Table 9. Cluster of Orthologous Groups (COG) represented in the *M. smithii* proteome

A. Summary

Number of *M. smithii* genes in COG	**Code**	**Functional Category**
136	J	Translation
60	K	Transcription
78	L	Replication, Recombination and Repair
3	B	Chromatin Structure and Dynamics
6	D	Cell Cycle Control
26	V	Defense Mechanisms
8	T	Signal Transduction Mechanisms
59	M	Cell Wall/Membrane Biogenesis
3	N	Cell Motility
1	Z	Cytoskeleton
17	U	Intracellular Trafficking and Secretion
41	O	Post-translational Modification, Protein Turnover, Chaperones
121	C	Energy Production and Conversion
30	G	Carbohydrate Transport and Metabolism
82	E	Amino Acid Transport and Metabolism
42	F	Nucleic Acid Transport and Metabolism
92	H	Coenzyme Transport and Metabolism
18	I	Lipid Transport and Metabolism
57	P	Inorganic Ion Transport and Metabolism
1	Q	Secondary Metabolites Biosynthesis, Transport and Catabolism
201	R	General Function Prediction Only
171	S	Function Unknown
491	-	Not in COGs

B. *M. smithii* genes in each COG

# in COG	COG	Description	*M. smithii* gene(s)
Translation (J)			
1	COG0008	Glutamyl- and glutaminyl-tRNA synthetases	MSM1452
1	COG0009	Putative translation factor (SUA5)	MSM0612
1	COG0012	Predicted GTPase, probable translation factor	MSM1164
1	COG0013	Alanyl-tRNA synthetase	MSM0619
1	COG0016	Phenylalanyl-tRNA synthetase alpha subunit	MSM1478
1	COG0017	Aspartyl/asparaginyl-tRNA synthetases	MSM1236
1	COG0018	Arginyl-tRNA synthetase	MSM1231
1	COG0023	Translation initiation factor 1 (eIF-1/SUI1) and related proteins	MSM0754
1	COG0024	Methionine aminopeptidase	MSM1120
1	COG0030	Dimethyladenosine transferase (rRNA methylation)	MSM1374
1	COG0042	tRNA-dihydrouridine synthase	MSM0972
1	COG0048	Ribosomal protein S12	MSM0901
1	COG0049	Ribosomal protein S7	MSM0900
1	COG0051	Ribosomal protein S10	MSM0897
1	COG0060	Isoleucyl-tRNA synthetase	MSM1341
1	COG0064	Asp-tRNAAsn/Glu-tRNAGln amidotransferase B subunit (PET112 homolog)	MSM1101
1	COG0072	Phenylalanyl-tRNA synthetase beta subunit	MSM0277
1	COG0080	Ribosomal protein L11	MSM0623
1	COG0081	Ribosomal protein L1	MSM0622
1	COG0087	Ribosomal protein L3	MSM0762
1	COG0088	Ribosomal protein L4	MSM0761
1	COG0089	Ribosomal protein L23	MSM0760
1	COG0090	Ribosomal protein L2	MSM0759
1	COG0091	Ribosomal protein L22	MSM0757
1	COG0092	Ribosomal protein S3	MSM0756
1	COG0093	Ribosomal protein L14	MSM0751
1	COG0094	Ribosomal protein L5	MSM0748
1	COG0096	Ribosomal protein S8	MSM0746
1	COG0097	Ribosomal protein L6P/L9E	MSM0745
1	COG0098	Ribosomal protein S5	MSM0741
1	COG0099	Ribosomal protein S13	MSM1425
1	COG0100	Ribosomal protein S11	MSM1427
1	COG0101	Pseudouridylate synthase	MSM0855
1	COG0102	Ribosomal protein L13	MSM1430
1	COG0103	Ribosomal protein S9	MSM1431
1	COG0124	Histidyl-tRNA synthetase	MSM1181
1	COG0130	Pseudouridine synthase	MSM0732
1	COG0143	Methionyl-tRNA synthetase	MSM0071
1	COG0154	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit and related amidases	MSM1253
1	COG0162	Tyrosyl-tRNA synthetase	MSM0513
1	COG0172	Seryl-tRNA synthetase	MSM1710
1	COG0180	Tryptophanyl-tRNA synthetase	MSM0216
1	COG0182	Predicted translation initiation factor 2B subunit, eIF-2B alpha/beta/delta family	MSM0804
1	COG0184	Ribosomal protein S15P/S13E	MSM1194
1	COG0185	Ribosomal protein S19	MSM0758
1	COG0186	Ribosomal protein S17	MSM0752
1	COG0197	Ribosomal protein L16/L10E	MSM0989
1	COG0198	Ribosomal protein L24	MSM0750
1	COG0199	Ribosomal protein S14	MSM0747
1	COG0200	Ribosomal protein L15	MSM0739
1	COG0215	Cysteinyl-tRNA synthetase	MSM0268
1	COG0231	Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A)	MSM0877
1	COG0244	Ribosomal protein L10	MSM0621
1	COG0255	Ribosomal protein L29	MSM0755
1	COG0256	Ribosomal protein L18	MSM0742
1	COG0293	23S rRNA methylase	MSM0508
1	COG0343	Queuine/archaeosine tRNA-ribosyltransferase	MSM1557
1	COG0423	Glycyl-tRNA synthetase (class II)	MSM0403
1	COG0441	Threonyl-tRNA synthetase	MSM1214
1	COG0442	Prolyl-tRNA synthetase	MSM0287
1	COG0480	Translation elongation factors (GTPases)	MSM0899
1	COG0495	Leucyl-tRNA synthetase	MSM1172
1	COG0522	Ribosomal protein S4 and related proteins	MSM1426
1	COG0525	Valyl-tRNA synthetase	MSM0275
1	COG0532	Translation initiation factor 2 (IF-2; GTPase)	MSM0202
1	COG0565	rRNA methylase	MSM0394
1	COG0621	2-methylthioadenine synthetase	MSM0845
1	COG0689	RNase PH	MSM0242
1	COG1093	Translation initiation factor 2, alpha subunit (eIF-2alpha)	MSM1133

1	COG1096	Predicted RNA-binding protein (consists of S1 domain and a Zn-ribbon domain)	MSM1357
1	COG1097	RNA-binding protein Rrp4 and related proteins (contain S1 domain and KH domain)	MSM0243
1	COG1258	Predicted pseudouridylate synthase	MSM1361
1	COG1325	Predicted exosome subunit	MSM0297
1	COG1358	Ribosomal protein HS6-type (S12/L30/L7a)	MSM0206
1	COG1369	RNase P/RNase MRP subunit POP5	MSM0246
1	COG1383	Ribosomal protein S17E	MSM0833
1	COG1384	Lysyl-tRNA synthetase (class I)	MSM1387
1	COG1471	Ribosomal protein S4E	MSM0749
1	COG1491	Predicted RNA-binding protein	MSM1375
1	COG1498	Protein implicated in ribosomal biogenesis, Nop56p homolog	MSM1046
1	COG1500	Predicted exosome subunit	MSM0244
1	COG1503	Peptide chain release factor 1 (eRF1)	MSM0891
1	COG1514	2'-5' RNA ligase	MSM0054
1	COG1534	Predicted RNA-binding protein containing KH domain, possibly ribosomal protein	MSM0710
2	COG1549	Queuine tRNA-ribosyltransferases, contain PUA domain	MSM0633, MSM0797
1	COG1552	Ribosomal protein L40E	MSM0125
1	COG1588	RNase P/RNase MRP subunit p29	MSM0753
1	COG1601	Translation initiation factor 2, beta subunit (eIF-2beta)/eIF-5 N-terminal domain	MSM0511
1	COG1603	RNase P/RNase MRP subunit p30	MSM0247
1	COG1631	Ribosomal protein L44E	MSM1135
1	COG1632	Ribosomal protein L15E	MSM0298
1	COG1670	Acetyltransferases, including N-acetylases of ribosomal proteins	MSM1573
1	COG1676	tRNA splicing endonuclease	MSM0217
1	COG1717	Ribosomal protein L32E	MSM0744
1	COG1727	Ribosomal protein L18E	MSM1429
1	COG1736	Diphthamide synthase subunit DPH2	MSM1358
1	COG1746	tRNA nucleotidyltransferase (CCA-adding enzyme)	MSM0053
1	COG1798	Diphthamide biosynthesis methyltransferase	MSM0801
1	COG1841	Ribosomal protein L30/L7E	MSM0740
1	COG1867	N2,N2-dimethylguanosine tRNA methyltransferase	MSM1031
1	COG1889	Fibrillarin-like rRNA methylase	MSM1047
1	COG1890	Ribosomal protein S3AE	MSM0661
1	COG1911	Ribosomal protein L30E	MSM0907
1	COG1976	Translation initiation factor 6 (eIF-6)	MSM0704
1	COG1997	Ribosomal protein L37AE/L43A	MSM1630
1	COG1998	Ribosomal protein S27AE	MSM0193
1	COG2004	Ribosomal protein S24E	MSM0194
1	COG2007	Ribosomal protein S8E	MSM1486
1	COG2016	Predicted RNA-binding protein (contains PUA domain)	MSM0183
1	COG2023	RNase P subunit RPR2	MSM0711
1	COG2051	Ribosomal protein S27E	MSM1134
1	COG2053	Ribosomal protein S28E/S33	MSM0205
1	COG2075	Ribosomal protein L24E	MSM0204
1	COG2092	Translation elongation factor EF-1beta	MSM0602
1	COG2097	Ribosomal protein L31E	MSM0705
1	COG2117	Predicted subunit of tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase, contains the PP-loop ATPase domain	MSM0707
1	COG2123	RNase PH-related exoribonuclease	MSM0241
1	COG2125	Ribosomal protein S6E (S10)	MSM0201
1	COG2126	Ribosomal protein L37E	MSM0181
1	COG2139	Ribosomal protein L21E	MSM1377
1	COG2147	Ribosomal protein L19E	MSM0743
1	COG2157	Ribosomal protein L20A (L18A)	MSM0703
1	COG2163	Ribosomal protein L14E/L6E/L27E	MSM0733
1	COG2167	Ribosomal protein L39E	MSM0706
1	COG2174	Ribosomal protein L34E	MSM0735
1	COG2238	Ribosomal protein S19E (S16A)	MSM0709
1	COG2260	Predicted Zn-ribbon RNA-binding protein	MSM1132
1	COG2263	Predicted RNA methylase	MSM0764
1	COG2511	Archaeal Glu-tRNAGln amidotransferase subunit E (contains GAD domain)	MSM0335
1	COG2519	tRNA(1-methyladenosine) methyltransferase and related methyltransferases	MSM1173
1	COG2888	Predicted Zn-ribbon RNA-binding protein with a function in translation	MSM0603
1	COG2890	Methylase of polypeptide chain release factors	MSM1373
1	COG3277	RNA-binding protein involved in rRNA processing	MSM0425
1	COG5256	Translation elongation factor EF-1alpha (GTPase)	MSM0898
1	COG5257	Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)	MSM0200
Transcription (K)			
2	COG0085	DNA-directed RNA polymerase, beta subunit/140 kD subunit	MSM0910, MSM0911
2	COG0086	DNA-directed RNA polymerase, beta' subunit/160 kD subunit	MSM0908, MSM0909
1	COG0195	Transcription elongation factor	MSM0906
1	COG0202	DNA-directed RNA polymerase, alpha subunit/40 kD subunit	MSM1428

1	COG0250	Transcription antiterminator	MSM0624
1	COG0571	dsRNA-specific ribonuclease	MSM0176
1	COG0583	Transcriptional regulator	MSM1390
3	COG0640	Predicted transcriptional regulators	MSM0819, MSM1126, MSM1350
1	COG0789	Predicted transcriptional regulators	MSM0949
1	COG0846	NAD-dependent protein deacetylases, SIR2 family	MSM1087
1	COG0864	Predicted transcriptional regulators containing the CopG/Arc/MetJ DNA-binding domain and a metal-binding domain	MSM0364
1	COG1095	DNA-directed RNA polymerase, subunit E'	MSM0197
1	COG1293	Predicted RNA-binding protein homologous to eukaryotic snRNP	MSM0778
1	COG1308	Transcription factor homologous to NACalpha-BTF3	MSM0384
2	COG1309	Transcriptional regulator	MSM0094, MSM0650
1	COG1321	Mn-dependent transcriptional regulator	MSM0218
1	COG1378	Predicted transcriptional regulators	MSM1445
1	COG1395	Predicted transcriptional regulator	MSM0453
3	COG1396	Predicted transcriptional regulators	MSM0026, MSM0329, MSM1528
1	COG1405	Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiation factor TFIIB	MSM0424
1	COG1476	Predicted transcriptional regulators	MSM1150
1	COG1497	Predicted transcriptional regulator	MSM1499
1	COG1522	Transcriptional regulators	MSM1032
1	COG1581	Archaeal DNA-binding protein	MSM1245
3	COG1594	DNA-directed RNA polymerase, subunit M/Transcription elongation factor TFIIS	MSM1354, MSM1720, MSM1763
1	COG1644	DNA-directed RNA polymerase, subunit N (RpoN/RPB10)	MSM1432
1	COG1675	Transcription initiation factor IIE, alpha subunit	MSM0631
1	COG1695	Predicted transcriptional regulators	MSM1250
1	COG1733	Predicted transcriptional regulators	MSM0864
1	COG1758	DNA-directed RNA polymerase, subunit K/omega	MSM1433
1	COG1761	DNA-directed RNA polymerase, subunit L	MSM1356
1	COG1777	Predicted transcriptional regulators	MSM1107
1	COG1813	Predicted transcription factor, homolog of eukaryotic MBF1	MSM0355
3	COG1846	Transcriptional regulators	MSM0413, MSM0600, MSM1230
2	COG1958	Small nuclear ribonucleoprotein (snRNP) homolog	MSM0182, MSM1220
1	COG1996	DNA-directed RNA polymerase, subunit RPC10 (contains C4-type Zn-finger)	MSM1631
1	COG2012	DNA-directed RNA polymerase, subunit H, RpoH/RPB5	MSM0912
1	COG2093	DNA-directed RNA polymerase, subunit E''	MSM0196
1	COG2101	TATA-box binding protein (TBP), component of TFIID and TFIIIB	MSM0720
1	COG2183	Transcriptional accessory protein	MSM1292
1	COG2207	AraC-type DNA-binding domain-containing proteins	MSM0775
1	COG2524	Predicted transcriptional regulator, contains C-terminal CBS domains	MSM1614
2	COG2865	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen	MSM0540, MSM1315
1	COG4008	Predicted metal-binding transcription factor	MSM0969
3	COG4742	Predicted transcriptional regulator	MSM0404, MSM0817, MSM0818
Replication, Recombination and Repair (L)			
2	COG0084	Mg-dependent DNase	MSM0097, MSM0416
1	COG0122	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase	MSM1365
1	COG0164	Ribonuclease HII	MSM0979
2	COG0177	Predicted EndoIII-related endonuclease	MSM0272, MSM1584
1	COG0178	Excinuclease ATPase subunit	MSM1581
2	COG0188	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit	MSM1353, MSM1775
5	COG0210	Superfamily I DNA and RNA helicases	MSM0058, MSM0113, MSM0731, MSM1420, MSM1771
1	COG0258	5'-3' exonuclease (including N-terminal domain of PolI)	MSM0725
1	COG0270	Site-specific DNA methylase	MSM0531
1	COG0322	Nuclease subunit of the excinuclease complex	MSM1695
1	COG0350	Methylated DNA-protein cysteine methyltransferase	MSM1185
1	COG0358	DNA primase (bacterial type)	MSM0427
2	COG0417	DNA polymerase elongation subunit (family B)	MSM1041, MSM1481
3	COG0419	ATPase involved in DNA repair	MSM0120, MSM0693, MSM1761
1	COG0420	DNA repair exonuclease	MSM0121
2	COG0468	RecA/RadA recombinase	MSM0611, MSM1333
2	COG0470	ATPase involved in DNA replication	MSM1176, MSM1177
1	COG0550	Topoisomerase IA	MSM0717
1	COG0556	Helicase subunit of the DNA excision repair complex	MSM1579
3	COG0582	Integrase	MSM0428, MSM1640, MSM1742
1	COG0592	DNA polymerase sliding clamp subunit (PCNA homolog)	MSM1137
2	COG0608	Single-stranded DNA-specific exonuclease	MSM1193, MSM1500
1	COG0648	Endonuclease IV	MSM0963
1	COG0708	Exonuclease III	MSM1479
1	COG1041	Predicted DNA modification methylase	MSM0352
1	COG1107	Archaea-specific RecJ-like exonuclease, contains DnaJ-type Zn finger domain	MSM0260
1	COG1111	ERCC4-like helicases	MSM1187

2	COG1112	Superfamily I DNA and RNA helicases and helicase subunits	MSM1081, MSM1694
1	COG1193	Mismatch repair ATPase (MutS family)	MSM0524
1	COG1241	Predicted ATPase involved in replication control, Cdc46/Mcm family	MSM0510
1	COG1311	Archaeal DNA polymerase II, small subunit/DNA polymerase delta, subunit B	MSM1271
1	COG1343	Uncharacterized protein predicted to be involved in DNA repair	MSM0163
1	COG1389	DNA topoisomerase VI, subunit B	MSM0955
2	COG1468	RecB family exonuclease	MSM0165, MSM1059
2	COG1518	Uncharacterized protein predicted to be involved in DNA repair	MSM0023, MSM0164
1	COG1525	Micrococcal nuclease (thermonuclease) homologs	MSM1495
1	COG1533	DNA repair photolyase	MSM0543
1	COG1570	Exonuclease VII, large subunit	MSM0001
1	COG1583	Uncharacterized protein predicted to be involved in DNA repair (RAMP superfamily)	MSM0170
1	COG1591	Holliday junction resolvase - archaeal type	MSM1098
1	COG1599	Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subunit and related ssDNA-binding proteins	MSM1332
1	COG1637	Predicted nuclease of the RecB family	MSM0497
1	COG1688	Uncharacterized protein predicted to be involved in DNA repair (RAMP superfamily)	MSM0167
1	COG1697	DNA topoisomerase VI, subunit A	MSM0956
1	COG1793	ATP-dependent DNA ligase	MSM0645
1	COG1857	Uncharacterized protein predicted to be involved in DNA repair	MSM0168
1	COG1933	Archaeal DNA polymerase II, large subunit	MSM1384
1	COG2219	Eukaryotic-type DNA primase, large subunit	MSM0073
1	COG2231	Uncharacterized protein related to Endonuclease III	MSM1475
2	COG3335	Transposase and inactivated derivatives	MSM0460, MSM1589
1	COG3359	Predicted exonuclease	MSM0138
2	COG3415	Transposase and inactivated derivatives	MSM0458, MSM1588
5	COG3464	Transposase and inactivated derivatives	MSM0087, MSM0230, MSM0396, MSM1093, MSM1566
1	COG3666	Transposase and inactivated derivatives	MSM1523
Chromatin Structure and Dynamics (B)			
3	COG2036	Histones H3 and H4	MSM0213, MSM0844, MSM1260
Cell Cycle Control (D)			
3	COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	MSM0553, MSM1028, MSM1178
1	COG0489	ATPases involved in chromosome partitioning	MSM0045
1	COG1077	Actin-like ATPase involved in cell morphogenesis	MSM0980
1	COG1192	ATPases involved in chromosome partitioning	MSM1241
Defense Mechanisms (V)			
5	COG0534	Na+-driven multidrug efflux pump	MSM0152, MSM0252, MSM0414, MSM1228, MSM1229
2	COG0577	ABC-type antimicrobial peptide transport system, permease component	MSM0856, MSM1400
2	COG0732	Restriction endonuclease S subunits	MSM0157, MSM0158
2	COG0842	ABC-type multidrug transport system, permease component	MSM1248, MSM1484
6	COG1002	Type II restriction enzyme, methylase subunits	MSM1743, MSM1744, MSM1745, MSM1746, MSM1747, MSM1748
3	COG1131	ABC-type multidrug transport system, ATPase component	MSM0593, MSM1249, MSM1483
2	COG1132	ABC-type multidrug transport system, ATPase and permease components	MSM0773, MSM0774
1	COG1136	ABC-type antimicrobial peptide transport system, ATPase component	MSM0857
1	COG1715	Restriction endonuclease	MSM1752
1	COG1968	Uncharacterized bacitracin resistance protein	MSM1201
1	COG4845	Chloramphenicol O-acetyltransferase	MSM0047
Signal Transduction Mechanisms (T)			
3	COG0589	Universal stress protein UspA and related nucleotide-binding proteins	MSM0485, MSM0887, MSM1699
5	COG3448	CBS-domain-containing membrane protein	MSM0305, MSM0484, MSM0790, MSM1053, MSM1054
Cell Wall/Membrane Biogenesis (M)			
1	COG0381	UDP-N-acetylglucosamine 2-epimerase	MSM0853
3	COG0399	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	MSM0347, MSM1030, MSM1536
4	COG0438	Glycosyltransferase	MSM0836, MSM1313, MSM1317, MSM1322
1	COG0449	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains	MSM1551
14	COG0463	Glycosyltransferases involved in cell wall biogenesis	MSM0423, MSM1290, MSM1294, MSM1297, MSM1310, MSM1311, MSM1312, MSM1316, MSM1323, MSM1324, MSM1328, MSM1545, MSM1623, MSM1627
2	COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	MSM0066, MSM0360
1	COG0562	UDP-galactopyranose mutase	MSM1502
1	COG0668	Small-conductance mechanosensitive channel	MSM0493
1	COG0677	UDP-N-acetyl-D-mannosaminuronate dehydrogenase	MSM1303

1	COG0707	pfam match to MurG; not predicted to be a carbohydrate active enzyme by CAZy	MSM0638
1	COG0750	Predicted membrane-associated Zn-dependent proteases 1	MSM1344
3	COG0769	UDP-N-acetylmuramyl tripeptide synthase	MSM0359, MSM1139, MSM1570
1	COG0770	UDP-N-acetylmuramyl pentapeptide synthase	MSM0880
1	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase	MSM0118
1	COG0773	UDP-N-acetylmuramate-alanine ligase	MSM1190
1	COG0794	Predicted sugar phosphate isomerase involved in capsule formation	MSM1391
1	COG1004	Predicted UDP-glucose 6-dehydrogenase	MSM1612
1	COG1083	CMP-N-acetylneuraminic acid synthetase	MSM0944
1	COG1087	UDP-glucose 4-epimerase	MSM1702
1	COG1088	dTDP-D-glucose 4,6-dehydratase	MSM1309
1	COG1091	dTDP-4-dehydrorhamnose reductase	MSM1304
1	COG1209	dTDP-glucose pyrophosphorylase	MSM1307
1	COG1210	UDP-glucose pyrophosphorylase	MSM1604
1	COG1861	Spore coat polysaccharide biosynthesis protein F, CMP-KDO synthetase homolog	MSM1537
1	COG1887	Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC	MSM1327
1	COG1898	dTDP-4-dehydrorhamnose 3,5-epimerase and related enzymes	MSM1308
1	COG2089	Sialic acid synthase	MSM1539
1	COG2148	Sugar transferases involved in lipopolysaccharide synthesis	MSM1331
1	COG2222	Predicted phosphosugar isomerases	MSM0872
2	COG2230	Cyclopropane fatty acid synthase and related methyltransferases	MSM0274, MSM0490
1	COG2843	Putative enzyme of poly-gamma-glutamate biosynthesis (capsule formation)	MSM0700
1	COG3049	Penicillin V acylase and related amidases	MSM0986
3	COG3475	LPS biosynthesis protein	MSM1512, MSM1515, MSM1544
1	COG3764	Sortase (surface protein transpeptidase)	MSM0984
1	COG3980	Spore coat polysaccharide biosynthesis protein, predicted glycosyltransferase	MSM1538
Cell Motility (N)			
1	COG3351	Putative archaeal flagellar protein D/E	MSM0137
2	COG5651	PPE-repeat proteins	MSM1586, MSM1590
Cytoskeleton (Z)			
1	COG5023	Tubulin	MSM1794
Intracellular Trafficking and Secretion (U)			
1	COG0201	Preprotein translocase subunit SecY	MSM0738
1	COG0541	Signal recognition particle GTPase	MSM1360
1	COG0552	Signal recognition particle GTPase	MSM0701
2	COG0681	Signal peptidase I	MSM0232, MSM1232
3	COG0811	Biopolymer transport proteins	MSM0978, MSM1401, MSM1718
1	COG0848	Biopolymer transport protein	MSM0977
1	COG1400	Signal recognition particle 19 kDa protein	MSM1501
1	COG2443	Preprotein translocase subunit Sss1	MSM0625
2	COG3210	Large exoproteins involved in heme utilization or adhesion	MSM0461, MSM1398
1	COG4023	Preprotein translocase subunit Sec61beta	MSM1363
1	COG4962	Flp pilus assembly protein, ATPase CpaF	MSM0597
2	COG4965	Flp pilus assembly protein TadB	MSM0471, MSM0596
Post-translational Modification, Protein Turnover, Chaperones (O)			
1	COG0068	Hydrogenase maturation factor	MSM1106
1	COG0071	Molecular chaperone (small heat shock protein)	MSM0870
1	COG0225	Peptide methionine sulfoxide reductase	MSM0582
1	COG0298	Hydrogenase maturation factor	MSM0636
1	COG0309	Hydrogenase maturation factor	MSM1492
1	COG0396	ABC-type transport system involved in Fe-S cluster assembly, ATPase component	MSM1003
1	COG0409	Hydrogenase maturation factor	MSM0945
1	COG0443	Molecular chaperone	MSM1109
3	COG0459	Chaperonin GroEL (HSP60 family)	MSM0220, MSM0826, MSM1533
1	COG0464	ATPases of the AAA+ class	MSM0642
1	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain	MSM1110
1	COG0492	Thioredoxin reductase	MSM0340
2	COG0501	Zn-dependent protease with chaperone function	MSM1174, MSM1203
1	COG0533	Metal-dependent proteases with possible chaperone activity	MSM1198
1	COG0576	Molecular chaperone GrpE (heat shock protein)	MSM1108
1	COG0602	Organic radical activating enzymes	MSM1055
2	COG0638	20S proteasome, alpha and beta subunits	MSM0245, MSM1037
1	COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	MSM1367
1	COG0719	ABC-type transport system involved in Fe-S cluster assembly, permease component	MSM1002
1	COG0785	Cytochrome c biogenesis protein	MSM0549
3	COG0826	Collagenase and related proteases	MSM0522, MSM0523, MSM1705
1	COG1047	FKBP-type peptidyl-prolyl cis-trans isomerases 2	MSM0930
1	COG1067	Predicted ATP-dependent protease	MSM1569
3	COG1180	Pyruvate-formate lyase-activating enzyme	MSM0538, MSM0652, MSM1284

1	COG1222	ATP-dependent 26S proteasome regulatory subunit	MSM0354
1	COG1382	Prefoldin, chaperonin cofactor	MSM1634
1	COG1397	ADP-ribosylglycohydrolase	MSM1572
1	COG1730	Predicted prefoldin, molecular chaperone implicated in de novo protein folding	MSM0702
1	COG1899	Deoxyhypusine synthase	MSM1615
1	COG1973	Hydrogenase maturation factor	MSM1158
1	COG2143	Thioredoxin-related protein	MSM0550
1	COG4070	Predicted peptidyl-prolyl cis-trans isomerase (rotamase), cyclophilin family	MSM0813
1	COG4930	Predicted ATP-dependent Lon-type protease	MSM1754
Energy Production and Conversion (C)			
1	COG0045	Succinyl-CoA synthetase, beta subunit	MSM0924
1	COG0074	Succinyl-CoA synthetase, alpha subunit	MSM0228
1	COG0221	Inorganic pyrophosphatase	MSM0198
1	COG0240	Glycerol-3-phosphate dehydrogenase	MSM1540
2	COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing	MSM1404, MSM1463
1	COG0247	Fe-S oxidoreductase	MSM1625
1	COG0371	Glycerol dehydrogenase and related enzymes	MSM0286
1	COG0372	Citrate synthase	MSM0446
2	COG0426	Uncharacterized flavoproteins	MSM0222, MSM1349
1	COG0479	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit	MSM0393
1	COG0636	F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K	MSM0439
1	COG0644	Dehydrogenases (flavoproteins)	MSM1701
2	COG0650	Formate hydrogenlyase subunit 4	MSM0317, MSM1062
3	COG0674	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit	MSM0332, MSM0559, MSM0927
1	COG0680	Ni,Fe-hydrogenase maturation factor	MSM1123
3	COG0716	Flavodoxins	MSM0062, MSM0503, MSM0861
1	COG0731	Fe-S oxidoreductases	MSM0922
4	COG0778	Nitroreductase	MSM0445, MSM1293, MSM1574, MSM1722
1	COG0822	NifU homolog involved in Fe-S cluster formation	MSM0263
1	COG1012	NAD-dependent aldehyde dehydrogenases	MSM0467
3	COG1013	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit	MSM0333, MSM0560, MSM0926
3	COG1014	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit	MSM0391, MSM0557, MSM0925
1	COG1029	Formylmethanofuran dehydrogenase subunit B	MSM1412
2	COG1032	Fe-S oxidoreductase	MSM0696, MSM0787
4	COG1035	Coenzyme F420-reducing hydrogenase, beta subunit	MSM0135, MSM1121, MSM1405, MSM1462
1	COG1036	Archaeal flavoproteins	MSM1338
1	COG1042	Acyl-CoA synthetase (NDP forming)	MSM1471
1	COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	MSM1258
1	COG1139	Uncharacterized conserved protein containing a ferredoxin-like domain	MSM1626
2	COG1142	Fe-S-cluster-containing hydrogenase components 2	MSM0561, MSM0562
2	COG1143	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	MSM0998, MSM1065
1	COG1144	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit	MSM0558
12	COG1145	Ferredoxin	MSM0136, MSM0306, MSM0310, MSM0311, MSM0395, MSM0579, MSM0783, MSM0784, MSM1066, MSM1409, MSM1410, MSM1700
5	COG1146	Ferredoxin	MSM0085, MSM0209, MSM0331, MSM0928, MSM1408
2	COG1148	Heterodisulfide reductase, subunit A and related polyferredoxins	MSM0082, MSM1336
2	COG1150	Heterodisulfide reductase, subunit C	MSM0084, MSM0796
1	COG1151	6Fe-6S prismane cluster-containing protein	MSM1446
1	COG1153	Formylmethanofuran dehydrogenase subunit D	MSM1411
1	COG1155	Archaeal/vacuolar-type H+-ATPase subunit A	MSM0435
1	COG1156	Archaeal/vacuolar-type H+-ATPase subunit B	MSM0434
1	COG1229	Formylmethanofuran dehydrogenase subunit A	MSM1413
1	COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	MSM0637
1	COG1269	Archaeal/vacuolar-type H+-ATPase subunit I	MSM0440
1	COG1304	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases	MSM1441
1	COG1390	Archaeal/vacuolar-type H+-ATPase subunit E	MSM0438
1	COG1394	Archaeal/vacuolar-type H+-ATPase subunit D	MSM0433
2	COG1413	FOG: HEAT repeat	MSM0372, MSM0501
1	COG1436	Archaeal/vacuolar-type H+-ATPase subunit F	MSM0436
2	COG1526	Uncharacterized protein required for formate dehydrogenase activity	MSM0295, MSM1392
1	COG1527	Archaeal/vacuolar-type H+-ATPase subunit C	MSM0437
2	COG1592	Rubrerythrin	MSM1348, MSM1733

1	COG1600	Uncharacterized Fe-S protein	MSM0609
1	COG1625	Fe-S oxidoreductase, related to NifB/MoaA family	MSM1020
2	COG1773	Rubredoxin	MSM0187, MSM0188
2	COG1838	Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal domain	MSM0769, MSM0929
2	COG1908	Coenzyme F420-reducing hydrogenase, delta subunit	MSM1001, MSM1461
2	COG1941	Coenzyme F420-reducing hydrogenase, gamma subunit	MSM1000, MSM1122
2	COG1951	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain	MSM0447, MSM0563
1	COG2033	Desulfoferrodoxin	MSM0262
2	COG2037	Formylmethanofuran:tetrahydromethanopterin formyltransferase	MSM0308, MSM1092
2	COG2048	Heterodisulfide reductase, subunit B	MSM0083, MSM0795
1	COG2055	Malate/L-lactate dehydrogenases	MSM1040
1	COG2141	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases	MSM0542
1	COG2191	Formylmethanofuran dehydrogenase subunit E	MSM1396
1	COG2218	Formylmethanofuran dehydrogenase subunit C	MSM1414
1	COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	MSM1160
1	COG2811	Archaeal/vacuolar-type H+-ATPase subunit H	MSM0441
2	COG3259	Coenzyme F420-reducing hydrogenase, alpha subunit	MSM0999, MSM1124
1	COG3260	Ni,Fe-hydrogenase III small subunit	MSM1064
1	COG3261	Ni,Fe-hydrogenase III large subunit	MSM1063
2	COG4231	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits	MSM0392, MSM1460
1	COG5016	Pyruvate/oxaloacetate carboxyltransferase	MSM0939
Carbohydrate Transport and Metabolism (G)			
1	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase	MSM0962
1	COG0063	Predicted sugar kinase	MSM1091
1	COG0120	Ribose 5-phosphate isomerase	MSM0284
1	COG0126	3-phosphoglycerate kinase	MSM0918
1	COG0148	Enolase	MSM1435
1	COG0149	Triosephosphate isomerase	MSM0919
1	COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	MSM1270
1	COG0483	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family	MSM0879
3	COG0524	Sugar kinases, ribokinase family	MSM0307, MSM1389, MSM1693
2	COG0574	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	MSM0823, MSM0988
1	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	MSM1085
2	COG1082	Sugar phosphate isomerases/epimerases	MSM1184, MSM1251
2	COG1109	Phosphomannomutase	MSM0648, MSM0656
1	COG1363	Cellulase M and related proteins	MSM0134
1	COG1830	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes	MSM0056
1	COG1980	Archaeal fructose 1,6-bisphosphatase	MSM0615
2	COG2074	2-phosphoglycerate kinase	MSM0408, MSM0791
2	COG2730	Endoglucanase	MSM1051, MSM1125
2	COG2814	Arabinose efflux permease	MSM1459, MSM1465
2	COG3635	Predicted phosphoglycerate mutase, AP superfamily	MSM0153, MSM0657
1	COG5297	Cellobiohydrolase A (1,4-beta-cellobiosidase A)	MSM0958
Amino Acid Transport and Metabolism (E)			
1	COG0002	Acetylglutamate semialdehyde dehydrogenase	MSM0860
1	COG0006	Xaa-Pro aminopeptidase	MSM0472
1	COG0019	Diaminopimelate decarboxylase	MSM1371
1	COG0031	Cysteine synthase	MSM0271
1	COG0040	ATP phosphoribosyltransferase	MSM1261
2	COG0065	3-isopropylmalate dehydratase large subunit	MSM0723, MSM1300
2	COG0066	3-isopropylmalate dehydratase small subunit	MSM0847, MSM1299
1	COG0067	Glutamate synthase domain 1	MSM0370
2	COG0069	Glutamate synthase domain 2	MSM0027, MSM0368
1	COG0070	Glutamate synthase domain 3	MSM0369
2	COG0075	Serine-pyruvate aminotransferase/archaeal aspartate aminotransferase	MSM0677, MSM1513
1	COG0076	Glutamate decarboxylase and related PLP-dependent proteins	MSM0987
1	COG0077	Prephenate dehydratase	MSM1052
1	COG0078	Ornithine carbamoyltransferase	MSM1226
2	COG0079	Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase	MSM0653, MSM1516
1	COG0082	Chorismate synthase	MSM1474
1	COG0106	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase	MSM0858
1	COG0107	Imidazoleglycerol-phosphate synthase	MSM1364
1	COG0112	Glycine/serine hydroxymethyltransferase	MSM1337
1	COG0118	Glutamine amidotransferase	MSM1159
3	COG0119	Isopropylmalate/homocitrate/citramalate synthases	MSM0350, MSM0722, MSM1246
1	COG0128	5-enolpyruvylshikimate-3-phosphate synthase	MSM0273
1	COG0131	Imidazoleglycerol-phosphate dehydratase	MSM1206
1	COG0133	Tryptophan synthase beta chain	MSM1142

1	COG0134	Indole-3-glycerol phosphate synthase	MSM1143
1	COG0136	Aspartate-semialdehyde dehydrogenase	MSM0829
1	COG0137	Argininosuccinate synthase	MSM1084
1	COG0139	Phosphoribosyl-AMP cyclohydrolase	MSM1182
1	COG0140	Phosphoribosyl-ATP pyrophosphohydrolase	MSM1103
1	COG0141	Histidinol dehydrogenase	MSM1238
1	COG0165	Argininosuccinate lyase	MSM0192
1	COG0169	Shikimate 5-dehydrogenase	MSM1179
1	COG0174	Glutamine synthetase	MSM1418
1	COG0253	Diaminopimelate epimerase	MSM1372
1	COG0287	Prephenate dehydrogenase	MSM0641
1	COG0289	Dihydrodipicolinate reductase	MSM0830
1	COG0334	Glutamate dehydrogenase/leucine dehydrogenase	MSM0888
1	COG0345	Pyrroline-5-carboxylate reductase	MSM0089
1	COG0346	Lactoylglutathione lyase and related lyases	MSM1366
1	COG0347	Nitrogen regulatory protein PII	MSM0233
1	COG0367	Asparagine synthase (glutamine-hydrolyzing)	MSM0160
3	COG0436	Aspartate/tyrosine/aromatic aminotransferase	MSM0610, MSM0788, MSM1455
1	COG0440	Acetolactate synthase, small (regulatory) subunit	MSM1224
1	COG0460	Homoserine dehydrogenase	MSM0154
1	COG0498	Threonine synthase	MSM0214
1	COG0527	Aspartokinases	MSM0832
1	COG0547	Anthranilate phosphoribosyltransferase	MSM1144
1	COG0548	Acetylglutamate kinase	MSM0375
1	COG0560	Phosphoserine phosphatase	MSM0719
1	COG0620	Methionine synthase II (cobalamin-independent)	MSM0102
1	COG0710	3-dehydroquinate dehydratase	MSM0231
1	COG0747	ABC-type dipeptide transport system, periplasmic component	MSM0300
1	COG0765	ABC-type amino acid transport system, permease component	MSM0806
1	COG1045	Serine acetyltransferase	MSM0270
1	COG1104	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes	MSM0264
1	COG1125	ABC-type proline/glycine betaine transport systems, ATPase components	MSM0990
1	COG1126	ABC-type polar amino acid transport system, ATPase component	MSM0805
1	COG1168	Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities	MSM0044
1	COG1174	ABC-type proline/glycine betaine transport systems, permease component	MSM0991
2	COG1305	Transglutaminase-like enzymes, putative cysteine proteases	MSM0219, MSM0786
1	COG1465	Predicted alternative 3-dehydroquinate synthase	MSM0055
1	COG1605	Chorismate mutase	MSM0834
1	COG1812	Archaeal S-adenosylmethionine synthetase	MSM1340
1	COG1921	Selenocysteine synthase [seryl-tRNASer selenium transferase]	MSM0767
1	COG2021	Homoserine acetyltransferase	MSM0496
1	COG2061	ACT-domain-containing protein, predicted allosteric regulator of homoserine dehydrogenase	MSM0155
1	COG2303	Choline dehydrogenase and related flavoproteins	MSM0865
1	COG2423	Predicted ornithine cyclodeaminase, mu-crystallin homolog	MSM1517
1	COG2856	Predicted Zn peptidase	MSM1529
2	COG2873	O-acetylhomoserine sulfhydrylase	MSM0174, MSM0265
1	COG4992	Ornithine/acetylornithine aminotransferase	MSM1368
Nucleic Acid Transport and Metabolism (F)			
1	COG0005	Purine nucleoside phosphorylase	MSM0665
1	COG0015	Adenylosuccinate lyase	MSM1151
1	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase	MSM1704
1	COG0035	Uracil phosphoribosyltransferase	MSM0398
1	COG0041	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase	MSM1287
1	COG0044	Dihydroorotase and related cyclic amidohydrolases	MSM0997
1	COG0046	Phosphoribosylformylglycinamidine (FGAM) synthase, synthetase domain	MSM1342
1	COG0047	Phosphoribosylformylglycinamidine (FGAM) synthase, glutamine amidotransferase domain	MSM1549
1	COG0104	Adenylosuccinate synthase	MSM1468
1	COG0105	Nucleoside diphosphate kinase	MSM0203
2	COG0125	Thymidylate kinase	MSM0077, MSM0520
1	COG0127	Xanthosine triphosphate pyrophosphatase	MSM1195
1	COG0150	Phosphoribosylaminoimidazole (AIR) synthetase	MSM1039
1	COG0151	Phosphoribosylamine-glycine ligase	MSM1227
1	COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	MSM1547
1	COG0167	Dihydroorotate dehydrogenase	MSM1044
1	COG0207	Thymidylate synthase	MSM1734
1	COG0274	Deoxyribose-phosphate aldolase	MSM0843
1	COG0284	Orotidine-5'-phosphate decarboxylase	MSM1617
1	COG0461	Orotate phosphoribosyltransferase	MSM0821
1	COG0503	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	MSM1359
1	COG0504	CTP synthase (UTP-ammonia lyase)	MSM0147
1	COG0516	IMP dehydrogenase/GMP reductase	MSM1629
1	COG0518	GMP synthase - Glutamine amidotransferase domain	MSM0343

1	COG0519	GMP synthase, PP-ATPase domain/subunit	MSM0345
1	COG0528	Uridylate kinase	MSM0415
1	COG0540	Aspartate carbamoyltransferase, catalytic chain	MSM1263
2	COG0717	Deoxycytidine deaminase	MSM0402, MSM0687
1	COG0856	Orotate phosphoribosyltransferase homologs	MSM0883
1	COG1001	Adenine deaminase	MSM0874
1	COG1051	ADP-ribose pyrophosphatase	MSM1355
1	COG1102	Cytidylate kinase	MSM0734
1	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase	MSM1383
1	COG1437	Adenylate cyclase, class 2 (thermophilic)	MSM0721
1	COG1781	Aspartate carbamoyltransferase, regulatory subunit	MSM0862
1	COG1828	Phosphoribosylformylglycinamidine (FGAM) synthase, PurS component	MSM1548
1	COG1936	Predicted nucleotide kinase (related to CMP and AMP kinases)	MSM0713
1	COG2019	Archaeal adenylate kinase	MSM0737
1	COG2233	Xanthine/uracil permeases	MSM0397
1	COG3363	Archaeal IMP cyclohydrolase	MSM0976
Coenzyme Transport and Metabolism (H)			
1	COG0001	Glutamate-1-semialdehyde aminotransferase	MSM1233
1	COG0007	Uroporphyrinogen-III methylase	MSM1550
1	COG0043	3-polyprenyl-4-hydroxybenzoate decarboxylase and related decarboxylases	MSM1286
1	COG0054	Riboflavin synthase beta-chain	MSM1296
1	COG0108	3,4-dihydroxy-2-butanone 4-phosphate synthase	MSM1256
1	COG0113	Delta-aminolevulinic acid dehydratase	MSM1476
1	COG0142	Geranylgeranyl pyrophosphate synthase	MSM1443
1	COG0157	Nicotinate-nucleotide pyrophosphorylase	MSM0491
1	COG0163	3-polyprenyl-4-hydroxybenzoate decarboxylase	MSM0237
1	COG0171	NAD synthase	MSM1171
1	COG0181	Porphobilinogen deaminase	MSM0881
1	COG0237	Dephospho-CoA kinase	MSM0141
1	COG0294	Dihydropteroate synthase and related enzymes	MSM0556
1	COG0301	Thiamine biosynthesis ATP pyrophosphatase	MSM0617
2	COG0303	Molybdopterin biosynthesis enzyme	MSM0950, MSM1343
1	COG0311	Predicted glutamine amidotransferase involved in pyridoxine biosynthesis	MSM0371
1	COG0314	Molybdopterin converting factor, large subunit	MSM0130
1	COG0315	Molybdenum cofactor biosynthesis enzyme	MSM1362
1	COG0340	Biotin-(acetyl-CoA carboxylase) ligase	MSM0766
1	COG0351	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	MSM0289
1	COG0352	Thiamine monophosphate synthase	MSM0917
1	COG0373	Glutamyl-tRNA reductase	MSM0967
1	COG0379	Quinolinate synthase	MSM0494
1	COG0382	4-hydroxybenzoate polyprenyltransferase and related prenyltransferases	MSM0941
1	COG0407	Uroporphyrinogen-III decarboxylase	MSM0518
2	COG0422	Thiamine biosynthesis protein ThiC	MSM0644, MSM1388
2	COG0452	Phosphopantothenoylcysteine synthetase/decarboxylase	MSM1048, MSM1049
1	COG0476	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	MSM0729
1	COG0499	S-adenosylhomocysteine hydrolase	MSM0727
2	COG0502	Biotin synthase and related enzymes	MSM0573, MSM1099
1	COG0521	Molybdopterin biosynthesis enzymes	MSM0820
1	COG0611	Thiamine monophosphate kinase	MSM1283
1	COG0684	Demethylmenaquinone methyltransferase	MSM0426
1	COG0720	6-pyruvoyl-tetrahydropterin synthase	MSM1056
1	COG0746	Molybdopterin-guanine dinucleotide biosynthesis protein A	MSM0240
1	COG1010	Precorrin-3B methylase	MSM1273
1	COG1056	Nicotinamide mononucleotide adenylyltransferase	MSM0129
1	COG1270	Cobalamin biosynthesis protein CobD/CbiB	MSM1266
2	COG1429	Cobalamin biosynthesis protein CobN and related Mg-chelatases	MSM1117, MSM1715
1	COG1488	Nicotinic acid phosphoribosyltransferase	MSM1792
2	COG1492	Cobyric acid synthase	MSM1254, MSM1565
2	COG1541	Coenzyme F390 synthetase	MSM0387, MSM1714
1	COG1587	Uroporphyrinogen-III synthase	MSM1504
1	COG1648	Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain)	MSM0968
1	COG1731	Archaeal riboflavin synthase	MSM1622
1	COG1763	Molybdopterin-guanine dinucleotide biosynthesis protein	MSM1407
1	COG1767	Triphosphoribosyl-dephospho-CoA synthetase	MSM1477
1	COG1797	Cobyrinic acid a,c-diamide synthase	MSM1215
1	COG1893	Ketopantoate reductase	MSM0033
2	COG1962	Tetrahydromethanopterin S-methyltransferase, subunit H	MSM0627, MSM1007
1	COG1985	Pyrimidine reductase, riboflavin biosynthesis	MSM0065
1	COG2038	NaMN:DMB phosphoribosyltransferase	MSM1200
1	COG2073	Cobalamin biosynthesis protein CbiG	MSM1267
1	COG2082	Precorrin isomerase	MSM1234
1	COG2099	Precorrin-6x reductase	MSM0896
1	COG2104	Sulfur transfer protein involved in thiamine biosynthesis	MSM0552
1	COG2145	Hydroxyethylthiazole kinase, sugar kinase family	MSM0916

3	COG2226	Methylase involved in ubiquinone/menaquinone biosynthesis	MSM1448, MSM1558, MSM1564
1	COG2241	Precorrin-6B methylase 1	MSM1167
1	COG2242	Precorrin-6B methylase 2	MSM0238
1	COG2243	Precorrin-2 methylase	MSM1351
1	COG2266	GTP:adenosylcobinamide-phosphate guanylyltransferase	MSM1005
1	COG2875	Precorrin-4 methylase	MSM0101
1	COG2896	Molybdenum cofactor biosynthesis enzyme	MSM1406
1	COG3161	4-hydroxybenzoate synthetase (chorismate lyase)	MSM0724
1	COG3252	Methenyltetrahydromethanopterin cyclohydrolase	MSM1723
2	COG4054	Methyl coenzyme M reductase, beta subunit	MSM0905, MSM1019
2	COG4055	Methyl coenzyme M reductase, subunit D	MSM0904, MSM1018
1	COG4056	Methyl coenzyme M reductase, subunit C	MSM1017
2	COG4057	Methyl coenzyme M reductase, gamma subunit	MSM0903, MSM1016
2	COG4058	Methyl coenzyme M reductase, alpha subunit	MSM0902, MSM1015
1	COG4059	Tetrahydromethanopterin S-methyltransferase, subunit E	MSM1014
1	COG4060	Tetrahydromethanopterin S-methyltransferase, subunit D	MSM1013
1	COG4061	Tetrahydromethanopterin S-methyltransferase, subunit C	MSM1012
1	COG4062	Tetrahydromethanopterin S-methyltransferase, subunit B	MSM1011
1	COG4063	Tetrahydromethanopterin S-methyltransferase, subunit A	MSM1010
1	COG4064	Tetrahydromethanopterin S-methyltransferase, subunit G	MSM1008
1	COG4218	Tetrahydromethanopterin S-methyltransferase, subunit F	MSM1009
Lipid Transport and Metabolism (I)			
1	COG0020	Undecaprenyl pyrophosphate synthase	MSM0096
1	COG0170	Dolichol kinase	MSM0078
1	COG0183	Acetyl-CoA acetyltransferase	MSM1562
1	COG0365	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases	MSM0330
1	COG0439	Biotin carboxylase	MSM0765
2	COG0558	Phosphatidylglycerophosphate synthase	MSM0613, MSM1706
1	COG0575	CDP-diglyceride synthetase	MSM0850
1	COG1183	Phosphatidylserine synthase	MSM0982
2	COG1211	4-diphosphocytidyl-2-methyl-D-erithritol synthase	MSM0377, MSM1542
1	COG1250	3-hydroxyacyl-CoA dehydrogenase	MSM0965
1	COG1257	Hydroxymethylglutaryl-CoA reductase	MSM0227
1	COG1260	Myo-inositol-1-phosphate synthase	MSM0940
1	COG1267	Phosphatidylglycerophosphatase A and related proteins	MSM0934
1	COG1577	Mevalonate kinase	MSM1439
1	COG1924	Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)	MSM0810
1	COG2084		MSM0548
1	COG3425	3-hydroxy-3-methylglutaryl CoA synthase	MSM1561
Inorganic Ion Transport and Metabolism (P)			
1	COG0003	Oxyanion-translocating ATPase	MSM1170
1	COG0004	Ammonia permease	MSM0234
1	COG0038	Chloride channel protein EriC	MSM1721
1	COG0053	Predicted Co/Zn/Cd cation transporters	MSM0789
1	COG0168	Trk-type K+ transport systems, membrane components	MSM1095
1	COG0226	ABC-type phosphate transport system, periplasmic component	MSM0568
1	COG0288	Carbonic anhydrase	MSM1223
4	COG0310	ABC-type Co2+ transport system, permease component	MSM0583, MSM0584, MSM1488, MSM1618
1	COG0370	Fe2+ transport system protein B	MSM0589
1	COG0474	Cation transport ATPase	MSM0895
1	COG0475	Kef-type K+ transport systems, membrane components	MSM1186
1	COG0530	Ca2+/Na+ antiporter	MSM1027
1	COG0569	K+ transport systems, NAD-binding component	MSM1096
1	COG0573	ABC-type phosphate transport system, permease component	MSM0567
1	COG0581	ABC-type phosphate transport system, permease component	MSM0566
1	COG0600	ABC-type nitrate/sulfonate/bicarbonate transport system, permease component	MSM0291
1	COG0609	ABC-type Fe3+-siderophore transport system, permease component	MSM1394
1	COG0614	ABC-type Fe3+-hydroxamate transport system, periplasmic component	MSM1393
3	COG0619	ABC-type cobalt transport system, permease component CbiQ and related transporters	MSM0585, MSM0771, MSM1620
2	COG0704	Phosphate uptake regulator	MSM0564, MSM0569
1	COG0715	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	MSM1469
1	COG0725	ABC-type molybdate transport system, periplasmic component	MSM1609
1	COG0798	Arsenite efflux pump ACR3 and related permeases	MSM1078
1	COG0855	Polyphosphate kinase	MSM1424
1	COG1006	Multisubunit Na+/H+ antiporter, MnhC subunit	MSM1072
1	COG1116	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	MSM0290
1	COG1117	ABC-type phosphate transport system, ATPase component	MSM0565
1	COG1118	ABC-type sulfate/molybdate transport systems, ATPase component	MSM1611
2	COG1122	ABC-type cobalt transport system, ATPase component	MSM0586, MSM1621
1	COG1230	Co/Zn/Cd efflux system component	MSM1639

1	COG1320	Multisubunit Na+/H+ antiporter, MnhG subunit	MSM1074
1	COG1348	Nitrogenase subunit NifH (ATPase)	MSM1707
1	COG1528	Ferritin-like protein	MSM1712
1	COG1563	Predicted subunit of the Multisubunit Na+/H+ antiporter	MSM1073
1	COG1824	Permease, similar to cation transporters	MSM1275
1	COG1863	Multisubunit Na+/H+ antiporter, MnhE subunit	MSM1076
1	COG1918	Fe2+ transport system protein A	MSM0588
1	COG1930	ABC-type cobalt transport system, periplasmic component	MSM1619
2	COG2111	Multisubunit Na+/H+ antiporter, MnhB subunit	MSM1068, MSM1069
1	COG2116	Formate/nitrite family of transporters	MSM1403
1	COG2212	Multisubunit Na+/H+ antiporter, MnhF subunit	MSM1075
4	COG2217	Cation transport ATPase	MSM0293, MSM0960, MSM1127, MSM1153
1	COG2608	Copper chaperone	MSM0961
1	COG3263	NhaP-type Na+/H+ and K+/H+ antiporters with a unique C-terminal domain	MSM0618
1	COG3420	Nitrous oxidase accessory protein	MSM1397
1	COG4149	ABC-type molybdate transport system, permease component	MSM1610
Secondary Metabolites Biosynthesis, Transport and Catabolism (Q)			
1	COG1228	Imidazolonepropionase and related amidohydrolases	MSM1154
General Function Prediction Only (R)			
2	COG0110	Acetyltransferase (isoleucine patch superfamily)	MSM0189, MSM1600
2	COG0312	Predicted Zn-dependent proteases and their inactivated homologs	MSM0866, MSM0947
1	COG0375	Zn finger protein HypA/HybF (possibly regulating hydrogenase expression)	MSM0108
1	COG0388	Predicted amidohydrolase	MSM0500
1	COG0433	Predicted ATPase	MSM0122
1	COG0446	Uncharacterized NAD(FAD)-dependent dehydrogenases	MSM0046
2	COG0456	Acetyltransferases	MSM0893, MSM1104
11	COG0457	FOG: TPR repeat	MSM0530, MSM0651, MSM0914, MSM1449, MSM1451, MSM1740, MSM1766, MSM1776, MSM1786, MSM1787, MSM1788
2	COG0491	Zn-dependent hydrolases, including glyoxylases	MSM0421, MSM1097
1	COG0496	Predicted acid phosphatase	MSM1218
2	COG0517	FOG: CBS domain	MSM0175, MSM1102
4	COG0535	Predicted Fe-S oxidoreductases	MSM0663, MSM0808, MSM1301, MSM1497
1	COG0561	Predicted hydrolases of the HAD superfamily	MSM0946
1	COG0595	Predicted hydrolase of the metallo-beta-lactamase superfamily	MSM1442
1	COG0603	Predicted PP-loop superfamily ATPase	MSM0936
1	COG0613	Predicted metal-dependent phosphoesterases (PHP family)	MSM1244
1	COG0622	Predicted phosphoesterase	MSM0507
1	COG0627	Predicted esterase	MSM0149
1	COG0628	Predicted permease	MSM1042
1	COG0641	Arylsulfatase regulator (Fe-S oxidoreductase)	MSM1606
5	COG0655	Multimeric flavodoxin WrbA	MSM0267, MSM0664, MSM0923, MSM1209, MSM1727
1	COG0661	Predicted unusual protein kinase	MSM0525
1	COG0663	Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	MSM0654
1	COG0666	FOG: Ankyrin repeat	MSM0266
1	COG0673	Predicted dehydrogenases and related proteins	MSM0882
1	COG0679	Predicted permeases	MSM1334
1	COG0714	MoxR-like ATPases	MSM0555
1	COG0730	Predicted permeases	MSM0420
3	COG0733	Na+-dependent transporters of the SNF family	MSM0699, MSM1531, MSM1532
1	COG0824	Predicted thioesterase	MSM0133
1	COG1011	Predicted hydrolase (HAD superfamily)	MSM1480
1	COG1019	Predicted nucleotidyltransferase	MSM0785
1	COG1078	HD superfamily phosphohydrolases	MSM0236
1	COG1084	Predicted GTPase	MSM0869
1	COG1094	Predicted RNA-binding protein (contains KH domains)	MSM0954
1	COG1099	Predicted metal-dependent hydrolases with the TIM-barrel fold	MSM0405
3	COG1123	ATPase components of various ABC-type transport systems, contain duplicated ATPase	MSM0770, MSM0971, MSM1698
2	COG1163	Predicted GTPase	MSM0714, MSM0715
1	COG1201	Lhr-like helicases	MSM0502
1	COG1202	Superfamily II helicase, archaea-specific	MSM1583
1	COG1203	Predicted helicases	MSM0166
1	COG1204	Superfamily II helicase	MSM0839
1	COG1205	Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster	MSM0112
5	COG1216	Predicted glycosyltransferases	MSM1321, MSM1329, MSM1330, MSM1503, MSM1507
1	COG1223	Predicted ATPase (AAA+ superfamily)	MSM0966
1	COG1234	Metal-dependent hydrolases of the beta-lactamase superfamily III	MSM0492
1	COG1235	Metal-dependent hydrolases of the beta-lactamase superfamily I	MSM1473
1	COG1244	Predicted Fe-S oxidoreductase	MSM0544

1	COG1245	Predicted ATPase, RNase L inhibitor (RLI) homolog	MSM0607
1	COG1253	Hemolysins and related proteins containing CBS domains	MSM1026
4	COG1266	Predicted metal-dependent membrane protease	MSM0292, MSM0803, MSM1148, MSM1180
1	COG1268	Uncharacterized conserved protein	MSM0429
2	COG1277	ABC-type transport system involved in multi-copper enzyme maturation, permease component	MSM0594, MSM0595
1	COG1287	Uncharacterized membrane protein, required for N-linked glycosylation	MSM0716
1	COG1310	Predicted metal-dependent protease of the PAD1/JAB1 superfamily	MSM0462
2	COG1323	Predicted nucleotidyltransferase	MSM0547, MSM0994
1	COG1326	Uncharacterized archaeal Zn-finger protein	MSM0846
2	COG1342	Predicted DNA-binding proteins	MSM0207, MSM0208
1	COG1350	Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB)	MSM1242
1	COG1355	Predicted dioxygenase	MSM1438
1	COG1365	Predicted ATPase (PP-loop superfamily)	MSM0190
9	COG1373	Predicted ATPase (AAA+ superfamily)	MSM0061, MSM0280, MSM0680, MSM1197, MSM1278, MSM1527, MSM1789, MSM1790, MSM1795
1	COG1402	Uncharacterized protein, putative amidase	MSM0184
2	COG1408	Predicted phosphohydrolases	MSM0964, MSM1165
1	COG1409	Predicted phosphohydrolases	MSM0383
1	COG1411	Uncharacterized protein related to proFAR isomerase (HisA)	MSM1636
1	COG1412	Uncharacterized proteins of PilT N-term./Vapc superfamily	MSM0199
1	COG1418	Predicted HD superfamily hydrolase	MSM0632
1	COG1439	Predicted nucleic acid-binding protein, consists of a PIN domain and a Zn-ribbon module	MSM0816
4	COG1453	Predicted oxidoreductases of the aldo/keto reductase family	MSM0148, MSM0728, MSM1450, MSM1608
1	COG1489	DNA-binding protein, stimulates sugar fermentation	MSM1090
1	COG1537	Predicted RNA-binding proteins	MSM0640
1	COG1545	Predicted nucleic-acid-binding protein containing a Zn-ribbon	MSM1279
2	COG1571	Predicted DNA-binding protein containing a Zn-ribbon domain	MSM0452, MSM1295
1	COG1606	ATP-utilizing enzymes of the PP-loop superfamily	MSM0482
1	COG1608	Predicted archaeal kinase	MSM1440
1	COG1611	Predicted Rossmann fold nucleotide-binding protein	MSM0004
1	COG1634	Uncharacterized Rossmann fold enzyme	MSM0672
1	COG1646	Predicted phosphate-binding enzymes, TIM-barrel fold	MSM0124
2	COG1672	Predicted ATPase (AAA+ superfamily)	MSM1196, MSM1646
1	COG1691	NCAIR mutase (PurE)-related proteins	MSM1105
1	COG1707	ACT domain-containing protein	MSM1060
1	COG1759	ATP-utilizing enzymes of ATP-grasp superfamily (probably carboligases)	MSM0506
1	COG1779	C4-type Zn-finger protein	MSM0409
1	COG1782	Predicted metal-dependent RNase, consists of a metallo-beta-lactamase domain and an RNA-binding KH domain	MSM1038
1	COG1821	Predicted ATP-utilizing enzyme (ATP-grasp superfamily)	MSM0852
1	COG1829	Predicted archaeal kinase (sugar kinase superfamily)	MSM0060
1	COG1855	ATPase (PilT family)	MSM1183
1	COG1878	Predicted metal-dependent hydrolase	MSM0827
1	COG1907	Predicted archaeal sugar kinases	MSM0848
1	COG1942	Uncharacterized protein, 4-oxalocrotonate tautomerase homolog	MSM0688
1	COG1964	Predicted Fe-S oxidoreductases	MSM0849
1	COG1988	Predicted membrane-bound metal-dependent hydrolases	MSM1079
1	COG1994	Zn-dependent proteases	MSM0479
2	COG2005	N-terminal domain of molybdenum-binding protein	MSM0131, MSM1207
1	COG2047	Uncharacterized protein (ATP-grasp superfamily)	MSM1131
1	COG2054	Uncharacterized archaeal kinase related to aspartokinases, uridylate kinases	MSM0604
1	COG2068	Uncharacterized MobA-related protein	MSM0116
1	COG2079	Uncharacterized protein involved in propionate catabolism	MSM0449
1	COG2081	Predicted flavoproteins	MSM1235
1	COG2085	Predicted dinucleotide-binding enzymes	MSM0049
1	COG2102	Predicted ATPases of PP-loop superfamily	MSM0142
1	COG2118	DNA-binding protein	MSM0708
1	COG2129	Predicted phosphoesterases, related to the Icc protein	MSM0792
1	COG2150	Predicted regulator of amino acid metabolism, contains ACT domain	MSM0635
1	COG2151	Predicted metal-sulfur cluster biosynthetic enzyme	MSM0634
1	COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold	MSM0779
1	COG2232	Predicted ATP-dependent carboligase related to biotin carboxylase	MSM0431
3	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid	MSM1208, MSM1559, MSM1560
1	COG2252	Permeases	MSM1736
1	COG2403	Predicted GTPase	MSM0091
1	COG2405	Predicted nucleic acid-binding protein, contains PIN domain	MSM1530
1	COG2517	Predicted RNA-binding protein containing a C-terminal EMAP domain	MSM0466
2	COG2520	Predicted methyltransferase	MSM0802, MSM1036
1	COG2522	Predicted transcriptional regulator	MSM0269
3	COG3291	FOG: PKD repeat	MSM0281, MSM1716, MSM1735

1	COG3442	Predicted glutamine amidotransferase	MSM1138
1	COG3552	Protein containing von Willebrand factor type A (vWA) domain	MSM0554
1	COG3608	Predicted deacylase	MSM1080
1	COG3894	Uncharacterized metal-binding protein	MSM0517
1	COG3942	Surface antigen	MSM0921
1	COG3943	Virulence protein	MSM1645
1	COG4002	Predicted phosphotransacetylase	MSM0095
1	COG4015	Predicted dinucleotide-utilizing enzyme of the ThiF/HesA family	MSM0577
1	COG4026	Uncharacterized protein containing TOPRIM domain, potential nuclease	MSM1703
2	COG4032	Predicted thiamine-pyrophosphate-binding protein	MSM0080, MSM0081
1	COG4052	Uncharacterized protein related to methyl coenzyme M reductase subunit C	MSM1021
1	COG4076	Predicted RNA methylase	MSM0363
1	COG4085	Predicted RNA-binding protein, contains TRAM domain	MSM0647
1	COG4087	Soluble P-type ATPase	MSM1252
1	COG4277	Predicted DNA-binding protein with the Helix-hairpin-helix motif	MSM1239
2	COG4747	ACT domain-containing protein	MSM0388, MSM1713
1	COG4801	Predicted acyltransferase	MSM1385
1	COG4827	Predicted transporter	MSM1717
1	COG5012	Predicted cobalamin binding protein	MSM0516
3	COG5271	AAA ATPase containing von Willebrand factor type A (vWA) domain	MSM0993, MSM1240, MSM1454
1	COG5362	Phage-related terminase	MSM1671
1	COG5518	Bacteriophage capsid portal protein	MSM1672
2	COG5643	Protein containing a metal-binding domain shared with formylmethanofuran dehydrogenase subunit E	MSM1489, MSM1491
Function Unknown (S)			
1	COG0011	Uncharacterized conserved protein	MSM1029
2	COG0028		MSM0686, MSM1225
1	COG0059		MSM1222
1	COG0111		MSM0457
1	COG0147		MSM1146
1	COG0248		MSM1423
2	COG0318		MSM0025, MSM0374
1	COG0327	Uncharacterized conserved protein	MSM0576
1	COG0378		MSM0107
1	COG0391	Uncharacterized conserved protein	MSM0974
1	COG0392	Predicted integral membrane protein	MSM1094
2	COG0393	Uncharacterized conserved protein	MSM0418, MSM0456
1	COG0432	Uncharacterized conserved protein	MSM0279
1	COG0444		MSM0303
1	COG0451		MSM0327
2	COG0458		MSM0361, MSM0488
1	COG0462		MSM1577
2	COG0473		MSM0373, MSM1298
2	COG0477		MSM0772, MSM1210
2	COG0500		MSM0028, MSM1510
1	COG0505		MSM0489
1	COG0512		MSM1145
1	COG0513		MSM1498
1	COG0543		MSM1043
1	COG0585	Uncharacterized conserved protein	MSM1156
1	COG0591		MSM0386
1	COG0599	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	MSM0296
1	COG0601		MSM0301
2	COG0615		MSM0859, MSM1514
1	COG1028		MSM1731
2	COG1061		MSM0690, MSM0695
1	COG1063		MSM0376
1	COG1086		MSM1535
1	COG1120		MSM1395
1	COG1124		MSM0304
2	COG1134		MSM1326, MSM1592
1	COG1173		MSM0302
1	COG1199		MSM1352
1	COG1208		MSM0655
1	COG1243		MSM0842
1	COG1255	Uncharacterized protein conserved in archaea	MSM0894
2	COG1300	Uncharacterized membrane protein	MSM0215, MSM1526
1	COG1303	Uncharacterized protein conserved in archaea	MSM0932
1	COG1339		MSM1257
1	COG1359	Uncharacterized conserved protein	MSM1378
1	COG1371	Uncharacterized conserved protein	MSM0668
1	COG1379	Uncharacterized conserved protein	MSM1129
1	COG1387		MSM0063
1	COG1415	Uncharacterized conserved protein	MSM0931

1	COG1422	Predicted membrane protein	MSM0736
1	COG1430	Uncharacterized conserved protein	MSM1339
1	COG1460	Uncharacterized protein conserved in archaea	MSM1376
1	COG1469	Uncharacterized conserved protein	MSM1033
2	COG1474		MSM0671, MSM1264
1	COG1478	Uncharacterized conserved protein	MSM0975
1	COG1511	Predicted membrane protein	MSM0093
2	COG1520	FOG: WD40-like repeat	MSM1247, MSM1567
1	COG1548		MSM0851
1	COG1578	Uncharacterized conserved protein	MSM0551
1	COG1602	Uncharacterized conserved protein	MSM0346
2	COG1617	Uncharacterized conserved protein	MSM0348, MSM0349
1	COG1627	Uncharacterized protein conserved in archaea	MSM0983
1	COG1630	Uncharacterized protein conserved in archaea	MSM0123
1	COG1641	Uncharacterized conserved protein	MSM0935
1	COG1665	Uncharacterized protein conserved in archaea	MSM1058
1	COG1679	Uncharacterized conserved protein	MSM1192
1	COG1685		MSM0835
1	COG1690	Uncharacterized conserved protein	MSM0666
1	COG1693	Uncharacterized protein conserved in archaea	MSM1417
1	COG1698	Uncharacterized protein conserved in archaea	MSM1268
1	COG1701	Uncharacterized protein conserved in archaea	MSM0140
2	COG1704	Uncharacterized conserved protein	MSM0660, MSM1422
1	COG1710	Uncharacterized protein conserved in archaea	MSM0069
1	COG1711	Uncharacterized protein conserved in archaea	MSM1136
1	COG1714	Predicted membrane protein/domain	MSM1493
1	COG1718		MSM0952
1	COG1720	Uncharacterized conserved protein	MSM0132
2	COG1738	Uncharacterized conserved protein	MSM0646, MSM1382
1	COG1739	Uncharacterized conserved protein	MSM0186
1	COG1751	Uncharacterized conserved protein	MSM0628
1	COG1771	Uncharacterized protein conserved in archaea	MSM0070
1	COG1784	Predicted membrane protein	MSM0599
1	COG1786	Uncharacterized conserved protein	MSM1155
1	COG1795	Uncharacterized conserved protein	MSM1213
1	COG1809	Uncharacterized conserved protein	MSM0086
1	COG1817	Uncharacterized protein conserved in archaea	MSM0106
2	COG1822	Predicted archaeal membrane protein	MSM0581, MSM1216
1	COG1836	Predicted membrane protein	MSM0659
1	COG1844	Uncharacterized protein conserved in archaea	MSM0356
1	COG1849	Uncharacterized protein conserved in archaea	MSM0614
2	COG1852	Uncharacterized conserved protein	MSM0225, MSM0649
1	COG1860	Uncharacterized protein conserved in archaea	MSM0285
1	COG1865	Uncharacterized conserved protein	MSM0825
1	COG1872	Uncharacterized conserved protein	MSM1603
4	COG1873	Uncharacterized conserved protein	MSM0465, MSM0822, MSM0841, MSM1004
1	COG1891	Uncharacterized protein conserved in archaea	MSM1628
1	COG1909	Uncharacterized protein conserved in archaea	MSM0195
1	COG1915	Uncharacterized conserved protein	MSM0875
1	COG1916	Uncharacterized homolog of PrgY (pheromone shutdown protein)	MSM1024
1	COG1917	Uncharacterized conserved protein, contains double-stranded beta-helix domain	MSM1447
1	COG1920	Uncharacterized conserved protein	MSM0288
1	COG1937	Uncharacterized protein conserved in bacteria	MSM0959
1	COG1944	Uncharacterized conserved protein	MSM0480
1	COG1945	Uncharacterized conserved protein	MSM0878
1	COG1950	Predicted membrane protein	MSM1166
1	COG1971	Predicted membrane protein	MSM0030
1	COG1990	Uncharacterized conserved protein	MSM0605
1	COG1991	Uncharacterized conserved protein	MSM0145
1	COG2029	Uncharacterized conserved protein	MSM1057
1	COG2035	Predicted membrane protein	MSM1582
1	COG2042	Uncharacterized conserved protein	MSM0126
1	COG2043	Uncharacterized protein conserved in archaea	MSM0115
1	COG2078	Uncharacterized conserved protein	MSM0867
1	COG2090	Uncharacterized protein conserved in archaea	MSM1591
1	COG2098	Uncharacterized protein conserved in archaea	MSM0985
1	COG2106	Uncharacterized conserved protein	MSM0763
1	COG2122	Uncharacterized conserved protein	MSM0088
1	COG2136		MSM1632
2	COG2138	Uncharacterized conserved protein	MSM1280, MSM1281
1	COG2246	Predicted membrane protein	MSM1289
2	COG2314	Predicted membrane protein	MSM0109, MSM1739
2	COG2364	Predicted membrane protein	MSM0673, MSM0676
1	COG2429	Uncharacterized conserved protein	MSM0973

1	COG2450	Uncharacterized conserved protein	MSM0406
1	COG2456	Uncharacterized conserved protein	MSM1624
1	COG2457	Uncharacterized conserved protein	MSM0873
1	COG2892	Uncharacterized protein conserved in archaea	MSM1633
1	COG3273	Uncharacterized conserved protein	MSM1274
2	COG3274	Uncharacterized protein conserved in bacteria	MSM1370, MSM1556
1	COG3356	Predicted membrane protein	MSM0776
1	COG3367	Uncharacterized conserved protein	MSM0407
1	COG3482	Uncharacterized conserved protein	MSM0481
1	COG3543	Uncharacterized conserved protein	MSM0430
3	COG3548	Predicted integral membrane protein	MSM0468, MSM0469, MSM1205
1	COG3586	Uncharacterized conserved protein	MSM1741
1	COG3815	Predicted membrane protein	MSM1770
1	COG3874	Uncharacterized conserved protein	MSM0683
1	COG3976	Uncharacterized protein conserved in bacteria	MSM1637
1	COG4009	Uncharacterized protein conserved in archaea	MSM0794
1	COG4010	Uncharacterized protein conserved in archaea	MSM0793
1	COG4012	Uncharacterized protein conserved in archaea	MSM1243
1	COG4014	Uncharacterized protein conserved in archaea	MSM0840
1	COG4016	Uncharacterized protein conserved in archaea	MSM0578
1	COG4017	Uncharacterized protein conserved in archaea	MSM0575
1	COG4018	Uncharacterized protein conserved in archaea	MSM0571
1	COG4019	Uncharacterized protein conserved in archaea	MSM0574
1	COG4020	Uncharacterized protein conserved in archaea	MSM1221
1	COG4021	Uncharacterized conserved protein	MSM0463
1	COG4022	Uncharacterized protein conserved in archaea	MSM0643
1	COG4029	Uncharacterized protein conserved in archaea	MSM0812
1	COG4030	Uncharacterized protein conserved in archaea	MSM0309
1	COG4033	Uncharacterized protein conserved in archaea	MSM0103
1	COG4035	Predicted membrane protein	MSM0315
1	COG4036	Predicted membrane protein	MSM0320
1	COG4037	Predicted membrane protein	MSM0321
1	COG4038	Predicted membrane protein	MSM0322
1	COG4039	Predicted membrane protein	MSM0323
1	COG4040	Predicted membrane protein	MSM0324
1	COG4041	Predicted membrane protein	MSM0325
1	COG4042	Predicted membrane protein	MSM0326
2	COG4050	Uncharacterized protein conserved in archaea	MSM0811, MSM1130
1	COG4051	Uncharacterized protein conserved in archaea	MSM0809
1	COG4053	Uncharacterized protein conserved in archaea	MSM0229
1	COG4065	Uncharacterized protein conserved in archaea	MSM1006
2	COG4066	Uncharacterized protein conserved in archaea	MSM0064, MSM0367
1	COG4068	Uncharacterized protein containing a Zn-ribbon	MSM0417
1	COG4069	Uncharacterized protein conserved in archaea	MSM0815
1	COG4071	Uncharacterized protein conserved in archaea	MSM0630
1	COG4073	Uncharacterized protein conserved in archaea	MSM0726
1	COG4077	Uncharacterized protein conserved in archaea	MSM1034
1	COG4078	Predicted membrane protein	MSM0319
1	COG4079	Uncharacterized protein conserved in archaea	MSM1472
1	COG4081	Uncharacterized protein conserved in archaea	MSM0104
1	COG4084	Uncharacterized protein conserved in archaea	MSM0314
1	COG4121	Uncharacterized conserved protein	MSM1555
1	COG4289	Uncharacterized protein conserved in bacteria	MSM1302
1	COG4635		MSM1262
3	COG4713	Predicted membrane protein	MSM0521, MSM1291, MSM1444
2	COG4744	Uncharacterized conserved protein	MSM1402, MSM1719
1	COG4883	Uncharacterized protein conserved in archaea	MSM1086
1	COG4907	Predicted membrane protein	MSM1421
1	COG5015	Uncharacterized conserved protein	MSM0863
1	COG5305	Predicted membrane protein	MSM1288
1	COG5423	Predicted metal-binding protein	MSM0050
1	COG5440	Uncharacterized conserved protein	MSM1265
4	COG5464	Uncharacterized conserved protein	MSM0067, MSM0681, MSM1765, MSM1785