hypothetical protein
0039	0,86	Membrane alanine aminopeptidase
0040	0,62	DNA-cytosine methyltransferase
0041	0,96	T/G-specific DNA glycosylase
0042	1,00	Superfamily II DNA and RNA helicase
0043	1,11	Hypothetical protein

0044	1,07	Endonuclease (putative)
0047	1,15	Conserved protein
0048	1,01	Conserved protein
0049	1,00	Hypothetical protein
0050	0,90	Conserved protein
0051	0,99	Conserved protein
0052	1,00	Conserved protein
0053	0,86	Conserved protein
0054	0,91	Conserved protein
0055	0,76	Conserved protein
0056	1,00	Uncharacterized flavoprotein
0058	0,86	Dihydroxy-acid dehydratase
0059	0,98	Transposase
0060	1,00	Hypothetical protein
0061	1,13	N5-METHYL-H4MPT:COENZYME M METHYLTRANSFE
0062	1,14	N5-Methyl-H4MPT:coenzyme M methyltransferase, subunit A homolog
0067	0,82	Heme biosynthesis protein
0068	0,80	Heme biosynthesis protein
0073	0,95	Delta-aminolevulinic acid dehydratase
0074	0,95	Glutamate-1-semialdehyde 2_1-aminomutase
0075	1,01	Porphobilinogen deaminase
0076	1,07	Dihydroorotate dehydrogenase
0077	1,05	Dihydroorotate dehydrogenase electron tr
0078	0,62	Fumarylacetoacetate hydrolase family pro
0079	0,91	Conserved protein
0080	2,85	Glutamyl-tRNA synthetase
0084	0,78	Conserved protein
0085	0,31	D-3-phosphoglycerate dehydrogenase
0086	0,74	Conserved protein
0087	0,57	LSU ribosomal protein L18E
0088	0,82	LSU ribosomal protein L13P
0089	0,68	SSU ribosomal protein S9P
0090	0,69	DNA-directed RNA polymerase subunit N
0091	0,82	DNA-directed RNA polymerase subunit K
0092	0,69	SSU ribosomal protein S2P

0093	1,29	Conserved protein
0094	1,03	Mevalonate kinase
0095	1,39	PHOSPHOMEVALONATE KINASE
0096	1,82	Isopentenyl-diphosphate delta-isomerase
0097	0,50	Zn-dependent hydrolase
0098	0,77	Geranyltranstransferase
0099	1,15	Hypothetical protein
0100	0,86	Pyruvate_ phosphate dikinase
0101	1,19	Transcription initiation factor IIB
0101	0,85	Transcription initiation factor IIB
0102	1,09	Conserved protein
0103	1,05	Hypothetical protein
0104	0,87	METHYLTRANSFERASE
0105	0,96	Thiol-specific antioxidant protein
0107	1,05	Cobalt-zinc-cadmium resistance protein
0108	1,19	Hypothetical protein
0109	2,20	Hypothetical protein
0111	0,93	Sodium/glutamate symport carrier protein
0113	0,89	Hypothetical protein
0114	1,02	Hypothetical protein
0115	0,83	Transposase
0116	0,61	HTH DNA-binding protein
0117	0,96	Hypothetical protein
0118	1,34	Conserved protein
0119	1,35	Conserved protein
0121	1,00	Hypothetical protein
0123	1,13	Iron-sulfur cluster-binding protein
0124	0,99	Conserved protein
0125	0,78	10 kDa chaperonin
0126	2,50	60 kDa chaperonin
0127	1,16	Conserved protein
0128	1,13	Transporter
0129	1,52	Conserved protein
0130	1,53	Aspartate aminotransferase
0131	1,94	Hypothetical protein

0132	1,01	Rubryerythrin
0133	0,71	Conserved protein
0134	0,93	Conserved protein
0136	0,54	protein Translation Initiation Factor 2
0137	0,99	SSU ribosomal protein S27E
0138	0,41	LSU ribosomal protein L44E
0139	1,82	Conserved protein
0140	0,78	DNA primase small subunit
0141	0,98	Conserved protein
0142	0,77	Conserved protein
0144	1,10	Cell division protein
0146	1,50	Conserved protein
0146	1,30	empt
0147	0,91	Conserved protein
0148	0,94	Conserved protein
0150	0,99	tRNA nucleotidyltransferase
0151	0,89	Replicatiom factor C subunit
0152	1,00	PUTATIVE SMALL MULTI-DRUG EXPORT PROTEIN
0152	0,94	PUTATIVE SMALL MULTI-DRUG EXPORT PROTEIN
0153	0,58	Ferredoxin
0154	0,83	DNA binding protein
0155	1,01	Methyltransferase
0156	0,99	Pyruvate carboxylase (biotin-containing)
0157	0,33	Pyruvate carboxylase_ subunit A
0158	1,07	BIOTIN--[ACETYL-COA-CARBOXYLASE] SYNTHET
0159	0,76	Conserved protein
0160	0,51	Transposase
0161	1,37	Phosphoserine phosphatase
0162	1,53	Conserved protein
0162	0,97	Conserved protein
0163	2,18	Conserved protein
0164	1,47	CELL DIVISION CONTROL PROTEIN (MCM famil
0165	0,95	RNA methylase
0166	1,00	Ferredoxin
0167	1,12	Conserved protein

0168	1,11	Conserved protein
0169	1,09	Sulfite reductase_ assimilatory-type
0170	0,84	Heterodisulfide reductase_ subunit HdrE
0171	1,52	Heterodisulfide reductase_ subunit HdrD
0172	0,93	Conserved protein
0173	1,27	Conserved protein
0174	0,52	Hypothetical protein
0175	1,19	Geranylgeranyl reductase
0176	0,95	Hypothetical protein
0177	0,70	Conserved protein
0178	1,00	Conserved protein
0179	0,96	Archaeal flavoprotein
0180	1,28	Dipeptide/oligopeptide ABC transporter_
0181	2,00	Dipeptide/ oligopeptide ABC transporter_
0182	2,78	Dipeptide/ oligopeptide ABC transporter_
0183	3,11	Dipeptide/ oligopeptide ABC transporter_
0184	1,47	Dipeptide/ oligopeptide binding protein
0185	1,00	Conserved protein
0186	0,74	Conserved protein
0187	1,00	Transporter
0187	0,70	Transporter
0188	1,00	Transcriptional regulator_ MarR family
0189	1,00	Conserved protein
0190	1,06	Conserved protein
0191	1,02	Hypothetical protein
0192	1,07	Conserved protein
0193	1,79	Conserved protein
0194	2,30	Conserved protein
0195	1,99	Vanillate decarboxylase protein
0196	4,74	Conserved protein
0197	5,06	Phosphohydrolase
0198	1,82	METHYLTRANSFERASE
0200	3,03	Conserved protein
0201	1,49	Purine phosphoribosyltransferase
0202	1,33	Diphthamide synthase subunit

0203	0,95	Methyltransferase
0204	0,87	putative RNA-binding protein
0205	1,02	DNA-directed RNA polymerase subunit L
0206	1,14	Conserved protein
0207	1,00	Conserved protein
0208	1,06	Conserved protein
0209	0,45	Diaminopimelate decarboxylase
0211	0,98	Hypothetical protein
0212	0,80	Transposase
0213	1,08	Conserved protein
0214	1,06	Conserved protein
0216	1,06	Arylsulfatase
0220	0,85	MOLYBDENUM-CONTAINING FORMYLMETHANOFURAN
0221	0,86	MOLYBDENUM FORMYLMETHANOFURAN DEHYDROGEN
0221	0,71	MOLYBDENUM FORMYLMETHANOFURAN DEHYDROGEN
0222	1,02	Conserved protein
0223	0,74	Conserved protein
0224	1,03	Conserved protein
0226	0,92	Conserved protein
0227	1,00	Conserved protein
0228	1,10	Conserved protein
0229	1,00	Nicotinate-nucleotide pyrophosphorylase
0229	1,00	Nicotinate-nucleotide pyrophosphorylase
0230	1,03	Molybdate ABC transporter_ ATP-binding p
0231	0,96	Molybdate ABC transporter_ permease prot
0232	0,98	Molybdate-binding protein
0233	1,47	Putative NAD(P)H oxidoreductase
0234	1,03	IRON-SULFUR FLAVOPROTEIN
0235	1,40	NADPH-flavin oxidoreductase
0236	1,81	IRON-SULFUR FLAVOPROTEIN
0238	1,03	DNA REPAIR HELICASE
0239	1,05	SURFACE LAYER PROTEIN B
0240	3,48	SURFACE LAYER PROTEIN B
0241	1,23	Conserved protein
0242	1,38	Conserved protein

0243	0,96	Conserved protein
0244	0,95	probable RNA processing protein
0245	1,00	Fibrillarin
0246	0,97	Conserved protein
0247	1,05	Conserved protein
0248	1,01	Integral membrane protein
0249	1,02	Conserved protein
0250	0,99	Integral membrane protein
0251	1,02	Hypothetical protein
0252	1,00	Cobalamin biosynthesis protein
0253	1,00	Cobalamin biosynthesis protein CobN
0254	1,01	Conserved protein
0255	0,76	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENAS
0256	1,25	Conserved protein
0257	1,55	Archaeal protein Translation Initiation
0258	1,05	Acetyltransferase
0259	1,18	ABC transporter_ ATP-binding protein
0260	1,13	ABC transporter_ permease protein
0261	1,11	HYPOTHETICAL BINDING PROTEIN OF ABC TRAN
0262	0,70	Uridylate kinase
0263	1,08	Conserved protein
0264	1,00	Conserved protein
0265	1,00	Transcriptional regulator_ TetR family
0266	1,86	OXIDOREDUCTASE_ ALDO/KETO REDUCTASE FAMI
0267	0,95	Phosphoribosylaminoimidazole carboxylase
0268	1,06	Conserved protein
0269	1,65	Aspartate-semialdehyde dehydrogenase
0270	3,99	Ferredoxin
0271	1,01	Conserved protein
0272	0,32	DIVALENT CATION TRANSPORT PROTEIN
0273	0,96	Conserved protein
0275	1,13	Conserved protein
0276	1,04	Conserved protein
0277	0,82	Fructose-bisphosphate aldolase
0278	0,72	Deoxycytidine triphosphate deaminase

0279	1,10	Conserved protein
0280	1,00	Conserved protein
0282	1,38	IRON-SULFUR FLAVOPROTEIN
0283	1,10	ABC transporter_ ATP-binding protein
0283	1,02	ABC transporter_ ATP-binding protein
0284	1,25	Transcriptional regulator
0284	0,85	Transcriptional regulator
0285	1,68	Beta-phosphoglucomutase / Glucose-1-pho
0286	1,13	GLYCOSYLTRANSFERASE
0287	1,00	Glycosyltransferase involved in cell wal
0288	1,04	Putative acetyltransferase
0289	1,00	Putative polysaccharide deacetylase
0290	1,00	GLYCOSYL TRANSFERASE
0291	1,04	OLIGOSACCHARIDE REPEAT UNIT TRANSPORTER
0292	1,16	METHYLTRANSFERASE
0293	1,07	Hypothetical protein
0294	0,05	Methanol:corrinoid methyltransferase Mta
0295	0,31	Methanol corrinoid protein MtaC
0296	0,67	Conserved protein
0297	0,70	Conserved protein
0298	1,00	Conserved protein
0299	1,00	Ferredoxin
0300	1,05	Conserved protein
0301	1,00	GLYCOSYL TRANSFERASE
0302	0,97	Conserved protein
0303	1,00	OXIDOREDUCTASE
0304	1,00	POSSIBLE SERINE\THREONINE PROTEIN PHOSPH
0305	0,99	methyl-accepting chemotaxis protein
0306	1,00	MG2+ TRANSPORTER MGTE
0307	1,28	TYPE I RESTRICTION-MODIFICATION SYSTEM R
0308	1,02	TRANSCRIPTIONAL REGULATORY PROTEIN_ ASNC
0309	1,08	Conserved protein
0310	1,09	Conserved protein
0311	1,00	Conserved protein
0314	1,01	TYPE I RESTRICTION-MODIFICATION SYSTEM S

0315	1,01	ATP-dependent DNA helicase RecG
0316	1,03	TYPE I RESTRICTION-MODIFICATION SYSTEM M
0317	0,93	Conserved protein
0318	1,29	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
0319	1,04	Methyltransferase
0320	0,91	Galactoside O-acetyltransferase
0321	1,00	Conserved protein
0321	0,79	Conserved protein
0322	1,00	Conserved protein
0324	1,21	Conserved protein
0325	1,07	Transposase
0326	1,05	Precorrin-6Y C5_15-methyltransferase [de
0327	0,92	CbiD protein
0328	0,88	DNA mismatch repair protein
0329	0,85	DNA mismatch repair protein
0330	1,26	O-acetyl transferase
0331	1,19	CDP-diacylglycerol--glycerol-3-phosphate
0332	1,13	Iron-sulfur binding reductase
0333	0,78	DIMETHYLAMINE CORRINOID PROTEIN
0333	0,14	DIMETHYLAMINE CORRINOID PROTEIN
0334	0,83	Trimethylamine:corrinoid methyltransfera
0335	0,50	Trimethylamine:corrinoid methyltransfera
0336	0,29	TRIMETHYLAMINE CORRINOID PROTEIN
0337	0,93	Trimethylamine permease
0338	0,95	Conserved protein
0340	0,51	Dimethylamine:Corrinoid Methyltransferas
0341	0,44	Dimethylamine:corrinoid methyltransferas
0342	0,80	Conserved protein
0343	0,89	Lysyl-tRNA synthetase_ class I
0344	4,39	Conserved protein
0345	3,50	Conserved protein
0346	0,99	PROTEASE
0347	1,00	Putative nucleoside-diphosphate-sugar ep
0348	3,21	Conserved protein
0349	0,94	Conserved protein

0350	0,95	Histidine biosynthesis protein
0351	1,31	Conserved protein
0352	1,79	Protein-L-isoaspartate O-methyltransferase
0353	1,43	Conserved protein
0354	0,96	Conserved protein
0355	0,89	Conserved protein
0356	1,03	3_4 dihydroxy-2-butanone 4-phosphate synthase
0357	1,07	Cobalt-zinc-cadmium resistance protein
0357	1,00	Cobalt-zinc-cadmium resistance protein
0358	0,94	Chorismate synthase
0359	1,49	Conserved protein
0360	1,37	Conserved protein
0361	1,32	Transcriptional regulator_ ArsR family
0362	1,20	Conserved protein
0363	0,99	Conserved protein
0364	0,86	Hypothetical protein
0366	0,97	Hypothetical protein
0367	1,03	Conserved protein
0368	1,51	Heme biosynthesis protein
0369	0,89	Heme biosynthesis protein
0378	1,00	Dienelactone hydrolase
0379	1,00	Conserved protein
0380	0,99	Conserved protein
0381	1,06	Superoxide dismutase
0382	1,00	Conserved protein
0383	1,06	Chaperone protein
0386	2,08	DNA gyrase_ subunit B
0387	1,04	Type II DNA topoisomerase VI_ subunit A
0388	1,03	Type II DNA topoisomerase VI_ subunit B
0389	0,99	TRANSCRIPTIONAL REGULATORY PROTEIN_ ASNC
0390	2,24	Hypothetical protein
0392	1,00	Conserved protein
0393	1,81	Conserved protein
0394	1,06	Conserved protein
0395	1,05	Conserved protein

0396	1,00	Conserved protein
0397	1,04	Cation transporter
0399	0,95	Potassium channel protein
0400	1,04	Hypothetical protein
0401	1,00	Conserved protein
0402	3,90	Hypothetical protein
0403	1,81	Peptide methionine sulfoxide reductase
0404	2,13	ABC transporter_ ATP-binding protein
0405	1,45	Heme exporter_ protein B
0406	1,89	empty
0406	1,31	Heme exporter_ protein C
0407	1,31	NADH:flavin oxidoreductases
0408	0,66	Transcriptional regulator_ MerR family
0409	0,89	Conserved protein
0410	0,75	Long-chain-fatty-acid--CoA ligase
0412	1,02	Conserved protein
0413	1,76	Cobalt transport protein
0414	6,97	Cobalt transport ATP-binding protein
0415	1,90	Hypothetical protein
0417	1,53	Conserved protein
0418	0,84	Small nuclear riboprotein (snRNA) homolo
0419	1,00	Conserved protein
0420	1,00	ATP-dependent DNA helicase
0421	1,18	5'-methylthioadenosine phosphorylase
0422	1,61	Conserved transmembrane protein
0423	1,00	Hypothetical protein
0424	1,00	Conserved protein
0425	0,76	Conserved protein
0426	1,00	Conserved protein
0427	0,63	3-isopropylmalate dehydratase
0428	1,00	Phosphoribosyl-ATP pyrophosphatase
0429	1,01	Conserved protein
0430	0,40	GTP-binding protein
0431	0,99	Cytochrome c-type biogenesis protein
0432	0,97	Aspartate aminotransferase

0433	0,79	HEXULOSE-6-PHOSPHATE ISOMERASE
0434	0,91	Conserved protein
0435	0,88	Conserved protein
0436	1,02	GTP-binding protein
0437	0,90	Conserved protein
0438	1,46	Shikimate kinase
0439	1,18	Chorismate mutase / prephenate dehydrata
0440	1,06	Phosphoribosylaminoimidazole carboxylase
0441	0,95	Conserved protein
0442	0,40	6-phosphofructokinase (ADP)
0443	0,83	Hypothetical protein
0444	0,99	Conserved protein
0445	0,82	Diphthine synthase
0446	1,00	Thioredoxin
0447	1,24	Thioredoxin reductase
0448	1,25	Conserved protein
0449	1,27	Transcriptional regulator
0450	1,24	O-linked N-acetylglucosamine transferase
0451	1,13	Putative phosphatase
0452	0,87	O-linked N-acetylglucosamine transferase
0453	1,40	Ribosomal protein S6 modification protei
0454	1,00	METHYLTRANSFERASE
0457	1,00	Hypothetical protein
0458	1,19	Oligosaccharyl transferase
0459	2,34	Conserved protein
0460	1,30	putative sugar kinase
0461	1,00	Conserved protein
0462	1,25	Molybdenum cofactor biosynthesis protein
0463	1,04	Ribose-phosphate pyrophosphokinase
0464	1,11	Hypothetical protein
0465	1,02	Hypothetical protein
0466	1,00	Hypothetical protein
0467	0,97	Hypothetical protein
0468	0,88	TYPE I RESTRICTION-MODIFICATION SYSTEM S
0469	0,99	TYPE I RESTRICTION-MODIFICATION SYSTEM M

0470	2,12	Conserved protein
0471	1,59	Conserved protein
0472	1,13	F420-DEPENDENT GLUCOSE-6-PHOSPHATE DEHYD
0473	1,50	DNA repair protein RAD50
0474	1,25	DNA REPAIR PROTEIN (MRE11/RAD32 family)
0476	1,43	Hypothetical protein
0477	1,11	Rubrerythrin
0478	0,98	Conserved protein
0479	1,00	Conserved protein
0480	0,98	Conserved protein
0481	1,02	Hypothetical protein
0482	1,00	TATA-box binding protein
0482	1,00	TATA-box binding protein
0483	0,84	Hypothetical protein
0484	2,17	Fructose-1_6-bisphosphatase
0484	0,72	Fructose-1_6-bisphosphatase
0485	0,98	GMP synthase [glutamine-hydrolyzing]
0486	1,00	Conserved protein
0487	1,71	Two component system histidine kinase
0488	1,00	F420-NONREDUCING HYDROGENASE III_ SUBUNI
0489	1,00	F420-NONREDUCING HYDROGENASE III_ LARGE
0490	1,00	F420-NONREDUCING HYDROGENASE III PRECURS
0491	1,31	Conserved protein
0492	1,00	Conserved protein
0493	0,97	HYDROGENASE EXPRESSION/FORMATION PROTEIN
0494	1,30	F420-NONREDUCING HYDROGENASE II_ SUBUNIT
0494	1,06	F420-NONREDUCING HYDROGENASE II_ SUBUNIT
0494	0,99	F420-NONREDUCING HYDROGENASE II_ SUBUNIT
0499	2,76	Hydrogenase expression/formation protein
0500	1,06	Hypothetical protein
0500	1,00	Hypothetical protein
0501	1,00	Hypothetical protein
0502	5,44	Hypothetical protein
0503	0,90	DNA-directed RNA polymerase_ subunit D
0504	1,00	SSU ribosomal protein S11P

0505	0,82	SSU ribosomal protein S4P
0506	0,78	SSU ribosomal protein S13P
0507	1,18	TRNA PSEUDOURIDINE SYNTHASE
0508	1,04	Cytidylate kinase
0509	0,69	Hypothetical protein
0510	0,97	Carbonic anhydrase
0511	0,66	Conserved protein
0512	0,70	Phosphoribosylaminoimidazole carboxylase
0513	0,76	Adenylate kinase
0514	1,30	PROTEIN TRANSLOCASE SUBUNIT SECY
0514	1,04	PROTEIN TRANSLOCASE SUBUNIT SECY
0515	0,73	LSU ribosomal protein L15P
0516	0,75	LSU ribosomal protein L30P
0517	0,73	SSU ribosomal protein S5P
0518	0,53	LSU ribosomal protein L18P
0519	0,55	LSU ribosomal protein L19E
0520	0,59	LSU ribosomal protein L32E
0521	0,68	LSU ribosomal protein L6P
0522	0,73	SSU ribosomal protein S8P
0523	0,54	SSU ribosomal protein S14P
0524	0,80	LSU ribosomal protein L5P
0525	0,70	SSU ribosomal protein S4E
0526	0,80	LSU ribosomal protein L14P
0527	0,83	SSU ribosomal protein S17P
0528	0,46	Ribonuclease P protein subunit P29
0529	0,36	LSU ribosomal protein L29P
0530	0,80	SSU ribosomal protein S3P
0531	0,58	LSU ribosomal protein L22P
0532	0,82	SSU ribosomal protein S19P
0533	0,74	LSU ribosomal protein L2P
0534	1,02	LSU ribosomal protein L23P
0535	0,84	LSU ribosomal protein L4
0536	0,72	LSU ribosomal protein L3P
0537	1,01	Hypothetical protein
0538	0,93	PUTATIVE SERINE/THREONINE PROTEIN KINASE

0539	0,77	Hypothetical protein
0540	0,82	Hypothetical protein
0541	18,43	Hypothetical protein
0542	0,58	Hypothetical protein
0543	0,99	Hypothetical protein
0544	1,01	Protease HTPX homolog
0544	0,92	Protease HTPX homolog
0545	1,51	Hypothetical protein
0546	0,97	Hypothetical protein
0547	0,93	Hypothetical protein
0548	1,00	GALACTOSIDE-O-ACETYLTRANSFERASE
0549	0,87	Conserved protein
0550	0,88	Glycosyl transferase
0551	0,95	Glycosyl transferase
0552	0,93	Putative glycosyl transferase
0553	0,95	Putative glycosyl transferase
0554	1,19	Putative Methyltransferase
0555	0,75	Glycosyl Transferase
0556	0,89	Heteropolysaccharide repeat unit export
0557	0,90	Conserved protein
0558	1,00	Conserved protein
0559	0,82	Hypothetical protein
0560	2,22	UDP-N-Acetylglucosamine-1-phosphate tran
0561	1,02	Hypothetical protein
0562	0,88	Indolepyruvate oxidoreductase_ subunit
0563	0,34	Indolepyruvate oxidoreductase_ subunit
0564	1,58	CODH nickel-insertion accessory protein
0565	1,00	probable transport channel protein
0566	1,23	HTH DNA-binding protein
0567	9,81	CO DEHYDROGENASE/ACETYL-COA SYNTHASE ALP
0568	0,76	CO DEHYDROGENASE/ACETYL-COA SYNTHASE EPS
0571	13,24	CO DEHYDROGENASE/ACETYL-COA SYNTHASE DEL
0573	0,77	Orotidine 5'-phosphate decarboxylase
0574	0,96	DEOXYHYPUSINE SYNTHASE
0575	1,82	ABC transporter_ ATP-binding protein

0576	1,22	Galactoside O-acetyltransferase
0577	1,00	Thioredoxin
0578	9,22	Conserved protein
0579	1,48	Conserved protein
0580	0,69	S-adenosylmethionine synthetase
0581	1,00	4-hydroxybenzoate octaprenyltransferase
0582	1,14	Conserved protein
0583	0,45	Quinolinate synthetase A
0584	0,85	putative dinucleotide-utilizing enzyme
0585	1,21	Conserved protein
0586	0,90	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE
0587	3,96	Iron(III) dicitrate-binding protein
0587	2,37	Iron(III) dicitrate-binding protein
0588	15,97	Iron(III) dicitrate transport system per
0589	10,69	Iron(III) dicitrate transport ATP-bindin
0590	0,35	SSU ribosomal protein S15P
0591	0,86	Conserved protein
0592	1,02	Conserved protein
0593	1,00	Conserved protein
0594	1,00	Conserved protein
0595	1,05	Histidyl-tRNA synthetase
0596	0,88	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE
0597	1,00	CbiB protein
0598	0,61	Hypothetical protein
0599	1,06	Cobalamin [5'-phosphate] synthase
0600	0,94	PUTATIVE NUCLEOTIDYLTRANSFERASE
0601	0,66	ABC transporter_ ATP-binding protein
0602	0,79	ABC transporter_ ATP-binding protein
0603	0,25	Conserved protein
0604	0,98	DIMETHYLAMINE CORRINOID PROTEIN
0605	0,80	Dimethylamine:corrinoide methyltransferas
0607	0,95	Trimethylamine:corrinoide methyltransfera
0608	0,94	Trimethylamine:Corrinoide Methyltransfera
0609	0,86	TRIMETHYLAMINE CORRINOID PROTEIN
0610	1,00	Trimethylamine Permease

0610	1,00	Trimethylamine Permease
0611	1,00	Conserved protein
0613	1,00	Conserved protein
0614	1,00	Hypothetical protein
0615	1,12	ARCHAEAL TRANSCRIPTIONAL REGULATOR
0616	1,15	Aspartate aminotransferase
0618	0,58	SSU ribosomal protein S8E
0619	0,93	Conserved protein
0620	0,94	Conserved protein
0621	0,86	Conserved protein
0622	1,40	Orotate phosphoribosyltransferase
0623	0,78	Conserved protein
0624	1,98	STOMATIN LIKE-PROTEIN
0625	1,37	NODULATION PROTEIN
0625	1,28	NODULATION PROTEIN
0626	0,78	Hydrogenase expression/formation protein
0626	0,71	Hydrogenase expression/formation protein
0627	0,56	Amidotransferase hisH
0628	1,35	Hypothetical protein
0629	1,00	Hypothetical protein
0629	0,78	Hypothetical protein
0630	1,06	Hypothetical protein
0631	1,00	Conserved protein
0632	1,00	Conserved protein
0633	0,81	TRANSPORTER_ LysE family
0634	0,97	Conserved protein
0635	0,85	TWITCHING MOBILITY (PilT) related protei
0635	0,83	TWITCHING MOBILITY (PilT) related protei
0636	0,87	Phosphoribosyl-AMP cyclohydrolase
0637	2,82	Conserved protein
0638	0,39	Conserved protein
0641	1,13	Hypothetical protein
0641	0,73	Hypothetical protein
0642	0,84	Hypothetical protein
0643	0,99	Hypothetical protein

0644	0,85	Hypothetical protein
0645	1,19	Hypothetical protein
0646	1,00	Hypothetical protein
0648	1,27	Surface layer protein (putative)
0649	1,01	Sec-independent protein translocase_ pro
0650	0,98	Sec-independent protein translocase_ pro
0651	0,72	Sec-independent protein translocase prot
0652	0,76	Sec-independent protein translocase_ pro
0653	0,85	Hypothetical protein
0654	1,17	Pyruvate formate-lyase activating enzyme
0656	1,00	Ferrous iron transport protein A
0657	1,00	Ferrous iron transport protein A
0658	1,05	Ferrous iron transport protein B
0659	1,00	Hypothetical protein
0660	1,00	Iron dependent transcriptional repressor
0661	0,98	METHYLTRANSFERASE
0662	1,02	ABC transporter_ ATP-binding protein
0663	1,40	ABC transporter_ ATP-binding protein
0664	1,97	ABC transporter_ permease protein
0664	1,95	ABC transporter_ permease protein
0665	2,52	ABC transporter_ permease protein
0666	1,88	ABC transporter_ periplasmic binding pro
0666	1,10	ABC transporter_ periplasmic binding pro
0668	1,49	CODH nickel-insertion accessory protein
0668	1,28	CODH nickel-insertion accessory protein
0669	1,09	Pyruvate formate-lyase activating enzyme
0669	1,00	Pyruvate formate-lyase activating enzyme
0670	0,97	Hypothetical protein
0671	1,04	Ferredoxin
0672	0,61	Hypothetical protein
0673	1,00	Conserved hypothetical protein
0674	0,98	Hypothetical protein
0675	1,18	Hypothetical protein
0675	1,17	Hypothetical protein
0676	1,00	Hypothetical protein

0677	1,25	Catalase
0678	0,78	ATP-dependent RNA helicase
0679	0,94	Hypothetical protein
0680	0,81	Acetyltransferase
0681	1,01	Putative hydrolase
0682	1,04	Hypothetical protein
0683	1,00	Acetyltransferase
0684	1,01	Hypothetical protein
0685	1,00	Conserved hypothetical protein
0686	1,00	Hypothetical protein
0688	1,00	Conserved hypothetical protein
0689	1,00	Hypothetical protein
0690	1,11	PHOSPHOHYDROLASE (MUTT/NUDIX family prot
0691	0,95	Cation-transporting ATPase
0692	1,07	Conserved hypothetical protein
0693	0,91	Dimethyladenosine transferase
0694	1,36	Conserved hypothetical protein
0695	1,00	Hypothetical protein
0696	0,87	LSU ribosomal protein L21E
0697	0,79	Conserved hypothetical protein
0698	0,85	Conserved hypothetical protein
0699	1,05	Hypothetical protein
0700	0,95	Hypothetical protein
0701	1,47	Hypothetical protein
0703	0,47	Hypothetical protein
0704	0,80	N2_N2-dimethylguanosine tRNA methyltrans
0705	0,82	Hypothetical protein
0706	1,00	Conserved protein
0707	1,24	hypothetical protein
0708	1,17	Phage shock protein A
0709	1,17	Hypothetical protein
0710	1,04	Universal stress protein
0711	1,02	Conserved protein
0712	0,81	GTP-binding protein homolog
0713	1,00	Sensory transduction histidine kinases

0714	1,15	Thiamine biosynthesis protein
0715	0,75	Probable transcriptional regulator
0716	0,91	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
0717	0,56	Archaeal protein Translation Elongation
0718	0,72	1-pyrroline-5-carboxylate synthetase
0719	0,69	Hypothetical protein
0720	0,78	Hypothetical protein
0722	0,97	Heat shock protein
0724	0,72	GrpE protein
0725	0,75	Chaperone protein
0726	0,25	Chaperone protein
0727	0,28	Trk system potassium uptake protein
0728	0,37	Trk system potassium uptake protein
0729	1,11	Trk system potassium uptake protein
0730	1,11	Trk system potassium uptake protein
0731	1,66	Geranylgeranyl reductase
0732	0,91	Conserved protein
0733	0,48	Hypothetical protein
0734	0,86	Biotin synthase / thiamine biosynthesis
0735	0,44	Biotin synthase / thiamine biosynthesis
0736	0,98	Biotin synthase / thiamine biosynthesis
0737	0,95	Oxidoreductase (hypothetical)
0738	0,69	F420H2 dehydrogenase_ subunitA
0739	0,12	F420H2 dehydrogenase_ subunitB
0740	0,16	F420H2 dehydrogenase_ subunitC
0741	0,06	F420H2 dehydrogenase_ subunitD
0742	0,51	F420H2 dehydrogenase_ subunitH
0743	0,97	F420H2 dehydrogenase_ subunitI
0744	0,95	F420H2 dehydrogenase_ subunitJ1
0745	0,81	F420H2 dehydrogenase_ subunitJ2
0746	0,34	F420H2 dehydrogenase_ subunitK
0747	0,14	F420H2 dehydrogenase_ subunitL
0748	0,13	F420H2 dehydrogenase_ subunitM
0749	0,07	F420H2 dehydrogenase_ subunitN
0750	0,08	F420h2 dehydrogenase_ subunitO

0751	12,46	Chloride channel (putative)
0752	1,92	Hypothetical protein
0753	1,00	Ribosomal-protein-alanine acetyltransfer
0754	1,00	Hypothetical protein
0755	1,00	Ribosomal-protein-alanine acetyltransfer
0756	1,17	Hypothetical protein
0757	1,17	NUCLEOTIDYLTRANSFERASE
0758	1,00	Hypothetical protein
0759	1,00	Surface layer protein (putative)
0762	1,02	Metallo cofactor biosynthesis protein (m
0763	6,54	Hypothetical protein
0764	3,94	ABC transporter_ permease protein
0765	0,93	Hypothetical protein
0766	2,20	Endonuclease III
0767	1,00	Conserved protein
0768	1,00	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
0769	1,00	Metalloendopeptidases (putative)
0770	1,05	Conserved protein
0771	0,92	Hypothetical protein
0772	0,89	Conserved protein
0773	1,00	Sensor histidine kinase/response regulat
0774	1,04	Response regulator
0775	2,49	TETRATRICOPEPTIDE REPEAT FAMILY PROTEIN
0776	1,30	Hypothetical protein
0777	0,96	Hypothetical protein
0778	0,96	DNA polymerase IV
0779	0,99	Hypothetical protein
0781	0,99	Putative ribosomal-protein-alanine acety
0782	1,38	Conserved protein
0783	1,00	Conserved protein
0784	1,59	Iron-sulfur cluster-binding protein
0785	1,35	O6-methylguanine-DNA methyltransferase
0786	1,96	Conserved protein
0787	1,00	Conserved protein
0788	1,88	Conserved protein

0791	1,41	Dolichol-phosphate mannosyltransferase
0792	1,29	Transcription initiation factor TFIIIB
0793	0,78	Transcription initiation factor TFIIIB
0794	1,16	Hypothetical protein
0795	2,98	Conserved protein
0796	3,19	Chromosome partition protein
0797	2,58	Conserved protein
0798	0,79	Ferrous iron transport protein B
0799	0,99	Transcriptional repressor
0800	0,71	Amino-acid acetyltransferase
0801	0,88	BIOY PROTEIN
0802	0,84	Cobalt transporter_ ATP-binding protein
0803	1,03	Cobalt transporter_ ATP-binding protein
0804	0,95	Cobalt transport protein
0805	0,87	Predicted transcriptional regulator
0806	1,24	Transporter
0807	1,00	Transcriptional regulator
0810	0,36	Branched-chain amino acid aminotransfera
0811	0,94	Molybdopterin biosynthesis protein
0812	0,84	GTP-binding protein
0813	0,82	D-alanine-D-alanine ligase related prote
0814	1,00	Arsenite permease
0815	1,00	Conserved protein
0816	1,66	Putative Sensory protein
0817	1,01	SURFACE LAYER PROTEIN B
0818	1,00	TRIMETHYLAMINE CORRINOID PROTEIN
0819	1,44	Putative ATP-dependent Na ⁺ efflux pump
0820	0,95	ABC transporter_ ATP-binding protein
0821	0,38	N-5-phosphoribosylamino)uracil reductase
0822	0,58	Formate hydrogenlyase subunit 3
0823	0,34	Formate hydrogenlyase subunit 4
0824	0,59	Hydrogenase-4 component E
0825	0,72	Hydrogenase-4 component F
0826	0,78	Formate hydrogenlyase subunit 5 precurs
0827	0,86	Formate hydrogenlyase subunit 7

0828	1,10	Conserved protein
0829	1,06	Two-component response regulator
0830	1,00	Cation-transporting ATPase
0831	0,08	Methylcobalamin: Coenzyme M Methyltransf
0832	0,69	Conserved protein
0833	0,52	Conserved protein
0836	1,17	Methanol:corrinoid methyltransferase
0837	12,20	putative regulatory protein
0838	4,18	Cation efflux system protein
0839	0,99	Conserved protein
0840	1,21	Conserved protein
0841	0,72	Conserved protein
0842	1,08	Conserved protein
0843	1,03	Conserved protein
0844	1,48	GTP-binding protein
0845	1,16	Undecaprenyl pyrophosphate synthetase
0846	1,10	Hypothetical protein
0847	0,74	Conserved protein
0848	1,22	METAL DEPENDENT HYDROLASE
0849	1,32	ABC transporter_ ATP-binding protein
0850	1,96	ABC transporter_ ATP-binding protein
0851	1,00	Putative DNA integration/recombination/i
0852	1,03	Putative DNA integration/recombination/i
0853	1,00	Thiol-disulfide isomerase/thioredoxin re
0854	1,00	Thiol-disulfide isomerase/thioredoxin re
0855	0,99	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
0856	0,71	Putative transcriptional regulator
0857	0,74	Iron-sulfur-binding protein
0858	0,37	Thermosome_ gamma subunit
0859	1,04	Conserved protein
0860	1,01	Conserved protein
0861	1,02	Hypothetical protein
0862	0,97	Archaeosine tRNA-ribosyltransferase
0863	1,17	Hypothetical protein
0864	1,01	Oxidoreductase (flavoprotein)

0865	1,03	Metallo cofactor biosynthesis protein (m
0866	0,38	Putative phosphoserine phosphatase
0867	0,28	Putative phosphoserine phosphatase
0868	0,65	F420-dependent methylenetetrahydromethan
0869	1,00	Conserved protein
0870	1,44	Conserved protein
0871	0,38	Thymidylate kinase
0872	6,36	Conserved protein
0873	0,97	Phosphoribosylformimino-5-aminoimidazole
0874	0,32	Conserved protein
0875	1,08	Conserved protein
0875	1,00	Conserved protein
0876	0,35	Hypothetical protein
0877	1,06	Polysaccharide deacetylase
0878	0,72	Conserved protein
0879	1,00	Conserved protein
0880	1,68	Conserved protein
0881	0,97	Glycosyl transferase
0882	1,08	OXIDOREDUCTASE
0883	0,96	Hypothetical protein
0884	1,72	O-antigen translocase
0884	0,89	O-antigen translocase
0885	0,48	Conserved protein
0886	1,29	GLYCOSYL TRANSFERASE
0887	1,33	Glycosyl transferase
0888	1,00	Conserved protein
0889	0,87	Conserved protein
0890	1,00	Hypothetical protein
0890	0,97	Hypothetical protein
0891	0,29	UDP-glucose 6-dehydrogenase
0892	0,73	UTP--glucose-1-phosphate uridylyltransfe
0893	0,55	UDP-glucose 4-epimerase
0894	0,81	Transporter
0895	1,00	Disaggregase-like protein
0895	0,99	Disaggregase-like protein

0896	0,63	GLYCOSYL TRANSFERASE
0897	0,56	GLYCOSYL TRANSFERASE
0898	0,52	Dolichyl-phosphate mannose synthase rela
0899	0,68	Dolichyl-phosphate mannose synthase rela
0900	0,36	GLYCOSYL TRANSFERASE
0901	0,42	GLYCOSYL TRANSFERASE
0902	0,68	GLYCOSYL TRANSFERASE
0903	1,00	Disaggregase
0904	1,01	Conserved protein
0914	1,63	Conserved protein
0915	1,70	Methyl-coenzyme M reductase_ beta subuni
0915	1,49	Methyl-coenzyme M reductase_ beta subuni
0916	2,23	Methyl-coenzyme M reductase operon prote
0917	2,07	Methyl-coenzyme M reductase operon prote
0918	2,37	Methyl-coenzyme M reductase_ gamma subun
0919	1,08	Methyl-coenzyme M reductase_ alpha subun
0920	1,35	METHYLTRANSFERASE
0921	1,15	3-phosphoshikimate 1-carboxyvinyltransfe
0922	1,19	Thymidylate synthase
0923	1,20	PROTEASE HTPX
0924	1,02	5-methylcytosine-specific restriction en
0925	1,01	Conserved protein
0926	0,98	Hypothetical protein
0927	1,00	Conserved protein
0928	1,00	SAM-dependent methyltransferases
0929	1,67	Nitrilase
0930	2,16	Glutamyl-tRNA (Gln) amidotransferase_ su
0931	1,98	Glutamyl-tRNA (Gln) amidotransferase_ su
0932	1,08	Glutamyl-tRNA (Gln) amidotransferase_ su
0933	0,94	Coenzyme F420 hydrogenase_ beta subunit
0934	1,21	Conserved protein
0935	0,99	Conserved protein
0936	0,40	Conserved protein
0937	1,18	Chromosomal protein
0938	1,00	Acetylglutamate kinase

0939	0,67	Fe-S OXIDOREDUCTASE
0940	1,71	GMP synthase [glutamine-hydrolyzing]
0941	0,97	ATP-dependent DNA helicase
0942	1,00	Conserved protein
0943	0,69	HEXULOSE-6-PHOSPHATE SYNTHASE
0944	1,10	Conserved protein
0945	0,99	Aspartate carbamoyltransferase_ catalyti
0946	1,02	Aspartate carbamoyltransferase_ regulato
0947	1,00	Conserved protein
0948	1,03	Conserved protein
0949	1,00	Conserved protein
0950	1,06	Conserved protein
0951	1,20	Conserved protein
0952	1,00	Conserved protein
0953	0,45	Dihydropicolinate reductase
0954	0,49	Dihydropicolinate synthase
0955	0,85	SSU ribosomal protein S17E
0958	1,00	Conserved protein
0959	1,00	Conserved protein
0960	1,00	Conserved protein
0961	1,00	Conserved protein
0962	1,00	dTDP-glucose 4_6-dehydratase
0965	1,00	Conserved protein
0966	1,03	Conserved protein
0967	1,00	Conserved protein
0968	1,16	Conserved protein
0970	1,75	Dolichyl-phosphate mannose synthase rela
0971	1,00	Dolichyl-phosphate mannose synthase rela
0972	1,00	GLYCOSYL TRANSFERASE
0973	1,00	Conserved protein
0974	4,69	OXIDOREDUCTASE
0975	1,00	GLYCOSYL TRANSFERASE
0976	1,71	GLYCOSYL TRANSFERASE
0977	1,52	GLYCOSYL TRANSFERASE
0978	1,00	Oligosaccharide repeat unit transporter

0979	1,00	UDP-N-acetyl-D-mannosamine 6-dehydrogena
0980	1,12	UDP-N-acetylglucosamine 2-epimerase
0981	1,15	Glucose-1-phosphate thymidyltransferas
0982	0,86	dTDP-4-dehydrorhamnose reductase
0983	1,00	dTDP-glucose 4_6-dehydratase
0984	1,01	dTDP-4-dehydrorhamnose 3_5-epimerase
0985	2,64	Dolichyl-phosphate mannose synthase rela
0986	0,96	hypothetical nucleotidyltransferase
0987	1,00	NUCLEOTIDYLTRANSFERASE
0988	0,97	UDP-N-acetylglucosamine 4-epimerase
0989	2,80	ABC transporter_ ATP-binding protein
0990	1,00	Transcriptional regulator
0991	1,00	Hypothetical protein
0992	1,14	Pirin
0993	1,00	Conserved protein
0994	1,04	Conserved protein
0999	1,03	Transposase
1002	1,00	Pirin
1003	1,00	Hypothetical protein
1004	1,03	Conserved protein
1005	1,00	Adenine deaminase
1005	0,66	Adenine deaminase
1006	1,00	Phosphoserine aminotransferase
1007	1,05	5-oxoprolinase
1008	1,23	Conserved protein
1009	1,00	Conserved protein
1010	1,00	Hypothetical protein
1011	1,11	FLAVOREDOXIN
1012	1,12	OXIDOREDUCTASE_ ALDO/KETO REDUCTASE FAMI
1013	1,11	OXIDOREDUCTASE_ ALDO/KETO REDUCTASE FAMI
1014	1,09	Hypothetical protein
1015	1,00	Ribosomal-protein-alanine acetyltransfer
1016	1,00	Hypothetical protein
1018	0,99	Ribonuclease BN
1022	0,88	Hypothetical protein

1023	1,08	Hydrolase
1024	1,05	Conserved protein
1025	0,85	Conserved protein
1026	1,00	Hypothetical protein
1027	1,01	Conserved protein
1028	1,21	Conserved protein
1029	1,00	Serine O-acetyltransferase
1030	3,54	METAL DEPENDENT HYDROLASE
1031	1,95	Conserved protein
1032	1,05	Lipopolysaccharide N-acetylglucosaminylt
1033	1,40	Conserved protein
1034	1,00	Mannosyltransferase
1035	1,00	Hypothetical protein
1036	0,97	Conserved protein
1037	1,05	Conserved protein
1038	2,89	Hypothetical protein
1039	1,39	Conserved protein
1040	0,97	Hypothetical protein
1041	1,13	Conserved protein
1042	0,88	Transcriptional regulator
1043	0,87	Transcriptional regulator
1044	0,91	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
1045	0,88	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
1046	0,79	Conserved protein
1048	1,40	Conserved protein
1049	1,35	Hypothetical protein
1050	1,00	Hypothetical protein
1051	0,85	Dimethylamine corrinoid protein
1052	0,47	Dimethylamine:corrinoid methyltransferas
1053	0,74	Dimethylamine:corrinoid methyltransferas
1054	0,85	Dimethylamine permease
1055	1,00	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
1056	1,00	Conserved protein
1057	1,42	Isoleucyl-tRNA synthetase
1058	1,16	Conserved protein

1059	1,41	Hypothetical protein
1060	0,91	Hypothetical protein
1061	1,00	Hypothetical protein
1062	1,00	Hypothetical protein
1063	1,14	TYPE I RESTRICTION-MODIFICATION SYSTEM R
1064	1,03	Hypothetical protein
1064	1,00	Hypothetical protein
1065	1,02	TYPE I RESTRICTION-MODIFICATION SYSTEM S
1066	0,83	Hypothetical protein
1069	0,85	Transposase
1070	1,00	Hypothetical protein
1071	0,87	Hypothetical protein
1072	0,84	Coenzyme F420 hydrogenase_ beta subunit
1073	0,47	Coenzyme F420 hydrogenase_ gamma subunit
1074	0,96	Coenzyme F420 hydrogenase_ delta subunit
1075	0,24	Coenzyme F420 hydrogenase_ alpha subunit
1076	1,51	Conserved protein
1078	1,02	Hypothetical protein
1079	1,00	GLYCOSYL TRANSFERASE
1080	1,00	Hypothetical protein
1081	1,08	OXIDOREDUCTASE
1082	1,00	CapK protein
1083	0,98	Competence-like protein
1084	0,83	Hypothetical protein
1085	1,22	IRON-SULFUR FLAVOPROTEIN
1086	1,51	Conserved protein
1087	1,18	Hypothetical protein
1088	1,00	Hypothetical protein
1089	1,00	Hypothetical protein
1090	1,00	CALCIUM DEPENDENT PROTEASE
1091	1,14	Hypothetical protein
1092	0,97	Hypothetical protein
1093	1,01	FUMARATE HYDRATASE_ ALPHA SUBUNIT
1094	1,01	FUMARATE HYDRATASE_ BETA SUBUNIT
1095	1,04	Conserved protein

1096	1,00	Cation-transporting ATPase
1097	1,00	Hypothetical protein
1098	1,00	Putative membrane transport protein
1099	1,00	Hypothetical protein
1100	1,01	SURFACE LAYER PROTEIN B
1101	0,88	RNASE P RNA COMPONENT
1102	1,19	Hypothetical protein
1103	0,72	DNA topoisomerase I
1104	0,89	Probable transcriptional regulator
1105	1,12	mRNA 3'-end processing factor
1106	1,50	Hypothetical protein
1107	1,12	Hypothetical protein
1108	1,08	Serine/threonine protein kinases
1110	1,20	Protease I
1111	1,13	Cystathionine gamma-synthase
1112	1,09	Nicotinate phosphoribosyltransferase
1113	0,39	not existing
1114	0,99	Hypothetical protein
1116	1,00	HELICASE (DEAD/DEAH FAMILY)
1117	0,95	RNase L inhibitor
1118	0,87	Hypothetical protein
1119	0,90	Conserved protein
1120	0,77	TYPE I RESTRICTION-MODIFICATION SYSTEM M
1121	0,86	TYPE I RESTRICTION-MODIFICATION SYSTEM S
1122	1,15	TYPE I RESTRICTION-MODIFICATION SYSTEM R
1123	1,00	Transcriptional regulator_ TetR/AcrR fam
1124	1,00	Conserved protein
1125	0,97	Conserved protein
1127	1,26	Thioredoxin
1128	1,21	Hypothetical protein
1129	1,87	Methylenetetrahydrofolate reductase
1130	1,13	ZINC-FINGER PROTEIN
1131	1,07	Dihydropteroate synthase
1132	0,49	Methylenetetrahydrofolate dehydrogenase
1133	0,59	Serine hydroxymethyltransferase

1134	0,64	Phosphoribosylglycinamide formyltransfer
1135	1,05	HTH DNA-binding protein
1136	1,02	Hypothetical protein
1137	1,00	NAD+ synthetase
1138	1,28	Cell division control protein (AAA famil
1139	0,87	Hypothetical protein
1140	0,94	SAM-dependent methyltransferases
1141	1,03	Conserved protein
1142	0,98	Hypothetical protein
1143	0,42	Hypothetical protein
1144	0,95	Hypothetical protein
1145	1,01	Hydrolase (HAD superfamily)
1146	0,45	RECOMBINATION/REPAIR PROTEIN RADA
1147	1,01	CYTIDYLYLTRANSFERASE
1148	0,98	Conserved protein
1149	2,72	Probable endonuclease IV
1150	1,00	5-methyltetrahydropteroyltriglutamate--h
1151	0,81	Cobalt transport ATP-binding protein
1152	0,73	Cobalt transport protein
1153	1,01	Cobalt transport protein
1155	1,00	CbiM protein
1156	2,83	Conserved protein
1157	1,00	Conserved protein
1158	0,64	Hypothetical protein
1159	1,36	tRNA nucleotidyltransferase
1160	2,74	8-OXOGUANINE DNA GLYCOSYLASE
1161	1,88	ADP-dependent phosphofructokinase
1161	1,45	Glucokinase
1162	1,32	Glutamate N-acetyltransferase / Amino-a
1163	1,79	Putative inosine-5'-monophosphate dehydr
1163	1,00	Putative inosine-5'-monophosphate dehydr
1164	0,89	N-acetyl-gamma-glutamyl-phosphate reduct
1165	1,25	Hypothetical protein
1166	0,95	Hypothetical protein
1167	1,00	Acetyltransferase

1167	1,00	Acetyltransferase
1168	1,00	Hypothetical protein
1169	1,00	Small heat shock protein
1170	0,85	Hypothetical protein
1171	0,85	Phosphoglycerate kinase
1172	0,63	DNA polymerase
1173	0,88	Heat shock protein
1176	16,13	Phycocyanin alpha-subunit phycocyanobili
1177	22,78	Conserved protein
1178	13,95	Conserved protein
1179	2,23	Acetyl-CoA synthetase_ beta subunit
1180	11,49	Acetate kinase
1181	15,78	Phosphate acetyltransferase
1182	0,79	IRON-SULFUR FLAVOPROTEIN
1183	0,88	Putative chloride channel protein
1184	1,00	Hypothetical protein
1185	2,11	3-demethylubiquinone-9 3-methyltransfera
1186	1,00	Translation initiation inhibitor
1187	2,30	Hypothetical protein
1188	1,00	Phycocyanin alpha-subunit phycocyanobili
1189	1,00	Methylcobalamin:Coenzyme M methyltransfe
1190	1,00	Conserved protein
1191	1,06	Conserved protein
1192	2,00	Isoleucyl-tRNA synthetase
1194	1,30	GTP-binding protein
1195	0,97	Conserved protein
1196	1,03	tRNA-intron endonuclease
1197	1,08	Cobyrinic acid a_c-diamide synthase
1198	2,15	NITROGENASE IRON PROTEIN 2
1199	1,10	Conserved protein
1200	1,40	Hypothetical protein
1201	0,82	Conserved protein
1202	1,00	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
1203	1,00	Hypothetical protein
1204	1,00	Hypothetical protein

1206	1,00	Hypothetical protein
1207	1,00	Hypothetical protein
1208	1,03	Hypothetical protein
1209	1,00	Conserved protein
1210	1,00	Hypothetical protein
1211	1,00	HYDROLASE
1212	0,61	Amino acid permease
1213	0,88	Conserved protein
1214	1,97	Hypothetical protein
1215	0,91	Conserved protein
1216	1,00	Conserved protein
1217	1,00	Hypothetical protein
1218	1,27	Hypothetical protein
1219	0,28	Hypothetical protein
1220	1,00	Conserved protein
1221	1,08	Conserved protein
1222	1,62	Hypothetical protein
1223	1,03	Exoribonuclease II
1224	1,00	Conserved protein
1224	1,00	Conserved protein
1226	1,48	Conserved protein
1229	1,06	Hypothetical protein
1231	1,00	Conserved protein
1232	1,01	Glutathione-regulated potassium-efflux s
1233	1,00	Nitrogen regulatory protein P-II
1234	1,29	Hypothetical protein
1235	1,34	Hypothetical protein
1236	0,83	Glutathione-regulated potassium-efflux s
1237	1,80	LYSINE 2_3-AMINOMUTASE
1238	1,17	Beta-lysine acetyltransferase
1239	1,00	Conserved protein
1240	1,09	PUTATIVE FLAGELLA-RELATED PROTEIN J
1241	1,00	PUTATIVE FLAGELLA RELATED PROTEIN FlaI
1242	1,00	Putative flagella-related protein H
1243	4,63	putative Flavoprotein

1244	0,72	Adenylosuccinate lyase
1246	0,51	GERANYLGERANYLGLYCERYL DIPHOSPHATE SYNTH
1247	0,62	METHYL COENZYME M REDUCTASE SYSTEM_ COMP
1248	0,86	IRON-SULFUR FLAVOPROTEIN
1249	1,00	PUTATIVE NADPH-FLAVIN OXIDOREDUCTASE
1250	1,00	Conserved protein
1251	1,14	Sensory transduction histidine kinases
1252	0,99	Hypothetical protein
1253	0,88	ABC transporter_ ATP-binding protein
1254	1,01	ABC transporter_ permease protein
1256	1,59	ABC transporter_ ATP-binding protein
1257	1,00	ABC transporter_ permease protein
1258	1,00	ABC transporter_ ATP-binding protein
1259	1,00	Ammonium transporter
1260	0,98	Nitrogen regulatory protein P-II
1261	1,02	Conserved protein
1262	0,98	Putative small heat shock protein
1263	1,00	Putative small heat shock protein
1263	0,87	Putative small heat shock protein
1264	0,90	Conserved protein
1265	1,00	Integral Membrane protein
1266	0,10	Glutamine synthetase
1267	0,13	Glutamate synthase_ large chain
1268	0,20	Glutamate synthase_ large chain
1269	0,98	Glutamate synthase_ large chain
1270	0,75	Coenzyme F420 hydrogenase beta subunit
1271	0,85	Hypothetical protein
1272	1,20	Hypothetical protein
1273	0,88	Conserved protein
1274	0,97	Conserved protein
1275	1,17	Xaa-Pro aminopeptidase
1276	1,24	Conserved protein
1277	1,00	Protease (putative)
1277	0,79	Protease (putative)
1278	1,00	F420-dependent NADP reductase

1279	1,25	HETERODISULFIDE REDUCTASE_ SUBUNIT HDRC
1280	2,80	HETERODISULFIDE REDUCTASE_ SUBUNIT HDRB
1281	0,52	Iron-sulfur binding protein
1283	0,58	Conserved protein
1284	1,15	Conserved protein
1285	0,46	Conserved protein
1286	0,39	Conserved protein
1287	0,73	Conserved protein
1288	0,23	Conserved protein
1289	0,35	HTH DNA-binding protein
1290	0,66	Nucleotide-binding protein
1291	1,08	Thiol-disulfide isomerase/thioredoxin
1291	0,98	Thiol-disulfide isomerase/thioredoxin
1292	1,27	Cytochrome c-type biogenesis protein
1293	0,33	Precorrin-8X methylmutase
1294	0,49	Precorrin-3B C17-methyltransferase
1295	0,91	COBALAMIN BIOSYNTHESIS PROTEIN G
1295	0,56	COBALAMIN BIOSYNTHESIS PROTEIN G
1296	0,98	COBALAMIN BIOSYNTHESIS PROTEIN G
1297	0,71	Precorrin-4 C11-methyltransferase
1298	0,65	Precorrin-2 C20-methyltransferase
1299	0,67	Precorrin-6Y C5_15-methyltransferase [de
1300	1,34	2-isopropylmalate synthase
1301	0,43	Isocitrate dehydrogenase [NADP]
1302	0,72	Putative molybdenum cofactor biosynthesi
1303	0,18	Zinc finger protein
1304	1,98	26S PROTEASOME REGULATORY SUBUNIT RPT2/S
1305	1,01	Conserved protein
1306	1,42	Cell division protein
1307	0,75	PROTEIN TRANSLOCASE SUBUNIT SECE
1308	0,44	Putative transcription antitermination p
1309	0,67	LSU ribosomal protein L11P
1310	0,39	LSU ribosomal protein L1P
1311	0,61	LSU ribosomal protein L10P
1312	0,34	LSU ribosomal protein L12AE

1313	0,83	Molybdenum cofactor biosynthesis enzyme
1314	0,44	Conserved protein
1315	1,00	Hypothetical protein
1316	1,00	Hypothetical protein
1317	1,01	Hypothetical protein
1318	1,00	Conserved protein
1320	0,99	TRANSLATION INITIATION FACTOR 1A (EIF-1A
1321	0,54	Serine/threonine protein kinase
1322	0,76	Putative RNA-binding protein
1323	1,02	Dihydroorotase
1324	0,89	Phosphate transport system protein
1325	1,85	Phosphate transporter_ ATP-binding prote
1326	1,26	Phosphate transporter_ permease protein
1327	1,23	Phosphate transporter_ permease protein
1328	4,83	Phosphate transporter_ permease protein
1329	1,66	Phosphate-binding protein
1330	1,01	DNA polymerase delta catalytic subunit
1331	1,39	Magnesium-chelatase subunit
1332	5,99	Conserved protein
1333	4,72	Hypothetical protein
1334	10,39	Hypothetical protein
1335	21,75	Hypothetical protein
1336	18,88	Cobalamin biosynthesis protein
1337	6,73	Conserved protein
1338	3,77	Cobalt transport ATP-binding protein
1339	4,99	Cobalt transport protein
1340	3,50	ABC transporter_ ATP-binding protein
1341	1,19	ABC transporter_ permease protein
1342	1,00	Hypothetical protein
1343	1,20	Hypothetical protein
1344	1,03	Hypothetical protein
1345	1,00	Conserved protein
1346	1,03	Hypothetical protein
1347	0,77	Regulatory protein (putative)
1348	0,90	Hypothetical Cytosolic protein

1349	0,94	Hypothetical Cytosolic protein
1350	0,93	Conserved protein
1351	1,06	Alkyl sulfatase
1352	0,84	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENAS
1353	0,67	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENAS
1354	0,40	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENAS
1355	1,50	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENAS
1356	1,05	Conserved protein
1357	1,56	Conserved protein
1358	1,55	Conserved protein
1359	1,00	HISTONE ACETYLTRANSFERASE (ELP3 faminly)
1359	0,59	HISTONE ACETYLTRANSFERASE (ELP3 faminly)
1360	0,81	Conserved protein
1361	0,70	Conserved protein
1362	0,71	Single-stranded-DNA-specific exonuclease
1363	0,90	Hypothetical protein
1364	1,15	Hypothetical protein
1365	1,06	Hypothetical protein
1366	0,47	Malate dehydrogenase
1367	0,97	Hypothetical protein
1368	1,93	hypothetical protein
1369	0,90	Tyrosyl-tRNA synthetase
1370	2,75	Conserved protein
1371	0,93	Hypothetical protein
1371	0,75	Hypothetical protein
1372	1,00	Conserved protein
1373	1,00	Hypothetical protein
1374	1,02	Hit-like protein_ involved in cell-cycle
1375	1,03	Hypothetical Transcriptional Regulatory
1376	1,00	Hypothetical protein
1377	1,00	Cysteine desulfurase NifS
1378	1,00	NifU protein
1379	2,39	Cobalt-zinc-cadmium resistance protein
1380	1,62	Cobalt-zinc-cadmium resistance protein
1381	1,00	Catalase

1382	1,00	METHYLTRANSFERASE
1383	1,47	OXIDOREDUCTASE_ ALDO/KETO REDUCTASE FAMI
1384	0,89	Integral membrane protein
1385	1,00	GLYCOSYL TRANSFERASE
1386	1,24	Hypothetical protein
1387	0,57	Transporter
1388	0,43	Conserved protein
1389	0,89	POLYPRENYLTRANSFERASE
1390	1,00	Glutamine transporter_ ATP-binding prote
1391	1,00	Glutamine transporter_ permease protein
1392	0,22	Glutamine-binding protein
1393	0,92	Hypothetical protein
1394	0,98	Hypothetical protein
1395	1,00	Conserved protein
1396	1,29	Acetyltransferase
1397	1,00	Hypothetical protein
1398	0,96	Integral membrane protein
1399	1,01	Methylcobalamin:coenzyme M methyltransfe
1400	3,73	Sensory Transduction protein Kinase
1402	0,37	Hypothetical protein
1403	1,02	PHOSPHINOTHRICIN ACETYLTRANSFERASE
1404	0,83	Cell surface glycoprotein
1405	1,00	Hypothetical protein
1406	1,00	hypothetical protein
1407	1,29	Hypothetical protein
1408	1,61	Hypothetical protein
1409	1,57	Hypothetical protein
1410	0,99	NUCLEOTIDYLTRANSFERASE
1412	1,10	Hypothetical protein
1413	1,50	ATP-dependent RNA helicase
1414	0,61	Lysyl-tRNA synthetase_ class II
1415	0,97	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
1416	0,84	Hypothetical protein
1417	1,12	ATP-dependent protease La
1418	1,00	Hypothetical protein

1419	1,07	CysteinyI-tRNA synthetase
1420	1,02	Maf protein
1421	1,02	Glutathione-regulated potassium-efflux s
1421	0,79	Glutathione-regulated potassium-efflux s
1422	0,94	Hypothetical protein
1423	0,98	Isochorismatase
1424	0,95	Conserved protein
1425	0,91	Hypothetical Membrane Spanning protein
1425	0,90	empty
1427	0,72	Hypothetical protein
1428	1,01	Transcriptional regulator_ MarR family
1429	1,19	Hypothetical protein
1430	1,07	Hypothetical protein
1431	0,86	Hypothetical protein
1432	1,34	Hypothetical protein
1434	0,85	Hypothetical protein
1435	1,00	Phenylacetic acid degradation protein
1436	0,95	ATP-dependent DNA ligase
1437	0,95	DNA polymerase beta
1441	19,31	Nitrogenase iron protein
1442	8,90	CO DEHYDROGENASE/ACETYL-COA SYNTHASE DEL
1445	1,04	Metallo cofactor biosynthesis protein (m
1446	1,13	Geranyltranstransferase/Farnesyltranstra
1447	0,92	Hypothetical protein
1450	1,02	ADP-ribosylglycohydrolase
1451	1,00	Hypothetical protein
1452	0,91	Hypothetical protein
1453	2,23	Hypothetical protein
1454	1,17	26S PROTEASOME REGULATORY SUBUNIT RPT2/S
1455	0,98	Hypothetical protein
1456	0,48	Adenylosuccinate synthetase
1457	0,38	SSU ribosomal protein S19E
1458	0,69	Conserved protein
1459	0,69	Hypothetical ATP-binding protein
1459	0,54	Hypothetical ATP-binding protein

1460	0,58	LSU ribosomal protein L39E
1461	0,94	LSU ribosomal protein L31E
1462	0,62	protein Translation Initiation Factor 6
1463	0,60	Prefoldin_ alpha subunit
1464	1,60	SIGNAL RECOGNITION PARTICLE_ SUBUNIT Ffh
1465	1,03	Stress-responsive transcriptional regula
1466	1,00	Conserved protein
1467	1,00	Conserved protein
1468	0,72	Probable peroxiredoxin
1472	0,94	Hypothetical protein
1472	0,86	Hypothetical protein
1474	0,93	Hypothetical protein
1475	0,89	Conserved protein
1476	1,05	Hypothetical protein
1476	1,00	Hypothetical protein
1476	0,94	Hypothetical protein
1480	1,01	Putative 6-aminohexanoate-dimer hydrolas
1483	0,99	Hypothetical protein
1484	1,01	Hypothetical protein
1485	1,00	Hypothetical protein
1486	1,00	Hypothetical protein
1487	1,00	Hypothetical protein
1488	1,01	METHYLTRANSFERASE
1489	1,93	Hypothetical protein
1490	1,11	Exodeoxyribonuclease III
1491	0,57	TYPE I RESTRICTION-MODIFICATION SYSTEM M
1492	1,00	Hypothetical protein
1493	1,04	Hypothetical protein
1494	1,68	Hypothetical protein
1495	0,67	TYPE I RESTRICTION-MODIFICATION SYSTEM S
1496	1,91	TYPE I RESTRICTION-MODIFICATION SYSTEM R
1497	1,14	Flavodoxin
1497	1,00	Flavodoxin
1498	1,09	Large-conductance mechanosensitive chann
1498	0,82	Large-conductance mechanosensitive chann

1499	1,00	Cob(I)alamin adenosyltransferase
1499	1,00	Cob(I)alamin adenosyltransferase
1500	1,19	TRANSPORTER_ LysE family
1501	1,10	ABC Transporter_ permease protein
1502	0,79	ABC Transporter_ ATP-binding protein
1503	0,58	PROTEASE HTPX
1504	1,09	Hypothetical protein
1505	0,51	Hypothetical protein
1506	1,04	Fructokinase
1507	0,83	Hypothetical protein
1508	1,05	Hypothetical protein
1509	0,98	Hypothetical protein
1510	1,00	Hypothetical protein
1511	1,00	Hypothetical protein
1512	1,01	Hypothetical protein
1513	0,92	Hypothetical protein
1514	0,93	Hypothetical protein
1515	0,97	Putative hydrolase
1516	0,41	Hypothetical protein
1517	0,86	Hypothetical protein
1518	0,95	IRON-SULFUR FLAVOPROTEIN
1519	1,21	ATP-dependent protease La
1520	0,91	Transcriptional regulator_ MarR family
1521	1,05	Hypothetical protein
1522	0,97	Hypothetical protein
1523	1,08	Oligoendopeptidase F
1524	0,56	Hypothetical protein
1525	0,85	Hypothetical protein
1526	1,94	Glycogen phosphorylase
1527	0,16	Hypothetical protein
1528	0,83	Hypothetical protein
1529	1,04	Hypothetical protein
1530	1,04	Probable cytosine deaminase
1531	2,69	Hypothetical protein
1532	2,04	Hypothetical protein

1533	1,61	Conserved protein
1534	1,03	Two component system histidine kinase
1535	1,12	Hypothetical protein
1536	1,00	Two component system histidine kinase
1536	1,00	Two component system histidine kinase
1537	1,25	Hypothetical protein (not in ERGO !)
1538	1,01	ABC transporter_ permease protein
1539	1,00	Hypothetical protein
1540	1,01	Hypothetical protein
1541	1,07	ABC transporter_ ATP-binding protein
1542	0,88	Hypothetical protein
1543	1,08	Transcriptional regulator
1543	0,97	Hypothetical protein
1544	1,00	Hypothetical protein
1545	0,95	Phycocyanin alpha-subunit phycocyanobili
1546	1,00	Hypothetical protein
1547	1,12	Carbonic anhydrase
1548	11,57	MOLYBDENUM FORMYLMETHANOFURAN DEHYDROGEN
1549	0,51	MOLYBDENUM FORMYLMETHANOFURAN DEHYDROGEN
1550	0,51	MOLYBDENUM FORMYLMETHANOFURAN DEHYDROGEN
1551	0,55	MOLYBDENUM-CONTAINING FORMYLMETHANOFURAN
1552	0,97	TUNGSTEN TRANSPORTER_ ATP BINDING PROTEI
1553	1,05	TUNGSTEN TRANSPORTER_ PERMEASE PROTEIN
1554	1,00	ABC TRANSPORTER_ TUNGSTEN-BINDING PROTEI
1555	1,00	Hypothetical protein
1556	0,98	Hypothetical protein
1557	1,00	Hypothetical protein
1558	0,86	Signal recognition particle SEC65 subuni
1559	0,88	PUTATIVE METAL DEPENDENT HYDROLASE
1560	0,96	Transcriptional regulator
1561	1,69	TRANSPORTER_ RND superfamily
1562	1,87	Hypothetical protein
1563	3,10	Hypothetical protein
1564	1,35	putative molybdenum transport protein Mo
1565	0,91	SODIUM/PROLINE SYMPORTER

1566	1,02	Conserved protein
1567	1,23	Tetrahydromethanopterin S-methyltransfer
1568	0,98	Tetrahydromethanopterin S-methyltransfer
1569	2,18	Tetrahydromethanopterin S-methyltransfer
1570	1,49	Tetrahydromethanopterin S-methyltransfer
1571	1,94	Tetrahydromethanopterin S-methyltransfer
1572	1,92	Tetrahydromethanopterin S-methyltransfer
1573	1,32	Tetrahydromethanopterin S-methyltransfer
1574	0,99	Tetrahydromethanopterin S-methyltransfer
1575	1,13	Hypothetical protein
1576	0,99	Replication factor C subunit
1577	1,08	Conserved protein
1578	1,20	CDP-diacylglycerol--glycerol-3-phosphate
1579	1,00	L-fucose phosphate aldolase
1580	1,03	Hypothetical protein
1581	1,11	Molybdopterin biosynthesis MoeB protein/
1582	1,00	Putative regulatory protein
1583	1,25	Hypothetical protein
1584	1,03	Hypothetical protein
1585	1,06	Aconitate hydratase
1586	0,96	Citrate synthase
1587	0,93	4-hydroxybenzoate decarboxylase
1588	1,78	Conserved protein
1589	1,04	Conserved protein
1590	1,49	Zinc metalloprotease
1591	1,07	Fe-S OXIDOREDUCTASE
1592	0,91	PHOSPHOGLUCOMUTASE / PHOSPHOMANNOMUTASE
1593	1,20	Conserved protein
1594	1,03	Amino-acid acetyltransferase
1595	0,77	Conserved protein
1596	0,50	Cysteine desulfurase
1597	0,96	Type II secretion system protein
1598	1,09	Transporter
1599	0,96	Hypothetical protein
1600	1,00	Hypothetical protein

1601	1,00	Hypothetical protein
1602	1,00	Hypothetical protein
1603	1,00	Hypothetical protein
1604	1,04	Hypothetical protein
1605	1,03	Hypothetical protein
1606	1,10	Hypothetical protein
1607	0,98	FdhD protein
1608	0,92	Imidazoleglycerol-phosphate dehydratase
1609	0,43	Phosphoribosylformimino-5-aminoimidazole
1611	0,84	S-adenosylmethionine synthetase
1612	1,03	Hypothetical protein
1613	0,87	Xaa-Pro aminopeptidase
1614	1,46	Methionine aminopeptidase
1615	0,69	Hypothetical protein
1616	1,00	Conserved protein
1617	0,76	PUTATIVE METHYLTRANSFERASE
1618	0,86	tRNA pseudouridine synthase A
1619	1,00	Hypothetical transcriptional regulatory
1620	0,82	Conserved protein
1622	1,08	PUTATIVE NUCLEOTIDYLTRANSFERASE
1623	1,04	3-isopropylmalate dehydratase
1625	1,00	Hypothetical protein
1626	1,05	METHYLTRANSFERASE
1627	0,90	Alanyl-tRNA synthetase
1629	1,13	Conserved protein
1630	1,00	Hypothetical protein
1631	1,01	Conserved protein
1632	1,00	SWF/SNF FAMILY HELICASE
1633	1,04	Molybdenum cofactor biosynthesis protein
1634	1,00	Pyruvate formate-lyase activating enzyme
1635	0,26	LSU ribosomal protein L10AE
1636	1,00	Probable translation initiation factor 2
1637	1,00	Metallo cofactor biosynthesis protein (m
1638	1,00	Conserved protein
1639	1,00	PUTATIVE NUCLEOTIDYLTRANSFERASE

1640	0,58	Tryptophanyl-tRNA synthetase
1641	0,96	Phenylalanyl-tRNA synthetase_ alpha chai
1642	1,02	Conserved protein
1643	1,00	Hypothetical protein
1644	1,01	Hypothetical protein
1645	1,00	Hypothetical protein
1646	1,00	Hypothetical membrane spanning protein
1647	1,73	Hypothetical protein
1648	1,00	Copper-exporting ATPase
1649	1,01	Cation-transporting ATPase
1650	1,00	Hypothetical protein
1651	0,93	Conserved protein
1652	1,00	Conserved protein
1653	1,47	Universal stress protein
1654	1,03	Universal stress protein
1655	0,89	Universal stress protein
1656	1,09	Universal stress protein
1657	1,14	Universal stress protein
1658	1,02	Universal stress protein
1659	1,01	Fe-S OXIDOREDUCTASE
1660	0,73	Hypothetical protein
1661	0,90	Hypothetical protein
1662	0,78	Lysly-tRNA synthetase (PylS)
1663	0,94	PylB (Pyrrolysine synthesis)
1664	0,60	PylC (Pyrrolysine synthesis)
1665	0,91	Hypothetical protein
1666	0,67	Inorganic pyrophosphatase
1666	0,13	Inorganic pyrophosphatase
1667	1,03	Conserved protein
1668	0,86	Methylcobalamin:coenzyme M methyltransfe
1669	0,78	Monomethylamine corrinoid protein
1669	0,68	Monomethylamine corrinoid protein
1671	0,70	Monomethylamine:corrinoid methyltransfer
1672	0,96	Monomethylamine permease
1673	1,00	Monomethylamine permease (C-terminal dom

1674	1,04	Hypothetical protein
1676	1,02	Transposase
1677	1,00	Conserved protein
1678	1,16	REPLICATION FACTOR C SUBUNIT
1679	1,62	PROTEIN TRANSLOCASE_ SUBUNIT SECD
1680	0,92	PROTEIN TRANSLOCASE_ SUBUNIT SECF
1681	0,65	dCMP DEAMINASE
1682	8,41	Hypothetical protein
1683	0,90	Conserved protein
1684	1,08	Hypothetical protein
1685	1,30	Small heat shock protein
1686	0,60	3-phosphonopyruvate decarboxylase
1687	0,58	Aspartate kinase
1688	0,83	Phosphoribosylformylglycinamide cyclo-
1689	0,99	Conserved protein
1690	1,02	Conserved protein
1691	1,00	Conserved protein
1692	1,00	Hypothetical protein
1693	1,21	Hypothetical protein
1694	1,12	Hypothetical protein
1695	0,88	Hypothetical protein
1696	1,22	archaeosine tRNA-ribosyltransferase
1697	0,71	Conserved protein
1698	0,96	Acetylornithine aminotransferase
1699	0,73	Histidinol-phosphate aminotransferase
1700	1,08	Conserved protein
1701	1,04	CDP-diacylglycerol--serine O-phosphatidy
1702	1,37	Phosphatidylserine decarboxylase
1703	0,89	Hypothetical protein
1704	0,70	MutT-like protein
1705	0,56	DNA-directed RNA polymerase subunit M
1706	0,98	DNA polymerase sliding clamp
1707	0,98	Conserved protein
1708	1,07	Conserved protein
1709	0,99	Cobyrinic acid a_c-diamide synthase

1710	0,55	Molybdenum cofactor biosynthesis protein
1712	0,77	Survival protein
1713	1,00	Probable transcriptional regulator
1714	1,00	Conserved protein
1715	0,91	Glycyl-tRNA synthetase
1716	0,97	ATP-DEPENDENT RNA HELICASE_ EIF-4A FAMIL
1717	0,90	Hypothetical protein
1718	0,30	Conserved protein
1719	0,99	Superfamily I DNA and RNA helicase
1720	1,09	Phenylalanyl-tRNA synthetase_ alpha chai
1721	1,04	Conserved protein
1722	1,05	Chaperone protein
1723	1,15	Chaperone protein
1723	0,99	Chaperone protein
1724	0,40	Thermosome_ alpha subunit
1725	1,74	ORIGIN RECOGNITION COMPLEX SUBUNIT
1726	1,15	Hypothetical protein
1727	1,04	Exopolyphosphatase
1727	0,89	Exopolyphosphatase
1728	0,89	Polyphosphate kinase
1728	0,87	Polyphosphate kinase
1729	1,58	DNA mismatch repair protein
1731	0,95	Hydrolase of the alpha/beta superfamily
1732	0,97	Hypothetical protein
1733	1,07	Archaeal protein Translation Initiation
1734	0,81	Myo-inositol-1-phosphate synthase
1735	0,89	DNA repair protein
1736	0,96	Glutaredoxin-like protein
1737	0,43	Anaerobic ribonucleoside-triphosphate re
1738	0,79	Ribonucleoside-triphosphate reductase ac
1739	1,11	THIAMIN-MONOPHOSPHATE KINASE
1740	2,74	Hypothetical protein
1741	1,03	Conserved hypothetical protein
1742	0,37	Putative aliphatic sulfonate binding pro
1743	1,18	ABC transporter_ permease protein

1744	1,07	ABC transporter_ ATP-binding protein
1745	1,03	Hypothetical protein
1746	0,35	PUTATIVE METHYLTRANSFERASE
1747	0,28	Conserved protein
1748	0,40	Conserved protein
1750	0,78	Conserved protein
1751	1,00	5-methyltetrahydropteroyltriglutamate--h
1752	1,01	5-methyltetrahydropteroyltriglutamate--h
1753	1,00	Conserved protein
1754	1,03	Arginyl-tRNA synthetase
1754	0,92	Arginyl-tRNA synthetase
1755	0,77	Peptide Chain Release Factor
1756	0,77	Fe-S OXIDOREDUCTASE
1757	1,00	DNA polymerase II small subunit
1758	1,00	SIGNAL SEQUENCE PEPTIDASE
1758	0,90	SIGNAL SEQUENCE PEPTIDASE
1759	1,10	NifR3-like protein
1760	0,54	Pyruvate synthase_ gamma subunit
1761	1,00	Pyruvate synthase_ delta subunit
1762	0,61	Pyruvate synthase_ alpha subunit
1763	0,85	Pyruvate synthase_ beta subunit
1763	0,59	Pyruvate synthase_ beta subunit
1764	1,03	Hypothetical protein
1765	1,04	Hypothetical protein
1766	0,86	Hypothetical protein
1767	0,77	Zinc ABC transporter_ permease protein
1768	0,70	Zinc ABC transporter_ ATP-binding protei
1769	0,64	Zinc ABC transporter_ zinc-binding prote
1770	0,92	Iron-dependent repressor
1771	1,35	Gluconate permease
1772	1,53	Chemotaxis protein CheW
1773	1,61	Methyl-accepting chemotaxis protein
1774	1,12	Two-component response regulator
1775	1,46	Chemotaxis protein
1776	2,51	protein-glutamate methylesterase

1777	1,07	Chemotaxis protein
1778	1,11	Chemotaxis protein methyltransferase
1779	1,00	Chemotaxis protein
1780	1,00	Chemotaxis protein
1781	1,63	Formylmethanofuran--tetrahydromethanopte
1781	0,20	Formylmethanofuran--tetrahydromethanopte
1782	0,68	Pheromone shutdown protein
1783	0,93	Conserved protein
1784	0,80	Glutamate decarboxylase
1785	1,09	Sodium/proline symporter
1785	0,80	Sodium/proline symporter
1787	0,97	ORIGIN RECOGNITION COMPLEX SUBUNIT
1788	0,99	UMP/CMP kinase related protein
1789	0,95	Conserved protein
1790	0,96	Conserved protein
1791	0,96	Hypothetical protein
1792	0,96	protein Translation Elongation Factor 1A
1794	1,00	Conserved protein
1795	0,99	HTH DNA-binding protein
1796	1,93	Conserved protein
1797	1,34	Conserved protein
1798	2,44	Conserved protein
1799	1,20	Conserved protein
1800	1,10	Conserved protein
1801	1,01	Transposase
1802	0,66	Replication factor-A protein
1803	1,52	Putative tRNA 2'phosphotransferase
1804	0,88	RNA 3'-terminal phosphate cyclase
1805	1,00	NADH oxidase
1806	2,02	DNA primase
1807	5,53	Conserved protein
1808	3,03	Acetyltransferase
1809	0,44	Archaeosine tRNA-ribosyltransferase
1810	0,76	(S)-2-hydroxy-acid dehydrogenase
1811	0,87	Fe-S oxidoreductase

1812	1,00	Conserved protein
1815	0,59	Sec-independent transport protein TatD
1816	0,62	2-isopropylmalate synthase
1822	1,20	Conserved protein
1823	1,22	Hypothetical protein
1824	1,01	Hypothetical protein
1825	1,10	Hypothetical protein
1826	1,09	Conserved protein
1827	1,51	Hypothetical protein
1828	0,74	Hypothetical protein
1831	0,71	Conserved protein
1832	1,39	Hypothetical protein
1833	1,00	Hypothetical protein
1834	1,05	Hypothetical protein
1835	0,88	Monomethylamine:corrinoid methyltransfer
1836	0,96	Monomethylamine:corrinoid methyltransfer
1837	1,04	Monomethylamine Corrinoid protein
1839	1,00	Putative ferredoxin
1840	0,78	Conserved protein
1841	1,03	O-linked N-acetylglucosamine transferase
1842	0,37	Phosphoglycolate phosphatase
1843	1,00	Conserved protein
1844	1,08	Ferredoxin
1845	1,54	ALDEHYDE FERREDOXIN OXIDOREDUCTASE
1846	1,47	permease_ Na ⁺ /H ⁺ -dicarboxylate symporter
1846	0,97	permease_ Na ⁺ /H ⁺ -dicarboxylate symporter
1847	0,81	Oligopeptide transporter_ ATP-binding pr
1848	1,00	Oligopeptide transporter_ ATP-binding pr
1850	1,00	Oligopeptide transporter_ permease prote
1851	1,00	Oligopeptide transporter_ permease prote
1852	1,01	Transport protein
1853	1,03	Conserved protein
1854	1,10	Hypothetical protein
1855	1,00	Hypothetical protein
1856	1,00	N-5'-phosphoribosyl)anthranilate isomera

1857	0,81	Hypothetical protein
1858	1,00	5-methylcytosine-specific restriction en
1859	1,00	Acetyltransferase
1860	1,00	Transcriptional regulator_ AraC family
1861	0,92	Ferredoxin
1862	1,02	Conserved protein
1863	1,00	Conserved protein
1864	1,07	Conserved protein
1865	0,79	Putative DNA or RNA helicase of superfam
1866	0,84	Threonyl-tRNA synthetase
1867	0,66	Hypothetical protein
1868	1,00	Hypothetical protein
1869	1,16	Phosphoadenosine phosphosulfate reductas
1870	0,98	Hypothetical protein
1871	1,00	Glutamate dehydrogenase
1872	0,96	Hypothetical protein
1873	1,50	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
1874	1,05	Hypothetical protein
1875	1,09	Iron-sulfur cluster-binding protein
1876	1,00	Excinuclease ABC_ subunit A
1877	1,99	Excinuclease ABC_ subunit C
1878	1,44	Excinuclease ABC_ subunit B
1878	1,32	Excinuclease ABC_ subunit B
1878	1,04	Excinuclease ABC_ subunit B
1879	1,15	Conserved protein
1880	2,00	Hypothetical protein
1881	1,27	Hypothetical protein
1882	0,99	Conserved protein
1883	1,06	Transcriptional regulator
1884	1,00	Putative inorganic pyrophosphatase
1885	0,96	Probable ATP-dependent helicase
1886	1,00	SAM-dependent methyltransferases
1887	1,06	Conserved protein
1888	1,00	Dihydrolipoamide dehydrogenase
1889	1,49	Hypothetical Membrane Spanning protein

1890	1,25	PROTEASE I
1891	1,73	Hypothetical protein
1892	1,27	Conserved protein
1893	1,17	Hypothetical protein
1894	1,00	Putative transport protein
1895	0,19	Glutaredoxin
1896	0,98	Ferredoxin-thioredoxin reductase_ cataly
1897	1,00	Serine O-acetyltransferase
1898	0,99	NADPH-flavin oxidoreductase
1899	1,00	Conserved protein
1900	1,00	Hypothetical protein
1902	0,81	Coenzyme F420 hydrogenase beta subunit
1903	1,10	Branched-chain amino acid transport prot
1904	0,79	Branched-chain amino acid transport prot
1905	1,00	Conserved protein
1906	1,00	Hypothetical protein
1907	1,14	Conserved protein
1908	1,02	Hypothetical protein
1909	1,00	Conserved protein
1910	1,00	Hypothetical protein
1911	1,16	Hypothetical protein
1912	1,02	Hypothetical protein
1913	1,00	Hypothetical protein
1914	1,06	Hypothetical protein
1915	1,00	Hypothetical protein
1916	1,24	Hypothetical protein
1917	1,00	Hypothetical protein
1918	1,11	Conserved protein
1920	1,07	Hypothetical protein
1921	0,98	Hypothetical protein
1922	1,00	Hypothetical protein
1923	1,17	Probable transcriptional regulator
1924	0,98	Hypothetical protein
1925	1,00	Conserved protein
1926	1,05	Thiamin-phosphate pyrophosphorylase

1927	0,89	Hydroxyethylthiazole kinase
1928	1,01	HTH DNA-binding protein
1929	1,14	Conserved protein
1930	0,82	Phosphate permease
1930	0,79	Phosphate permease
1932	0,96	Transposase
1933	1,00	Conserved protein
1934	1,25	Conserved protein
1935	1,00	Putative ketoreductase
1936	1,00	ABC Transporter_ permease protein)
1937	1,00	ABC transporter_ ATP-binding protein
1938	2,92	Conserved protein
1939	1,00	Conserved protein
1940	1,79	Transporter
1941	1,23	Conserved protein
1942	0,99	Conserved protein
1943	1,00	Conserved protein
1944	0,96	Conserved protein
1945	1,00	Conserved protein
1946	1,00	Ferredoxin
1947	0,93	Prismane protein
1948	0,98	Hypothetical protein
1949	1,00	Cation efflux protein
1950	0,97	Transporter
1951	0,88	Transcriptional regulator_ ArsR family
1952	0,91	PROTEASE
1953	1,00	Response regulator
1954	1,04	Two component system histidine kinase
1955	1,00	Conserved protein
1956	1,01	Hypothetical protein
1957	1,22	Conserved protein
1958	1,00	Conserved protein
1960	1,04	Transporter
1961	0,95	Hypothetical protein
1962	5,34	Hypothetical protein

1963	1,00	Hypothetical protein
1964	0,11	Transcriptional regulator_ MarR family
1965	0,16	DinF protein
1966	1,02	Hypothetical membrane spanning protein
1967	1,00	Hypothetical protein
1968	1,03	Hypothetical protein
1969	1,38	Potassium channel protein
1970	0,11	Glutamine synthetase
1971	1,88	Flavodoxin
1972	1,00	Transporter
1973	0,96	Ornithine decarboxylase
1974	1,00	KETOISOVALERATE OXIDOREDUCTASE SUBUNIT
1975	1,11	KETOISOVALERATE OXIDOREDUCTASE SUBUNIT
1976	0,96	Ketoisovalerate oxidoreductase subunit
1977	0,78	Putative Acetyl-CoA synthetase
1978	0,71	Transcriptional regulator
1979	1,15	Hypothetical protein
1980	1,15	Hypothetical protein
1981	1,00	Hypothetical protein
1982	1,41	Hypothetical protein
1983	1,00	Hypothetical protein
1984	1,00	Transcriptional regulator_ ArsR family
1985	1,00	PUTATIVE METHYLTRANSFERASE
1986	1,00	Hypothetical protein
1987	7,01	Transcriptional regulator_ MerR family
1988	1,25	Hypothetical protein
1991	0,98	Conserved protein
1992	1,00	Putative cation transport regulator
1993	0,62	Conserved protein
1996	1,10	Conserved protein
1997	1,00	Hydrogenase maturation protein
1998	4,40	A1AO H+ ATPASE_ SUBUNIT D
1998	3,53	A1AO H+ ATPASE_ SUBUNIT D
1999	4,05	A1AO H+ ATPASE_ SUBUNIT B
1999	1,24	A1AO H+ ATPASE_ SUBUNIT B

2000	2,33	A1AO H+ ATPASE_ SUBUNIT A
2001	2,83	A1AO H+ ATPASE_ SUBUNIT F
2002	2,05	A1AO H+ ATPASE_ SUBUNIT C
2003	1,92	A1AO H+ ATPASE_ SUBUNIT E
2004	2,83	A1AO H+ ATPASE_ SUBUNIT K
2008	1,09	Conserved protein
2009	0,98	Carbon monoxide dehydrogenase
2010	1,00	METAL DEPENDENT HYDROLASE
2011	0,98	Hypothetical protein
2012	1,00	Conserved protein
2013	1,00	Conserved protein
2014	1,01	Conserved protein
2015	1,00	SURFACE LAYER PROTEIN B
2016	1,07	TYPE I RESTRICTION-MODIFICATION SYSTEM M
2017	1,13	TYPE I RESTRICTION-MODIFICATION SYSTEM S
2018	1,26	TYPE I RESTRICTION-MODIFICATION SYSTEM R
2019	1,10	Zinc metalloprotease
2020	0,88	Cell surface protein
2021	1,10	Hypothetical protein
2022	0,97	Methyltransferase involved in cell divisi
2023	0,93	Hypothetical protein
2024	1,01	Conserved protein
2025	1,05	Conserved protein
2026	0,86	DNA/pantothenate metabolism flavoprotein
2027	0,99	Conserved protein
2028	1,02	Hypothetical protein
2029	1,07	Conserved protein
2030	1,27	Chlorohydrolase family protein
2031	0,77	Adenosylhomocysteinase
2032	1,16	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
2033	1,00	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
2034	1,41	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
2035	0,22	DNA-directed RNA polymerase_ subunit H
2036	0,72	DNA-directed RNA polymerase_ beta chain
2037	0,88	DNA-directed RNA polymerase_ beta chain

2038	2,52	DNA-directed RNA polymerase_ subunit A'
2039	0,97	DNA-directed RNA polymerase_ subunit A''
2039	0,42	DNA-directed RNA polymerase_ subunit A''
2040	0,27	LSU ribosomal protein L30E
2041	0,50	NusA protein homolog
2042	0,47	SSU ribosomal protein S12P
2043	0,38	SSU ribosomal protein S7P
2044	0,80	protein Translation Elongation factor 2
2045	0,55	protein Translation Elongation Factor 1A
2046	0,64	SSU ribosomal protein S10P
2047	1,00	Conserved protein
2048	1,00	Conserved protein
2049	1,04	Conserved protein
2050	1,03	Conserved protein
2051	0,99	Conserved protein
2052	1,09	Conserved protein
2053	1,00	Conserved protein
2054	1,00	Conserved protein
2055	1,03	Dihydropyrimidinase
2056	1,08	Conserved protein
2057	1,03	Tetrahydromethanopterin S-methyltransfer
2058	1,00	Conserved protein
2059	1,00	Hypothetical protein
2060	1,00	Conserved protein
2061	0,93	Conserved protein
2063	0,99	Transcriptional regulator_ ArsR family
2064	0,97	Conserved protein
2065	1,00	ARSENATE REDUCTASE
2066	1,14	Putative methyltransferase
2067	1,00	Transcriptional regulator_ ArsR family
2068	0,98	Cytochrome c-type biogenesis protein Ccd
2069	0,90	Conserved protein
2070	1,16	Conserved protein
2071	1,18	Hypothetical protein
2072	1,00	Transcriptional regulator_ ArsR family

2073	1,00	Conserved protein
2074	0,61	Conserved protein
2075	1,16	Conserved protein
2076	1,30	Conserved protein
2077	0,95	Transposase
2078	1,01	Transposase
2079	0,80	Transposase
2080	0,99	Conserved protein
2081	1,00	AMIDOHYDROLASE (putative)
2082	1,03	Acetyltransferase
2083	1,71	Glucoamylase
2084	1,02	Trp repressor binding protein
2085	1,02	Dolichyl-phosphate glucose synthetase
2086	0,95	Galactosyltransferase
2087	1,00	Glycosyltransferase
2088	1,09	Hypothetical protein
2089	1,04	Hypothetical protein
2090	1,01	Transposase
2091	1,05	Conserved protein
2092	1,00	Glucose-1-phosphate thymidyltransferase
2093	1,00	Polysaccharide ABC transporter_ ATP-bind
2097	0,98	REVERSE TRANSCRIPTASE
2098	4,24	Transposase
2099	1,00	Transposase
2100	1,05	Hypothetical protein
2101	1,00	Hypothetical protein
2102	1,01	TYPE I RESTRICTION-MODIFICATION SYSTEM S
2103	0,91	TYPE I RESTRICTION-MODIFICATION SYSTEM M
2106	0,98	Conserved protein
2107	0,94	Conserved protein
2108	1,20	Conserved protein
2109	0,91	Conserved protein
2110	1,01	Conserved protein
2111	0,97	Conserved protein
2112	0,50	Conserved protein

2113	0,70	Homoserine dehydrogenase
2114	0,87	ATP-dependent DNA ligase
2115	1,24	Hypothetical protein
2116	1,13	Conserved protein
2117	0,89	Conserved protein
2118	0,89	Hypothetical protein
2119	0,99	Conserved protein
2120	1,00	Hypothetical protein
2121	1,00	Conserved protein
2122	1,52	Hypothetical protein
2123	1,77	Phosphoenolpyruvate synthase
2124	0,89	Conserved protein
2125	0,98	Hypothetical protein
2126	1,00	Conserved protein
2127	1,93	Multiple antibiotic resistance protein
2128	1,24	Conserved protein
2129	1,18	Hypothetical protein
2130	1,00	Conserved protein
2131	1,00	Conserved protein
2133	1,00	Conserved protein
2134	1,00	Conserved protein
2135	0,97	TYPE I RESTRICTION-MODIFICATION SYSTEM S
2136	0,99	TYPE I RESTRICTION-MODIFICATION SYSTEM M
2137	1,00	Hypothetical protein
2138	0,97	Hypothetical protein
2139	1,00	Hypothetical protein
2140	1,03	Conserved protein
2141	1,03	Conserved protein
2142	1,32	Conserved protein
2143	0,85	Hypothetical protein
2144	1,02	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
2145	0,95	Aminoacyl-histidine dipeptidase
2146	1,00	Hypothetical protein
2147	0,98	Conserved protein
2148	1,00	Hypothetical protein

2150	1,05	Hypothetical protein
2151	0,86	Conserved protein
2152	1,07	Hypothetical protein
2153	1,49	Hypothetical protein
2154	0,93	Hypothetical protein
2155	1,00	Hypothetical protein
2156	1,00	Hypothetical protein
2157	1,00	Hypothetical protein
2158	0,94	Hypothetical protein
2159	0,98	Putative DNA recombinase
2160	1,00	Hypothetical protein
2161	1,00	Hypothetical protein
2162	1,00	Hypothetical protein
2163	1,00	Conserved protein
2164	1,00	Iron-containing alcohol dehydrogenase
2165	1,11	Glycogen debranching enzyme
2165	1,00	Glycogen debranching enzyme
2166	1,00	Conserved protein
2167	1,00	Conserved protein
2168	2,34	Two component system histidine kinase
2169	1,02	Conserved protein
2170	1,42	Conserved protein
2171	1,00	Acylphosphatase
2172	0,96	Cobalt-zinc-cadmium resistance protein
2173	0,96	Putative phosphoglycerate mutase
2174	1,01	Hypothetical protein
2175	1,03	Conserved protein
2176	1,02	Glyceraldehyde 3-phosphate dehydrogenase
2177	1,27	Suppressor protein SuhB homolog
2178	1,24	Hypothetical protein
2181	1,00	Conserved protein
2183	0,75	INDOLEPYRUVATE FERREDOXIN OXIDOREDUCTASE
2184	1,11	Hypothetical protein
2185	1,00	IRON-SULFUR FLAVOPROTEIN
2186	1,00	DNA repair protein

2187	0,91	Molybdopterin converting factor_ subunit
2188	0,98	Molybdopterin-guanine dinucleotide biosy
2189	0,97	Hypothetical protein
2190	0,88	Conserved protein
2191	1,00	Conserved protein
2192	1,00	Pirin
2193	0,98	Conserved protein
2193	0,67	empty
2194	1,06	Conserved protein
2195	1,02	Hypothetical protein
2196	1,01	Hypothetical protein
2197	1,52	Carbon monoxide dehydrogenase accessory
2198	1,04	Conserved protein
2199	1,00	Asparagine synthetase [glutamine-hydroly
2200	0,98	Hypothetical protein
2201	1,00	Phosphoribosylformylglycinamide synthase
2202	2,51	Conserved protein
2203	1,00	Conserved protein
2204	1,10	Conserved protein
2208	1,05	Glutamate 5-kinase
2209	1,25	Gamma-glutamyl phosphate reductase
2209	0,76	Gamma-glutamyl phosphate reductase
2210	0,99	Conserved protein
2211	1,00	Conserved protein
2212	1,00	Hypothetical protein
2213	0,99	Conserved protein
2214	1,24	Universal stress protein
2215	5,07	Conserved protein
2216	3,65	Conserved protein
2217	0,52	Conserved protein
2218	1,00	Conserved protein
2219	1,01	Conserved protein
2220	1,33	Molybdopterin biosynthesis MoeA protein
2221	1,08	Molybdopterin converting factor_ small s
2222	0,98	Conserved protein

2223	1,18	Conserved protein
2224	1,00	Na ⁺ /H ⁺ antiporter
2224	0,79	Na ⁺ /H ⁺ antiporter
2225	1,41	Cation-transporting ATPase
2226	1,00	Conserved protein
2226	0,99	Conserved protein
2227	1,54	Conserved protein
2228	1,27	Succinate-semialdehyde dehydrogenase [NA
2229	1,00	Conserved protein
2230	1,00	Glycosyltransferases involved in cell wa
2231	1,01	Transcriptional regulator_ ArsR family
2232	0,69	Conserved protein
2233	0,96	Coenzyme F390 synthetase/phenylacetyl-Co
2234	0,98	Hypothetical protein
2235	1,00	Conserved protein
2236	0,93	Conserved protein
2237	1,00	Conserved protein
2238	1,00	Conserved protein
2239	1,94	Bacterioferritin comigratory protein
2240	1,02	Conserved protein
2241	1,00	Conserved protein
2242	1,00	Deoxyribodipyrimidine photolyase
2243	1,13	Conserved protein
2244	1,26	Cell division cycle protein 48 homolog
2245	1,00	Phosphoribosylamidoimidazole-succinocarb
2246	1,18	Conserved protein
2247	1,20	Conserved protein
2248	1,12	protein Translation Initiation Factor 1
2249	1,33	Conserved protein
2250	1,00	Phosphoribosylformylglycinamide synthase
2251	1,42	Alpha-amylase
2252	1,01	Alpha-amylase
2253	1,03	Conserved protein
2254	1,12	Glucoamylase
2255	0,84	Seryl-tRNA synthetase

2256	1,76	Periplasmic serine protease
2257	0,70	Methionyl-tRNA synthetase
2258	0,95	Adenylate cyclase
2259	0,78	Conserved protein
2260	0,84	Beta-ketoacyl synthase/ thiolase
2261	0,52	Hydroxymethylglutaryl-CoA synthase
2262	0,62	Putative transcriptional regulator
2263	1,34	Conserved protein
2264	1,00	Conserved protein
2265	1,50	Hypothetical protein
2266	1,00	Transposase
2267	1,31	Conserved protein
2269	0,94	Conserved protein
2270	0,77	Conserved protein
2271	1,04	DNA polymerase IV
2272	1,15	Cobalt transporter_ ATP-binding protein
2273	1,45	Cobalt transport protein
2274	1,15	Hypothetical protein
2275	1,00	Putative methyltransferase
2276	1,03	Putative methyltransferase
2276	1,00	Putative methyltransferase
2277	3,73	Putative methyltransferase
2278	4,31	CbiM protein
2279	11,43	CbiM protein
2280	1,20	Endonuclease III
2281	1,00	Conserved protein
2282	1,00	Glutathione reductase
2283	0,33	PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE
2284	1,55	Conserved protein
2285	1,00	Conserved protein
2286	1,00	Cation-transporting ATPase
2287	0,92	Putative methyltransferase
2288	1,56	Transcriptional regulator
2289	0,84	Phosphoglycerate mutase
2290	0,81	Conserved protein

2291	1,10	FLAP ENDONUCLEASE-1 (RAD27/FEN1 family)
2292	0,91	Hypothetical protein
2293	1,04	Conserved protein
2294	1,03	Conserved protein
2295	1,38	POTASSIUM/COPPER-TRANSPORTING ATPASE
2296	2,36	ABC transporter_ ATP-binding protein
2297	0,98	Conserved protein
2298	1,12	Conserved protein
2299	1,19	Conserved protein
2300	1,19	Conserved protein
2301	1,65	Conserved protein
2302	1,15	Conserved protein
2303	1,27	4-carboxymuconolactone decarboxylase
2304	1,07	Conserved protein
2305	1,07	MutT related protein
2306	1,02	Aldehyde ferredoxin oxidoreductase
2307	0,59	protein Translation Initiation Factor 5A
2308	0,74	Agmatinase
2309	2,64	Conserved protein
2315	1,00	Hypothetical protein
2316	3,06	Hypothetical protein
2317	1,03	Hypothetical protein
2321	2,55	Transposase
2322	1,00	Hypothetical protein
2326	1,05	INTEGRAL MEMBRANE PROTEIN
2327	0,90	Conserved protein
2328	1,10	Conserved protein
2329	0,90	Conserved protein
2330	0,99	Conserved protein
2331	1,12	Acetolactate synthase small subunit
2332	1,03	Coenzyme F390 synthetase
2333	0,61	Conserved protein
2334	0,41	Prefoldin beta subunit
2335	0,97	Conserved protein
2336	1,08	Hypothetical protein

2337	0,72	2-isopropylmalate synthase
2338	0,97	Acetolactate synthase large subunit
2339	1,15	Acetolactate synthase small subunit
2340	0,95	Ketol-acid reductoisomerase
2341	1,05	Nitroreductase family protein
2342	1,45	Putative nickel-responsive regulator Nik
2343	1,07	Hypothetical protein
2344	0,86	Glutamate synthase [NADPH]
2345	0,84	Probable dihydroorotate dehydrogenase el
2347	1,00	Transcriptional regulator_ ArsR family
2348	1,00	METHYLTRANSFERASE
2349	1,18	MANNOSE-6-PHOSPHATE ISOMERASE/ MANNOSE-1
2350	0,99	GDP-mannose 4_6 dehydratase
2351	1,19	GDP-FUCOSE SYNTHETASE
2352	1,03	Polysaccharide ABC transporter_ permease
2353	1,47	Polysaccharide ABC transporter_ ATP-bind
2354	1,01	MANNOSYLTRANSFERASE
2355	1,00	Glycosyltransferase involved in cell wal
2356	1,28	Glycosyltransferase involved in cell wal
2357	1,32	Glycosyltransferase involved in cell wal
2358	1,33	MANNOSYLTRANSFERASE
2359	1,32	GLUCOSYLTRANSFERASE
2360	1,00	GLYCOSYL TRANSFERASE
2362	1,41	Oligosaccharyl transferase
2363	1,46	3-isopropylmalate dehydratase
2364	2,15	Conserved protein
2365	1,07	Conserved protein
2366	1,02	Isocitrate dehydrogenase [NADP]
2367	1,55	Alpha-acetolactate decarboxylase
2368	1,02	PUTATIVE FLAVODOXIN
2369	5,66	Conserved protein
2370	6,39	FLAVOPROTEIN
2371	5,78	IRON-SULFUR FLAVOPROTEIN
2372	2,98	Hypothetical protein
2373	2,67	Desulfoferrodoxin

2374	5,26	Hypothetical protein
2375	1,13	Zinc finger protein
2377	0,06	Coenzyme F420-dependent N5_N10-methylene
2377	0,05	Coenzyme F420-dependent N5_N10-methylene
2378	0,79	F420H2 Dehydrogenase Subunit FpoF
2378	0,11	F420H2 Dehydrogenase Subunit FpoF
2379	0,44	Nicotinamide-nucleotide adenyltransfer
2379	0,26	Nicotinamide-nucleotide adenyltransfer
2380	1,00	Conserved protein
2381	1,22	Hypothetical protein
2382	0,97	Transposase
2383	1,00	Transposase
2384	1,09	Hypothetical protein
2385	1,18	Conserved protein
2386	1,00	Conserved protein
2387	0,80	Undecaprenyl pyrophosphate synthetase
2388	1,03	Conserved protein
2389	1,00	Conserved protein
2390	1,07	Long-chain-fatty-acid--CoA ligase
2391	1,38	Conserved protein
2392	1,22	NH3-dependent NAD(+) synthetase
2393	1,11	Iron-sulfur cluster-binding protein
2394	0,98	Acetyltransferases
2395	1,00	Conserved protein
2396	0,92	Probable radical-forming protein
2397	1,00	Hypothetical protein
2398	1,00	Conserved protein
2399	1,01	Conserved protein
2400	0,96	Nucleoside-triphosphatase
2401	1,02	O-sialoglycoprotein endopeptidase
2402	1,00	Conserved protein
2404	0,95	SSU ribosomal protein S24E
2405	1,00	Hypothetical protein
2406	0,65	DNA-directed RNA polymerase subunit E
2407	0,91	DNA-directed RNA polymerase subunit E'

2408	0,74	Conserved protein
2409	0,76	protein Translation Initiation Factor 2
2410	0,72	Conserved protein
2411	0,98	Integral membrane protein
2412	0,70	Conserved membrane protein
2413	0,99	GLYCEROL 1-PHOSPHATE DEHYDROGENASE (puta
2414	0,96	Conserved protein
2415	1,46	Conserved protein
2417	1,42	Sulfate adenylyltransferase
2418	1,75	Conserved protein
2418	1,11	Conserved protein
2419	1,13	Conserved protein
2420	1,00	Conserved protein
2422	1,04	GLYCOSYLTRANSFERASE
2423	0,99	Conserved protein
2424	1,00	Hypothetical protein
2425	2,62	Transposase
2426	4,21	Phosphate-binding protein
2427	1,31	Phosphate transport ATP-binding protein
2428	1,04	Phosphate transport system protein
2429	1,13	PUTATIVE PHOSPHATE REGULATORY PROTEIN
2430	1,01	ARSENATE REDUCTASE
2431	0,95	Conserved protein
2432	1,00	Alkaline phosphatase
2433	1,00	Transcriptional regulator_ lcc related p
2434	0,79	ABC transporter_ ATP-binding protein
2435	1,00	ABC transporter_ ATP-binding protein
2436	1,38	Conserved protein
2436	1,00	Conserved protein
2437	1,00	Acetyltransferase
2438	1,00	Hypothetical protein
2439	2,58	Transcriptional regulator
2439	1,00	Transcriptional regulator
2440	2,49	Hypothetical protein
2441	2,11	Hypothetical protein

2442	1,39	Hypothetical protein
2443	2,14	Conserved protein
2444	1,48	Hypothetical protein
2445	1,26	Hypothetical protein
2446	0,99	Hypothetical protein
2447	1,02	Hypothetical protein
2449	1,14	Conserved protein
2450	2,74	Dipeptide ABC transporter_ binding prote
2451	0,98	Dipeptide ABC transporter_ binding prote
2452	1,64	Dipeptide ABC transporter_ permease prot
2453	1,33	Dipeptide ABC transporter_ permease prot
2454	1,04	Dipeptide ABC transporter_ ATP-binding p
2455	0,98	Dipeptide ABC transporter_ ATP-binding p
2456	1,08	Conserved protein
2457	1,02	Conserved protein
2458	1,02	Hypothetical protein
2459	1,85	Conserved protein
2460	1,00	RNA SIGNAL RECOGNITION PARTILCE 4.5S RNA
2461	1,00	Conserved protein
2462	1,00	Undecaprenyl pyrophosphate synthetase
2463	1,00	METHYLTRANSFERASE
2464	1,00	TRANSLATION INITIATION FACTOR 1A (EIF-1A
2465	0,78	Ubiquinone/menaquinone biosynthesis meth
2466	1,00	Conserved protein
2467	1,00	Conserved protein
2469	1,68	Hypothetical protein
2469	1,00	Hypothetical protein
2470	1,00	Hypothetical protein
2471	1,07	Conserved protein
2472	1,00	Conserved protein
2473	1,54	Superfamily I DNA and RNA helicase
2474	1,00	Conserved protein
2475	1,52	O-linked N-acetylglucosamine transferase
2476	1,00	Hypothetical protein
2477	1,00	Conserved protein

2478	1,00	Conserved protein
2479	1,01	Hypothetical protein
2480	0,35	Argininosuccinate synthase
2481	0,56	Carbamoyl-phosphate synthase large chain
2482	0,49	Carbamoyl-phosphate synthase small chain
2483	1,00	Glycine betaine transporter_ ATP-binding
2483	0,96	Glycine betaine transporter_ ATP-binding
2484	1,00	Glycine betaine transporter_ permease pr
2484	0,95	Glycine betaine transporter_ permease pr
2485	1,06	Glycine betaine transporter_ substrate-b
2486	0,93	Conserved protein
2487	1,00	Hypothetical protein
2488	2,84	Hypothetical protein
2489	1,27	Hypothetical protein
2490	0,99	Acetylornithine aminotransferase
2491	1,02	Aldehyde dehydrogenase
2492	1,00	Conserved protein
2492	1,00	Conserved protein
2493	2,24	Glutamyl-tRNA (Gln) amidotransferase
2494	1,00	Hypothetical protein
2496	1,14	Transposase
2497	1,21	Universal stress protein
2500	0,73	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENAS
2501	1,03	Ferredoxin-thioredoxin reductase_ cataly
2502	3,01	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENAS
2502	2,16	TUNGSTEN-CONTAINING FORMYLMETHANOFURAN D
2503	1,03	TUNGSTEN FORMYLMETHANOFURAN DEHYDROGENAS
2504	1,25	Conserved protein
2505	1,20	SAM-dependent methyltransferases
2506	0,71	SURFACE LAYER PROTEIN B
2507	1,00	SURFACE LAYER PROTEIN B
2508	1,00	CONSERVED PROTEIN
2509	1,13	Hypothetical protein
2510	2,67	N-methylhydantoinase (ATP hydrolyzing)
2511	1,00	Sodium-dependent transporter

2512	0,97	Putative ribosomal RNA methyltransferase
2514	0,36	Thermosome b-subunit
2515	0,98	Ribose 5-phosphate isomerase
2516	0,85	Aspartyl-tRNA synthetase
2517	1,02	Conserved protein
2518	1,00	Hypothetical protein
2519	1,47	Hypothetical protein
2520	1,00	Xanthine-guanine phosphoribosyltransferase
2521	1,07	Conserved protein
2522	6,86	Hypothetical protein
2523	1,18	Hypothetical Cytosolic protein
2524	0,98	Phosphoserine phosphatase
2525	1,04	Shikimate kinase
2526	1,00	Conserved protein
2527	1,06	Hypothetical protein
2528	1,06	Pyrimidine-nucleoside phosphorylase
2529	1,02	Transporter
2530	1,00	Conserved protein
2531	1,23	ABC transporter permease protein
2532	1,25	Conserved protein
2533	0,96	Cobamoyl synthase
2534	0,96	Conserved protein
2535	0,99	Transposase
2536	1,08	Ornithine cyclodeaminase
2537	1,60	Conserved protein
2538	1,06	O-linked N-acetylglucosamine transferase
2539	1,17	Conserved protein
2540	1,00	Conserved protein
2541	1,12	Serine/threonine protein phosphatase
2542	1,04	O-linked N-acetylglucosamine transferase
2543	1,12	Hypothetical protein
2544	1,00	FxsA protein
2545	0,87	Hypothetical protein
2546	0,97	Hypothetical protein
2547	1,10	Cysteine desulfhydrase

2548	1,19	NifU protein
2549	1,00	Ribosomal protein S6 modification protei
2550	0,97	Hypothetical protein
2551	0,99	Conserved protein
2553	0,62	Conserved protein
2554	1,04	Putative transmembrane efflux protein
2555	1,99	Transcriptional regulator_ MarR family
2556	0,84	Hypothetical protein
2558	0,38	CTP synthase
2559	0,88	Hypothetical protein
2560	1,05	Carbon monoxide dehydrogenase
2561	1,01	Iron-sulfur protein
2562	0,89	Universal stress protein
2563	1,00	Conserved protein
2564	0,70	Universal stress protein
2565	1,31	PmbA protein
2566	1,23	Zinc metalloprotease
2567	1,74	ATP-dependent protease La
2568	1,01	Conserved protein
2569	1,00	Conserved protein
2570	1,06	Conserved protein
2571	0,97	Conserved protein
2572	0,84	Threonine synthase
2573	1,00	Sulfolpyruvate decarboxylase alpha chain
2574	1,03	Ferredoxin oxidoreductase
2575	1,00	Zn-dependent hydrolase
2576	0,92	Conserved protein
2577	3,83	CONSERVED PROTEIN (Archaea)
2578	0,99	Cytochrome c-type biogenesis protein
2579	1,06	Putative Cytochrome c biogenesis factors
2580	1,09	Conserved protein
2581	0,56	Orotate phosphoribosyltransferase
2582	1,00	4-carboxymuconolactone decarboxylase
2584	1,02	Phosphoribosylamine--glycine ligase
2585	0,51	Ornithine carbamoyltransferase

2586	1,10	Transcriptional regulator
2587	0,94	IRON-SULFUR FLAVOPROTEIN
2588	0,97	Conserved protein
2589	1,02	putative nucleoside-diphosphate-sugar ep
2590	1,33	Conserved protein
2591	0,95	DNA integration/recombination/inversion
2592	1,01	Conserved protein
2593	1,00	Conserved protein
2594	1,12	Conserved protein
2595	0,87	TYPE IIS RESTRICTION ENZYME
2597	1,01	ATP-dependent DNA helicase
2598	1,00	ATP-dependent DNA helicase
2599	1,86	Hypothetical protein
2600	1,39	Conserved protein
2601	1,01	DNA repair protein
2602	1,30	ATP-dependent protease La
2603	1,05	HOMOSPERMIDINE SYNTHASE
2604	1,10	Cobalt-zinc-cadmium resistance protein
2605	1,04	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
2606	1,05	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
2609	1,07	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
2610	1,00	Transporter
2611	1,81	Methanol corrinoid protein
2613	1,56	Methylcobalamin:coenzyme M methyltransfe
2614	1,02	Conserved protein
2615	1,20	Conserved protein
2616	0,97	Conserved protein
2617	1,16	Diamine acetyltransferase
2618	1,18	Conserved protein
2619	0,48	Thiamine biosynthesis protein
2620	1,13	DNA topoisomerase III
2621	0,39	SSU ribosomal protein S3AE
2623	1,00	Short chain dehydrogenase/reductase
2624	1,00	Conserved protein
2625	0,98	NUCLEOTIDYLTRANSFERASE

2626	1,00	Hypothetical nucleotidyltransferase
2627	1,00	Conserved protein
2631	1,84	Transposase
2632	1,00	Hypothetical protein
2633	1,00	TYPE III RESTRICTION-MODIFICATION SYSTEM
2634	1,00	Conserved protein
2635	1,10	Conserved protein
2636	1,00	Conserved protein
2637	0,96	Conserved protein
2638	1,00	ATP-dependent DNA helicase
2640	1,10	Conserved protein
2641	1,01	Conserved protein
2642	1,02	Hypothetical protein
2643	0,99	Hypothetical protein
2644	1,07	Hypothetical protein
2645	1,00	Conserved protein
2646	2,09	Conserved protein
2646	1,00	Conserved protein
2648	1,02	Hypothetical protein
2649	1,02	Hypothetical protein
2650	1,00	Hypothetical protein
2651	1,00	Conserved protein
2652	2,01	Cysteine proteinase
2653	0,95	Conserved protein
2654	0,98	Putative single-stranded-DNA-specific ex
2655	1,05	Hypothetical protein
2656	1,00	Hypothetical protein
2657	1,00	Conserved protein
2658	1,00	Conserved protein
2659	1,08	Conserved protein
2660	0,96	Conserved protein
2661	1,04	Fe-S OXIDOREDUCTASE
2662	1,00	THIAZOLE BIOSYNTHETIC ENZYME
2663	1,14	Hypothetical protein
2664	1,00	Molybdenum-pterin-binding-protein

2665	1,00	Conserved protein
2667	1,00	Conserved protein
2668	0,53	SODIUM-CALCIUM EXCHANGER
2669	0,93	Hypothetical protein
2670	1,00	Hypothetical protein
2671	0,95	Alanyl-tRNA synthetase
2672	1,00	Conserved protein
2673	1,07	Conserved protein
2674	1,66	PUTATIVE MECHANOSENSITIVE ION CHANNEL
2675	1,15	Conserved protein
2676	1,09	Hypothetical protein
2677	1,06	Conserved protein
2678	0,37	Ferredoxin
2679	0,43	Hypothetical protein
2680	0,89	Glycerol-3-phosphate cytidyltransferase
2681	1,07	Aspartate aminotransferase
2682	0,78	Riboflavin synthase_ subunit beta
2683	0,78	Riboflavin synthase_ subunit alpha
2686	1,00	Hypothetical protein
2687	1,00	Conserved protein
2688	0,98	Conserved protein
2689	1,00	Conserved protein
2690	0,88	Conserved protein
2691	1,78	Serine protease inhibitor
2692	1,07	Conserved protein
2693	1,03	Hypothetical protein
2694	1,05	Conserved protein
2695	1,00	Hypothetical protein
2696	1,00	Hypothetical protein
2697	0,98	Conserved protein
2698	1,00	Hypothetical protein
2699	1,00	MoxR-like ATPase
2700	1,00	Conserved protein
2701	1,00	ABC transporter_ ATP-binding protein
2702	1,00	Conserved protein

2703	1,07	Conserved protein
2704	0,95	(Na ⁺)-linked D-alanine glycine permease
2705	1,00	Hypothetical protein
2706	1,02	SODIUM-CALCIUM EXCHANGER PROTEIN
2707	1,00	Acetyltransferase
2708	0,93	Acetyltransferase
2709	1,00	transcriptional regulator
2710	1,00	Peptidyl-prolyl cis-trans isomerase
2711	1,00	Hypothetical protein
2712	0,93	Hypothetical protein
2713	0,48	N5_N10-methenyltetrahydromethanopterin c
2713	0,47	N5_N10-methenyltetrahydromethanopterin c
2714	1,41	Hypothetical protein
2715	1,00	HYDROLASE
2716	0,70	Aspartate aminotransferase
2717	1,02	Hypothetical protein
2719	0,73	Sensory Transduction protein Kinase
2720	10,84	Aldehyde ferredoxin oxidoreductase
2720	7,16	Aldehyde ferredoxin oxidoreductase
2721	2,35	Putative molybdopterin converting factor
2722	8,23	Hypothetical protein
2723	2,25	Hypothetical protein
2724	4,17	Conserved protein
2725	1,08	Magnesium and cobalt transport protein C
2726	1,00	Conserved protein
2727	1,00	Hypothetical protein
2728	1,00	Hypothetical protein
2729	2,26	Coenzyme F390 synthetase
2730	1,38	Putative pyruvate:ferredoxin oxidoreduct
2731	4,52	Putative pyruvate:ferredoxin oxidoreduct
2732	1,04	Hypothetical protein
2735	1,06	NAD-dependent malic enzyme
2736	1,00	Hypothetical protein
2737	1,02	Conserved protein
2738	1,58	HYPOTHETICAL SENSORY TRANSDUCTION HISTID

2739	1,02	Conserved protein
2740	1,01	Conserved protein
2741	0,72	LSU ribosomal protein L37AE
2742	0,98	Ribonuclease
2743	1,25	Ribonuclease
2744	1,80	Hypothetical protein
2745	1,13	Hypothetical protein
2746	0,81	Proteasome_ subunit-alpha
2747	1,00	Hypothetical protein
2748	0,57	Hypothetical protein
2749	0,91	Hypothetical protein
2750	0,63	LSU ribosomal protein L15E
2750	0,51	LSU ribosomal protein L15E
2751	1,00	Hypothetical protein
2752	1,00	Hypothetical protein
2755	1,09	Probable ATP-dependent helicase
2756	1,16	Hypothetical protein
2757	1,17	Type I restriction enzyme
2758	1,06	NUCLEOTIDYLTRANSFERASE
2759	1,00	NUCLEOTIDYLTRANSFERASE
2760	1,03	NUCLEOTIDYLTRANSFERASE
2761	1,10	Hypothetical protein
2763	1,11	Hypothetical protein
2764	1,00	Hypothetical protein
2765	1,00	Zinc metalloprotease
2766	1,02	Conserved protein
2767	1,07	Hypothetical protein
2774	1,00	Transposase
2775	0,97	Conserved protein
2776	1,04	Conserved protein
2777	1,00	Transporter
2778	1,00	Conserved protein
2779	1,00	Hypothetical protein
2780	0,83	Ammonium transporter
2780	0,65	empty

2781	0,97	Nitrogen regulatory protein P-II
2782	1,20	SAM-dependent methyltransferases
2783	1,00	Conserved protein
2784	1,02	MOLYBDENUM TRANSPORTER_ ATP-BINDING PROT
2785	1,00	Molybdenum transporter_ permease protein
2786	0,97	Molybdate-binding protein
2787	0,97	Nitrogenase iron-molybdenum cofactor bio
2788	1,00	Nitrogenase iron-molybdenum cofactor bio
2789	0,87	Nitrogenase molybdenum-iron protein beta
2790	0,99	Nitrogenase molybdenum-iron protein alph
2791	1,00	Nifl(2)_ GlnB-like protein
2792	1,00	NITROGEN FIXATION NIFHD REGION GLNB-LIKE
2793	1,00	Nitrogenase iron protein
2794	1,35	Oxidoreductase (flavoprotein)
2795	1,06	Hypothetical protein
2795	1,02	Hypothetical protein
2796	1,09	Hypothetical protein
2797	1,02	Pyruvate kinase
2797	0,95	Pyruvate kinase
2798	0,96	Fructose-bisphosphate aldolase
2802	8,00	CO DEHYDROGENASE/ACETYL-COA SYNTHASE GAM
2802	5,05	CO DEHYDROGENASE/ACETYL-COA SYNTHASE GAM
2803	0,89	Conserved protein
2804	1,56	Hypothetical protein
2805	0,93	Transcription initiation factor IIE_ alp
2806	0,80	Conserved protein
2807	0,84	Proteasome_ beta subunit
2808	1,10	CLEAVAGE AND POLYADENYLATION SPECIFICITY
2809	1,22	Beta-phosphoglucomutase
2810	0,83	Cell division protein
2811	1,04	Dihydropteroate synthase
2812	0,96	Conserved protein
2813	0,63	VACUOLAR-TYPE H+-PYROPHOSPHATASE
2813	0,37	VACUOLAR-TYPE H+-PYROPHOSPHATASE
2814	1,05	VACUOLAR-TYPE H+-PYROPHOSPHATASE

2814	0,65	VACUOLAR-TYPE H ⁺ -PYROPHOSPHATASE
2815	0,95	Hypothetical permease
2816	1,13	Hypothetical permease
2820	0,62	Prolyl-tRNA synthetase
2821	0,76	Conserved protein
2824	0,81	Copper-binding protein
2825	1,00	Copper-binding protein
2826	0,98	Hypothetical protein
2827	1,03	Succinate-semialdehyde dehydrogenase [NA
2828	1,00	Acetolactate synthase
2829	0,82	TRANSLATION INITIATION FACTOR 1A
2830	0,68	DNA-directed RNA polymerases I_ II_ and
2831	1,00	TRANSLATION INITIATION FACTOR 1A (EIF-1A
2832	1,00	Multidrug efflux pump
2833	1,00	SAM-dependent methyltransferases
2834	0,97	Uncharacterized permease
2835	1,00	Copper-exporting ATPase
2836	1,20	COP associated protein
2837	0,85	COP associated protein
2838	3,04	Ech Hydrogenase_ Subunit
2839	2,05	Ech Hydrogenase_ Subunit
2840	1,52	Ech Hydrogenase_ Subunit
2841	4,26	Ech Hydrogenase_ Subunit
2842	3,96	Ech Hydrogenase_ Subunit
2843	4,31	Ech Hydrogenase_ Subunit
2844	1,26	Hydrogenase expression/formation protein
2845	1,02	HYDROGENASE EXPRESSION/FORMATION PROTEIN
2846	1,29	HYDROGENASE EXPRESSION/FORMATION PROTEIN
2847	2,14	Hydrogenase expression/formation protein
2847	1,00	Hydrogenase expression/formation protein
2848	1,13	Hydrogenase expression/formation protein
2849	1,07	F420-NONREDUCING HYDROGENASE I PRECURSOR
2850	1,06	F420-NONREDUCING HYDROGENASE I_ LARGE SU
2851	1,24	F420-NONREDUCING HYDROGENASE I_ CYTOCHRO
2853	1,04	UBIQUINONE BIOSYNTHESIS PROTEIN

2854	1,10	Hypothetical protein
2855	1,00	METHYLTRANSFERASE
2856	0,98	Argininosuccinate lyase
2857	1,26	L-asparaginase
2858	1,58	Sodium/proline symporter
2860	1,00	L-sorbose dehydrogenase
2861	1,00	METHYLTRANSFERASE
2862	1,04	Hypothetical protein
2863	1,04	Hypothetical protein
2864	0,78	Coenzyme F390 Synthetase/Phenylacetate-Co
2866	1,00	Conserved protein
2867	1,81	Conserved protein
2868	1,00	Hypothetical protein
2869	1,00	Transcriptional regulator_ ArsR family
2870	1,00	Conserved protein
2871	1,00	Hypothetical protein
2872	1,01	Potassium channel protein
2873	1,00	Hypothetical protein
2874	1,00	ABC transporter_ ATP-binding protein
2875	1,11	ABC Transporter_ permease protein
2876	0,97	Hypothetical protein
2877	1,07	Hypothetical protein
2878	1,93	Membrane protein related to SecD/SecE
2879	1,00	Transcriptional regulator_ MarR family
2880	1,19	ABC transporter_ permease protein
2881	1,16	Hypothetical permease
2882	0,83	Conserved protein
2883	1,00	Amino acid permease
2884	1,05	Putrescine-ornithine antiporter
2885	1,00	Hypothetical protein
2886	0,94	Hypothetical protein
2887	1,13	Hypothetical protein
2888	1,10	5-NITROIMIDAZOLE ANTIBIOTIC RESISTANCE P
2889	1,00	Acetolactate synthase
2890	1,00	Hypothetical protein

2891	1,00	MoxR-like ATPase
2893	1,90	Enolase
2894	0,66	Hypothetical protein
2895	0,94	Hypothetical protein
2896	1,73	ABC transporter_ ATP-binding protein
2897	0,98	ABC-Type transporter_ permease protein
2898	1,00	ABC-Type transporter_ permease protein
2899	1,00	Ribonucleoside-diphosphate
2900	1,06	Peptidyl-prolyl cis-trans isomerase
2901	0,97	Conserved protein
2902	1,00	Hypothetical protein
2903	1,00	Conserved protein
2904	1,00	Hypothetical protein
2905	0,92	GLUCOSE-6-PHOSPHATE DEHYDROGENASE [coenz
2906	21,50	Indole-3-glycerol phosphate synthase
2907	8,24	Tryptophan synthase_ beta chain
2908	1,00	Tryptophan synthase_ alpha chain
2910	14,42	Anthranilate phosphoribosyltransferase
2911	3,65	N-5'-phosphoribosyl)anthranilate isomera
2913	1,00	Conserved protein
2914	1,00	Transcriptional regulator_ ArsR family
2915	1,23	Conserved protein
2916	1,33	Conserved protein
2917	1,04	Transposase
2918	1,38	Transposase
2919	0,96	Conserved protein
2921	1,00	Conserved protein
2921	0,96	Conserved protein
2922	1,09	Conserved protein
2923	0,97	Conserved protein
2924	1,52	ABC transporter_ permease protein
2925	1,42	ABC transporter_ ATP-binding protein
2926	1,32	Dipeptide/oligopeptide transporter_ ATP-
2927	1,00	Dipeptide/oligopeptide transporter_ perm
2928	7,40	Dipeptide/oligopeptide transporter_ perm

2929	5,23	METHYLTRANSFERASE
2930	3,04	Dipeptide/oligopeptide-binding protein
2931	0,91	SSU ribosomal protein S6E
2932	0,40	protein Translation Initiation Factor IF
2933	0,91	Nucleoside diphosphate kinase
2934	0,19	SSU ribosomal protein S28E
2935	0,71	LSU ribosomal protein L7AE
2936	1,04	REPLICATION FACTOR C SUBUNIT
2937	1,00	CONSERVED PROTEIN (Archaea)
2939	1,00	BRAMP
2940	1,02	Cell division cycle protein (AAA family
2941	1,07	Putative inosine monophosphate dehydroge
2944	1,03	SUA5 protein
2945	1,00	Ribulose biphosphate carboxylase large
2945	0,90	Ribulose biphosphate carboxylase large
2946	1,02	Cation transporter
2947	0,47	Cation transporter
2955	0,85	Cation transporter
2956	1,62	Putative heat shock protein
2957	0,87	Putative heat shock protein
2958	0,89	CdcH protein
2959	1,00	Transcriptional regulator_ ArsR family
2962	1,02	Conserved protein
2963	0,17	Putative pyridoxine biosynthesis protein
2964	1,00	Imidazoleglycerol-phosphate synthase
2965	1,08	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
2969	0,97	Conserved protein
2970	1,00	Phosphohydrolase
2971	0,40	GLYCOSYL TRANSFERASE
2972	0,82	Conserved protein
2973	1,12	Transposase
2974	1,16	Conserved protein
2975	0,76	Conserved protein
2976	1,03	Conserved protein
2977	0,94	Conserved protein

2978	1,09	THIAMIN-MONOPHOSPHATE KINASE
2979	0,58	Ferredoxin
2980	1,36	NifB protein
2981	0,63	NifB protein
2982	0,70	6-pyruvoyltetrahydropterin synthase
2983	1,01	Conserved protein
2984	0,99	Conserved protein
2985	0,89	Conserved protein
2986	1,04	Conserved protein
2987	0,87	Putative serine/threonine protein phosph
2988	1,00	Dihydropyrimidinase
2989	1,06	Glutathione-independent formaldehyde deh
2990	0,91	Conserved protein
2991	0,90	ATP-dependent RNA helicase
2992	0,99	Conserved protein
2993	0,96	Conserved protein
2994	1,10	Conserved protein
2995	1,00	Conserved protein
2996	1,45	Arsenical-resistance protein
3001	0,98	Conserved protein
3002	1,00	Hypothetical protein
3004	1,00	Conserved protein
3005	1,02	SIGNAL RECOGNITION PARTICLE_ SUBUNIT FFH
3006	0,97	GMP synthase [glutamine-hydrolyzing]
3007	15,03	2-dehydro-3-desoxyphosphoheptanote aldol
3008	21,83	3-dehydroquinate synthase
3009	18,93	3-dehydroquinate dehydratase
3010	24,45	Shikimate 5-dehydrogenase
3011	18,54	Prephenate dehydrogenase
3012	3,80	Hypothetical protein
3013	1,02	METHYLTRANSFERASE
3014	0,60	Triosephosphate isomerase
3015	0,13	Conserved protein involved in sugar meta
3016	1,24	Endonuclease III
3017	1,76	Conserved protein

3018	1,03	Conserved protein
3019	0,94	Bacterioferritin
3019	0,74	Bacterioferritin
3021	0,42	Conserved protein
3022	0,36	Hypothetical protein
3023	1,00	Acetyltransferase
3024	0,69	Aspartate aminotransferase
3025	0,61	Myo-inositol 2-dehydrogenase
3026	0,67	NDP-N-acetyl-D-galactosaminuronic acid d
3027	1,08	Conserved protein
3028	0,99	O-antigen translocase
3029	0,64	Conserved protein
3030	1,16	Conserved protein
3031	1,68	Hypothetical protein
3036	1,00	ANTIBIOTIC RESISTANCE PROTEIN
3037	0,90	Putative ferredoxin
3038	0,99	Transcriptional regulator_ ArsR family
3040	2,22	Hypothetical protein
3041	1,00	Conserved protein
3042	1,46	Pyruvate formate-lyase activating enzyme
3043	1,00	HYPOTHETICAL SENSORY TRANSDUCTION HISTID
3044	1,00	Hypothetical protein
3045	1,08	Putative NADH oxidase
3046	1,02	Phosphoglycerate mutase
3047	1,03	Conserved protein
3049	1,02	Hypothetical protein
3050	1,00	Hypothetical protein
3051	1,03	Transposase
3052	1,02	Transposase
3053	0,94	DNA REPAIR HELICASE (RAD25/XPB family)
3054	1,07	Hypothetical protein
3055	1,26	Hypothetical protein
3056	1,12	Conserved protein
3057	1,14	Conserved protein
3058	0,97	Acetyltransferase

3059	0,89	Probable resolvase/ recombinase
3060	1,03	Probable transcriptional regulator
3060	1,00	Probable transcriptional regulator
3061	1,27	Probable resolvase/ recombinase
3062	0,99	Membrane metalloprotease
3063	1,00	Periplasmic divalent cation tolerance pr
3064	1,00	Hypothetical protein
3065	3,04	Hypothetical protein
3066	1,92	ABC transporter_ permease protein
3067	3,13	Conserved protein
3068	1,72	Hypothetical protein
3069	2,86	Cobalt transport ATP-binding protein
3069	1,52	Cobalt transport ATP-binding protein
3070	1,40	ABC transporter_ permease protein
3071	2,29	Conserved protein
3072	2,44	Conserved protein
3073	1,01	Conserved protein
3074	2,33	ABC transporter_ ATP-binding protein
3075	13,54	Conserved protein
3076	11,56	Conserved protein
3077	2,12	Conserved protein
3078	2,35	Hypothetical protein
3079	0,97	Hypothetical protein
3080	1,00	Transposase
3081	1,00	Deoxycytidylate deaminase
3082	1,00	Lactoylglutathione lyase
3083	1,04	Conserved protein
3085	1,00	Hypothetical protein
3087	1,21	Transposase
3088	1,03	Transcriptional regulator_ ArsR family
3089	0,95	Conserved protein
3092	1,14	Uroporphyrinogen-III synthase
3093	0,97	Metallo cofactor biosynthesis protein (m
3094	1,03	Hypothetical protein
3095	0,98	Conserved protein

3096	1,78	Hypothetical protein
3097	1,00	Hypothetical protein
3098	0,71	Valyl-tRNA synthetase
3099	0,99	Hypothetical protein
3100	1,00	FLAGELLA RELATED PROTEIN FlaJ
3101	0,92	FLAGELLA RELATED PROTEIN FlaI
3102	1,00	FLAGELLA RELATED PROTEIN FlaH
3103	1,00	Conserved protein
3104	1,25	Hypothetical protein
3105	0,97	Hypothetical protein
3106	1,00	Flagellin B1 precursor
3106	0,99	Flagellin B1 precursor
3107	0,96	Flagellin B1 precursor
3108	1,26	CHEMOTAXIS PROTEIN METHYLTRANSFERASE
3109	1,00	Chemotaxis protein
3110	1,00	Chemotaxis protein
3111	1,00	Chemotaxis protein
3112	1,10	Protein-glutamate methylesterase
3113	1,00	Chemotaxis protein
3114	1,00	Hypothetical Exported protein
3115	1,00	Chemotaxis protein
3115	1,00	Chemotaxis protein
3116	0,92	Methyl-accepting chemotaxis protein
3117	0,99	Hypothetical protein
3118	0,75	3-hydroxy-3-methylglutaryl-coenzyme A re
3119	1,02	Conserved protein
3120	2,80	Tryptophan synthase_ beta chain
3121	1,22	empty
3121	1,08	PUTATIVE PHOSPHOMETHYLPYRIMIDINE KINASE/
3122	1,00	Putative snRNP Sm-like protein
3123	1,03	Amidophosphoribosyltransferase
3124	1,00	Hypothetical protein
3125	0,81	Probable cation efflux pump
3126	0,92	Transcriptional regulator
3127	1,00	Transcriptional regulator_ MarR family

3128	1,00	Hypothetical protein
3129	1,81	Putative cation efflux pump
3130	1,02	Putative molybdopterin biosynthesis prot
3131	23,16	Conserved protein
3132	0,95	Conserved protein
3133	1,00	Hypothetical protein
3134	1,01	Conserved protein
3135	1,22	Glutamate dehydrogenase
3136	1,07	Acetyl-CoA synthetase_ alpha subunit
3137	1,00	Hypothetical protein
3138	1,06	Sulfite reductase_ assimilatory-type
3139	1,09	Transcriptional regulator_ MarR family
3140	1,27	Sulfite reductase_ assimilatory-type
3141	1,03	Hypothetical protein
3142	1,15	Hypothetical protein
3143	0,87	Conserved protein
3144	0,99	Ferredoxin
3145	1,11	Hypothetical protein
3146	0,76	Hypothetical protein
3147	1,00	Hypothetical protein
3148	1,08	CHORISMATE MUTASE/ PREPHENATE DEHYDRATAS
3149	1,14	Conserved protein
3150	0,94	MoxR-like ATPase
3151	1,02	Hypothetical Cytosolic protein
3152	1,14	Conserved protein
3153	1,18	Conserved protein
3154	1,07	Conserved protein
3155	1,32	Integral membrane protein
3156	1,11	SUGAR-PHOSPHATE NUCLEOTYDYL TRANSFERASE
3157	1,00	Conserved protein
3158	1,11	Peptidyl-prolyl cis-trans isomerase
3159	1,92	Peptidyl-prolyl cis-trans isomerase
3160	1,20	Peptidyl-prolyl cis-trans isomerase
3161	1,00	Hypothetical protein
3162	2,98	Conserved protein

3163	1,00	Hypothetical protein
3164	1,00	Hypothetical protein
3165	0,73	HETERODISULFIDE REDUCTASE_ SUBUNIT HDRA
3166	0,84	HETERODISULFIDE REDUCTASE_ SUBUNIT HDRC
3167	0,86	HETERODISULFIDE REDUCTASE_ SUBUNIT HDRB
3167	0,44	HETERODISULFIDE REDUCTASE_ SUBUNIT HDRB
3168	1,00	Surface layer protein (putative)
3169	1,13	Hypothetical protein
3170	1,06	Hypothetical protein similar to C-termin
3171	0,96	Conserved protein
3172	0,98	Conserved protein
3173	0,53	Surface layer protein (putative)
3174	0,82	Transposase
3175	2,60	Conserved protein
3176	1,03	Hypothetical protein similar to C-termin
3177	1,00	Conserved protein
3178	1,00	Conserved protein
3179	1,00	Conserved protein
3180	1,05	Hypothetical protein similar to C-termin
3181	1,00	Hypothetical protein
3182	0,95	Surface layer protein (putative)
3183	1,06	Conserved protein
3184	1,07	Hypothetical protein similar to C-termin
3184	1,03	Hypothetical protein similar to C-termin
3184	1,00	Hypothetical protein similar to C-termin
3184	1,00	Hypothetical protein similar to C-termin
3185	1,47	Hypothetical protein
3186	1,17	3-isopropylmalate dehydratase
3188	1,00	Conserved protein
3189	1,00	FLAGELLA RELATED PROTEIN FlaJ
3190	1,00	FLAGELLA RELATED PROTEIN FlaI
3191	1,04	FLAGELLA RELATED PROTEIN FlaH
3193	1,00	Conserved protein
3194	1,00	Conserved protein
3195	1,00	Flagillin B1

3196	1,03	Pyruvate synthase_ subunit beta
3197	1,14	Pyruvate synthase_ subunit alpha
3198	1,00	Transposase
3199	1,00	Transposase
3203	1,10	Conserved protein
3214	1,00	Hypothetical protein
3219	0,95	Hypothetical protein
3220	1,57	Hypothetical protein
3221	1,07	Hypothetical protein
3223	1,00	Conserved protein
3225	1,02	Hypothetical protein
3228	4,43	Conserved protein
3231	0,97	Hypothetical protein
3232	1,03	Ferrous iron transport protein B
3234	1,02	Oligopeptide-binding protein OppA
3235	1,00	Putative NADH oxidase
3238	1,05	Hypothetical protein
3240	0,31	Conserved protein
3243	1,00	Conserved protein
3244	1,00	Hypothetical protein
3245	0,93	Transposase
3246	0,72	Conserved protein
3247	1,00	TRANSCRIPTIONAL REGULATOR_ PBSX FAMILY
3249	1,06	Conserved protein
3250	1,00	Hypothetical protein
3251	1,00	Hypothetical protein
3252	1,02	Conserved protein
3253	1,11	Conserved protein
3254	1,00	Conserved protein
3255	1,01	Conserved protein
3256	0,99	Hypothetical protein
3257	1,00	Conserved protein
3258	1,02	Conserved protein
3261	1,00	Hypothetical protein
3262	1,00	Conserved protein

3263	1,00	Ferredoxin
3264	1,00	Hypothetical protein
3265	1,00	Conserved protein
3266	1,04	Hypothetical protein
3267	1,00	Hypothetical protein
3268	1,00	Hypothetical protein
3269	1,00	Conserved protein
3270	1,00	Hypothetical protein
3272	1,02	Hypothetical protein
3273	1,00	Hypothetical protein
3275	1,01	Hypothetical protein
3276	1,00	Conserved protein
3277	1,00	Hypothetical protein
3281	1,05	Transposase
3283	1,00	Hypothetical protein
3285	1,00	Hypothetical protein
3286	0,98	Hypothetical protein
3287	1,00	Conserved protein
3288	1,00	Conserved protein
3289	0,98	Transposase
3291	1,00	Iron-dependent repressor
3293	0,97	Hypothetical protein
3295	1,00	Hypothetical protein
3296	0,79	LSU ribosomal protein L24P
3297	0,46	Hypothetical protein
3299	1,00	Hypothetical protein
3304	1,23	Hypothetical protein
3307	0,91	Hypothetical membrane associated protein
3309	1,20	Hypothetical protein
3311	1,00	Hypothetical protein
3313	1,92	Zinc finger protein
3317	1,16	Hypothetical protein
3320	1,00	Conserved protein
3321	1,07	Hypothetical protein
3323	1,03	Conserved protein

3325	0,87	Hypothetical protein
3328	1,05	Hypothetical protein
3330	0,94	Conserved protein
3331	1,08	Conserved protein
3332	1,00	Hypothetical protein
3333	0,99	Chromosomal protein
3334	1,00	Conserved protein
3335	2,14	ABC transporter_ permease protein
3336	1,00	Hypothetical protein
3337	1,04	Hypothetical protein
3338	1,00	Conserved protein
3339	1,01	Conserved protein
3342	0,96	Hypothetical protein
3354	1,02	Hypothetical protein
3356	1,00	Hypothetical protein
3357	1,14	Conserved protein
3358	0,93	Conserved protein
3360	0,95	Conserved protein
3362	2,61	Putative Flavodoxin
3371	0,80	Polysaccharide ABC transporter_ permease
3372	0,75	Transposase
3374	1,00	Conserved protein
3375	1,00	Hypothetical protein
3379	1,02	Conserved protein
3380	0,94	Conserved protein
3381	1,02	Conserved protein
3383	1,13	Hypothetical protein
3386	0,95	Conserved protein
3390	1,04	Conserved protein
3393	1,00	Conserved protein
3394	0,76	Conserved protein
3395	1,03	Conserved protein
3396	1,00	Conserved protein
3397	1,09	Transcriptional regulator_ ArsR family
3400	1,00	Conserved protein

3402	1,25	Hypothetical protein
3403	1,03	glutamate dehydrogenase
3404	1,36	Conserved protein
3405	0,96	Hypothetical protein
3408	0,91	Conserved protein
3410	1,00	Conserved protein
3411	1,00	Hypothetical protein
3413	0,96	Conserved protein
3414	1,00	Hypothetical protein
3415	1,00	Conserved protein
3416	1,04	Conserved protein
3417	1,00	Conserved protein
3419	1,00	Conserved protein
3421	1,00	Transposase
3424	1,00	Conserved protein
3425	0,88	Conserved protein
3426	1,00	Conserved protein
3428	1,11	Hypothetical protein
3430	1,00	Conserved protein
3431	1,02	Conserved protein
3434	1,00	Hypothetical protein
3436	0,91	Conserved protein
3442	0,98	Hypothetical protein
3447	1,00	Hypothetical protein
3448	1,00	Transposase
3449	0,95	Conserved transmembrane protein
3454	1,48	Conserved protein
3456	1,00	Hypothetical protein
3458	1,00	Conserved protein
3459	0,94	Conserved protein
3466	1,00	Conserved protein
3475	1,00	Transposase
3477	1,00	Hypothetical protein
3479	1,00	Conserved protein
3481	1,00	Conserved protein

3484	1,00	Conserved transmembrane protein
3486	1,00	Conserved protein
3489	1,00	Conserved protein
3493	1,00	Conserved protein
3496	1,00	Conserved protein
3497	1,00	GLYCOSYL TRANSFERASE
3502	0,99	Endonuclease III
3509	0,81	Conserved protein
3511	1,00	Hypothetical protein
3514	1,00	Hypothetical protein
3515	1,00	Hypothetical protein
3529	1,00	Hypothetical protein
3535	1,00	Conserved protein
3536	1,00	Conserved protein
3545	0,99	Conserved protein
3547	1,00	Conserved protein
3551	1,00	METALLOPROTEINASE
3556	1,32	Conserved protein
3561	0,99	Hypothetical protein
3566	1,00	Hypothetical protein
3576	1,03	Hypothetical protein
3578	2,31	Hypothetical protein
3585	0,99	Hypothetical protein
3594	1,06	Conserved protein
3612	1,00	Hypothetical protein
3614	1,00	Hypothetical protein
3633	1,00	Hypothetical protein
3634	1,32	Conserved protein
3639	1,00	Hypothetical protein
3646	0,68	Conserved protein
3664	1,00	Hypothetical protein
3667	1,00	Hypothetical protein
3671	1,23	Hypothetical protein
3683	1,00	Hypothetical protein
3699	1,00	Conserved protein

3727	1,00	Hypothetical protein
3734	0,95	Hypothetical protein
3737	2,49	Hypothetical protein
3737	1,00	Hypothetical protein
3745	1,59	Hypothetical protein
3748	1,00	Hypothetical protein
3753	1,01	Hypothetical protein
3756	2,64	Conserved protein
3762	1,00	Hypothetical protein
3769	1,03	Hypothetical protein
3771	0,93	Hypothetical protein
3785	1,71	Hypothetical protein
3788	1,00	Hypothetical protein
3789	1,00	Hypothetical protein
3792	1,00	Hypothetical protein
3792	0,98	Hypothetical protein
3800	0,94	Transposase
3800	0,40	Transposase
3802	1,00	Putative ferredoxin
3802	0,93	Putative ferredoxin
3806	1,10	Hypothetical protein
3809	1,08	LemA PROTEIN
3814	1,66	Hypothetical protein
3817	1,00	Transposase
3819	1,08	TYPE I RESTRICTION-MODIFICATION SYSTEM R
3820	1,23	not existing
3829	0,43	2-isopropylmalate synthase
3830	1,18	Conserved protein
3830	1,03	Conserved protein
3843	1,19	Conserved protein
3847	1,01	Conserved protein
3847	1,00	Conserved protein
3851	0,91	Conserved protein
3878	0,93	TYPE I RESTRICTION-MODIFICATION SYSTEM M
3887	1,13	Hypothetical protein

3901	0,94	Hypothetical protein
3908	1,27	Conserved protein
3911	1,00	Conserved protein
3940	1,24	Heterodisulfate reductase_ subunit A
3946	1,00	Hypothetical protein
3956	1,00	DNA helicase II
3960	1,00	Hypothetical protein
3978	1,00	Hypothetical protein
3979	3,27	Hypothetical protein
3986	1,00	Conserved protein
3987	0,99	Conserved protein
3988	0,96	Histidinol dehydrogenase
3992	1,00	Hypothetical protein
3996	1,00	Conserved protein
4000	1,00	Hypothetical protein
4009	2,17	Conserved protein
4015	1,48	Oligosaccharyl transferase
4019	15,40	CO DEHYDROGENASE/ACETYL-COA SYNTHASE ALP
4019	4,96	CO DEHYDROGENASE/ACETYL-COA SYNTHASE ALP
4020	29,78	CO DEHYDROGENASE/ACETYL-COA SYNTHASE EPS
4020	15,63	CO DEHYDROGENASE/ACETYL-COA SYNTHASE EPS
4021	22,79	CO DEHYDROGENASE/ACETYL-COA SYNTHASE BET
4023	0,86	Conserved protein
4024	1,40	Conserved protein
4025	2,88	Thioredoxin 2
4028	1,91	Hypothetical protein
4029	1,04	Transposase
4029	1,00	Transposase
4030	0,97	Conserved protein
4032	1,00	Hypothetical protein
4034	3,28	Universal stress protein
4034	1,00	Universal stress protein
4039	0,90	Conserved protein
4041	3,53	A1AO H+ ATPASE_ SUBUNIT I
4042	1,86	A1AO H+ ATPASE_ SUBUNIT H

4043	1,00	Transposase
4044	1,05	Hypothetical protein
4047	0,85	Pyrroline-5-carboxylate reductase
4058	1,00	Hypothetical protein
4063	1,01	Hypothetical protein
4064	1,01	Hypothetical protein
4066	1,00	Hypothetical protein
4070	0,79	Hypothetical protein
4073	1,00	Hypothetical protein
4074	1,03	Thiamine biosynthesis protein
4076	1,00	Conserved protein
4081	1,00	Hypothetical protein
4082	7,96	Methanol corrinoid protein
4082	5,62	Methanol corrinoid protein
4086	0,96	Hypothetical protein
4087	1,05	Hypothetical protein
4088	1,00	Hypothetical protein
4090	0,73	Dolichol-phosphate mannosyltransferase
4093	1,03	NUCLEOTIDYLTRANSFERASE
4094	0,93	Conserved protein
4096	1,25	Hypothetical protein
4105	0,34	Conserved protein
4107	1,00	Conserved protein
4110	1,02	Conserved protein_ Archaea
4112	1,02	Xanthine-guanine phosphoribosyltransferase
4115	0,82	Hypothetical protein
4116	1,05	Fe-S OXIDOREDUCTASE
4141	0,35	MOLYBDENUM FORMYLMETHANOFURAN DEHYDROGEN
4151	0,98	ATPase involved in DNA repair
4163	0,94	Heme biosynthesis protein
4167	1,09	Heme biosynthesis protein
4168	1,23	Glutamyl-tRNA reductase
4168	0,67	Glutamyl-tRNA reductase
4182	1,00	Hypothetical protein
4182	1,00	Hypothetical protein

4183	1,00	Hypothetical protein
4184	0,89	RNase P
4201	0,96	Hypothetical protein
4214	1,00	Hypothetical protein
4223	1,10	empty
4223	1,02	Putative glycosyltransferase
4224	1,99	Glucoamylase
4228	0,99	Conserved protein
4230	0,82	Transcriptional regulator
4230	0,81	Transcriptional regulator
4237	0,90	Hypothetical protein
4242	1,63	DNA gyrase_ subunit A
4244	11,67	Methylthiol:coenzyme M methyltransferase
4245	5,26	Methylthiol:coenzyme M methyltransferase
4251	0,94	Hypothetical protein
4251	0,90	Hypothetical protein
4295	0,77	Hypothetical protein
4307	1,05	Transposase (N-terminal domain)
4312	1,10	Hypothetical protein
4313	0,99	Transposase
4317	0,80	Transposase (N-terminal domain)
4330	0,88	Transposase
4359	1,13	Transcriptional regulator_ ArsR family
4362	0,92	Transposase (N-terminal domain)
4388	0,94	Transposase
4414	1,11	REVERSE TRANSCRIPTASE
4417	1,06	REVERSE TRANSCRIPTASE
4417	1,00	REVERSE TRANSCRIPTASE
4433	0,44	Hypothetical protein
4434	1,00	Hypothetical protein
4438	1,00	Conserved protein
4441	1,18	Transposase
4460	0,80	Transposase (N-terminal domain)
4461	1,01	Transposase
4462	1,03	Transposase

[illegible]

[illegible][illegible]

empty	1,00
empty	1,00
empty	1,00
empty	1,00
empty	1,00
empty	1,00
empty	0,99
empty	0,99
empty	0,98
empty	0,75
Empty contr.	1,44
Empty contr.	1,09
Empty contr.	1,01
Empty contr.	1,00
Empty contr.	0,90
Empty contr.	0,85
Empty contr.	0,83
Empty contr.	0,80
Empty contr.	0,72
IGR	1,12
IGR	1,00
IGR	1,00
leer TS23_g6	1,00
pCR4.0 plasmid contr.	1,72
pCR4.0 plasmid contr.	1,10
pCR4.0 plasmid contr.	1,01
RNA060	1,05

empty
empty
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empty
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Internal control
Internal control
Internal control
Internal control
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Internal control
Internal control
Internal control
empty
2157221-2157373
2441886-2442005
leer
pCR4.0 plasmid contr.
pCR4.0 plasmid contr.
pCR4.0 plasmid contr.
RNA060