Table S2. Distribution of arCOGs in each archaeal phyla/domains; hyperthermophilic *Crenarchaeota*, *Euryarchaeaota*, *Thaumarchaeota*, *Korarchaeota* and *C. subteranneum*.

arCOG	COG	COG category	Anotation	Number of genomes in each archaeal order																
				Crenarchaeota (hyperthermophilic)			*"Thaumar chaeota"*	HWCGI	*"Korarc haeota"*	*Euryarchaeota*										*"Nanoar chaeota"*
				Desulfurococcales	*Sulfolobales*	*Thermoproteales*	*Nitrosopumilales*	*C. subterraneum*	*K. cryptophilum'*	*Archaeoglobales*	*Halobacteriales*	*Methanobacteriales*	*Methanococcales*	*Methanomicrobiales*	*Methanocellales*	*Methanosarcinales*	*Methanopyrales*	*Thermococcales*	*Thermoplasmatales*	*N. equitans*
			Number of species used in this study	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00001	COG1695	K	Predicted transcriptional regulator, PadR family	2	2	5	0	1	1	1	0	2	0	1	1	2	0	4	3	0
arCOG00002	COG1695	K	Predicted transcriptional regulator, PadR family	3	3	5	2	1	1	0	2	0	2	2	1	2	0	4	3	0
arCOG00004	COG1695	K	Predicted transcriptional regulator, PadR family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00005	COG1695	K	Predicted transcriptional regulator, PadR family	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00006	COG1695	K	Predicted transcriptional regulator, PadR family	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00007	COG1695	K	Predicted transcriptional regulator, PadR family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG00008	COG1695	K	Predicted transcriptional regulator, PadR family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00009	COG0531	E	Amino acid transporter	1	2	5	1	1	1	1	4	1	3	3	0	4	1	1	1	0
arCOG00011	COG0531	E	Amino acid transporter	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG00012	COG0531	E	Amino acid transporter	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG00013	COG0531	E	Amino acid transporter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG00014	COG0524	G	Sugar kinase, ribokinase family	3	3	5	2	1	1	1	4	2	3	3	1	4	1	4	3	0
arCOG00015	COG1105	G	Fructose-1-phosphate kinase or kinase (PfkB)	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
arCOG00016	COG0524	G	Sugar kinase, ribokinase family	3	3	5	2	1	1	0	0	2	0	0	0	1	0	4	0	0
arCOG00017	COG2522	R	Predicted transcriptional regulator	3	3	4	2	1	1	1	0	1	0	3	1	5	0	2	0	1
arCOG00018	COG0063	G	Predicted sugar kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00019	COG2145	H	Hydroxyethylthiazole kinase, sugar kinase family	0	0	1	0	0	0	1	2	1	2	3	1	3	0	3	0	0
arCOG00020	COG0351	H	Hydroxymethylpyrimidine/phosphomethylpyrimidir	3	3	4	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00021	COG1992	S	Uncharacterized conserved protein	2	3	5	0	1	1	0	4	1	0	3	0	1	0	4	0	0
arCOG00022		S	Uncharacterized conserved protein	2	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG00023		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00024	COG0554	C	Glycerol kinase	2	2	2	0	1	1	1	3	0	0	0	0	0	0	3	3	0
arCOG00025	COG1070	G	Sugar (pentulose and hexulose) kinase	1	1	1	0	1	0	1	0	0	0	0	0	1	0	0	0	0
arCOG00026	COG1070	G	Sugar (pentulose and hexulose) kinase	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG00027	COG0076	E	Glutamate decarboxylase, L-tyrosine decarboxylase	3	1	0	0	0	0	1	3	2	3	3	1	5	1	4	1	0
arCOG00028	COG0856	F	Orotate phosphoribosyltransferase homolog	0	0	0	0	0	0	1	3	2	3	3	1	5	0	0	3	0
arCOG00029	COG0461	F	Orotate phosphoribosyltransferase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00030	COG0503	F	Adenine/guanine phosphoribosyltransferase or relate	0	0	0	2	0	0	0	4	2	3	3	1	5	1	0	0	0
arCOG00031	COG0503	F	Adenine/guanine phosphoribosyltransferase or relate	3	3	5	0	1	1	0	3	0	0	0	0	0	0	4	0	0
arCOG00032	COG1092	R	SAM-dependent methyltransferase	2	0	0	0	0	1	0	0	0	3	0	0	0	1	4	0	0
arCOG00033	COG2520	J	Wybutosine (yW) biosynthesis enzyme, methyltrans	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00034	COG0311	H	Predicted glutamine amidotransferase involved in py	3	3	4	2	0	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00035	COG2102	R	Predicted ATPase of PP-loop superfamily	3	3	5	2	1	0	1	4	2	3	3	1	5	1	4	3	1
arCOG00036	COG2102	R	Predicted ATPase of PP-loop superfamily	1	0	3	0	1	0	1	0	0	0	1	0	2	0	4	0	0
arCOG00037	COG2117	J	Predicted subunit of tRNA(5-methylaminomethyl-2-	0	0	0	0	0	0	0	4	2	3	3	1	5	1	4	0	0
arCOG00038	COG0301	H	Thiamine biosynthesis ATP pyrophosphatase	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	1
arCOG00039	COG0603	R	Predicted PP-loop superfamily ATPase	2	3	4	2	1	0	1	2	2	3	3	1	5	1	4	3	0
arCOG00040	COG2236	R	Predicted phosphoribosyltransferase	3	3	5	1	1	1	1	4	0	0	0	1	4	0	4	3	0
arCOG00041	COG1926	R	Predicted phosphoribosyltransferase	1	0	1	0	1	0	0	2	0	0	1	1	3	0	0	2	0
arCOG00042	COG0037	D	tRNA(Ile)-lysidine synthase MesJ	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	1
arCOG00043	COG1606	R	ATP-utilizing enzyme of the PP-loop superfamily	0	0	0	2	0	1	1	2	2	3	3	1	5	1	0	0	0
arCOG00044	COG0037	D	tRNA(Ile)-lysidine synthase MesJ	0	0	0	0	0	0	0	0	0	3	0	0	0	1	4	0	0
arCOG00045	COG1365	R	Predicted ATPase (PP-loop superfamily)	0	0	0	0	0	0	0	0	2	3	0	0	0	1	4	0	0
arCOG00046	COG0037	D	tRNA(Ile)-lysidine synthase MesJ	0	0	0	0	0	0	0	0	0	3	0	1	3	1	4	0	0
arCOG00047	COG1041	L	Predicted DNA modification methylase	3	3	5	1	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00048	COG0116	L	Predicted N6-adenine-specific DNA methylase	3	0	4	0	1	1	1	1	0	1	0	1	0	1	4	0	1
arCOG00050	COG0421	E	Spermidine synthase	3	3	5	0	1	1	1	0	0	3	1	0	0	0	4	3	0
arCOG00051	COG4262	R	Predicted spermidine synthase with an N-terminal m	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00052	COG0166	G	Glucose-6-phosphate isomerase	3	3	5	2	1	0	0	4	0	3	0	0	0	0	0	3	0
arCOG00053	COG0269	G	3-hexulose-6-phosphate synthase or related protein	3	3	5	0	0	1	1	0	0	2	3	1	4	1	4	0	0
arCOG00054	COG2521	R	Predicted archaeal methyltransferase	3	0	5	0	1	0	0	0	0	1	0	0	0	1	4	0	0
arCOG00055	COG0421	E	Spermidine synthase	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG00056	COG1818	R	Predicted RNA-binding protein, contains THUMP d	3	0	4	0	0	0	1	0	0	1	0	0	0	1	4	0	0
arCOG00057	COG0449	M	Glucosamine 6-phosphate synthetase	3	3	5	2	1	1	0	4	2	3	3	1	5	1	4	3	0
arCOG00058	COG2222	M	Predicted phosphosugar isomerase	0	0	0	0	0	0	0	0	2	0	0	0	0	1	4	0	0
arCOG00059	COG2222	M	Predicted phosphosugar isomerase	1	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00060	COG0626	E	Cystathionine beta-lyase/cystathionine gamma-synth	2	3	4	0	0	1	0	3	0	0	0	0	3	0	4	3	0
arCOG00061	COG2873	E	O-acetylhomoserine sulfhydrylase	0	0	0	0	0	0	0	4	1	0	2	1	3	0	0	0	0
arCOG00062	COG0388	R	Predicted amidohydrolase	3	3	5	2	1	1	1	3	2	0	3	1	5	0	4	3	0
arCOG00063	COG0504	F	CTP synthase (UTP-ammonia lyase)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00064	COG0505	E	Carbamoylphosphate synthase small subunit	1	3	4	2	0	0	1	4	2	3	3	1	5	1	1	3	0
arCOG00065	COG0520	O	Selenocysteine lyase/Cysteine desulfurase	2	3	2	2	1	1	0	4	1	0	3	1	4	1	4	1	0
arCOG00066	COG1104	E	Cysteine sulfinate desulfinase/cysteine desulfurase o	0	0	0	2	0	1	1	0	1	0	3	1	5	0	0	0	0
arCOG00067	COG0462	F	Phosphoribosylpyrophosphate synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00068	COG0794	M	Predicted sugar phosphate isomerase involved in cap	3	3	5	0	1	1	1	0	2	1	3	1	5	1	0	0	0
arCOG00069	COG0171	H	NH3-dependent NAD+ synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00070	COG0112	E	Glycine/serine hydroxymethyltransferase	3	3	4	2	1	1	1	4	2	1	3	1	5	1	4	3	0
arCOG00071	COG0367	E	Asparagine synthase (glutamine-hydrolyzing)	1	0	3	2	1	0	1	4	2	3	3	1	4	1	4	3	0
arCOG00072	COG0175	E	3'-phosphoadenosine 5'-phosphosulfate sulfotransfer	3	0	0	0	0	0	0	0	0	0	0	0	0	1	4	0	1
arCOG00073	COG0175	E	PAPS reductase related enzyme fused to RNA-bindi	2	1	4	0	0	1	0	1	0	3	3	1	4	1	4	1	0
arCOG00074	COG0175	E	3'-phosphoadenosine 5'-phosphosulfate sulfotransfer	0	0	0	1	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG00075	COG0175	E	3'-phosphoadenosine 5'-phosphosulfate sulfotransfer	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00076	COG1003	E	Glycine cleavage system protein P (pyridoxal-bindir	2	3	0	0	1	1	0	3	0	0	0	0	0	0	4	3	0
arCOG00077	COG0403	E	Glycine cleavage system protein P (pyridoxal-bindir	2	3	0	0	1	1	0	3	0	0	0	0	0	0	4	3	0
arCOG00078	COG1889	J	Fibrillarin-like rRNA methylase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00079	COG0293	J	23S rRNA methylase	0	0	0	2	1	0	1	4	2	3	3	1	5	1	0	3	0
arCOG00080	COG1189	J	Predicted rRNA methylase	0	0	0	0	0	0	1	0	0	0	0	1	5	1	0	0	0
arCOG00081	COG0284	F	Orotidine-5'-phosphate decarboxylase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00082	COG0075	E	Serine-pyruvate aminotransferase/archaeal aspartate	3	3	4	2	1	0	1	4	2	3	3	1	5	1	4	3	0
arCOG00083	COG1932	H	Phosphoserine aminotransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00084	COG1818	R	Predicted RNA-binding protein, contains THUMP d	3	0	5	2	0	0	0	0	1	0	0	0	0	0	4	0	0
arCOG00085	COG0519	F	GMP synthase, PP-ATPase domain/subunit	1	3	4	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00086	COG0512	E	Anthranilate/para-aminobenzoate synthase compone	1	3	5	2	0	0	1	4	2	3	3	0	4	1	3	3	0
arCOG00087	COG0518	F	GMP synthase - Glutamine amidotransferase domair	1	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG00088	COG2071	R	Predicted glutamine amidotransferase	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0
arCOG00089	COG0118	E	Glutamine amidotransferase	0	3	4	2	1	0	1	4	2	3	3	1	5	1	2	1	0
arCOG00090	COG0518	F	GMP synthase - Glutamine amidotransferase domair	0	3	0	2	0	0	1	4	0	0	2	1	4	0	0	0	0
arCOG00091	COG1103	R	Archaea-specific pyridoxal phosphate-dependent en	0	0	0	0	0	0	1	0	1	3	3	1	5	1	0	0	0
arCOG00092	COG1982	E	Arginine/lysine/ornithine decarboxylase	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG00093	COG0034	F	Glutamine phosphoribosylpyrophosphate amidotran	0	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG00094	COG0034	F	Glutamine phosphoribosylpyrophosphate amidotran	0	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00095	COG0067	E	Glutamate synthase domain 1	0	3	4	0	1	0	1	0	2	3	2	1	4	1	1	1	0
arCOG00096	COG0070	E	Glutamate synthase domain 3	0	0	0	0	0	0	1	0	2	3	2	1	4	1	1	0	0
arCOG00097	COG2218	C	Formylmethanofuran dehydrogenase subunit C	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG00098	COG2218	C	Formylmethanofuran dehydrogenase subunit C	0	0	0	0	0	0	0	0	1	3	0	0	2	0	0	0	0
arCOG00099	COG0857	R	BioD-like N-terminal domain of phosphotransacetyl	0	0	0	0	0	0	1	3	0	0	0	1	1	0	0	0	0
arCOG00100	COG0132	H	Dethiobiotin synthetase	0	0	0	2	0	0	0	1	0	3	0	0	0	0	0	0	0
arCOG00101	COG1492	H	Cobyric acid synthase	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG00102	COG0047	F	Phosphoribosylformylglycinamidine (FGAM) synth	0	2	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG00103	COG0269	G	3-hexulose-6-phosphate synthase or related protein	0	0	0	0	0	0	1	0	2	1	3	1	5	0	0	0	0
arCOG00104	COG1795	C	Formaldehyde-activating enzyme nesessary for meth	0	0	0	0	0	0	0	0	0	0	1	1	3	1	0	0	0
arCOG00105	COG1492	H	Cobyric acid synthase	0	3	1	0	0	0	1	4	2	3	2	1	5	1	2	3	0
arCOG00106	COG1797	H	Cobyrinic acid a,c-diamide synthase	0	3	4	2	0	0	1	4	2	3	3	1	5	1	0	3	0
arCOG00107	COG1492	H	Cobyric acid synthase	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG00108	COG2189	L	Adenine specific DNA methylase Mod	0	0	0	1	0	0	1	0	1	0	3	1	1	0	0	1	0
arCOG00109	COG2890	J	Methylase of polypeptide chain release factors	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00110	COG2813	J	16S RNA G1207 methylase RsmC	2	3	0	0	0	0	0	0	0	3	0	0	0	1	4	0	0
arCOG00111	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	4	0	0
arCOG00112	COG0137	E	Argininosuccinate synthase	1	3	4	2	1	1	1	4	2	3	3	1	5	1	1	3	0
arCOG00113	COG0156	H	7-keto-8-aminopelargonate synthetase or related enz	0	0	0	2	0	1	0	2	0	3	0	0	0	0	4	2	0
arCOG00114	COG1921	E	Selenocysteine synthase [seryl-tRNASer selenium tr	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG00115	COG0863	L	DNA modification methylase	0	1	0	2	0	1	0	4	0	1	3	1	0	0	1	3	0
arCOG00116		R	Predicted pyridoxal phosphate-dependent enzyme	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG00117	COG0684	H	Demethylmenaquinone methyltransferase	0	0	1	0	1	0	0	0	2	1	0	0	0	1	0	0	0

arCOG00118	COG0399	M	Predicted pyridoxal phosphate-dependent enzyme ap	1	0	5	2	1	1	0	0	2	3	2	1	4	1	2	0	0
arCOG00119	COG0076	E	Glutamate decarboxylase, L-tyrosine decarboxylase	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG00120	COG4121	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG00121	COG0367	E	Asparagine synthase (glutamine-hydrolyzing)	0	0	0	0	0	0	0	0	0	1	1	0	2	0	1	0	0
arCOG00122	COG2265	J	SAM-dependent methyltransferase related to tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	1
arCOG00123	COG2265	J	SAM-dependent methyltransferase related to tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG00124	COG0175	E	3'-phosphoadenosine 5'-phosphosulfate sulfotransfer	0	3	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00125	COG1818	R	Predicted RNA-binding protein, contains THUMP d	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00126	COG0388	R	Predicted amidohydrolase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0
arCOG00127	COG0388	R	Predicted amidohydrolase	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
arCOG00128	COG0520	O	Selenocysteine lyase/Cysteine desulfurase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00129	COG0863	L	DNA modification methylase	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	2	0
arCOG00130	COG0477	G	permease of the major facilitator superfamily	3	3	5	2	1	1	1	4	1	3	3	1	5	1	4	3	0
arCOG00131	COG0477	G	permease of the major facilitator superfamily	0	0	1	0	0	0	0	2	0	0	0	1	1	0	0	0	0
arCOG00132	COG0477	G	permease of the major facilitator superfamily	2	3	4	0	0	1	0	2	0	0	0	1	2	0	4	3	0
arCOG00134	COG0477	G	permease of the major facilitator superfamily	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00135	COG0477	G	permease of the major facilitator superfamily	0	1	0	0	0	0	0	1	0	0	0	0	2	0	3	3	0
arCOG00136	COG0477	G	permease of the major facilitator superfamily	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0
arCOG00137	COG0477	G	permease of the major facilitator superfamily	0	0	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG00138	COG0477	G	permease of the major facilitator superfamily	0	3	1	0	0	0	0	0	0	0	0	0	0	0	1	3	0
arCOG00139	COG0477	G	permease of the major facilitator superfamily	2	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG00140	COG0477	G	permease of the major facilitator superfamily	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG00141	COG0477	G	permease of the major facilitator superfamily	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	2	0
arCOG00142	COG0477	G	permease of the major facilitator superfamily	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00143	COG0477	G	permease of the major facilitator superfamily	1	0	3	0	1	1	1	0	2	2	3	1	4	0	1	0	0
arCOG00144	COG0477	G	permease of the major facilitator superfamily	0	3	4	0	0	1	0	0	0	0	1	0	2	0	1	3	0
arCOG00145	COG0477	G	permease of the major facilitator superfamily	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00146	COG2211	G	Na+/melibiose symporter or related transporter	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00147	COG0477	G	permease of the major facilitator superfamily	0	3	1	0	0	0	1	3	0	0	2	0	1	0	0	3	0
arCOG00148	COG2223	P	Nitrate/nitrite transporter	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00149	COG1653	G	ABC-type sugar transport system, periplasmic comp	2	0	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG00150	COG1653	G	ABC-type sugar transport system, periplasmic comp	1	1	4	0	0	0	0	1	0	0	0	0	0	0	1	1	0
arCOG00151	COG1653	G	ABC-type sugar transport system, periplasmic comp	0	0	1	0	1	0	0	2	0	0	0	0	0	0	2	2	0
arCOG00152	COG2182	G	Maltose-binding periplasmic protein	3	0	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG00153	COG1653	G	ABC-type sugar transport system, periplasmic comp	3	1	1	0	0	0	0	2	0	0	0	0	0	0	3	2	0
arCOG00154	COG2182	G	Maltose-binding periplasmic protein	0	3	4	0	0	0	0	1	0	0	0	0	0	0	3	1	0
arCOG00155	COG1653	G	ABC-type sugar transport system, periplasmic comp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG00156	COG1653	G	ABC-type sugar transport system, periplasmic comp	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG00157	COG1175	G	ABC-type sugar transport system, permease compor	3	3	5	0	1	0	0	3	0	0	0	0	0	0	4	3	0
arCOG00158	COG0395	G	ABC-type sugar transport system, permease compor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG00159	COG0395	G	ABC-type sugar transport system, permease compor	3	1	4	0	1	0	0	3	0	0	0	0	0	0	3	3	0
arCOG00160	COG3833	G	ABC-type maltose transport system, permease comp	0	3	4	0	0	0	0	1	0	0	0	0	0	0	3	1	0
arCOG00161	COG1176	E	ABC-type spermidine/putrescine transport system, p	1	0	4	0	1	0	1	3	0	0	0	0	0	0	0	0	0
arCOG00162	COG1177	E	ABC-type spermidine/putrescine transport system, p	1	0	4	0	1	0	1	3	0	0	0	0	0	0	0	0	0
arCOG00163	COG1178	P	ABC-type Fe3+ transport system, permease compon	3	0	4	0	1	0	0	4	0	2	0	0	0	0	4	0	0
arCOG00164	COG0555	O	ABC-type sulfate transport system, permease compc	2	3	4	0	1	1	1	4	1	3	3	1	3	1	4	2	0
arCOG00165	COG4149	P	ABC-type molybdate transport system, permease co	1	0	0	0	0	0	0	0	0	2	0	0	4	0	0	0	0
arCOG00166	COG4662	H	ABC-type tungstate transport system, periplasmic co	1	0	3	0	0	0	0	2	1	0	3	1	2	0	0	0	0
arCOG00167	COG0573	P	ABC-type phosphate transport system, permease con	3	1	4	2	1	1	1	4	2	3	0	1	5	0	3	0	0
arCOG00168	COG0581	P	ABC-type phosphate transport system, permease con	3	1	4	2	1	1	1	4	2	3	3	1	5	1	3	0	0
arCOG00169	COG0600	P	ABC-type nitrate/sulfonate/bicarbonate transport sy	2	0	1	2	1	1	1	1	1	3	3	1	5	1	0	0	0
arCOG00170	COG4176	E	ABC-type proline/glycine betaine transport system,	0	0	0	0	0	0	0	0	0	2	2	0	4	0	0	0	0
arCOG00171	COG1174	E	ABC-type proline/glycine betaine transport system,	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG00172	COG1174	E	ABC-type proline/glycine betaine transport system,	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG00173	COG3639	P	ABC-type phosphate/phosphonate transport system,	0	0	1	2	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00174	COG4986	P	ABC-type anion transport system, duplicated perme	0	3	5	0	1	1	0	0	0	0	0	0	0	0	0	3	0
arCOG00175	COG3839	G	ABC-type sugar transport system, ATPase componer	3	3	5	0	1	1	0	3	1	3	3	1	4	0	4	3	0
arCOG00176	COG3842	E	ABC-type spermidine/putrescine transport system, A	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00177	COG3842	E	ABC-type spermidine/putrescine transport system, A	1	0	4	0	1	0	1	4	0	2	0	0	4	0	0	0	0
arCOG00178	COG3839	G	ABC-type sugar transport system, ATPase componer	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG00179	COG3839	G	ABC-type sugar transport system, ATPase componer	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00180	COG3839	G	ABC-type sugar transport system, ATPase componer	2	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
arCOG00181	COG0444	E	ABC-type dipeptide/oligopeptide/nickel transport sy	3	3	5	2	1	1	1	4	0	0	2	1	4	0	4	3	0
arCOG00182	COG0444	E	ABC-type dipeptide/oligopeptide/nickel transport sy	0	2	1	0	0	0	0	0	0	0	2	0	3	0	4	0	0
arCOG00183	COG0444	E	ABC-type dipeptide/oligopeptide/nickel transport sy	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0
arCOG00184	COG4608	E	ABC-type oligopeptide transport system, ATPase co	3	3	5	2	1	1	1	4	0	0	2	1	3	0	4	3	0
arCOG00185	COG1123	R	ATPase component of various ABC-type transport s	0	1	0	0	0	0	0	1	2	3	3	1	5	1	0	2	0
arCOG00186	COG3845	R	ABC-type uncharacterized transport system, ATPase	3	0	4	0	1	1	1	3	0	0	0	0	0	0	4	0	0
arCOG00187	COG1245	R	Predicted ATPase, RNase L inhibitor (RLI) homolog	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00188	COG1122	P	ABC-type cobalt transport system, ATPase compone	2	3	3	0	1	1	1	0	2	0	3	1	4	0	0	0	0
arCOG00189	COG1131	V	ABC-type multidrug transport system, ATPase comp	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG00191	COG4175	E	ABC-type proline/glycine betaine transport system,	0	0	0	0	0	0	0	0	0	2	2	0	4	0	0	0	0
arCOG00192	COG1125	E	ABC-type proline/glycine betaine transport system,	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG00193	COG1116	P	ABC-type nitrate/sulfonate/bicarbonate transport sy	1	3	5	2	1	1	1	1	1	3	3	1	5	1	0	3	0
arCOG00194	COG1131	V	ABC-type multidrug transport system, ATPase comp	3	3	5	2	1	1	1	4	2	2	3	1	5	1	4	3	0
arCOG00195	COG3842	E	ABC-type spermidine/putrescine transport system, A	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00196	COG1131	V	ABC-type multidrug transport system, ATPase comp	0	2	0	0	0	0	0	0	0	0	1	0	3	0	3	0	0
arCOG00197	COG4152	R	ABC-type uncharacterized transport system, ATPase	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG00198	COG1120	P	ABC-type cobalamin/Fe3+-siderophores transport s	3	3	3	0	1	0	1	2	0	3	3	1	5	0	4	3	0
arCOG00199	COG1120	P	ABC-type cobalamin/Fe3+-siderophores transport s	0	0	0	0	0	0	1	4	0	1	3	1	1	0	0	0	0
arCOG00201	COG1121	P	ABC-type Mn/Zn transport system, ATPase compon	3	0	4	2	1	1	1	3	1	0	3	1	5	0	4	0	0
arCOG00202	COG1122	P	ABC-type cobalt transport system, ATPase compone	3	0	2	0	1	1	1	4	2	3	3	1	5	1	4	0	0
arCOG00203	COG1122	P	ABC-type cobalt transport system, ATPase compone	0	0	0	0	0	0	0	0	0	0	3	0	5	0	0	0	0
arCOG00204	COG4608	E	ABC-type oligopeptide transport system, ATPase co	1	1	1	0	0	0	0	0	0	0	2	0	4	0	0	2	0
arCOG00205	COG3842	E	ABC-type spermidine/putrescine transport system, A	0	0	3	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG00206	COG3638	P	ABC-type phosphate/phosphonate transport system,	0	0	0	2	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00207	COG1131	V	ABC-type multidrug transport system, ATPase comp	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00208	COG1131	V	ABC-type multidrug transport system, ATPase comp	0	2	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0
arCOG00209	COG3839	G	ABC-type sugar transport system, ATPase componer	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00210	COG1134	G	ABC-type polysaccharide/polyol phosphate transpor	0	0	0	0	0	0	1	0	1	0	2	1	4	0	0	0	0
arCOG00211	COG3839	G	ABC-type sugar transport system, ATPase componer	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG00212	COG4608	E	ABC-type oligopeptide transport system, ATPase co	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG00213	COG0226	P	ABC-type phosphate transport system, periplasmic c	3	1	4	2	1	1	1	4	2	3	3	1	5	1	3	0	0
arCOG00214	COG0521	H	Molybdopterin biosynthesis enzyme	3	3	5	0	1	1	1	4	1	3	3	1	5	1	4	3	0
arCOG00215	COG1058	R	Predicted nucleotide-utilizing enzyme related to mol	2	3	5	0	1	1	1	4	0	0	0	1	0	0	4	3	0
arCOG00216	COG0303	H	Molybdopterin biosynthesis enzyme	3	3	5	0	1	1	1	4	1	3	3	1	4	1	4	3	0
arCOG00217	COG0303	H	Molybdopterin biosynthesis enzyme	1	3	5	0	1	1	1	4	1	3	3	1	5	0	1	3	0
arCOG00218	COG0303	H	Molybdopterin biosynthesis enzyme	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
arCOG00219	COG0725	P	ABC-type molybdate transport system, periplasmic c	3	3	1	0	0	1	1	4	1	3	3	1	4	1	4	2	0
arCOG00220	COG0687	E	Spermidine/putrescine-binding periplasmic protein	1	0	4	0	1	0	1	3	0	0	0	0	0	0	0	0	0
arCOG00221	COG1840	P	ABC-type Fe3+ transport system, periplasmic comp	3	0	4	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG00222	COG1840	P	ABC-type Fe3+ transport system, periplasmic comp	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00223	COG2005	R	N-terminal domain of molybdenum-binding protein	0	3	4	0	1	0	1	2	0	0	0	0	4	1	0	0	0
arCOG00224	COG0583	K	Transcriptional regulator (LysR family)	0	0	0	0	0	0	1	0	0	3	0	0	0	1	0	0	0
arCOG00225	COG0583	K	Transcriptional regulator (LysR family)	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG00226	COG4143	H	ABC-type thiamine transport system, periplasmic co	1	0	3	0	0	0	0	2	0	0	0	0	0	0	4	0	0
arCOG00227	COG1840	P	ABC-type Fe3+ transport system, periplasmic comp	0	0	1	0	1	0	0	4	0	2	0	0	0	0	0	0	0
arCOG00228	COG3585	H	Molybdopterin-binding protein	0	0	0	0	0	0	0	1	1	2	2	1	3	0	0	0	0
arCOG00229	COG2998	H	ABC-type tungstate transport system, permease com	1	0	3	0	0	0	0	2	1	0	3	1	2	0	0	0	0
arCOG00230	COG1910	P	Periplasmic molybdate-binding protein/domain	2	0	4	0	0	1	0	0	1	0	0	0	0	0	0	0	0
arCOG00231	COG1117	P	ABC-type phosphate transport system, ATPase comp	3	1	4	2	1	1	1	4	2	3	3	1	5	1	3	0	0
arCOG00232	COG0704	P	Phosphate uptake regulator	3	0	3	2	1	1	1	4	2	3	3	1	5	0	3	0	0
arCOG00233	COG1283	P	Na+/phosphate symporter	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0
arCOG00234	COG0704	P	Phosphate uptake regulator	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG00235	COG0179	Q	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7	2	3	4	2	1	1	1	4	2	3	0	1	5	1	4	3	0
arCOG00236	COG3970	R	Fumarylacetoacetate (FAA) hydrolase family protein	0	2	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0
arCOG00237	COG0471	P	Di- and tricarboxylate transporter	1	1	3	0	0	0	0	4	1	3	3	0	0	1	3	0	0
arCOG00238	COG1055	P	Na+/H+ antiporter NhaD or related arsenite permeas	3	2	5	0	1	1	1	0	0	0	3	1	3	0	3	3	0
arCOG00239	COG1024	I	Enoyl-CoA hydratase/carnithine racemase	1	3	3	2	1	0	1	4	0	0	0	0	0	0	0	3	0
arCOG00240	COG0447	H	Dihydroxynaphthoic acid synthase	0	0	0	0	1	0	1	4	0	0	0	0	0	0	0	0	0
arCOG00241	COG1024	I	Enoyl-CoA hydratase/carnithine racemase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00242	COG1024	I	Enoyl-CoA hydratase/carnithine racemase	0	2	3	0	0	0	1	0	0	0	0	0	0	0	0	1	0
arCOG00243	COG1748	E	Saccharopine dehydrogenase or related enzyme	2	0	5	0	1	1	1	0	0	0	0	0	0	0	2	2	0
arCOG00244	COG3268	S	Saccharopine dehydrogenase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00245	COG0287	E	Prephenate dehydrogenase	1	3	4	2	1	1	1	4	2	3	3	1	5	1	2	0	1
arCOG00246	COG0039	C	Malate/lactate dehydrogenase	1	3	4	2	1	0	1	4	2	3	3	0	3	1	0	3	0
arCOG00247	COG2084	I	3-hydroxyisobutyrate dehydrogenase or related beta	3	3	5	2	1	0	0	0	1	0	0	1	2	0	1	3	0
arCOG00248	COG1023	G	Predicted 6-phosphogluconate dehydrogenase	0	0	0	0	1	0	0	4	0	0	0	1	0	0	0	0	0

arCOG00249	COG1250	I	3-hydroxyacyl-CoA dehydrogenase	1	3	4	2	1	1	1	3	0	0	0	0	0	0	0	3	0
arCOG00250	COG1250	I	3-hydroxyacyl-CoA dehydrogenase	0	1	0	0	0	0	1	4	1	0	0	0	0	0	0	0	3	0
arCOG00251	COG1250	I	3-hydroxyacyl-CoA dehydrogenase	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00252	COG0677	M	UDP-N-acetyl-D-mannosaminuronate dehydrogenas	1	0	5	2	0	1	0	1	2	3	2	1	4	0	4	0	0
arCOG00253	COG1004	M	Predicted UDP-glucose 6-dehydrogenase	0	1	2	0	1	0	1	4	1	2	3	1	5	0	2	0	0
arCOG00254	COG1712	R	Predicted dinucleotide-utilizing enzyme	1	0	1	2	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG00255	COG0077	E	Prephenate dehydratase	0	3	4	2	1	1	0	4	2	3	3	1	5	1	1	3	1
arCOG00256	COG0287	E	Prephenate dehydrogenase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG00257	COG1744	R	Uncharacterized ABC-type transport system, peripla	3	0	3	0	1	1	1	1	0	0	0	0	0	0	0	0	0
arCOG00258	COG1744	R	Uncharacterized ABC-type transport system, peripla	3	0	3	0	1	1	0	3	0	0	0	0	0	0	4	0	0
arCOG00259	COG4603	R	ABC-type uncharacterized transport system, permea	3	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00260	COG4603	R	ABC-type uncharacterized transport system, permea	3	0	3	0	1	1	1	3	0	0	0	0	0	0	4	0	0
arCOG00261	COG1079	R	Uncharacterized ABC-type transport system, permea	3	0	3	0	1	1	1	3	0	0	0	0	0	0	4	0	0
arCOG00262	COG1079	R	Uncharacterized ABC-type transport system, permea	2	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00263	COG1172	G	Ribose/xylose/arabinose/galactoside ABC-type trans	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00264	COG2041	R	Sulfite oxidase or related enzyme	3	3	4	0	1	0	1	3	0	0	0	0	0	0	0	3	0
arCOG00266	COG2041	R	Sulfite oxidase or related enzyme	0	2	1	0	0	0	0	2	0	0	1	1	2	0	0	0	0
arCOG00267	COG0755	O	ABC-type transport system involved in cytochrome	2	0	2	0	0	0	1	2	0	0	0	1	3	0	0	0	0
arCOG00268	COG1138	O	Cytochrome c biogenesis factor	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00269	COG1138	O	Cytochrome c biogenesis factor, CcmF homolog	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00270	COG1138	O	Cytochrome c biogenesis factor	0	0	0	0	0	0	1	2	0	0	0	0	3	0	0	0	0
arCOG00271	COG0697	G	permease of the drug/metabolite transporter (DMT)	3	3	4	1	1	1	1	4	1	2	2	1	3	0	4	3	0
arCOG00272	COG0697	G	permease of the drug/metabolite transporter (DMT)	3	0	5	0	0	1	1	1	0	0	0	0	1	0	4	0	0
arCOG00273	COG0697	G	permease of the drug/metabolite transporter (DMT)	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0
arCOG00274	COG0697	G	permease of the drug/metabolite transporter (DMT)	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00275	COG0697	G	permease of the drug/metabolite transporter (DMT)	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG00276	COG0697	G	permease of the drug/metabolite transporter (DMT)	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00277	COG0697	G	permease of the drug/metabolite transporter (DMT)	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00278	COG0697	G	permease of the drug/metabolite transporter (DMT)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG00279	COG1586	E	S-adenosylmethionine decarboxylase	3	3	5	0	1	1	1	0	0	3	3	0	0	0	4	3	0
arCOG00280	COG0433	L	HerA helicase	3	3	5	2	1	1	1	4	2	3	2	1	5	1	4	3	1
arCOG00281		R	Predicted ATPase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG00282	COG0433	L	HerA helicase	2	0	4	0	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00283	COG0433	L	HerA helicase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00284	COG0433	L	HerA helicase	3	3	3	0	0	0	0	2	0	0	0	1	3	0	0	0	1
arCOG00285	COG0433	L	HerA helicase	2	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00286	COG0433	L	HerA helicase	2	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00287		S	Predicted NurA-like nuclease	3	3	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00288	COG0778	C	Nitroreductase	3	3	4	2	1	1	1	4	2	3	3	1	5	1	3	1	0
arCOG00289	COG0778	C	Nitroreductase	0	0	0	0	0	0	1	0	1	0	2	0	4	0	0	0	0
arCOG00291	COG1145	C	Ferredoxin	1	0	4	2	0	0	1	0	1	0	0	0	0	0	0	0	0
arCOG00292	COG1145	C	Ferredoxin domain containing protein	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG00295	COG2000	R	Predicted Fe-S protein	0	0	0	0	0	0	0	0	1	3	3	1	2	1	0	0	0
arCOG00296	COG1145	C	Ferredoxin	0	0	0	0	0	0	0	0	0	1	2	1	4	0	0	0	0
arCOG00297	COG4871	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	1	0	0	1	5	0	0	0	0
arCOG00298		Q	McbC-like oxidoreductase, duplicated domains (non	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00299		O	DsbA family protein	2	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00300	COG1145	C	Ferredoxin	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00301	COG0778	C	Nitroreductase	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG00302	COG0613	R	Metal-dependent phosphoesterase (PHP family)	3	3	1	2	0	0	1	4	2	3	3	1	5	0	0	0	0
arCOG00304	COG1387	E	Histidinol phosphatase or related hydrolase of the PH	0	0	0	0	0	0	1	0	2	3	3	1	5	1	4	0	0
arCOG00305	COG1796	L	DNA polymerase IV (family X)	0	0	0	0	0	0	0	3	1	0	1	1	4	0	0	2	0
arCOG00306	COG0613	R	Metal-dependent phosphoesterase (PHP family)	0	0	0	0	0	0	0	4	1	2	0	0	0	0	0	0	0
arCOG00307	COG1603	J	RNase P/RNase MRP subunit p30	3	3	1	0	1	1	1	4	2	3	3	1	5	1	4	0	0
arCOG00308	COG0613	R	Metal-dependent phosphoesterase (PHP family)	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00309	COG0613	R	Metal-dependent phosphoesterase (PHP family)	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00310	COG1225	O	Peroxiredoxin	2	3	4	2	1	0	0	4	0	0	3	1	4	0	2	3	0
arCOG00312	COG0450	O	Peroxiredoxin	3	2	5	0	0	1	1	0	1	3	2	1	5	0	4	3	1
arCOG00313	COG1999	R	Cu2+-binding oxygen sensor (SCO1/SenC/PrrC fam	0	0	2	0	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00314	COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	0	2	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00315	COG1225	O	Peroxiredoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00316	COG1225	O	Peroxiredoxin	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00317	COG4847	S	Uncharacterized protein conserved in archaea	1	2	4	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG00318	COG0704	P	Phosphate uptake regulator	3	3	5	2	1	1	1	4	2	3	3	1	4	1	4	3	0
arCOG00319	COG0704	P	Phosphate uptake regulator	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00320	COG0704	P	Phosphate uptake regulator	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0
arCOG00321	COG0312	R	Predicted Zn-dependent protease or their inactivated	3	3	5	1	1	1	1	0	2	3	3	1	5	1	4	3	0
arCOG00322	COG0312	R	Predicted Zn-dependent protease or their inactivated	3	3	5	1	1	1	1	0	2	3	3	1	5	1	4	2	0
arCOG00323	COG0312	R	Predicted Zn-dependent protease or their inactivated	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00324	COG0123	R	Deacetylase, including yeast histone deacetylase and	3	3	5	0	1	1	1	4	1	1	2	1	4	1	4	0	1
arCOG00325	COG0123	R	Deacetylase, including yeast histone deacetylase and	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00326	COG0123	R	Deacetylase, including yeast histone deacetylase and	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00327	COG0123	R	Deacetylase, including yeast histone deacetylase and	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG00328	COG0417	L	DNA polymerase elongation subunit (family B)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00329	COG0417	L	DNA polymerase elongation subunit (family B)	2	2	0	0	1	0	1	2	0	1	1	0	0	0	0	2	0
arCOG00331	COG0417	L	DNA polymerase elongation subunit (family B), C-t	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1
arCOG00332	COG0247	C	Membrane associated Fe-S oxidoreductase	1	0	4	0	1	1	1	3	0	0	1	0	0	0	0	2	0
arCOG00333	COG0247	C	Fe-S oxidoreductase	1	3	5	0	0	1	1	3	2	3	3	1	5	1	0	3	0
arCOG00334	COG0247	C	Fe-S oxidoreductase	2	3	4	0	0	1	1	0	1	0	0	0	0	0	0	3	0
arCOG00335	COG1139	C	Uncharacterized conserved protein containing ferred	2	3	4	0	1	1	1	0	1	0	0	0	0	0	0	3	0
arCOG00336	COG0247	C	Fe-S oxidoreductase	0	0	0	0	1	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00337	COG0277	C	FAD/FMN-containing dehydrogenase	2	3	5	2	1	1	1	4	0	0	0	1	5	0	0	3	0
arCOG00338	COG2048	C	Heterodisulfide reductase, subunit B	0	3	0	0	0	1	1	0	2	3	3	1	5	1	0	1	0
arCOG00339	COG0247	C	Fe-S oxidoreductase	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0
arCOG00340	COG0277	C	FAD/FMN-containing dehydrogenase fused to Hetei	0	2	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG00341	COG0277	C	FAD/FMN-containing dehydrogenase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00342	COG2048	C	Heterodisulfide reductase, subunit B	0	3	0	0	0	0	0	0	1	0	0	1	3	0	0	0	0
arCOG00343	COG0247	C	Fe-S oxidoreductase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00344	COG0277	C	FAD/FMN-containing dehydrogenase	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00345	COG0277	C	FAD/FMN-containing dehydrogenase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00346		S	Uncharacterized conserved protein, DUF1121	0	0	0	0	0	0	0	1	0	2	1	0	0	0	0	0	0
arCOG00347	COG1938	R	Archaeal enzyme of ATP-grasp superfamily	3	3	5	2	1	1	1	4	1	3	3	1	5	1	4	2	0
arCOG00348	COG2047	R	Uncharacterized protein (ATP-grasp superfamily)	0	0	1	1	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00349	COG1141	C	Ferredoxin	3	0	4	0	0	1	1	4	2	0	1	1	1	0	4	0	1
arCOG00350	COG1161	R	Predicted GTPase	3	3	4	0	0	1	0	0	0	3	0	0	4	1	4	0	1
arCOG00351	COG1162	R	Predicted GTPase	0	0	0	0	0	0	0	0	0	0	2	1	3	0	0	0	0
arCOG00352	COG1084	R	Predicted GTPase	3	3	5	0	0	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00353	COG2262	R	GTP-binding protein protease modulator	3	3	5	2	1	1	0	4	0	1	0	1	4	1	4	0	0
arCOG00354	COG1100	R	GTPase SAR1 or related small G protein	0	0	0	0	0	1	1	4	1	3	3	1	5	1	4	0	0
arCOG00355	COG0218	R	GTP-binding protein YscX, possible signaling factor	0	0	0	0	0	0	1	4	0	3	3	1	5	1	4	0	0
arCOG00357	COG0012	J	Predicted GTPase, probable translation factor	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00358	COG1163	R	Predicted GTPase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00359	COG0370	P	Fe2+ transport system protein B	2	0	4	0	0	1	1	1	2	3	3	1	5	1	4	0	0
arCOG00360	COG3366	S	Uncharacterized protein conserved in archaea	0	0	1	0	0	0	1	4	0	3	1	0	5	1	0	0	0
arCOG00361	COG3366	S	Uncharacterized protein conserved in archaea	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG00362	COG2229	R	Predicted GTPase	0	0	2	0	0	1	0	0	1	3	1	1	0	1	0	0	0
arCOG00363	COG1100	R	GTPase SAR1 or related small G protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00364	COG1100	R	GTPase SAR1 or related small G protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00365	COG1100	R	GTPase SAR1 or related small G protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00366	COG1100	R	GTPase SAR1 or related small G protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00367	COG1630	L	NurA 5'-3' nuclease	3	3	5	2	1	1	1	4	2	3	2	1	5	1	4	3	0
arCOG00368	COG0419	L	ATPase involved in DNA repair, SbcC	3	3	5	2	1	1	1	4	2	3	2	1	5	1	4	3	1
arCOG00369	COG4717	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	3	0	0	0	0
arCOG00370	COG1196	D	Chromosome segregation ATPase	1	0	1	0	0	0	1	0	1	0	1	0	2	0	1	0	0
arCOG00371	COG1196	D	Chromosome segregation ATPase	0	0	0	2	1	1	1	4	0	3	3	1	5	0	4	3	0
arCOG00379		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00372		S	Uncharacterized conserved protein	3	0	0	0	1	0	0	0	0	0	0	1	1	1	2	0	0
arCOG00373		R	Predicted ATPase	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
arCOG00374	COG2512	K	Predicted membrane-associated trancriptional regula	3	0	5	2	0	1	0	0	0	0	0	0	0	0	4	0	0
arCOG00375	COG2512	K	Predicted trancriptional regulator	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00376	COG2512	K	Predicted membrane-associated trancriptional regula	0	0	0	0	0	0	1	0	0	0	0	1	4	0	0	0	0
arCOG00377	COG2512	K	Predicted membrane-associated trancriptional regula	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00378	COG2512	K	Predicted membrane-associated trancriptional regula	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00380		S	Uncharacterized conserved protein	0	3	5	0	0	0	0	4	1	1	1	0	3	0	0	0	0
arCOG00381		K	Predicted trancriptional regulator, ArsR family	0	0	0	0	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00382		K	Predicted trancriptional regulator, ArsR family	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00383	COG4026	R	Uncharacterized protein containing TOPRIM domai	0	0	0	0	0	0	0	0	1	0	0	0	0	1	4	0	0
arCOG00385		S	Uncharacterized conserved protein	0	1	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0

arCOG00386	COG2512	K	Predicted membrane-associated trancriptional regula	0	0	0	0	0	0	0	1	0	0	1	0	5	0	0	0	0
arCOG00387	COG2512	K	Predicted membrane-associated trancriptional regula	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0
arCOG00388	COG2247	M	Putative cell wall-binding domain	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3	0	0
arCOG00391		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG00393	COG2512	K	Predicted membrane-associated trancriptional regula	1	3	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00394	COG0640	K	Transcriptional regulator containing HTH domain, A	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG00395	COG2512	K	Predicted membrane-associated trancriptional regula	0	0	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0
arCOG00396	COG3355	K	Predicted transcriptional regulator	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG00397	COG0420	L	DNA repair exonuclease, SbcD	3	3	5	2	1	1	1	4	2	3	2	1	5	1	4	3	1
arCOG00398	COG2411	S	Uncharacterized conserved protein	3	0	4	0	1	1	1	1	0	0	0	0	0	1	4	0	1
arCOG00399	COG2411	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG00400	COG2411	S	Uncharacterized conserved protein	0	0	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG00401	COG0441	J	Threonyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00402	COG0442	J	Prolyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00403	COG0172	J	Seryl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00404	COG0124	J	Histidyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00405	COG0423	J	Glycyl-tRNA synthetase (class II)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00406	COG0017	J	Aspartyl/asparaginyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00407	COG0017	J	Aspartyl/asparaginyl-tRNA synthetase	1	0	5	0	1	1	0	0	0	0	0	1	0	0	4	3	0
arCOG00408	COG1190	J	Lysyl-tRNA synthetase (class II)	0	3	4	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG00409	COG0017	J	Aspartyl/asparaginyl-tRNA synthetase	1	0	5	0	1	1	0	0	0	0	0	0	0	0	4	3	0
arCOG00410	COG0016	J	Phenylalanyl-tRNA synthetase alpha subunit	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00411	COG2024	J	Phenylalanyl-tRNA synthetase alpha subunit (archae	0	0	0	0	0	0	1	0	1	3	3	1	5	1	0	0	0
arCOG00412	COG0072	J	Phenylalanyl-tRNA synthetase beta subunit	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00413		J	Phenylalanyl-tRNA synthetase (PheRS) alpha chain	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG00415	COG0468	L	RecA/RadA recombinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00416	COG0550	L	Uncharachterized domain associated with topoisome	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG00417	COG0468	L	RecA/RadA recombinase	2	0	1	2	1	0	1	4	2	3	3	1	5	0	4	3	0
arCOG00418	COG0468	L	RecA/RadA recombinase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00419	COG0537	F	HIT family hydrolase	3	3	5	2	1	1	1	4	1	3	2	1	5	0	4	3	1
arCOG00420	COG1085	C	Galactose-1-phosphate uridylyltransferase	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0
arCOG00421	COG1085	C	Galactose-1-phosphate uridylyltransferase	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG00422	COG1085	C	Galactose-1-phosphate uridylyltransferase	1	0	4	2	0	0	0	0	0	0	0	1	5	0	3	0	0
arCOG00423	COG2404	R	Predicted phosphohydrolase (DHH superfamily)	3	3	1	0	0	1	0	4	0	0	3	0	0	0	0	0	0
arCOG00424	COG0608	L	DHH superfamily phosphohydrolase/exonuclease	1	0	3	2	0	0	0	0	0	0	0	1	3	1	0	0	1
arCOG00425		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00426	COG0608	L	DHH superfamily phosphohydrolase/exonuclease	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG00427	COG0608	L	Single-stranded DNA-specific exonuclease RecJ	1	0	1	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00428		S	Protein similar to exonuclease RecJ central domain	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	1
arCOG00429	COG1107	L	Archaea-specific RecJ-like exonuclease, contains D	0	0	0	0	0	0	1	4	2	3	3	1	5	1	4	0	0
arCOG00430	COG2404	R	Predicted phosphohydrolase (DHH superfamily)	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00431	COG2404	R	Predicted phosphohydrolase (DHH superfamily)	0	0	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00432		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00433	COG0608	L	Protein similar to exonuclease RecJ central domain	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG00434	COG0714	R	MoxR-like ATPase	3	3	5	2	1	0	1	4	0	2	3	1	5	0	4	3	1
arCOG00435	COG0714	R	MoxR-like ATPase	1	0	1	0	0	0	0	2	0	0	3	0	0	0	0	0	0
arCOG00436	COG0714	R	MoxR-like ATPase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00437	COG0714	R	MoxR-like ATPase	0	0	0	0	0	0	0	0	0	1	1	1	3	0	0	0	0
arCOG00438	COG1239	R	AAA family ATPase	0	0	1	1	0	0	1	4	1	1	1	0	5	1	0	3	1
arCOG00439	COG1241	L	Predicted ATPase involved in replication control, Cd	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00441	COG0714	R	MoxR-like ATPase	3	0	4	2	1	1	0	2	2	0	0	1	3	1	0	0	0
arCOG00442	COG2425	R	Uncharacterized protein containing a von Willebran	3	3	4	0	0	0	0	0	0	1	0	1	0	1	0	1	0
arCOG00443	COG2425	R	Uncharacterized protein containing a von Willebran	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG00444	COG2425	R	Uncharacterized protein containing a von Willebran	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00445	COG1240	H	Von Willebrand factor type A (vWA) domain	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00446	COG2086	C	Electron transfer flavoprotein, beta subunit	1	3	4	0	1	1	1	3	0	0	0	0	0	0	0	3	0
arCOG00447	COG2025	C	Electron transfer flavoprotein, alpha subunit	1	3	4	0	1	1	1	3	0	0	0	0	0	0	0	3	0
arCOG00448	COG2086	C	Electron transfer flavoprotein, alpha and beta subuni	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0
arCOG00449	COG0589	T	Nucleotide-binding protein, UspA family	3	0	0	0	0	1	1	4	0	1	2	1	3	0	3	3	0
arCOG00450	COG0589	T	Nucleotide-binding protein, UspA family	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0
arCOG00451	COG0589	T	Nucleotide-binding protein, UspA family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00452	COG5491	N	Conserved protein implicated in secretion	3	3	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00453	COG5491	N	Conserved protein implicated in secretion	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00454	COG5491	N	Conserved protein implicated in secretion	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00455	COG0345	E	Pyrroline-5-carboxylate reductase	2	2	5	0	0	1	0	2	2	0	2	0	4	0	2	3	0
arCOG00456	COG0240	C	NAD(P)H-dependent glycerol-3-phosphate dehydro	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0
arCOG00457	COG2085	R	Predicted dinucleotide-binding enzyme	0	0	1	2	1	0	1	4	2	3	3	1	5	1	0	0	0
arCOG00458	COG1913	R	Predicted Zn-dependent protease	3	2	3	0	1	1	1	4	0	1	3	1	1	1	4	0	1
arCOG00459	COG0177	L	Predicted EndoIII-related endonuclease	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00461	COG2231	L	Uncharacterized protein related to Endonuclease III	0	3	1	0	0	0	0	0	1	3	2	1	4	0	0	3	0
arCOG00462	COG1194	L	A/G-specific DNA glycosylase	1	0	2	0	0	0	0	4	1	0	3	1	1	0	0	0	0
arCOG00463	COG1833	L	Uri superfamily endonuclease	1	2	5	0	0	1	1	4	2	0	3	1	4	1	4	1	1
arCOG00464	COG0122	L	3-methyladenine DNA glycosylase/8-oxoguanine DI	1	1	0	2	0	0	1	4	2	0	3	0	4	0	4	0	0
arCOG00465	COG2231	L	Uncharacterized protein related to Endonuclease III	2	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00466	COG0122	L	3-methyladenine DNA glycosylase/8-oxoguanine DI	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00467	COG1474	L	Cdc6-related protein, AAA superfamily ATPase	3	3	5	2	1	1	1	4	2	0	3	1	5	0	4	3	1
arCOG00468		R	Predicted ATPase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00469	COG0470	L	ATPase involved in DNA replication HolB, small su	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00470	COG0470	L	ATPase involved in DNA replication HolB, large sul	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00471	COG1474	L	Cdc6-related protein, AAA superfamily ATPase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00472		R	Predicted ATPase	0	0	0	0	0	1	0	1	0	3	1	0	0	0	4	0	0
arCOG00473	COG2255	L	Holliday junction resolvasome, helicase subunit Ruv	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG00474	COG0212	H	5-formyltetrahydrofolate cyclo-ligase	3	3	5	2	1	1	0	3	0	0	3	0	0	1	0	0	0
arCOG00475	COG0685	E	5,10-methylenetetrahydrofolate reductase	3	3	4	2	0	1	0	0	0	0	0	0	4	0	4	3	0
arCOG00476	COG0382	H	4-hydroxybenzoate polyprenyltransferase or related	3	3	5	0	1	1	1	3	2	3	3	1	5	1	4	3	0
arCOG00477	COG0382	H	4-hydroxybenzoate polyprenyltransferase or related	2	3	3	0	0	1	1	0	0	0	0	0	0	0	0	3	0
arCOG00478	COG0382	H	4-hydroxybenzoate polyprenyltransferase or related	0	0	0	0	1	0	1	4	1	0	1	0	1	0	0	0	0
arCOG00479	COG0109	O	Polyprenyltransferase (cytochrome oxidase assembl	2	3	5	2	1	1	1	4	0	0	0	0	0	0	0	3	0
arCOG00480	COG1575	H	1,4-dihydroxy-2-naphthoate octaprenyltransferase	1	0	2	2	1	0	0	4	0	0	0	1	0	0	0	1	0
arCOG00481	COG0382	H	4-hydroxybenzoate polyprenyltransferase or related	0	0	0	0	0	0	0	1	1	0	1	1	5	0	0	0	0
arCOG00482	COG0382	H	4-hydroxybenzoate polyprenyltransferase or related	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG00483	COG0382	H	4-hydroxybenzoate polyprenyltransferase or related	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG00484	COG0382	H	4-hydroxybenzoate polyprenyltransferase or related	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG00485	COG1384	J	Lysyl-tRNA synthetase (class I)	3	0	1	2	1	1	1	4	2	3	1	1	5	1	4	3	1
arCOG00486	COG0215	J	Cysteinyl-tRNA synthetase	3	3	5	2	1	1	1	4	1	2	1	1	3	0	4	3	1
arCOG00487	COG0018	J	Arginyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00488	COG0592	L	DNA polymerase sliding clamp subunit (PCNA hom	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00489	COG2096	H	cob(I)alamin adenosyltransferase	2	3	4	2	1	0	1	4	0	0	0	0	0	0	4	3	0
arCOG00491		S	Uncharacterized conserved protein	3	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00492	COG1167	K	Transcriptional regulators containing a DNA-bindin	3	3	4	0	0	1	0	0	0	2	2	1	0	0	4	3	0
arCOG00493	COG0057	G	Glyceraldehyde-3-phosphate dehydrogenase/erythro	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00494	COG0136	E	Aspartate-semialdehyde dehydrogenase	1	3	4	2	1	1	1	4	2	3	3	1	5	1	4	2	0
arCOG00495	COG0002	E	Acetylglutamate semialdehyde dehydrogenase	1	3	4	2	1	1	1	3	2	3	3	1	5	1	4	1	0
arCOG00496	COG0126	G	3-phosphoglycerate kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00497	COG2220	R	Zn-dependent hydrolase of the beta-lactamase fold	3	3	5	0	1	1	1	4	2	1	3	1	5	1	4	3	1
arCOG00498	COG0491	R	Zn-dependent hydrolase, glyoxylase family	2	3	4	0	1	1	1	4	0	0	0	1	0	0	1	3	0
arCOG00499	COG1235	R	Metal-dependent hydrolase of the beta-lactamase su	0	0	0	0	0	0	1	4	2	3	3	1	5	1	4	0	1
arCOG00500	COG1234	R	Metal-dependent hydrolase of the beta-lactamase su	2	3	5	0	1	0	1	4	0	0	1	1	5	0	0	1	0
arCOG00501	COG1234	R	Metal-dependent hydrolase of the beta-lactamase su	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00502	COG1235	R	Metal-dependent hydrolase of the beta-lactamase su	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3	0
arCOG00503	COG1237	R	Metal-dependent hydrolase of the beta-lactamase su	2	1	2	0	0	1	1	0	1	3	3	1	5	1	4	0	0
arCOG00504	COG0491	R	Zn-dependent hydrolase, glyoxylase family	1	3	4	0	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00505	COG0491	R	Zn-dependent hydrolase, glyoxylase family	2	2	3	0	1	0	1	4	0	0	0	0	0	0	0	0	0
arCOG00506	COG0426	C	Uncharacterized flavoprotein	1	2	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG00507	COG0491	R	Zn-dependent hydrolase, glyoxylase family	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
arCOG00508	COG2015	Q	Alkyl sulfatase or related hydrolase	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG00509	COG0426	C	Uncharacterized flavoprotein	2	0	1	0	0	1	1	0	2	3	3	1	5	0	4	0	0
arCOG00510	COG0655	R	Multimeric flavodoxin WrbA	0	2	0	0	0	0	1	0	0	0	1	1	4	0	0	0	0
arCOG00511	COG0491	R	Zn-dependent hydrolase, glyoxylase family	0	1	1	0	0	0	1	3	0	0	0	0	0	0	0	3	0
arCOG00512	COG3467	R	Predicted flavin-nucleotide-binding protein	0	0	0	0	0	0	0	3	0	0	0	0	2	0	0	0	0
arCOG00513	COG3467	R	Predicted flavin-nucleotide-binding protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00514	COG3467	R	Predicted flavin-nucleotide-binding protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00515	COG2220	R	Zn-dependent hydrolase of the beta-lactamase fold	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00516	COG3467	R	Predicted flavin-nucleotide-binding protein	0	0	0	2	1	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00517	COG0491	R	Rhodanese Homology Domain fused to Zn-depende	0	2	0	2	0	0	0	4	0	0	2	1	4	0	0	0	0
arCOG00518	COG3576	R	Predicted flavin-nucleotide-binding protein structura	0	0	0	2	0	0	0	0	1	3	3	1	5	0	0	0	0
arCOG00519	COG0716	C	Flavodoxin	0	0	0	0	0	0	0	0	2	2	3	1	1	0	1	0	0
arCOG00520	COG3467	R	Predicted flavin-nucleotide-binding protein	0	0	0	2	0	1	0	0	1	2	3	1	4	0	0	1	0

arCOG00521	COG3467	R	Predicted flavin-nucleotide-binding protein	0	0	0	2	0	0	0	1	0	0	0	0	4	0	0	0	0
arCOG00522	COG0716	C	Flavodoxin	0	0	0	0	0	0	0	0	1	1	0	1	1	1	1	0	0
arCOG00523	COG0716	C	Flavodoxin	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0
arCOG00524	COG4635	C	Flavodoxin	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG00525	COG3467	R	Pyridoxamine 5'-phosphate oxidase fused to flavodo	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG00526	COG3467	R	Pyridoxamine 5'-phosphate oxidase related protein	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG00527	COG0491	R	Zn-dependent hydrolase, glyoxylase family	0	0	0	0	0	0	0	0	0	0	3	0	3	0	0	0	0
arCOG00528	COG5015	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	1	1	2	0	0	0	0
arCOG00529	COG0491	R	Zn-dependent hydrolase, glyoxylase family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG00530	COG2220	R	Zn-dependent hydrolase of the beta-lactamase fold	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00531	COG3576	R	Predicted flavin-nucleotide-binding protein structura	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG00532	COG1763	H	Molybdopterin-guanine dinucleotide biosynthesis pr	3	3	4	0	1	0	1	4	1	3	2	1	2	1	4	2	0
arCOG00533	COG0314	H	Molybdopterin converting factor, large subunit	0	0	0	0	0	0	1	3	0	0	1	1	4	0	0	0	0
arCOG00534	COG0314	H	Molybdopterin converting factor, large subunit	2	3	4	0	1	1	0	0	1	3	3	0	1	0	4	3	0
arCOG00535	COG2104	H	Sulfur transfer protein involved in thiamine biosynth	3	2	0	0	0	1	1	3	2	2	0	1	5	0	4	3	0
arCOG00536	COG1977	H	Molybdopterin converting factor, small subunit	2	0	5	1	1	1	1	4	0	2	3	1	5	0	4	3	0
arCOG00537	COG1977	H	Molybdopterin converting factor, small subunit	0	0	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00538	COG1977	H	Molybdopterin converting factor, small subunit	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG00539	COG1977	H	Molybdopterin converting factor, small subunit	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00540	COG5131	O	Ubiquitin-like protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00541	COG1236	J	Predicted exonuclease of the beta-lactamase fold inv	3	3	5	2	1	1	1	4	0	3	0	1	4	0	0	3	0
arCOG00542	COG1782	R	Predicted metal-dependent RNase, consists of a met	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG00543	COG1782	R	Predicted metal-dependent RNase, consists of a met	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00544	COG1236	J	Predicted exonuclease of the beta-lactamase fold inv	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG00545	COG1236	J	Predicted exonuclease of the beta-lactamase fold inv	3	3	5	2	1	1	1	1	0	0	0	1	5	1	3	0	0
arCOG00546	COG0595	J	mRNA degradation ribonuclease J1/J2 (metallo-beta	0	0	0	0	0	0	0	4	2	3	3	1	5	1	4	0	1
arCOG00547	COG0595	J	mRNA degradation ribonuclease J1/J2 (metallo-beta	0	0	0	1	1	1	0	0	1	0	0	1	1	0	3	0	0
arCOG00551	COG1711	L	DNA replication initiation complex subunit, GINS f	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00552	COG1711	L	DNA replication initiation complex subunit, GINS f	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00553	COG1204	L	Replicative SFII helicase	2	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00554	COG1202	R	Superfamily II helicase, archaea-specific	0	0	0	0	0	0	0	4	2	3	3	1	5	1	4	0	0
arCOG00555	COG1205	R	Distinct helicase family with a unique C-terminal do	2	3	5	2	1	1	1	3	2	3	2	1	4	1	4	0	0
arCOG00557	COG1201	R	Lhr-like helicase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00558	COG0513	L	Superfamily II DNA and RNA helicase	0	3	1	2	0	0	1	0	2	3	3	1	4	0	1	3	0
arCOG00560	COG0514	L	Superfamily II DNA helicase	1	0	0	0	0	1	0	0	0	0	3	1	4	0	0	0	0
arCOG00561	COG4346	O	Predicted membrane-bound dolichyl-phosphate-man	2	3	4	0	1	1	0	0	0	0	0	0	0	0	4	0	0
arCOG00562	COG4745	O	Predicted membrane-bound mannosyltransferase	0	0	0	0	0	0	1	4	0	0	3	1	3	0	0	0	0
arCOG00563	COG5427	S	Uncharacterized membrane protein	0	0	0	0	0	0	1	4	0	0	3	0	3	0	0	0	0
arCOG00564	COG5427	S	Uncharacterized membrane protein	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
arCOG00565		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	2	3	0	1	0	0	4	0	0
arCOG00566	COG1807	M	4-amino-4-deoxy-L-arabinose transferase or related	0	0	1	0	0	0	1	1	0	0	0	1	1	0	3	0	0
arCOG00567	COG5305	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG00568		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG00569		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00570	COG0644	C	Dehydrogenase (flavoprotein)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00571	COG1053	C	Succinate dehydrogenase/fumarate reductase, flavop	2	3	4	2	1	1	1	4	2	3	3	0	0	1	0	3	0
arCOG00572	COG0029	H	Aspartate oxidase	0	3	1	0	0	0	0	4	0	0	0	0	0	0	4	0	0
arCOG00573	COG1053	C	Succinate dehydrogenase/fumarate reductase, flavop	0	0	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG00574	COG1635	G	Ribulose 1,5-bisphosphate synthetase, converts PRP	3	3	4	2	0	1	1	4	1	3	3	0	5	1	4	0	0
arCOG00575	COG2081	R	Predicted flavoprotein	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0
arCOG00576	COG0428	P	Predicted divalent heavy-metal cations transporter	1	2	3	2	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG00577	COG0428	P	Predicted divalent heavy-metal cations transporter	2	0	3	0	0	1	0	4	1	3	0	1	4	0	4	0	0
arCOG00578	COG1645	R	Uncharacterized Zn-finger containing protein	3	3	5	2	1	1	1	4	0	3	3	1	5	1	4	0	0
arCOG00579	COG1594	K	DNA-directed RNA polymerase, subunit M/Transcri	3	3	5	2	1	1	1	4	2	3	3	1	5	0	4	3	1
arCOG00580	COG1594	K	DNA-directed RNA polymerase, subunit M/Transcri	3	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00581	COG2513	G	PEP phosphonomutase or related enzyme	1	3	4	2	0	0	0	1	0	0	0	0	0	0	0	3	0
arCOG00582	COG2513	G	PEP phosphonomutase or related enzyme	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00583	COG2224	C	Isocitrate lyase	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00584	COG0413	H	Ketopantoate hydroxymethyltransferase	3	3	4	2	0	0	0	3	0	0	0	0	0	0	4	0	0
arCOG00585	COG0489	D	Mrp family protein, ATPase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00586	COG1192	D	ATPase involved in chromosome partitioning, ParA	1	3	3	0	1	0	0	4	2	1	2	0	1	1	4	2	0
arCOG00587	COG3640	D	CO dehydrogenase maturation factor	0	0	0	0	0	1	1	0	1	3	1	1	5	1	0	0	0
arCOG00588	COG3640	D	CO dehydrogenase maturation factor	0	0	0	0	0	0	0	0	1	2	1	1	5	0	0	0	0
arCOG00589	COG0455	N	Antiactivator of flagellar biosynthesis FleN, an ATP	0	0	1	0	0	0	1	4	1	3	1	1	1	1	4	0	1
arCOG00590	COG1348	P	Nitrogenase subunit NifH (ATPase)	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG00591	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG00592	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00593	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	1	2	2	0	0	0	0	0	0
arCOG00594	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	1	2	0	1	3	0	0	0	0
arCOG00595	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG00596	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00597	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00598	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	1	2	2	1	3	0	0	0	0
arCOG00599	COG1192	D	ATPase involved in chromosome partitioning, ParA	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00600	COG0517	R	CBS domain	3	3	4	2	0	1	1	3	2	3	3	1	5	1	4	3	0
arCOG00601	COG0517	R	CBS domain	0	3	2	0	1	0	1	4	1	3	0	1	0	1	4	3	1
arCOG00602	COG0517	R	CBS domain containing protein	3	0	3	0	0	0	0	0	1	0	1	1	5	0	0	0	0
arCOG00603	COG0167	F	Dihydroorotate dehydrogenase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00604	COG0042	J	tRNA-dihydrouridine synthase	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG00605	COG0042	J	tRNA-dihydrouridine synthase	0	0	0	0	0	0	1	4	2	3	3	1	5	1	0	0	0
arCOG00606	COG0517	R	CBS domain	3	3	4	1	1	1	1	4	2	3	2	1	5	1	4	3	0
arCOG00607	COG0517	R	Zn-dependent protease fused to CBS domain	0	0	0	0	0	0	1	4	1	3	2	1	5	0	0	0	0
arCOG00608	COG3620	K	Predicted transcriptional regulator with C-terminal C	0	0	1	2	0	1	1	4	0	0	1	1	4	0	4	3	0
arCOG00609	COG0750	M	Predicted membrane-associated Zn-dependent prote	2	0	0	2	1	0	1	4	0	0	0	1	4	1	4	3	0
arCOG00610	COG2524	K	Predicted transcriptional regulator, contains C-termi	2	3	5	0	0	0	1	4	2	3	3	1	5	1	0	0	0
arCOG00612	COG0516	F	IMP dehydrogenase/GMP reductase	1	0	2	2	1	1	0	4	2	3	3	1	0	1	4	3	0
arCOG00613	COG1304	H	Isopentenyl diphosphate isomerase	3	3	5	0	1	1	1	3	2	3	3	1	5	1	4	3	0
arCOG00614	COG1994	R	Zn-dependent protease	3	3	5	0	1	0	0	4	2	3	3	1	0	0	2	3	1
arCOG00615	COG1902	C	NADH:flavin oxidoreductase, Old Yellow Enzyme f	0	3	1	0	0	0	1	3	0	0	0	1	4	0	0	3	0
arCOG00616	COG1411	R	Uncharacterized protein related to proFAR isomeras	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG00617	COG0107	E	Imidazoleglycerol-phosphate synthase	0	3	4	2	1	0	1	4	2	3	3	1	5	1	2	1	0
arCOG00618	COG0106	E	Phosphoribosylformimino-5-aminoimidazole carbox	0	3	4	2	1	0	1	4	2	3	3	1	5	1	2	1	0
arCOG00619	COG0069	E	Glutamate synthase domain 2 and ferredoxin domai	0	3	5	0	1	1	1	0	2	3	2	1	5	1	1	1	0
arCOG00620	COG1900	S	Uncharacterized conserved DUF39 domain fused to	0	0	0	0	0	0	1	0	1	3	3	1	5	1	0	0	0
arCOG00621	COG1900	S	Uncharacterized conserved DUF39 domain fused to	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG00622	COG1475	K	Stage 0 sporulation protein J (antagonist of Soj) con	1	0	0	0	0	0	1	3	2	0	3	1	0	0	3	0	0
arCOG00623	COG0517	R	ParB-like nuclease domain fused to CBS domain	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0
arCOG00624	COG1824	P	Permease, similar to cation transporter	2	0	0	0	0	1	1	4	1	0	2	0	4	1	4	0	0
arCOG00625	COG2239	P	Mg/Co/Ni transporter MgtE (contains CBS domain)	1	0	0	0	0	0	0	1	1	0	0	1	1	0	0	0	0
arCOG00626	COG1253	R	Hemolysins or related protein containing CBS doma	0	0	0	2	0	0	0	4	0	0	3	1	2	0	0	0	1
arCOG00627	COG2021	E	Homoserine acetyltransferase	0	0	0	0	0	0	0	4	2	0	2	1	3	0	0	0	0
arCOG00628	COG0517	R	CBS domain	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG00629	COG0517	R	CBS domain	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG00630	COG1253	R	Hemolysins or related protein containing CBS doma	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG00631	COG0517	R	CBS domain	0	0	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00632	COG0477	G	permease of the major facilitator superfamily	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00633	COG0517	R	CBS domain	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00634	COG2239	P	Mg/Co/Ni transporter MgtE (contains CBS domain)	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
arCOG00635	COG2070	R	Dioxygenase related to 2-nitropropane dioxygenase	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG00636	COG0309	O	Hydrogenase maturation factor	3	3	5	0	1	1	1	3	2	3	3	1	3	1	4	3	0
arCOG00637	COG1973	O	Hydrogenase maturation factor	0	3	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG00638	COG0611	H	Thiamine monophosphate kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00639	COG0150	F	Phosphoribosylaminoimidazole (AIR) synthetase	0	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG00640	COG2144	R	Selenophosphate synthetase-related protein	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG00641	COG0046	F	Phosphoribosylformylglycinamidine (FGAM) synth	0	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG00642	COG2144	R	Selenophosphate synthetase-related protein	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG00643	COG0709	E	Selenophosphate synthase	0	3	3	0	0	0	0	1	0	3	0	0	0	1	0	0	0
arCOG00644	COG0007	H	Uroporphyrinogen-III methylase	2	3	4	2	0	0	1	4	2	3	3	1	5	1	0	3	0
arCOG00645	COG2875	H	Precorrin-4 methylase	0	3	2	2	0	0	1	4	2	3	3	0	5	1	0	3	0
arCOG00646	COG0007	H	Uroporphyrinogen-III methylase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00647	COG1010	H	Precorrin-3B methylase	0	3	2	2	0	0	1	4	2	3	3	0	5	1	0	3	0
arCOG00648	COG2243	H	Precorrin-2 methylase	0	3	2	2	0	0	1	4	2	3	3	0	5	1	0	3	0
arCOG00649	COG0007	H	Uroporphyrinogen-III methylase	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00650	COG2241	H	Precorrin-6B methylase 1	0	3	2	2	0	0	1	4	2	3	3	0	4	1	0	1	0
arCOG00651	COG2073	H	Cobalamin biosynthesis protein CbiG	0	3	2	2	0	0	1	4	2	3	3	0	2	1	0	3	0
arCOG00652	COG2073	H	Cobalamin biosynthesis protein CbiG	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00653		S	Uncharacterized conserved protein	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00654	COG2107	R	Predicted periplasmic solute-binding protein	1	3	4	2	0	0	1	0	0	0	0	0	0	0	0	3	0

arCOG00655	COG1427	R	Predicted periplasmic solute-binding protein	1	0	4	1	0	0	1	0	0	0	0	0	0	0	0	2	0
arCOG00656	COG1060	H	Thiamine biosynthesis enzyme ThiH, FO synthase o	1	0	4	2	0	0	1	4	2	3	3	1	5	1	0	2	0
arCOG00657	COG1060	H	Thiamine biosynthesis enzyme ThiH, FO synthase o	0	0	0	2	0	0	1	4	2	3	3	1	5	1	0	0	0
arCOG00658	COG0502	H	Biotin synthase or related enzyme	0	0	0	2	0	0	0	2	2	3	1	0	4	1	0	0	0
arCOG00659	COG0502	H	Biotin synthase or related enzyme	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG00660	COG0320	H	Lipoate synthase	1	2	2	0	1	0	0	3	0	0	0	1	0	0	0	1	0
arCOG00661	COG4277	R	Predicted DNA-binding protein with the Helix-hairp	1	0	0	0	0	0	0	0	0	2	0	2	1	2	0	0	0
arCOG00662	COG2516	R	Biotin synthase-related enzyme	2	3	0	0	0	1	0	0	0	0	3	1	5	0	4	0	0
arCOG00663	COG1208	M	Nucleoside-diphosphate-sugar pyrophosphorylase in	3	3	5	2	1	0	0	0	2	0	1	1	1	0	0	3	1
arCOG00664	COG1209	M	dTDP-glucose pyrophosphorylase	0	3	1	0	0	0	0	4	1	1	2	1	5	0	0	3	0
arCOG00665	COG1210	M	UDP-glucose pyrophosphorylase	0	1	2	0	1	0	0	0	2	3	2	0	5	0	2	0	0
arCOG00666	COG1208	M	Nucleoside-diphosphate-sugar pyrophosphorylase in	3	3	5	0	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00667	COG1209	M	dTDP-glucose pyrophosphorylase	1	3	1	1	0	0	1	0	1	0	0	0	1	0	2	2	0
arCOG00668	COG1208	M	Nucleoside-diphosphate-sugar pyrophosphorylase in	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG00669	COG1209	M	dTDP-glucose pyrophosphorylase	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG00670	COG0558	I	Phosphatidylglycerophosphate synthase	3	3	5	2	1	1	1	4	2	0	3	1	5	0	4	3	0
arCOG00671	COG1183	I	Phosphatidylserine synthase	0	0	0	0	0	0	1	4	2	3	0	0	5	1	0	0	0
arCOG00672	COG0558	I	Phosphatidylglycerophosphate synthase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00673	COG1213	M	Predicted sugar nucleotidyltransferase	2	0	1	1	0	1	1	1	1	0	1	0	0	0	4	0	0
arCOG00674	COG0558	I	Phosphatidylglycerophosphate synthase	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG00675	COG1095	K	DNA-directed RNA polymerase, subunit E'	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00676	COG1096	J	Predicted RNA-binding protein (consists of S1 doma	3	3	5	2	1	1	1	0	2	0	0	1	5	1	4	3	0
arCOG00678	COG1097	J	RNA-binding protein Rrp4 or related protein (contai	3	3	5	2	1	1	1	0	2	0	0	1	5	1	4	3	1
arCOG00679	COG0675	L	Transposase	1	3	4	0	0	1	0	4	0	1	0	0	2	1	3	2	0
arCOG00680	COG0675	L	Transposase	0	2	0	0	0	0	0	0	0	1	0	0	3	0	0	2	0
arCOG00681	COG0675	L	Transposase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00682	COG0675	L	Transposase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00683	COG0675	L	Transposase	0	3	2	0	0	1	0	4	0	0	0	0	0	0	3	2	0
arCOG00684	COG0675	L	Transposase	0	3	1	0	0	0	0	3	1	0	0	0	5	0	1	2	0
arCOG00686	COG0675	L	Transposase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00687	COG0675	L	Transposase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00689	COG0044	F	Dihydroorotase or related cyclic amidohydrolase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00690	COG3653	Q	N-acyl-D-aspartate/D-glutamate deacylase	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
arCOG00691	COG1574	R	Predicted metal-dependent hydrolase with the TIM-l	3	0	1	0	0	1	0	3	0	0	1	0	2	0	3	2	0
arCOG00692	COG0402	F	Cytosine deaminase or related metal-dependent hyd	3	3	3	2	0	0	1	4	2	3	3	1	5	1	0	1	0
arCOG00693	COG1001	F	Adenine deaminase	1	0	0	2	1	1	1	0	2	1	1	0	5	1	0	1	0
arCOG00694	COG3454	P	Metal-dependent hydrolase involved in phosphonate	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00695	COG0402	F	Cytosine deaminase or related metal-dependent hyd	2	3	2	0	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00696	COG1228	Q	Imidazolonepropionase or related amidohydrolase	0	3	1	0	0	0	1	2	1	0	0	0	1	0	1	3	0
arCOG00697	COG0402	F	Cytosine deaminase or related metal-dependent hyd	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00698	COG0804	E	Urea amidohydrolase (urease) alpha subunit	0	1	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00699	COG1820	G	N-acetylglucosamine-6-phosphate deacetylase	1	2	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG00700	COG0402	F	Cytosine deaminase related metal-dependent hydrol	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00701	COG0584	C	Glycerophosphoryl diester phosphodiesterase	3	2	5	0	0	0	0	4	0	0	2	1	1	0	3	3	0
arCOG00702	COG1404	O	Subtilisin-like serine protease	2	0	3	1	1	0	1	2	0	0	2	1	5	0	2	0	0
arCOG00704	COG1404	O	Ssurface layer-associated subtilisin-like serine prote	3	0	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00705	COG1404	O	Subtilisin-like serine protease, fragment	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
arCOG00706	COG2414	C	Aldehyde:ferredoxin oxidoreductase	3	0	5	0	1	1	1	2	0	0	3	1	3	0	4	2	0
arCOG00707	COG2414	C	Aldehyde:ferredoxin oxidoreductase	2	0	5	0	0	1	1	2	0	0	0	1	0	0	3	0	0
arCOG00708	COG2414	C	Aldehyde:ferredoxin oxidoreductase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00709	COG2414	C	Aldehyde:ferredoxin oxidoreductase	1	0	3	0	0	0	0	0	0	0	0	0	0	0	4	2	0
arCOG00710	COG1848	V	PIN domain containing protein	1	0	0	0	0	0	1	0	0	1	2	0	0	0	2	0	0
arCOG00711	COG1848	V	PIN domain containing protein	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0
arCOG00712	COG1848	V	PIN domain containing protein	0	0	0	0	0	0	0	0	0	1	1	0	0	0	3	0	0
arCOG00713	COG1848	V	PIN domain containing protein	1	2	2	0	1	1	1	0	0	0	1	0	0	0	2	0	0
arCOG00714	COG5573	V	PIN domain containing protein	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG00715	COG1848	V	PIN domain containing protein	1	0	0	0	0	0	1	0	0	0	0	0	0	0	3	0	0
arCOG00716	COG1848	V	PIN domain containing protein	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG00717	COG2405	V	PIN domain containing protein	1	0	0	0	1	0	1	3	0	0	1	0	0	0	1	0	0
arCOG00719	COG2405	V	PIN domain containing protein	0	0	0	0	0	0	1	2	0	0	0	0	0	0	1	0	0
arCOG00720	COG1458	V	PIN domain containing protein	3	0	0	0	0	0	1	1	1	3	0	0	5	1	4	0	0
arCOG00721	COG1439	V	Predicted nucleic acid-binding protein, consists of a	3	3	4	2	1	0	1	4	2	3	3	1	5	1	4	3	1
arCOG00722	COG2886	S	Uncharacterized small protein	1	0	1	0	0	0	1	2	0	0	2	0	0	0	1	0	0
arCOG00723	COG5483	S	Uncharacterized conserved protein	2	2	4	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG00724	COG1695	K	Predicted transcriptional regulator, PadR family	1	1	0	0	0	1	0	1	0	0	0	0	3	0	0	2	0
arCOG00725	COG3465	S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0
arCOG00726	COG4113	V	PIN domain containing protein	2	3	3	0	1	0	0	0	0	0	0	0	0	0	3	0	0
arCOG00727	COG4113	V	PIN domain containing protein	1	3	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00728	COG4113	V	PIN domain containing protein	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG00729	COG4113	V	PIN domain containing protein	2	3	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00730	COG1848	V	PIN domain containing protein	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0
arCOG00731	COG0640	K	Transcriptional regulator containing HTH domain, A	2	3	1	1	1	0	0	1	1	0	0	0	0	0	1	3	0
arCOG00732	COG1846	K	Transcriptional regulator, MarR family	0	3	2	0	0	1	1	1	0	1	0	0	0	0	4	2	0
arCOG00733	COG1695	K	Predicted transcriptional regulator, PadR family	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG00734	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	1	0	1	2	2	1	4	0	4	0	0
arCOG00735	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00736	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00737	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00738	COG0640	K	Transcriptional regulator containing HTH domain, A	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00739	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00740	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00741	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00742	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00743		K	Predicted transcriptional regulator	2	0	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0
arCOG00744		K	Transcriptional regulator containing HTH domain	0	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00746		K	Predicted transcriptional regulator, paREP10 subfam	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00747	COG3432	K	Predicted transcriptional regulator	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00748	COG1173	E	ABC-type dipeptide/oligopeptide/nickel transport sy	3	3	5	0	0	1	1	4	1	0	2	1	4	0	4	3	0
arCOG00749	COG1173	E	ABC-type dipeptide/oligopeptide/nickel transport sy	2	3	5	2	1	1	0	0	0	0	0	0	0	0	4	0	0
arCOG00750	COG1173	E	ABC-type dipeptide/oligopeptide/nickel transport sy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG00751	COG0601	E	ABC-type dipeptide/oligopeptide/nickel transport sy	3	3	5	2	1	1	1	4	1	0	2	1	4	0	4	3	0
arCOG00752	COG0601	E	ABC-type dipeptide/oligopeptide/nickel transport sy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG00753	COG0578	C	Glycerol-3-phosphate dehydrogenase	0	2	2	0	0	0	0	3	0	0	0	1	0	0	0	3	0
arCOG00754	COG0579	R	Malate/quinone oxidoreductase or related dehydroge	2	0	1	2	1	1	1	0	0	0	0	0	0	0	3	1	0
arCOG00755	COG0665	E	Glycine/D-amino acid oxidase (deaminating)	3	3	5	0	1	1	1	2	0	0	1	1	3	0	4	3	0
arCOG00756	COG0404	E	Glycine cleavage system T protein (aminomethyltra	3	3	0	0	1	1	0	4	0	0	0	0	0	0	4	3	0
arCOG00757	COG0404	E	Glycine cleavage system T protein (aminomethyltra	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00758	COG0665	E	Glycine/D-amino acid oxidase (deaminating)	0	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00759	COG0665	E	Glycine/D-amino acid oxidase (deaminating)	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00760	COG2301	G	Citrate lyase beta subunit	1	3	0	2	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00761	COG1720	S	Uncharacterized conserved protein	3	3	4	0	1	1	1	1	1	3	3	1	4	1	4	0	0
arCOG00762	COG2191	C	Formylmethanofuran dehydrogenase subunit E	0	0	2	0	0	0	1	0	1	2	3	1	5	0	3	2	0
arCOG00763	COG2191	C	Formylmethanofuran dehydrogenase subunit E	0	0	0	0	0	0	0	0	1	2	2	1	4	0	0	0	0
arCOG00764	COG2191	C	Formylmethanofuran dehydrogenase subunit E	0	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0
arCOG00765	COG5643	R	Protein containing a metal-binding domain shared w	0	0	0	0	0	0	0	0	1	0	2	0	4	1	0	0	0
arCOG00767	COG1109	G	Phosphomannomutase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00768	COG1109	G	Phosphomannomutase, alpha/beta/alpha domain I or	1	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG00769	COG0693	R	Putative intracellular protease/amidase	2	3	4	0	1	1	1	4	0	3	3	1	5	1	4	3	1
arCOG00770	COG1199	K	Rad3-related DNA helicase	2	3	5	2	1	1	0	4	2	3	3	1	5	0	4	3	0
arCOG00771	COG1680	V	Beta-lactamase class C and other penicillin binding	2	0	2	0	0	0	0	1	0	0	2	0	1	0	2	1	0
arCOG00772	COG1680	V	Beta-lactamase class C and other penicillin binding	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00773	COG1607	I	Acyl-CoA hydrolase	2	3	4	1	1	0	0	4	0	0	0	0	0	0	0	3	0
arCOG00774	COG2030	I	Acyl dehydratase	0	3	0	0	1	0	1	3	0	0	0	0	0	0	0	0	0
arCOG00775	COG2030	I	Acyl dehydratase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00776	COG2030	I	Acyl dehydratase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00777	COG2050	Q	HGG motif-containing thioesterase, possibly involve	0	3	2	0	0	0	1	3	0	0	3	1	5	0	4	3	0
arCOG00778	COG2030	I	Acyl dehydratase	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG00779	COG0200	J	Ribosomal protein L15	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00780	COG1727	J	Ribosomal protein L18E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00781	COG1717	J	Ribosomal protein L32E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00782	COG0199	J	Ribosomal protein S14	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00784	COG1588	J	RNase P/RNase MRP subunit p29	3	1	4	2	0	1	1	3	2	3	2	1	5	1	4	2	0
arCOG00785	COG0255	J	Ribosomal protein L29	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00786	COG1468	V	CRISPR-associated protein Cas4 (RecB family exor	3	3	3	0	1	1	1	1	1	1	2	0	3	0	0	0	0
arCOG00787	COG2887	L	UvrD/Rep family helicase fused to exonuclease fam	0	0	0	1	0	0	0	1	0	0	2	0	0	0	0	0	1
arCOG00790	COG1468	V	CRISPR-associated protein Cas4 (RecB family exor	2	3	4	2	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG00791	COG0210	L	Superfamily I DNA and RNA helicase	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG00792	COG1112	L	Superfamily I DNA/RNA helicase	1	1	1	1	0	0	1	0	2	3	0	1	0	1	4	1	0

arCOG00793	COG1468	R	RecB family exonuclease	0	0	0	0	0	0	1	0	1	0	3	1	5	0	0	0	0
arCOG00794	COG1468	V	CRISPR-associated protein Cas4 (RecB family exor	0	0	0	0	0	0	1	1	2	1	0	0	3	0	3	1	1
arCOG00795	COG1112	L	UvrD/REP helicase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG00796	COG1112	L	UvrD/REP helicase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00797	COG0210	L	Superfamily I DNA and RNA helicase	0	0	0	0	0	0	0	4	1	0	0	0	0	0	0	0	0
arCOG00798	COG0210	L	Superfamily I DNA and RNA helicase	0	0	0	1	0	0	0	2	2	0	2	1	3	0	0	3	0
arCOG00800	COG1468	L	RecB family exonuclease	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG00801	COG0210	L	RecB family exonuclease	0	0	0	1	0	0	0	0	0	0	1	1	2	0	0	1	0
arCOG00802	COG1074	L	ATP-dependent exoDNAse (exonuclease V) beta sul	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG00803	COG1112	L	Superfamily I DNA/RNA helicase fused Vsr family	0	0	0	1	0	0	0	0	2	0	2	0	3	0	0	1	0
arCOG00805	COG3857	L	ATP-dependent nuclease, subunit B	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG00806	COG1112	L	Superfamily I DNA/RNA helicase fused to RecB far	0	0	0	0	0	0	0	0	0	0	2	0	0	0	3	0	0
arCOG00807	COG0060	J	Isoleucyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00808	COG0525	J	Valyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00809	COG0495	J	Leucyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00810	COG0143	J	Methionyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00811	COG0440	E	Acetolactate synthase, small subunit	3	0	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0
arCOG00812	COG2002	K	Transcriptional regulator AbrB	2	0	1	0	0	1	0	1	0	0	0	0	0	0	2	0	0
arCOG00813	COG1707	R	ACT domain-containing protein	0	0	0	0	0	0	1	0	2	3	3	1	1	1	0	0	0
arCOG00814	COG1707	K	HTH and ACT domains	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG00815	COG2002	K	Transcriptional regulator AbrB	1	3	2	0	0	0	1	0	0	0	0	1	0	0	4	0	0
arCOG00816	COG2002	K	Transcriptional regulator AbrB	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG00817	COG2002	K	Transcriptional regulator AbrB	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00818	COG2002	K	Transcriptional regulator AbrB	1	2	0	0	0	0	0	3	0	0	1	0	0	0	1	0	0
arCOG00819	COG2002	K	AbrB family transcriptional regulator	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
arCOG00820	COG2002	K	Transcriptional regulator AbrB	2	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00821		K	AbrB family transcriptional regulator	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00822	COG2002	K	Transcriptional regulator AbrB	0	0	0	0	0	0	1	0	0	0	2	1	0	0	0	0	0
arCOG00823	COG2002	K	Transcriptional regulator AbrB	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00824	COG2002	K	Transcriptional regulator AbrB	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG00825	COG2002	K	Transcriptional regulator AbrB	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00826	COG0454	K	Acetyltransferase (GNAT) family	1	3	5	2	1	1	1	4	2	3	2	1	5	0	4	3	0
arCOG00827	COG1246	E	Acetyltransferase (GNAT family)	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG00828	COG3393	R	Predicted acetyltransferase	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG00830	COG1247	M	Sortase or related acyltransferase	0	0	0	0	0	0	0	1	0	0	2	1	3	0	0	0	0
arCOG00831	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00832	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG00833	COG0456	R	Acetyltransferase (GNAT) family	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00834	COG0454	K	Acetyltransferase (GNAT) family	1	0	0	0	0	1	0	0	0	0	1	0	2	0	1	0	0
arCOG00836	COG1247	M	Sortase or related acyltransferase	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00837	COG0456	R	Acetyltransferase (GNAT) family	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG00838	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	1	4	0	0	1	0	3	0	0	0	0
arCOG00839	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	3	0	0	3	1	3	0	0	0	0
arCOG00840	COG1246	E	Acetyltransferase (GNAT family)	0	0	0	0	0	0	0	4	0	0	1	0	0	0	0	0	0
arCOG00842	COG1670	J	Acetyltransferase, RimL family	0	0	0	0	0	0	0	2	0	2	3	1	3	0	2	3	0
arCOG00843	COG1670	J	Acetyltransferase, RimL family	0	0	0	0	0	0	0	0	0	0	2	1	2	0	0	0	0
arCOG00844	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	1	0	4	0	0	1	1	1	0	4	2	0
arCOG00845	COG0454	K	Acetyltransferase (GNAT) family	0	0	4	2	0	0	0	4	0	0	0	0	0	0	4	2	0
arCOG00846	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG00847	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	1	0	0	0	0	1	0	1	1	0	0	0	0	0
arCOG00848	COG0456	R	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00849	COG3153	R	Predicted acetyltransferase	0	0	1	0	0	0	0	0	1	0	0	0	3	0	0	0	0
arCOG00850	COG3153	R	Predicted acetyltransferase	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG00851	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG00852	COG0456	R	Acetyltransferase (GNAT) family	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00853	COG0281	C	Malic enzyme	2	3	4	0	1	1	1	4	0	0	1	0	4	0	4	3	0
arCOG00854	COG4002	R	Predicted phosphotransacetylase	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG00855	COG0280	C	Phosphotransacetylase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00856	COG0318	I	Acyl-CoA synthetase (AMP-forming)/AMP-acid lig	1	3	3	1	1	0	1	4	2	2	3	1	4	0	0	3	0
arCOG00857	COG0318	I	Acyl-CoA synthetase (AMP-forming)/AMP-acid lig	1	3	1	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG00858	COG0528	F	Uridylate kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00859	COG2054	R	Uncharacterized archaeal kinase related to aspartoki	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG00860	COG1608	R	Predicted archaeal kinase	3	1	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00861	COG0527	E	Aspartokinase	2	3	4	2	1	1	1	4	2	3	3	1	5	1	4	2	0
arCOG00862	COG0548	E	Acetylglutamate kinase	1	3	4	2	1	1	1	3	2	3	3	1	5	1	4	1	0
arCOG00863	COG0549	E	Carbamate kinase	3	0	5	0	1	1	0	1	0	0	1	0	0	0	4	3	0
arCOG00864	COG0263	E	Glutamate 5-kinase	0	0	0	0	0	0	0	2	0	0	0	0	4	0	0	0	0
arCOG00865	COG1156	C	Archaeal/vacuolar-type H+-ATPase subunit B	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00866	COG0055	C	F0F1-type ATP synthase, beta subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00867	COG0056	C	F0F1-type ATP synthase, alpha subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00868	COG1155	C	Archaeal/vacuolar-type H+-ATPase subunit A	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00869	COG1390	C	Archaeal/vacuolar-type H+-ATPase subunit E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00871	COG0553	K	Superfamily II DNA/RNA helicase, SNF2 family	1	0	2	1	0	1	1	4	0	0	0	0	0	0	3	0	0
arCOG00872	COG1111	L	ERCC4-like helicase	0	0	0	2	1	1	1	4	2	3	3	1	5	1	4	2	1
arCOG00873	COG0322	L	Excinuclease-associated helix-hairpin-helix domain	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG00874	COG1061	K	DNA or RNA helicase of superfamily II	3	3	4	1	0	1	1	4	0	0	0	1	4	0	3	3	0
arCOG00876	COG1061	K	DNA or RNA helicase of superfamily II	0	0	5	0	0	1	0	0	0	0	0	0	0	0	4	0	0
arCOG00877	COG1061	K	DNA or RNA helicase of superfamily II	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
arCOG00878	COG0610	V	Type I site-specific restriction-modification system,	1	0	0	1	0	0	1	1	2	2	1	1	4	0	1	1	0
arCOG00879	COG0610	V	Type I site-specific restriction-modification system,	0	0	0	0	0	0	0	0	0	1	1	0	3	0	0	0	0
arCOG00880	COG4096	V	Type I site-specific restriction-modification system,	0	0	0	0	0	0	0	0	0	1	2	1	4	0	0	0	0
arCOG00881	COG1061	K	DNA or RNA helicase of superfamily II	0	1	0	1	0	0	0	0	1	0	1	0	1	0	0	0	0
arCOG00883	COG0553	K	Superfamily II DNA/RNA helicase, SNF2 family	0	1	0	2	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG00884	COG1061	K	DNA or RNA helicase of superfamily II	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG00885		K	DNA or RNA helicase of superfamily II	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	1	0
arCOG00886	COG0553	K	Superfamily II DNA/RNA helicase, SNF2 family	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG00887	COG1483	R	Predicted ATPase (AAA+ superfamily)	2	0	2	0	0	1	1	0	0	0	0	0	0	0	3	0	0
arCOG00888	COG1483	R	Predicted ATPase (AAA+ superfamily)	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0
arCOG00889	COG1743	L	Adenine-specific DNA methylase containing a Zn-ri	2	0	2	0	0	1	1	1	0	0	1	0	0	1	3	0	0
arCOG00890	COG0863	L	DNA modification methylase	1	0	0	1	1	0	0	0	0	1	1	0	0	0	0	1	0
arCOG00891	COG0084	L	Mg-dependent DNase	3	3	5	2	1	1	0	0	2	3	0	0	5	1	4	0	1
arCOG00892	COG1099	R	Predicted metal-dependent hydrolase with the TIM-l	0	0	0	0	0	0	1	0	2	3	0	1	0	1	0	0	0
arCOG00893	COG1831	R	Predicted metal-dependent hydrolase (urease superfa	3	0	4	0	0	0	1	4	1	3	3	1	4	1	4	3	0
arCOG00894	COG0463	M	Glycosyltransferase	2	0	5	2	1	1	1	4	2	1	3	1	5	1	4	1	0
arCOG00895	COG0463	M	Glycosyltransferase	1	3	0	0	1	0	0	4	2	3	2	1	2	1	4	3	0
arCOG00896	COG0463	M	Glycosyltransferase	0	0	0	0	0	1	0	1	1	0	2	1	4	0	4	0	0
arCOG00897	COG0463	M	Glycosyltransferase	0	0	0	0	0	0	1	4	0	0	3	0	3	0	0	0	0
arCOG00898	COG0392	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG00899	COG0392	S	Uncharacterized conserved membrane protein	1	0	1	2	0	1	1	3	2	3	3	1	5	1	4	0	0
arCOG00901	COG0392	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG00902	COG0392	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00903	COG0392	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG00904	COG0463	M	Glycosyltransferase	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0
arCOG00905	COG1573	L	Uracil-DNA glycosylase	3	3	5	2	1	1	1	4	0	0	1	1	5	0	4	3	1
arCOG00906	COG2260	J	Predicted Zn-ribbon RNA-binding protein	3	3	5	2	0	0	1	4	2	3	3	1	5	1	4	3	1
arCOG00908	COG3286	S	Uncharacterized protein conserved in archaea	3	0	5	0	0	1	0	0	0	3	0	0	0	1	4	0	0
arCOG00910	COG2263	J	Predicted RNA methylase	3	3	5	2	0	1	1	4	1	3	3	1	5	1	4	3	1
arCOG00911	COG0540	F	Aspartate carbamoyltransferase, catalytic chain	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00912	COG0078	E	Ornithine carbamoyltransferase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00913	COG1568	R	Predicted methyltransferase	0	0	0	0	0	0	1	0	0	3	0	0	0	0	4	0	0
arCOG00914	COG4992	E	Ornithine/acetylornithine aminotransferase	1	3	4	2	1	1	1	3	2	3	3	1	5	1	4	1	0
arCOG00915	COG0160	E	4-aminobutyrate aminotransferase or related aminoti	3	3	5	1	1	1	0	3	0	0	1	0	3	0	4	3	0
arCOG00916	COG0160	E	4-aminobutyrate aminotransferase or related aminoti	0	3	0	0	1	0	0	0	0	0	0	0	0	0	4	0	0
arCOG00917	COG0161	H	Adenosylmethionine-8-amino-7-oxononanoate amin	0	0	0	2	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG00918	COG0001	H	Glutamate-1-semialdehyde aminotransferase	2	3	4	2	1	1	1	4	2	3	3	1	5	1	0	3	0
arCOG00919	COG1591	L	Holliday junction resolvase - archaeal type	3	3	4	2	1	1	1	4	2	3	0	0	0	1	4	0	1
arCOG00920	COG1591	L	Holliday junction resolvase - archaeal type	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG00921	COG1318	K	Predicted transcriptional regulator	3	0	5	0	0	1	0	0	0	1	0	0	0	1	4	0	1
arCOG00922	COG1136	V	ABC-type antimicrobial peptide transport system, A	3	2	5	2	1	1	1	4	1	3	3	1	5	1	1	0	1
arCOG00923	COG1126	E	ABC-type polar amino acid transport system, ATPas	3	0	4	0	0	1	1	3	1	2	3	1	2	0	0	0	0
arCOG00924	COG0410	E	ABC-type branched-chain amino acid transport syste	2	1	4	1	1	1	1	3	0	1	1	0	0	0	0	0	0
arCOG00925	COG0411	E	ABC-type branched-chain amino acid transport syste	2	1	4	1	1	1	1	3	0	1	1	0	0	0	0	0	0
arCOG00926	COG0411	E	ABC-type branched-chain amino acid transport syste	1	0	3	0	1	1	1	3	0	0	0	0	0	0	0	0	0
arCOG00927	COG4674	R	Uncharacterized ABC-type transport system, ATPase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG00928	COG1628	L	Endonuclease V homolog	3	3	5	1	1	1	1	4	1	3	2	1	4	1	4	3	1
arCOG00929	COG1515	L	Deoxyinosine 3'endonuclease (endonuclease V)	3	3	5	0	1	1	1	4	0	0	1	1	1	1	4	3	1
arCOG00930	COG2896	H	Molybdenum cofactor biosynthesis enzyme	3	3	5	0	1	1	1	4	1	3	3	1	5	1	4	3	0
arCOG00931	COG0535	R	Radical SAM superfamily enzyme	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0

arCOG00932	COG2108	R	Uncharacterized conserved protein related to pyruva	2	3	4	0	0	1	1	4	0	3	3	1	5	1	4	0	0
arCOG00933	COG1964	R	Radical SAM superfamily enzyme	3	3	5	2	1	1	1	1	2	1	3	0	3	1	4	3	0
arCOG00934	COG1313	C	Radical SAM superfamily enzyme	3	0	5	0	1	1	1	0	1	1	2	1	4	1	3	0	0
arCOG00935	COG1180	O	Pyruvate-formate lyase-activating enzyme	0	0	0	0	0	0	0	0	1	0	1	0	0	1	0	0	0
arCOG00936	COG1180	O	Pyruvate-formate lyase-activating enzyme	2	0	4	0	1	1	1	0	0	0	0	0	1	1	1	0	0
arCOG00937	COG1180	C	Radical SAM superfamily enzyme fused to ferredox	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
arCOG00938	COG0535	R	Radical SAM superfamily enzyme	3	3	5	1	0	1	1	3	0	1	3	1	5	1	4	3	1
arCOG00939	COG0641	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0
arCOG00940	COG0535	R	Radical SAM superfamily enzyme	1	0	1	0	0	1	1	0	1	0	0	0	2	1	2	0	0
arCOG00941	COG0535	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	0	0	1	5	0	1	0	0
arCOG00942	COG0535	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	0	0	0	5	1	0	0	0
arCOG00943	COG0535	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG00944	COG0535	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG00945	COG0641	R	Radical SAM superfamily enzyme	0	1	0	0	0	0	1	0	2	1	3	1	4	0	3	0	0
arCOG00946	COG1180	O	Pyruvate-formate lyase-activating enzyme	3	3	5	2	1	1	1	0	2	3	3	1	5	1	4	3	1
arCOG00947	COG1180	O	Pyruvate-formate lyase-activating enzyme	2	0	4	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG00948	COG1180	O	Pyruvate-formate lyase-activating enzyme	0	0	0	0	0	0	0	0	0	1	2	0	3	0	0	0	0
arCOG00949	COG1180	O	Pyruvate-formate lyase-activating enzyme	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00950	COG1625	C	Fe-S oxidoreductase, related to NifB/MoaA family	0	0	0	0	0	0	0	0	2	3	3	1	5	1	3	0	0
arCOG00951	COG2100	R	Radical SAM superfamily enzyme	3	1	4	0	0	1	1	0	0	3	0	1	0	1	4	0	0
arCOG00952	COG1180	O	Pyruvate-formate lyase-activating enzyme	2	0	2	0	0	1	1	0	2	3	2	1	5	1	4	0	1
arCOG00953	COG0731	J	Homolog of Wybutosine (yW) biosynthesis enzyme.	1	0	1	0	0	0	1	0	0	1	3	0	5	1	3	1	0
arCOG00954	COG2896	H	Molybdenum cofactor biosynthesis enzyme	0	0	1	0	0	0	0	0	1	1	0	0	0	0	2	0	0
arCOG00955	COG0535	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	1	0	0	3	0	0	4	1	4	0	0
arCOG00956	COG0535	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG00957	COG0535	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG00958	COG1145	C	Ferredoxin	0	0	0	0	0	0	0	0	2	3	3	1	4	0	4	3	0
arCOG00959	COG1146	C	Ferredoxin	0	0	0	0	0	1	1	0	2	3	3	0	3	1	4	1	0
arCOG00960	COG1146	C	Ferredoxin	0	0	0	0	0	0	0	0	1	2	0	0	4	0	0	0	0
arCOG00961	COG1145	C	Ferredoxin	2	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00962	COG0479	C	Succinate dehydrogenase/fumarate reductase, Fe-S p	2	3	5	2	1	1	1	4	0	0	0	0	1	0	0	3	0
arCOG00963	COG0479	C	Succinate dehydrogenase/fumarate reductase, Fe-S p	0	0	0	0	0	0	0	0	2	3	3	0	0	1	0	0	0
arCOG00964	COG1150	C	Heterodisulfide reductase, subunit C	0	0	0	0	0	1	1	0	2	3	3	1	5	1	0	0	0
arCOG00965	COG1150	C	Heterodisulfide reductase, subunit C	0	3	0	0	0	0	0	0	1	0	0	1	3	0	0	0	0
arCOG00966	COG1150	C	Heterodisulfide reductase, subunit C	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00967	COG2419	J	tRNA m(1)G methyltransferase	2	3	4	0	0	0	1	0	0	0	0	0	0	1	4	0	1
arCOG00968	COG2428	S	Uncharacterized conserved protein	3	0	1	0	0	0	0	0	0	0	0	0	0	1	4	0	0
arCOG00969	COG2248	R	Predicted hydrolase (metallo-beta-lactamase superfa	3	3	5	0	0	1	1	0	0	1	0	0	3	1	4	0	1
arCOG00970	COG0638	O	20S proteasome, alpha and beta subunit	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00971	COG0638	O	20S proteasome, alpha and beta subunit	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00972	COG1056	H	Nicotinamide mononucleotide adenylyltransferase	3	3	5	2	1	1	1	4	2	3	3	1	5	0	4	3	1
arCOG00973	COG0144	J	tRNA or rRNA cytosine-C5-methylase	3	3	5	0	1	1	1	4	0	3	0	1	1	1	4	0	1
arCOG00974	COG0144	J	tRNA or rRNA cytosine-C5-methylase	3	0	0	0	0	0	1	0	0	0	0	0	0	1	4	0	0
arCOG00975	COG0144	J	tRNA or rRNA cytosine-C5-methylase	2	3	5	0	0	0	0	0	0	0	0	0	0	1	4	0	0
arCOG00976	COG2518	O	Protein-L-isoaspartate carboxylmethyltransferase	3	3	4	0	0	1	1	4	1	3	2	1	5	1	4	0	0
arCOG00977	COG2242	H	Precorrin-6B methylase 2	0	3	2	2	0	0	1	4	2	3	3	0	5	1	0	3	0
arCOG00978	COG2519	J	tRNA(1-methyladenosine) methyltransferase or rela	3	3	5	2	1	1	1	4	2	3	3	1	1	1	4	3	1
arCOG00979	COG4122	R	Predicted O-methyltransferase	1	0	0	2	0	0	0	3	0	0	0	0	1	0	0	0	0
arCOG00980	COG1047	O	FKBP-type peptidyl-prolyl cis-trans isomerase 2	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00981	COG1047	O	FKBP-type peptidyl-prolyl cis-trans isomerase 2	0	0	0	0	0	0	0	3	0	3	3	1	5	0	1	0	0
arCOG00982	COG0371	C	Glycerol dehydrogenase or related enzyme	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG00983	COG0337	E	3-dehydroquinate synthetase	1	3	4	0	0	0	0	0	0	0	0	0	0	0	3	3	0
arCOG00984	COG1454	C	Alcohol dehydrogenase, class IV	2	3	2	2	0	0	1	2	1	1	2	1	3	0	4	2	0
arCOG00985	COG2016	J	Predicted RNA binding protein (contains PUA doma	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00986	COG0144	J	RNA methylase associated PUA domain	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0
arCOG00987	COG0130	J	Pseudouridine synthase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG00988	COG0144	J	RNA methylase associated PUA domain	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG00989	COG0343	J	Queuine/archaeosine tRNA-ribosyltransferase	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	1
arCOG00990	COG1549	J	Queuine tRNA-ribosyltransferase, contain PUA dom	0	0	1	0	0	0	1	3	2	3	3	1	5	1	4	3	1
arCOG00991	COG1370	O	Prefoldin, molecular chaperone implicated in de nov	3	3	5	2	1	0	1	3	2	3	3	1	5	1	4	3	1
arCOG00993	COG1374	J	Protein involved in ribosomal biogenesis, contains P	3	3	0	0	0	0	1	0	0	3	0	1	0	1	4	0	1
arCOG00995	COG1549	J	Queuine tRNA-ribosyltransferase related protein	1	2	0	0	0	0	0	0	0	0	3	1	4	0	0	0	0
arCOG00996	COG0343	J	Queuine/archaeosine tRNA-ribosyltransferase	1	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG00997	COG0343	J	Queuine/archaeosine tRNA-ribosyltransferase	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG00998	COG1958	K	Small nuclear ribonucleoprotein (snRNP) homolog	3	3	5	2	1	1	1	4	2	2	3	1	5	1	4	3	1
arCOG00999	COG1958	K	Small nuclear ribonucleoprotein (snRNP) homolog	2	3	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01000	COG0006	E	Xaa-Pro aminopeptidase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01001	COG0024	J	Methionine aminopeptidase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01002	COG0006	E	Xaa-Pro aminopeptidase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01003	COG0006	E	Xaa-Pro aminopeptidase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01004	COG2421	C	Predicted acetamidase/formamidase	1	3	0	0	0	1	0	3	0	0	0	0	0	0	3	1	0
arCOG01005	COG0803	P	ABC-type metal ion transport system, periplasmic c	3	0	4	2	1	1	1	3	1	0	3	1	5	0	4	0	0
arCOG01006	COG1108	P	ABC-type Mn2+/Zn2+ transport system, permease c	3	0	4	2	1	1	1	3	1	0	3	1	5	0	4	0	0
arCOG01007	COG0609	P	ABC-type Fe3+-siderophore transport system, perm	3	3	5	0	1	0	1	4	0	3	3	1	5	0	4	3	0
arCOG01008	COG0864	K	Transcriptional regulator, CopG/Arc/MetJ family (D	3	3	4	2	0	1	1	4	2	3	3	1	5	1	4	0	0
arCOG01009	COG3609	K	Predicted transcriptional regulators containing the C	3	2	5	0	1	0	1	4	0	0	3	0	0	0	4	0	0
arCOG01010	COG2161	K	Antitoxin (DNA-binding domain) of toxin-antitoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01011	COG3609	K	Predicted transcriptional regulators containing the C	0	0	0	0	0	0	0	0	0	1	0	0	0	0	3	0	0
arCOG01012	COG3609	K	Predicted transcriptional regulators containing the C	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01013	COG4352	J	Protein containg a domain similar to ribosomal prote	3	2	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01015	COG1258	J	Predicted pseudouridylate synthase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01016	COG1460	K	DNA-directed RNA polymerase, subunit F (rpoF)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01018	COG0565	J	rRNA methylase	3	3	1	0	0	1	1	4	2	3	3	1	5	1	1	3	1
arCOG01019	COG4080	R	SpoU rRNA Methylase family enzyme	3	3	5	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG01020	COG0683	E	ABC-type branched-chain amino acid transport syst	1	0	3	0	1	1	1	3	0	0	1	0	0	0	0	0	0
arCOG01021	COG0683	E	ABC-type branched-chain amino acid transport syst	2	1	4	1	1	1	1	4	0	1	2	0	0	0	0	0	0
arCOG01022	COG0683	E	ABC-type branched-chain amino acid transport syst	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01023	COG0683	E	ABC-type branched-chain amino acid transport syst	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01024	COG0683	E	ABC-type branched-chain amino acid transport syst	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01025	COG1685	E	Archaeal shikimate kinase	1	3	4	2	1	1	1	4	2	3	1	1	5	1	3	3	0
arCOG01026	COG1907	R	Predicted sugar kinase	2	3	0	0	1	0	1	3	2	3	3	1	5	1	4	0	0
arCOG01027	COG0083	E	Homoserine kinase	2	3	4	2	1	1	0	4	0	3	0	1	0	1	4	3	0
arCOG01028	COG1577	I	Mevalonate kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	0	0
arCOG01029	COG0153	G	Galactokinase	1	0	4	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01030	COG2605	R	Predicted kinase related to galactokinase and mevalk	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01031	COG3161	H	4-hydroxybenzoate synthetase (chorismate lyase)	0	0	0	0	0	0	1	0	1	3	0	0	4	1	0	0	0
arCOG01032	COG3890	I	Phosphomevalonate kinase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01033	COG0169	E	Shikimate 5-dehydrogenase	1	3	4	2	1	1	1	4	2	3	3	1	5	1	3	3	0
arCOG01034	COG1618	F	Predicted nucleotide kinase	3	3	5	0	1	1	1	0	1	1	2	0	2	1	4	3	0
arCOG01035	COG2423	E	Alanine dehydrogenase, mu-crystallin homolog	1	3	5	0	1	1	1	4	1	0	2	1	5	1	0	3	0
arCOG01036	COG0373	H	Glutamyl-tRNA reductase	2	3	4	2	0	0	1	4	2	3	3	1	5	1	0	3	0
arCOG01037	COG1102	F	Cytidylate kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01038	COG1936	F	Predicted nucleotide kinase (CMP/AMP kinase relat	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01039	COG2019	F	Archaeal adenylate kinase	2	3	4	2	1	0	0	1	2	3	3	0	0	1	4	3	1
arCOG01040	COG0529	P	Adenylylsulfate kinase or related kinase	3	0	1	2	0	0	1	1	0	1	0	1	1	0	1	0	0
arCOG01041	COG4088	F	Predicted nucleotide kinase	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG01042	COG1325	J	Predicted exosome subunit	3	3	5	2	1	1	1	4	2	3	0	1	5	1	4	0	1
arCOG01043	COG1931	S	Uncharacterized protein conserved in archaea	3	3	5	2	1	1	0	4	2	3	0	0	5	1	4	0	0
arCOG01044	COG1648	H	Siroheme synthase (precorrin-2 oxidase/ferrochelata	2	2	4	2	0	0	1	4	2	3	3	1	4	1	0	2	0
arCOG01045	COG0237	H	Dephospho-CoA kinase	3	3	5	2	0	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01046	COG0563	F	Adenylate kinase or related kinase	1	0	1	0	0	1	1	4	0	0	0	1	5	0	4	0	0
arCOG01047	COG0703	E	Shikimate kinase	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG01048		S	Uncharacterized conserved protein	1	0	5	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG01049	COG2876	E	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAI	1	3	4	0	0	0	0	0	0	0	0	0	0	0	3	3	0
arCOG01050	COG2089	M	Sialic acid synthase	0	0	0	1	0	0	0	1	0	2	1	0	2	0	0	0	0
arCOG01051	COG3958	G	Transketolase, C-terminal subunit	1	3	4	2	0	0	0	0	0	3	0	0	0	0	3	3	0
arCOG01052	COG0022	C	Pyruvate/2-oxoglutarate dehydrogenase complex, de	1	1	2	0	1	0	0	3	0	0	0	1	0	0	0	3	0
arCOG01053	COG3959	G	Transketolase, N-terminal subunit	1	3	4	1	0	0	0	0	0	3	0	0	0	0	3	3	0
arCOG01054	COG1071	C	Pyruvate/2-oxoglutarate dehydrogenase complex, de	1	1	2	0	1	0	0	3	0	0	0	1	0	0	0	3	0
arCOG01055	COG3432	K	Predicted transcriptional regulator	2	3	4	2	1	0	1	0	0	1	1	0	5	0	0	3	0
arCOG01057	COG1733	K	Predicted transcriptional regulator	1	3	3	1	1	0	1	4	1	3	3	1	4	0	0	3	0
arCOG01059	COG3432	K	Predicted transcriptional regulator	0	0	0	0	0	0	1	0	0	0	0	1	5	0	0	0	0
arCOG01060	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	1	0	0	0	1	0	0	0	0	1	5	1	0	0	0
arCOG01061	COG3432	K	Predicted transcriptional regulator	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01062	COG3432	K	Predicted transcriptional regulator	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01063	COG3432	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01064	COG0446	R	NAD(FAD)-dependent dehydrogenase	2	3	4	1	1	1	1	1	0	0	0	0	0	0	0	3	0
arCOG01065	COG0446	R	NAD(FAD)-dependent dehydrogenase	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	3	1

arCOG01066	COG0446	R	NAD(FAD)-dependent dehydrogenase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01067	COG1252	C	NADH dehydrogenase, FAD-containing subunit	1	3	1	2	0	0	0	4	0	0	0	0	1	0	0	1	0
arCOG01068	COG1249	C	Pyruvate/2-oxoglutarate dehydrogenase complex, di	3	3	4	0	1	0	1	4	2	3	3	1	5	1	0	3	0
arCOG01069	COG0446	R	CoA-dependent NAD(P)H Sulfur Oxidoreductase	1	3	5	0	0	1	1	3	2	3	0	1	4	1	4	3	0
arCOG01070	COG0446	R	NAD(FAD)-dependent dehydrogenase	0	3	0	0	0	0	1	4	0	0	0	0	1	0	3	0	0
arCOG01071	COG0446	R	NAD(FAD)-dependent dehydrogenase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01072	COG0494	L	NUDIX family hydrolase	1	3	4	2	1	0	1	4	0	0	0	0	0	0	0	3	0
arCOG01073	COG0494	L	NUDIX family hydrolase	3	3	4	1	1	1	0	4	0	0	3	0	0	0	0	0	0
arCOG01074	COG0494	L	NUDIX family hydrolase	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01075	COG1051	F	NUDIX family hydrolase	3	3	5	0	1	1	1	2	2	3	0	1	5	1	4	1	0
arCOG01076	COG2816	L	NTP pyrophosphohydrolase containing a Zn-finger,	0	0	0	0	0	0	0	0	1	0	1	0	4	0	0	0	0
arCOG01077	COG0494	L	NUDIX family hydrolase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01078	COG0494	L	NUDIX family hydrolase	0	0	3	2	1	0	0	4	2	0	2	1	3	0	0	2	0
arCOG01080	COG0494	L	NUDIX family hydrolase	0	0	3	0	0	0	0	3	0	0	0	0	3	0	0	0	0
arCOG01081	COG1443	I	Isopentenyldiphosphate isomerase	0	0	0	2	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01082	COG0494	L	NUDIX family hydrolase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01083	COG0494	L	NUDIX family hydrolase	2	0	0	0	0	0	0	3	0	0	0	0	2	0	0	0	0
arCOG01084	COG1694	R	Predicted pyrophosphatase	3	3	3	0	1	1	1	1	0	0	0	1	4	1	4	1	0
arCOG01085	COG1646	R	Predicted phosphate-binding enzyme, TIM-barrel fo	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01086	COG0159	E	Tryptophan synthase alpha chain	1	3	4	2	1	0	1	4	2	3	3	1	5	1	3	3	0
arCOG01087	COG0149	G	Triosephosphate isomerase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01088	COG0134	E	Indole-3-glycerol phosphate synthase	1	3	4	2	1	0	1	4	2	3	3	1	5	1	3	3	0
arCOG01089	COG0352	H	Thiamine monophosphate synthase	0	0	1	0	1	0	1	3	1	2	3	1	3	0	3	3	0
arCOG01090	COG0800	G	2-keto-3-deoxy-6-phosphogluconate aldolase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01091	COG1814	S	Uncharacterized membrane protein	2	3	4	0	1	1	1	1	2	3	0	0	2	1	0	0	0
arCOG01093	COG2406	R	Protein distantly related to bacterial ferritins	1	2	2	2	1	0	0	0	1	2	1	0	2	0	2	0	0
arCOG01094	COG2193	P	Bacterioferritin (cytochrome b1)	1	0	0	0	0	1	0	0	1	0	0	1	2	0	0	0	0
arCOG01095	COG1528	P	Ferritin	0	0	0	2	0	0	1	0	2	2	1	0	4	0	2	0	0
arCOG01096	COG1814	S	Uncharacterized membrane protein	3	3	5	0	1	1	0	0	1	0	1	0	0	0	4	3	0
arCOG01097	COG1592	C	Rubrerythrin	1	3	2	0	0	1	1	0	2	3	3	1	5	1	3	0	0
arCOG01098		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG01099	COG4802	C	Ferredoxin-thioredoxin reductase, catalytic subunit	0	0	0	0	0	0	1	0	0	0	3	1	4	0	0	0	0
arCOG01100	COG4802	C	Ferredoxin-thioredoxin reductase, catalytic subunit f	0	0	0	0	0	0	1	0	1	0	2	1	4	0	0	0	0
arCOG01101	COG0783	P	DNA-binding ferritin-like protein (oxidative damag	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01102	COG1633	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	3	0	4	0	0
arCOG01103	COG1633	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01104	COG1633	S	Ferritin-like domain	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG01105	COG1633	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01106		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01107	COG0624	E	Acetylornithine deacetylase/Succinyl-diaminopimel	3	3	5	2	1	1	1	3	0	3	3	1	1	1	4	3	1
arCOG01108	COG1473	R	Metal-dependent amidase/aminoacylase/carboxypep	0	1	1	0	0	1	0	4	0	0	0	0	3	0	4	3	0
arCOG01109	COG0624	E	Acetylornithine deacetylase/Succinyl-diaminopimel	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG01110	COG0624	E	Acetylornithine deacetylase/Succinyl-diaminopimel	0	3	0	2	1	0	0	0	0	0	0	1	0	0	0	1	0
arCOG01111	COG0574	G	Phosphoenolpyruvate synthase/pyruvate phosphate	2	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01112	COG0469	G	PEP-utilising enzyme associated, "swivelling" beta/l	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG01113	COG1080	G	Phosphoenolpyruvate-protein kinase (PTS system E	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01114	COG0574	G	Phosphoenolpyruvate synthase/pyruvate phosphate	1	2	0	1	0	0	0	1	0	0	0	1	2	0	0	0	0
arCOG01115	COG1571	R	Predicted DNA-binding protein containing a Zn-ribt	3	3	5	2	1	0	1	4	2	3	3	1	5	1	4	3	0
arCOG01116	COG1571	R	Predicted DNA-binding protein containing a Zn-ribt	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG01117	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	3	3	5	2	1	0	1	3	0	0	0	1	4	0	4	2	1
arCOG01118	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	0	5	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01119	COG4274	S	Uncharacterized conserved protein	0	1	1	0	0	0	1	0	0	0	1	0	1	0	0	0	0
arCOG01120	COG5431	S	Uncharacterized metal-binding protein	3	3	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01121	COG5431	S	Uncharacterized metal-binding protein	0	0	0	0	1	0	1	2	0	0	3	1	0	0	0	0	0
arCOG01122	COG0120	G	Ribose 5-phosphate isomerase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01123	COG0182	J	Translation initiation factor eIF-2B alpha subunit	3	3	5	2	1	1	1	0	2	3	3	1	5	1	4	3	0
arCOG01124	COG1184	J	Translation initiation factor 2B subunit, eIF-2B alph	2	0	1	0	1	0	1	4	0	1	3	1	5	0	4	0	0
arCOG01125	COG1184	J	Translation initiation factor 2B subunit, eIF-2B alph	2	0	4	0	0	1	0	0	0	0	0	0	0	0	4	1	0
arCOG01126	COG1184	J	Translation initiation factor 2B subunit, eIF-2B alph	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG01127	COG1184	J	Translation initiation factor 2B subunit, eIF-2B alph	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01128	COG0819	K	Transcriptional activator TenA	2	3	4	0	0	0	0	3	0	0	0	0	0	0	3	3	0
arCOG01129	COG0819	K	Transcriptional activator TenA	0	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01130	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01131	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	0	0	2	2	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01132	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG01133	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	0	0	0	0	0	0	1	0	2	3	3	1	5	0	0	0	0
arCOG01134	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01135	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG01136	COG0073	R	EMAP domain RNA-binding protein	3	3	5	1	1	1	0	1	0	0	0	0	0	0	4	3	0
arCOG01137	COG0824	R	Thioesterase superfamily enzyme	1	3	3	0	0	0	0	3	2	2	0	0	4	0	0	2	0
arCOG01138	COG1310	R	Predicted metal-dependent protease of the PAD1/JA	1	2	3	2	1	1	0	3	0	0	0	1	0	0	4	0	0
arCOG01139	COG1310	R	Predicted metal-dependent protease of the PAD1/JA	0	0	0	2	1	0	1	4	2	0	3	1	5	1	4	3	0
arCOG01140		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG01141	COG0622	R	Predicted phosphoesterase	3	0	5	0	0	1	1	4	2	3	1	1	5	1	4	0	0
arCOG01142	COG1409	R	Predicted phosphohydrolase	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01143	COG0639	T	Serine/threonine protein phosphatase PP2A family	3	3	5	0	1	1	1	2	0	0	0	0	3	0	0	1	0
arCOG01144	COG1409	R	Predicted phosphohydrolase	3	0	4	0	0	0	0	0	0	0	0	1	0	0	0	1	0
arCOG01145	COG2129	R	Icc family phosphoesterase	3	2	5	0	1	1	1	1	2	3	3	1	5	1	4	0	1
arCOG01147	COG1409	R	Predicted phosphohydrolase	3	3	1	0	0	1	1	0	0	0	0	1	0	0	0	0	0
arCOG01148	COG0639	T	Serine/threonine protein phosphatase PP2A family	3	0	0	0	0	1	1	3	0	1	0	1	3	1	4	3	0
arCOG01149		R	Calcineurin-like phosphoesterase	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01150	COG1407	R	Predicted ICC-like phosphoesterase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01151	COG2908	S	Uncharacterized protein conserved in bacteria	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG01153	COG1409	R	Predicted phosphohydrolase	0	0	0	1	1	0	1	2	2	0	0	0	4	1	4	0	0
arCOG01154	COG4186	R	Predicted phosphoesterase or phosphohydrolase	0	1	0	0	0	0	0	2	0	1	0	1	1	0	0	0	0
arCOG01156	COG1408	R	Calcineurin-like phosphohydrolase	0	0	3	0	1	1	0	0	2	0	1	0	1	0	0	0	0
arCOG01157	COG1408	R	Calcineurin-like phosphohydrolase	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG01158	COG0560	E	Phosphoserine phosphatase	2	0	3	2	0	1	1	4	0	3	0	1	5	1	4	3	0
arCOG01159	COG1340	S	Uncharacterized archaeal coiled-coil protein	3	3	5	1	1	1	1	4	2	0	3	1	5	1	4	3	1
arCOG01161	COG4030	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	2	0	0	0	0	1	0	0	0
arCOG01162	COG1340	S	Uncharacterized archaeal coiled-coil protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG01163	COG0473	C	Isocitrate/isopropylmalate dehydrogenase	0	3	4	2	1	1	1	3	2	3	3	1	5	1	4	1	0
arCOG01164	COG0538	C	Isocitrate dehydrogenase	1	3	4	0	0	0	1	4	0	0	0	0	0	0	1	3	0
arCOG01165	COG1389	L	DNA topoisomerase VI, subunit B	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	0	1
arCOG01166	COG0323	L	DNA mismatch repair enzyme (predicted ATPase)	0	0	0	0	0	0	0	4	0	0	3	0	5	0	0	0	0
arCOG01167	COG1529	C	Aerobic-type carbon monoxide dehydrogenase, larg	2	3	3	0	1	0	0	2	0	0	0	0	0	0	0	1	0
arCOG01168	COG4948	M	L-alanine-DL-glutamate epimerase or related enzym	3	3	2	0	0	1	1	4	0	0	0	0	0	1	0	3	0
arCOG01169	COG0148	G	Enolase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01170	COG0148	G	Enolase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	4	0	0
arCOG01171	COG0467	T	RecA-superfamily ATPase implicated in signal trans	3	3	5	0	1	1	1	2	1	1	2	1	5	1	4	0	1
arCOG01172		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	3	0	0	2	1	0	0	0	0	0
arCOG01173	COG0467	T	RecA-superfamily ATPase implicated in signal trans	1	0	0	0	1	0	1	3	0	0	0	0	1	0	3	0	0
arCOG01174	COG0467	T	RecA-superfamily ATPase implicated in signal trans	2	0	4	0	0	0	1	2	1	0	0	1	2	0	3	0	0
arCOG01175	COG0467	T	RecA-superfamily ATPase implicated in signal trans	0	0	0	0	0	0	1	2	0	0	2	1	1	0	0	0	0
arCOG01176	COG0467	T	RecA-superfamily ATPase implicated in signal trans	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01177	COG0467	T	RecA-superfamily ATPase implicated in signal trans	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01178	COG0467	T	GvpD gas vesicle protein, contains RecA/KaiC fami	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2	0
arCOG01179	COG0361	J	Translation initiation factor 1 (IF-1)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01180	COG1718	T	Serine/threonine protein kinase involved in cell cycl	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01181	COG0478	T	RIO-like serine/threonine protein kinase fused to N-	3	3	5	0	0	0	1	4	0	3	3	1	5	1	4	0	1
arCOG01182	COG2112	T	Predicted Ser/Thr protein kinase	2	3	5	2	1	0	1	0	0	3	0	0	0	0	4	0	1
arCOG01183	COG0533	L	Iron containing AP-endonuclease	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01185	COG3642	T	Mn2+-dependent serine/threonine protein kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01186	COG3642	T	Mn2+-dependent serine/threonine protein kinase	2	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG01187	COG0068	O	Hydrogenase maturation factor	2	0	3	0	1	1	1	0	2	3	3	1	3	1	4	0	0
arCOG01188	COG2192	O	Predicted carbamoyl transferase, NodU family	0	1	0	1	0	0	0	0	0	3	0	0	0	1	4	0	1
arCOG01189	COG0661	R	Predicted unusual protein kinase	0	3	0	2	0	0	0	4	2	0	2	0	4	0	0	3	0
arCOG01190	COG1718	T	Serine/threonine protein kinase involved in cell cycl	0	0	0	0	0	0	0	4	1	0	0	1	0	0	0	0	0
arCOG01191	COG2250	S	HEPN domain containing protein	2	3	5	0	1	1	1	0	0	1	2	1	0	1	4	0	0
arCOG01192	COG2250	S	HEPN domain containing protein	0	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01193	COG2250	S	HEPN domain containing protein	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01194	COG2250	S	HEPN domain containing protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01195	COG1708	R	Predicted nucleotidyltransferase	1	0	3	0	0	1	0	0	0	1	2	1	0	0	3	0	0
arCOG01197	COG1708	R	Predicted nucleotidyltransferase	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01198	COG1708	R	Predicted nucleotidyltransferase	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG01199	COG1708	R	Predicted nucleotidyltransferase	1	0	5	0	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01200	COG1708	R	Predicted nucleotidyltransferase	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01201	COG1708	R	Predicted nucleotidyltransferase	0	1	0	0	0	0	1	0	0	1	1	0	1	0	2	0	0

arCOG01202	COG1708	R	Predicted nucleotidyltransferase	0	2	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0
arCOG01203	COG1708	R	Predicted nucleotidyltransferase	0	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01204	COG1708	R	Predicted nucleotidyltransferase	1	3	4	0	1	1	1	0	0	0	0	0	0	0	2	0	1
arCOG01205	COG1708	R	Predicted nucleotidyltransferase	3	3	4	0	1	1	1	0	0	0	0	0	0	1	4	0	0
arCOG01206	COG1669	R	Nucleotidyltransferase	0	0	0	0	0	0	1	0	0	2	3	0	3	0	1	0	0
arCOG01207		K	Predicted transcriptional regulator, MarR family	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG01208	COG1708	R	Predicted nucleotidyltransferase	0	0	0	0	1	0	0	1	0	0	1	1	1	0	1	0	0
arCOG01210		R	Predicted nucleotidyltransferase and HTH domain	0	0	1	0	0	0	0	2	1	2	0	1	2	0	0	0	0
arCOG01211	COG1708	R	Predicted nucleotidyltransferase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01212		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01213	COG0561	R	HAD superfamily hydrolase	3	3	5	2	0	0	1	4	1	0	3	1	5	1	4	3	0
arCOG01214	COG0561	R	HAD superfamily hydrolase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01215	COG3769	R	Predicted hydrolase (HAD superfamily)	2	0	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0
arCOG01216	COG1877	G	Trehalose-6-phosphatase	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	3	0
arCOG01217	COG1400	U	Signal recognition particle 19 kDa protein	3	2	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01218	COG0526	O	Thiol-disulfide isomerase or thioredoxin	3	3	5	0	1	1	1	0	0	0	0	0	0	0	4	3	1
arCOG01219	COG1867	J	N2,N2-dimethylguanosine tRNA methyltransferase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01220	COG2264	J	Ribosomal protein L11 methylase	0	0	0	0	0	0	0	0	2	2	2	1	4	0	0	0	0
arCOG01221	COG1986	F	Inosine/xanthosine triphosphatase	3	3	5	0	1	1	1	0	1	3	0	1	0	1	1	3	0
arCOG01222	COG0615	M	Cytidylyltransferase fused to conserved domain of I	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01223	COG1019	R	Predicted nucleotidyltransferase	0	0	5	2	0	1	1	4	2	3	3	1	5	1	4	0	0
arCOG01224	COG1849	S	Uncharacterized protein conserved in archaea	3	3	5	0	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG01225	COG1100	R	GTPase SAR1 or related small G protein	3	3	5	2	1	1	1	0	0	0	0	0	0	0	4	3	0
arCOG01226	COG1703	E	Putative periplasmic protein kinase ArgK or related	1	3	0	2	0	0	1	4	0	0	0	0	0	0	4	3	0
arCOG01227	COG0552	U	Signal recognition particle GTPase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01228	COG0541	U	Signal recognition particle GTPase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01229	COG2403	R	Predicted GTPase	3	0	4	0	1	1	0	0	0	0	0	0	1	0	4	0	0
arCOG01230	COG2403	R	Predicted GTPase	0	0	0	0	0	0	0	0	2	0	0	0	0	1	4	0	0
arCOG01231	COG0378	O	Ni2+-binding GTPase involved in regulation of expr	1	1	0	1	0	0	1	3	2	3	3	1	5	1	0	0	0
arCOG01232	COG0523	R	GTPase (G3E type)	0	0	0	0	0	0	0	0	0	1	0	0	4	0	0	0	0
arCOG01233	COG0523	R	GTPase (G3E type)	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01234	COG0523	R	GTPase (G3E type)	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01235	COG1622	C	Heme/copper-type cytochrome/quinol oxidase, subu	1	3	2	0	1	0	0	4	0	0	0	0	0	0	0	1	0
arCOG01236	COG1622	C	Heme/copper-type cytochrome/quinol oxidase, subu	1	3	3	2	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG01237	COG0843	C	Heme/copper-type cytochrome/quinol oxidase, subu	1	3	2	0	1	0	0	4	0	0	0	0	0	0	0	1	0
arCOG01238	COG0843	C	Heme/copper-type cytochrome/quinol oxidase, subu	1	3	3	2	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01239	COG1901	S	Uncharacterized conserved protein	2	0	4	0	0	0	1	4	0	3	3	1	5	1	4	0	0
arCOG01240	COG1901	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01241	COG0582	L	Integrase	3	3	1	2	1	1	1	4	2	3	3	1	4	0	4	3	0
arCOG01242	COG0582	L	Integrase	0	0	0	1	0	0	0	1	0	0	2	1	2	0	0	2	0
arCOG01243	COG4973	L	Site-specific recombinase XerC	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01244	COG4342	S	Uncharacterized protein conserved in archaea	3	2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG01245	COG0582	L	Integrase	0	0	0	2	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG01247	COG4974	L	Site-specific recombinase XerD	1	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
arCOG01248	COG0582	L	Integrase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01250	COG0582	L	Integrase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01251	COG0582	L	Integrase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01252	COG1012	C	NAD-dependent aldehyde dehydrogenase	2	3	4	1	1	1	0	4	1	3	3	1	5	1	2	3	0
arCOG01253	COG0014	E	Gamma-glutamyl phosphate reductase	0	0	0	0	0	0	0	2	0	0	0	0	4	0	0	0	0
arCOG01254	COG2872	R	Predicted metal-dependent hydrolase related to alany	3	2	5	0	1	1	0	0	0	0	0	1	5	0	4	3	0
arCOG01255	COG0013	J	Alanyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01256	COG2872	R	Predicted metal-dependent hydrolase related to alany	0	2	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01257	COG0459	O	Chaperonin GroEL (HSP60 family)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01258	COG0459	O	Chaperonin GroEL (HSP60 family)	0	0	0	0	0	0	0	4	0	0	3	0	4	0	0	0	0
arCOG01259	COG1028	I	Short-chain alcohol dehydrogenase	3	3	5	2	1	1	1	4	1	0	3	0	3	0	4	3	1
arCOG01260	COG1028	I	Short-chain alcohol dehydrogenase	2	3	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01261	COG1028	I	Short-chain alcohol dehydrogenase	0	1	1	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01262	COG1028	I	Short-chain alcohol dehydrogenase	0	3	4	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01263	COG0300	R	Short-chain dehydrogenase	0	3	2	2	1	0	0	2	0	0	0	0	1	0	2	0	0
arCOG01264	COG1028	I	Short-chain alcohol dehydrogenase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01265	COG4221	R	Short-chain alcohol dehydrogenase	0	0	0	2	0	0	0	4	0	0	0	0	0	0	1	0	0
arCOG01266	COG1028	I	Short-chain alcohol dehydrogenase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01267	COG1028	I	Short-chain alcohol dehydrogenase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01268	COG1758	K	DNA-directed RNA polymerase, subunit K/omega	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01269	COG0559	E	Branched-chain amino acid ABC-type transport syst	1	1	4	1	1	1	1	3	0	1	1	0	0	0	0	0	0
arCOG01270	COG0559	E	Branched-chain amino acid ABC-type transport syst	1	0	3	0	1	1	1	3	0	0	0	0	0	0	0	0	0
arCOG01271	COG0559	E	Branched-chain amino acid ABC-type transport syst	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG01272	COG0559	E	Branched-chain amino acid ABC-type transport syst	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01273	COG4177	E	ABC-type branched-chain amino acid transport syste	1	1	4	1	1	1	1	3	0	1	0	0	0	0	0	0	0
arCOG01274	COG4177	E	ABC-type branched-chain amino acid transport syste	1	0	3	0	1	1	1	3	0	0	1	0	0	0	0	0	0
arCOG01275	COG4177	E	ABC-type branched-chain amino acid transport syste	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01276	COG4177	E	ABC-type branched-chain amino acid transport syste	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01278	COG0183	I	Acetyl-CoA acetyltransferase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01279	COG0183	I	Acetyl-CoA acetyltransferase	1	3	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0
arCOG01280	COG0183	I	Acetyl-CoA acetyltransferase	1	3	1	0	1	0	1	0	0	0	0	0	0	0	0	3	0
arCOG01281	COG0183	I	Acetyl-CoA acetyltransferase	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01282	COG0183	I	Acetyl-CoA acetyltransferase	1	3	4	0	0	1	1	3	0	0	0	0	0	0	0	3	0
arCOG01283	COG1545	R	Predicted nucleic-acid-binding protein containing a	1	3	3	0	1	0	1	0	0	0	0	0	0	0	0	2	0
arCOG01284	COG1545	R	Predicted nucleic-acid-binding protein containing a	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01285	COG1545	V	Predicted nucleic-acid-binding protein containing a	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	0
arCOG01286	COG1545	R	Predicted nucleic-acid-binding protein containing a	0	0	1	0	0	0	1	4	0	0	0	0	0	0	0	0	0
arCOG01287	COG1545	R	Predicted nucleic-acid-binding protein containing a	1	3	1	0	1	0	1	0	0	0	0	0	0	0	0	3	0
arCOG01288	COG1545	R	Predicted nucleic-acid-binding protein containing a	1	3	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0
arCOG01289	COG1545	R	Predicted nucleic-acid-binding protein containing a	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01290	COG1533	L	DNA repair photolyase	3	3	5	0	0	1	1	0	1	1	1	1	4	0	4	2	0
arCOG01291	COG1533	L	DNA repair photolyase	3	0	4	0	0	1	0	0	0	0	0	0	0	1	0	0	0
arCOG01292	COG0493	E	NADPH-dependent glutamate synthase beta chain o	3	0	5	0	0	1	0	0	0	0	3	1	5	0	4	2	0
arCOG01293	COG0446	R	NAD(FAD)-dependent dehydrogenase	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG01294	COG0446	R	NAD(FAD)-dependent dehydrogenase	1	0	1	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG01295	COG0446	R	NAD(FAD)-dependent dehydrogenase	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01296	COG0492	O	Thioredoxin reductase	3	3	5	2	1	1	1	4	2	3	1	1	5	1	4	3	1
arCOG01297	COG3634	O	Alkyl hydroperoxide reductase, large subunit	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
arCOG01299	COG0446	R	NAD(FAD)-dependent dehydrogenase	1	3	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01300		R	Pyridine nucleotide-disulphide oxidoreductase and F	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01301	COG0492	O	Thioredoxin reductase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01302	COG1531	S	Uncharacterized protein conserved in archaea	3	3	5	0	0	1	1	0	1	3	2	1	1	1	4	0	0
arCOG01303	COG0509	E	Glycine cleavage system H protein (lipoate-binding)	3	3	0	0	1	1	0	3	0	0	0	0	0	0	4	3	0
arCOG01304	COG1637	L	Predicted nuclease of the RecB family	3	3	5	0	1	0	0	4	2	2	0	1	1	1	4	0	0
arCOG01305	COG1637	L	Topoisomerase DNA binding C4 zinc finger fused to	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01306	COG1222	O	ATP-dependent 26S proteasome regulatory subunit	3	3	0	0	0	0	1	4	2	3	3	1	5	1	4	0	1
arCOG01307	COG0464	O	ATPase of the AAA+ class	3	3	0	2	1	0	0	0	0	0	0	0	0	0	3	2	0
arCOG01308	COG0464	O	ATPase of the AAA+ class	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01310		S	Uncharacterized conserved protein	2	0	4	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG01311	COG0616	O	Periplasmic serine protease (ClpP class)	0	0	4	0	0	0	0	4	1	3	0	1	4	0	4	3	1
arCOG01312		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01313		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01314		S	Uncharacterized conserved membrane protein	1	0	1	0	0	0	0	2	0	2	3	1	0	0	4	0	0
arCOG01315		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01316	COG0591	E	Na+/proline symporter	2	3	1	1	0	0	1	4	2	2	3	0	5	0	4	3	0
arCOG01317	COG4147	R	Sodium:solute symporter	0	0	0	0	0	0	1	2	0	0	0	1	0	0	0	0	0
arCOG01318	COG4145	H	Na+/panthothenate symporter	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG01319	COG0591	E	Na+/proline symporter	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0
arCOG01320	COG0108	H	3,4-dihydroxy-2-butanone 4-phosphate synthase	3	3	3	2	0	0	1	4	2	3	3	1	4	1	0	1	0
arCOG01321	COG0807	H	GTP cyclohydrolase II	0	0	0	0	0	0	1	0	0	0	0	0	1	0	2	3	0
arCOG01322	COG1731	H	Archaeal riboflavin synthase	3	3	3	0	0	0	1	0	2	3	2	1	5	1	0	1	0
arCOG01323	COG0054	H	Riboflavin synthase beta-chain	3	3	3	2	0	1	1	4	2	3	3	1	5	1	2	1	0
arCOG01324	COG2820	F	Uridine phosphorylase	3	3	5	0	1	1	0	4	0	0	0	0	0	0	1	1	0
arCOG01325	COG0813	F	Purine-nucleoside phosphorylase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01327	COG0005	F	Purine nucleoside phosphorylase	3	3	5	2	0	1	1	2	2	3	3	1	5	1	4	3	0
arCOG01328	COG2386	O	ABC-type transport system involved in cytochrome	0	0	0	0	0	0	1	2	0	0	0	0	3	0	0	0	0
arCOG01329	COG2386	O	ABC-type transport system involved in cytochrome	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01330	COG2426	S	Predicted membrane protein	3	1	0	0	0	0	1	0	0	0	3	0	4	0	4	0	0
arCOG01331	COG0501	O	Zn-dependent protease with chaperone function	3	3	5	0	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01333	COG0501	O	Zn-dependent protease with chaperone function	0	2	4	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG01334	COG0501	O	Zn-dependent protease with chaperone function	0	0	0	0	0	1	0	3	0	0	0	0	0	0	1	1	0
arCOG01336	COG2078	S	Uncharacterized conserved protein	3	3	5	2	1	1	1	2	2	3	3	1	5	1	4	3	1
arCOG01337	COG0045	C	Succinyl-CoA synthetase, beta subunit	3	3	5	2	1	1	1	4	2	3	3	0	0	1	0	3	0
arCOG01338	COG1042	C	Acyl-CoA synthetase, ATP-grasp containing subunit	2	0	5	1	0	1	1	0	0	0	3	1	3	1	4	0	0

arCOG01339	COG0074	C	Succinyl-CoA synthetase, alpha subunit	3	3	5	2	1	1	1	4	2	3	3	0	0	1	0	3	0
arCOG01340	COG1042	C	Acyl-CoA synthetase (NDP forming)	2	2	5	2	1	1	1	3	1	3	3	1	4	1	4	3	0
arCOG01341	COG1730	O	Predicted prefoldin, molecular chaperone implicated	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01342	COG1382	O	Prefoldin, chaperonin cofactor	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01344	COG2238	J	Ribosomal protein S19E (S16A)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01345	COG3388	K	Predicted transcriptional regulator	0	0	0	0	0	0	1	4	0	0	3	1	5	1	0	3	0
arCOG01346	COG1534	J	Predicted RNA-binding protein containing KH dom	3	3	1	0	0	0	1	4	2	3	2	1	4	1	4	0	1
arCOG01347	COG1793	L	ATP-dependent DNA ligase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01348	COG0061	H	NAD kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01349	COG0483	G	Archaeal fructose-1,6-bisphosphatase or related enz	3	3	5	2	0	1	1	4	2	1	3	1	5	1	4	0	0
arCOG01350	COG3199	R	Predicted inorganic polyphosphate/ATP-NAD kinas	3	3	0	0	0	1	0	4	0	0	2	0	1	0	4	3	0
arCOG01351	COG0460	E	Homoserine dehydrogenase	1	3	4	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01352	COG0334	E	Glutamate dehydrogenase/leucine dehydrogenase	3	3	5	2	1	1	1	4	1	0	1	1	4	0	4	3	1
arCOG01354	COG2892	S	Uncharacterized protein conserved in archaea	3	0	3	0	0	0	1	4	2	0	3	1	5	0	0	0	0
arCOG01355	COG1032	C	Radical SAM superfamily enzyme	3	0	4	0	0	1	1	0	2	3	0	0	0	1	0	1	0
arCOG01356	COG1032	C	Radical SAM superfamily enzyme	3	2	4	0	1	1	0	0	1	3	3	1	5	1	4	2	1
arCOG01357	COG1032	C	Radical SAM superfamily enzyme	2	3	5	2	1	1	0	0	0	0	0	0	1	1	4	3	0
arCOG01358	COG0621	J	2-methylthioadenine synthetase	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	1
arCOG01359	COG1031	C	Radical SAM superfamily enzyme	3	0	4	0	0	0	1	4	0	3	3	1	4	1	4	0	0
arCOG01360	COG1244	R	MiaB family, Radical SAM enzyme	0	0	0	0	0	0	1	4	2	3	3	1	5	1	4	3	1
arCOG01361	COG1243	K	Histone acetyltransferase	1	3	4	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01362	COG1242	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG01363	COG1032	C	Radical SAM superfamily enzyme	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	3	0
arCOG01364	COG1032	C	Radical SAM superfamily enzyme	0	0	3	0	0	1	0	0	0	0	0	0	0	0	0	2	0
arCOG01365	COG1369	J	RNase P/RNase MRP subunit POP5	2	0	0	0	1	0	1	4	2	3	3	1	5	1	4	0	0
arCOG01366	COG1369	J	RNase P/RNase MRP subunit POP5	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01367	COG1091	M	dTDP-4-dehydrorhamnose reductase	1	3	2	0	0	1	1	1	2	1	2	1	5	0	2	2	0
arCOG01368	COG1091	M	dTDP-4-dehydrorhamnose reductase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01369	COG0451	M	Nucleoside-diphosphate-sugar epimerase	1	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01370	COG1087	M	UDP-glucose 4-epimerase	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG01371	COG1088	M	dTDP-D-glucose 4,6-dehydratase	1	3	0	1	0	1	1	0	2	1	2	1	5	0	2	2	0
arCOG01372	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	0	0	0	0	0	0	2	0	0	1	1	0	0	0	0
arCOG01373	COG1089	M	GDP-D-mannose dehydratase	0	0	1	1	0	0	1	0	2	1	1	1	4	0	0	0	0
arCOG01374	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0
arCOG01375	COG1086	M	Predicted nucleoside-diphosphate sugar epimerase	0	0	0	1	0	0	0	0	0	2	1	0	1	0	0	0	0
arCOG01376	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	1	0	0	0	0	2	2	0	0	0	0	0	0	0	0
arCOG01377	COG3379	S	Uncharacterized conserved protein	3	3	1	0	0	0	0	4	0	0	0	0	0	0	2	0	0
arCOG01378	COG1524	R	Uncharacterized protein of the AP superfamily	0	3	1	0	0	0	1	0	0	0	0	1	0	0	4	3	1
arCOG01379	COG1524	R	Uncharacterized protein of the AP superfamily	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG01380	COG3379	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01381	COG0463	M	Glycosyltransferase	2	3	4	0	1	0	0	3	1	2	2	1	4	0	4	3	1
arCOG01383	COG1216	R	Predicted glycosyltransferase	1	1	2	1	1	1	1	0	2	1	2	1	5	0	2	1	0
arCOG01384	COG0463	M	Glycosyltransferase	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0
arCOG01385	COG0463	M	Glycosyltransferase	0	0	2	0	0	0	0	0	2	0	2	1	2	0	1	0	0
arCOG01386	COG1215	M	Glycosyltransferase	0	0	0	0	0	1	0	1	1	0	2	0	0	0	0	0	0
arCOG01387	COG0463	M	Glycosyltransferase	0	0	0	0	0	0	1	4	0	0	0	0	0	0	0	0	0
arCOG01388	COG0463	M	Glycosyltransferase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01389	COG1215	M	Glycosyltransferase	1	3	5	1	1	1	1	2	1	0	3	1	4	1	4	3	0
arCOG01390	COG0463	M	Glycosyltransferase	0	0	0	2	1	0	0	0	1	0	0	0	0	0	0	0	0
arCOG01391	COG1215	M	Glycosyltransferase	1	3	5	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG01392	COG0381	M	UDP-N-acetylglucosamine 2-epimerase	0	0	1	1	0	1	0	2	2	3	2	1	4	0	4	0	0
arCOG01393	COG1819	G	Glycosyl transferase, related to UDP-glucuronosyltr	0	0	0	2	1	1	0	1	1	3	0	0	5	1	0	0	0
arCOG01394	COG0707	M	UDP-N-acetylglucosamine:LPS N-acetylglucosamir	2	3	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
arCOG01395	COG1817	R	Lipid-A-disaccharide synthase related glycosyltrans	2	0	5	2	1	1	0	0	2	3	1	1	4	0	4	0	0
arCOG01396		R	UDP-N-acetylglucosamine 2-epimerase, MurG fami	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG01397	COG0463	M	Glycosyltransferase	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01398	COG0463	M	Glycosyltransferase	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG01400	COG0500	Q	SAM-dependent methyltransferase	2	3	3	0	0	0	1	0	0	0	0	0	0	0	1	3	0
arCOG01401	COG0500	Q	SAM-dependent methyltransferase	0	1	3	0	0	0	0	0	0	0	1	0	1	0	0	1	0
arCOG01402	COG0500	Q	SAM-dependent methyltransferase	0	0	1	1	0	0	0	4	0	0	1	0	1	1	0	0	0
arCOG01403	COG0438	M	Glycosyltransferase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01405	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	1	0	0	1	1	1	0	0	0	0
arCOG01406	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG01407	COG0438	M	Glycosyltransferase	1	3	3	0	0	0	0	4	1	0	3	1	2	0	2	1	0
arCOG01408	COG0438	M	Glycosyltransferase	1	3	1	0	1	0	0	2	1	0	0	0	2	0	1	0	0
arCOG01409	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	2	1	1	0	2	0	1	1	0
arCOG01410	COG0438	M	Glycosyltransferase	0	0	0	0	1	0	0	1	0	1	2	0	3	0	2	0	0
arCOG01411	COG0438	M	Glycosyltransferase	0	1	3	0	0	0	0	0	0	0	2	0	4	0	2	3	0
arCOG01412	COG0438	M	Glycosyltransferase, fused to cupin domain	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG01413	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01414	COG0438	M	Glycosyltransferase	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01415	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG01416	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG01417	COG0438	M	Glycosyltransferase	1	3	3	0	0	0	1	0	0	0	0	0	0	0	0	1	0
arCOG01418	COG0438	M	Glycosyltransferase	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01419	COG0438	M	Glycosyltransferase	0	3	0	0	0	0	0	0	1	0	0	0	0	0	0	3	0
arCOG01420	COG0297	G	Glycogen synthase	1	3	4	0	0	0	0	0	0	3	0	0	0	0	4	0	0
arCOG01421	COG0058	G	Glucan phosphorylase	1	3	5	0	0	0	0	0	0	3	2	0	4	0	4	0	0
arCOG01422	COG5493	S	Uncharacterized conserved protein containing a coil	1	3	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01423	COG5493	S	Uncharacterized conserved protein containing a coil	1	0	3	0	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01424		S	Uncharacterized conserved protein	0	3	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01425		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG01426		S	Uncharacterized conserved protein	0	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01427		S	Uncharacterized conserved protein	0	1	4	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG01429		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01430	COG0031	E	Cysteine synthase	3	3	5	2	1	1	0	4	1	0	2	0	3	0	3	3	0
arCOG01431	COG1171	E	Threonine dehydratase	3	3	5	2	1	1	0	4	0	0	1	0	0	0	0	3	0
arCOG01432	COG1350	R	Predicted alternative tryptophan synthase beta-subu	2	3	5	0	1	1	1	0	1	0	2	1	5	0	4	3	0
arCOG01433	COG0133	E	Tryptophan synthase beta chain	0	0	0	2	0	0	1	4	2	3	3	1	5	1	3	0	0
arCOG01434	COG0498	E	Threonine synthase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01435	COG2515	E	1-aminocyclopropane-1-carboxylate deaminase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01436	COG0498	E	Threonine synthase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG01437	COG5551	V	CRISPR system related protein, RAMP superfamily	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01438	COG5551	V	CRISPR system related protein, RAMP superfamily	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01439	COG5551	V	CRISPR system related protein, RAMP superfamily	0	3	4	0	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01440	COG5551	V	CRISPR system related protein, RAMP superfamily	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01441		V	CRISPR system related protein, AF0070 family	1	0	2	0	0	0	0	0	0	1	0	0	0	0	1	0	0
arCOG01442	COG2254	L	Predicted HD superfamily hydrolase, possibly a nuc	1	2	1	0	0	1	0	0	0	1	0	0	0	0	1	0	0
arCOG01443	COG2254	L	Predicted HD superfamily hydrolase, possibly a nuc	2	2	4	0	1	0	1	0	0	0	0	0	0	0	3	0	0
arCOG01444	COG1203	V	CRISPR-associated helicase Cas3	3	2	4	1	1	1	1	0	0	1	0	0	1	0	4	0	0
arCOG01445	COG1203	V	CRISPR-associated helicase Cas3	0	0	0	0	0	0	1	1	2	2	1	1	5	0	3	0	1
arCOG01446	COG0640	K	Transcriptional regulator containing HTH domain, A	3	3	3	0	1	1	1	1	1	1	1	1	0	2	0	4	0
arCOG01448	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG01449		S	Uncharacterized conserved protein	0	0	0	1	0	0	0	4	0	2	2	1	1	0	0	0	0
arCOG01450	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01451	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01452	COG1518	V	CRISPR-associated protein Cas1	3	3	3	0	1	1	1	2	2	2	3	1	5	1	3	2	1
arCOG01453	COG1518	V	CRISPR-associated protein Cas1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0
arCOG01454		V	CRISPR-associated protein/domain	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG01455	COG1064	R	Zn-dependent alcohol dehydrogenase	3	3	4	2	1	0	0	3	0	0	0	0	3	0	0	3	0
arCOG01456	COG1062	C	Zn-dependent alcohol dehydrogenase	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01457	COG1064	R	Zn-dependent alcohol dehydrogenase	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01458	COG0604	C	NADPH:quinone reductase or related Zn-dependent	0	3	2	2	1	1	0	4	0	0	0	1	2	0	0	3	0
arCOG01459	COG1063	E	Threonine dehydrogenase or related Zn-dependent d	2	3	4	2	1	1	1	3	1	0	1	1	3	0	4	3	0
arCOG01460	COG1063	E	Threonine dehydrogenase or related Zn-dependent d	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG01461	COG2130	R	Putative NADP-dependent oxidoreductase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01462	COG1668	C	ABC-type Na+ efflux pump, permease component	3	3	3	0	1	1	0	0	1	1	0	1	3	0	4	0	0
arCOG01463	COG0842	V	ABC-type multidrug transport system, permease cor	1	3	1	0	1	1	1	0	2	0	2	1	4	1	3	0	0
arCOG01464		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0
arCOG01465	COG0842	V	ABC-type multidrug transport system, permease cor	3	3	4	0	1	1	1	2	0	0	0	0	1	0	4	0	0
arCOG01466		S	Uncharacterized conserved protein	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01467	COG0842	V	ABC-type multidrug transport system, permease cor	1	3	5	2	1	1	1	4	1	2	2	1	5	0	4	3	0
arCOG01468	COG0842	V	ABC-type multidrug transport system, permease cor	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01469	COG0842	V	ABC-type multidrug transport system, permease cor	0	3	5	0	0	0	0	0	0	0	0	0	0	0	2	3	0
arCOG01470	COG1668	C	ABC-type Na+ efflux pump, permease component	0	0	0	0	0	0	1	3	1	0	2	1	0	0	0	0	0
arCOG01471	COG3945	S	Hemerythrin HHE cation binding domain containing	1	1	3	2	1	0	0	0	0	0	0	1	3	0	0	0	0
arCOG01472	COG2461	S	Hemerythrin HHE cation binding domain containing	1	0	0	0	0	1	1	0	0	0	0	0	0	0	2	0	0
arCOG01474	COG0053	P	Predicted Co/Zn/Cd cation transporter	3	0	5	1	0	1	1	4	2	3	3	1	4	1	3	0	0

arCOG01475	COG0053	P	Predicted Co/Zn/Cd cation transporter	0	0	0	0	0	0	1	0	1	0	1	0	4	0	0	0	0
arCOG01476	COG0053	P	Predicted Co/Zn/Cd cation transporter	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01477	COG1230	P	Co/Zn/Cd efflux system component	0	3	1	1	0	0	0	1	0	0	0	0	3	0	3	0	0
arCOG01478	COG0053	P	Predicted Co/Zn/Cd cation transporter	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01479	COG0053	P	Predicted Co/Zn/Cd cation transporter	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01480	COG0053	P	Predicted Co/Zn/Cd cation transporter	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01481	COG1488	H	Nicotinic acid phosphoribosyltransferase	3	3	5	0	1	1	1	4	0	0	2	0	4	1	4	3	0
arCOG01482	COG0157	H	Nicotinate-nucleotide pyrophosphorylase	1	3	3	2	0	0	1	3	2	3	3	1	5	1	4	0	0
arCOG01483	COG0157	H	Nicotinate-nucleotide pyrophosphorylase	0	0	1	0	0	0	0	0	0	2	1	0	4	0	1	0	0
arCOG01484	COG1985	H	Pyrimidine reductase, riboflavin biosynthesis	3	3	4	2	0	0	1	4	2	3	3	1	5	1	0	1	0
arCOG01485	COG0117	H	Pyrimidine deaminase and reductase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG01486	COG1658	L	Ribonuclease M5 (contains TOPRIM domain)	0	0	0	1	1	1	1	0	1	1	0	1	5	0	4	2	0
arCOG01487	COG2131	F	Deoxycytidylate deaminase	0	0	0	2	0	0	1	0	0	0	1	1	5	0	4	3	0
arCOG01488	COG0590	F	Cytosine/adenosine deaminase	0	0	0	0	0	0	0	2	0	2	3	1	4	0	0	0	0
arCOG01489	COG1985	H	Pyrimidine reductase, riboflavin biosynthesis	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG01490	COG0262	H	Dihydrofolate reductase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01491	COG0243	C	Anaerobic dehydrogenase	2	3	4	0	1	1	1	4	1	3	3	1	2	1	4	2	0
arCOG01492	COG3383	R	Uncharacterized anaerobic dehydrogenase	0	3	0	0	0	0	0	2	1	0	1	0	1	0	0	3	0
arCOG01493	COG0243	C	Formate dehydrogenase alpha subunit, contains mol	0	0	1	0	0	0	1	1	0	0	0	0	1	0	0	0	0
arCOG01495	COG0243	C	Molybdopterin oxidoreductase	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01496	COG0243	C	Molybdopterin oxidoreductase, contains molybdopte	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG01497	COG5013	C	Nitrate reductase alpha subunit	1	0	2	0	1	0	0	1	0	0	0	0	0	0	0	0	0
arCOG01498	COG1029	C	Formylmethanofuran dehydrogenase subunit B	0	0	0	0	0	0	1	0	0	0	0	0	5	0	0	0	0
arCOG01499	COG1029	C	Formylmethanofuran dehydrogenase subunit B	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG01500	COG0437	C	Fe-S-cluster-containing hydrogenase component 1	3	3	4	0	1	1	1	3	0	0	1	1	3	0	2	0	0
arCOG01501	COG1140	C	Nitrate reductase beta subunit	1	0	2	0	1	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01502	COG1142	C	Fe-S-cluster-containing hydrogenase component 2	0	0	1	0	0	1	1	0	1	3	0	1	4	1	3	0	0
arCOG01503	COG0437	C	Fe-S-cluster-containing hydrogenase component 1	1	3	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01504	COG2180	C	Nitrate reductase delta subunit	1	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG01505	COG3381	R	Uncharacterized component of anaerobic dehydroge	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01506	COG3381	R	Uncharacterized component of anaerobic dehydroge	0	1	1	0	1	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01507	COG4904	S	Uncharacterized protein conserved in archaea	1	0	2	0	1	0	1	0	0	0	0	0	0	0	0	0	0
arCOG01510	COG1599	L	Single-stranded DNA-binding replication protein A (	3	3	1	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01511	COG0145	E	N-methylhydantoinase A/acetone carboxylase, beta :	2	3	4	0	1	0	1	3	0	1	1	0	5	1	0	2	0
arCOG01512	COG0146	E	N-methylhydantoinase B/acetone carboxylase, alpha	2	3	4	0	1	0	0	3	0	1	0	0	0	1	0	2	0
arCOG01513	COG0145	E	N-methylhydantoinase A/acetone carboxylase, beta :	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG01514	COG0145	E	N-methylhydantoinase A/acetone carboxylase, beta :	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG01515	COG0145	E	N-methylhydantoinase A/acetone carboxylase, beta :	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01516	COG0145	E	N-methylhydantoinase A/acetone carboxylase, beta :	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01517	COG0145	E	N-methylhydantoinase A/acetone carboxylase, beta :	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG01518	COG1363	G	Cellulase M or related protein	3	0	5	0	0	1	1	4	2	3	3	0	5	1	4	0	0
arCOG01519	COG1363	G	Cellulase M or related protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01520	COG1363	G	Cellulase M or related protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01521	COG1233	Q	Phytoene dehydrogenase or related enzyme	1	3	1	1	1	1	0	4	1	3	2	1	4	0	2	1	0
arCOG01522	COG1232	H	Protoporphyrinogen oxidase	0	0	2	0	1	0	1	4	0	1	3	0	3	0	1	0	0
arCOG01523	COG1233	Q	Phytoene dehydrogenase or related enzyme	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01524	COG1233	Q	Phytoene dehydrogenase or related enzyme	0	0	0	0	0	0	0	0	0	2	0	0	4	0	0	0	0
arCOG01525	COG0562	M	UDP-galactopyranose mutase	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG01526	COG1110	L	Reverse gyrase	3	3	5	0	1	1	1	0	0	1	0	0	0	1	4	0	1
arCOG01527	COG0550	L	Topoisomerase IA	3	3	5	1	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01529	COG0365	I	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligas	1	3	3	1	0	0	1	3	1	0	0	0	0	0	0	3	0
arCOG01530	COG0315	H	Molybdenum cofactor biosynthesis enzyme	3	3	5	0	1	1	1	4	1	3	3	1	5	1	4	3	0
arCOG01531		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01532	COG0020	I	Undecaprenyl pyrophosphate synthase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01533	COG0747	E	ABC-type dipeptide transport system, periplasmic co	3	1	3	0	0	0	0	0	0	0	0	0	0	0	3	2	0
arCOG01534	COG0747	E	ABC-type dipeptide transport system, periplasmic co	2	2	5	0	0	1	1	4	1	0	2	1	4	0	4	2	0
arCOG01535	COG0747	E	ABC-type dipeptide transport system, periplasmic co	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01536	COG0747	E	ABC-type dipeptide transport system, periplasmic co	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG01537	COG0651	C	NADH:ubiquinone oxidoreductase subunit 4 (chain	3	1	5	2	1	1	1	4	2	3	2	1	3	0	4	2	0
arCOG01538	COG1008	C	NADH dehydrogenase subunit M	0	0	0	0	0	0	0	4	0	0	0	0	5	0	0	3	0
arCOG01539	COG1009	C	NADH dehydrogenase subunit L	2	3	5	2	1	1	1	4	0	0	3	1	5	0	1	3	0
arCOG01540	COG1007	C	NADH dehydrogenase subunit N	2	3	5	2	0	1	1	4	0	0	0	0	5	0	0	3	0
arCOG01541	COG0651	C	Multisubunit Na+/H+ antiporter, MnhD subunit	0	0	0	0	0	0	0	4	0	0	0	0	0	0	4	0	0
arCOG01542	COG1009	C	NADH dehydrogenase subunit L	0	0	2	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01543	COG1143	C	NADH dehydrogenase subunit I	3	3	5	2	1	1	1	4	2	3	3	1	5	0	4	3	0
arCOG01544	COG1143	C	NADH dehydrogenase subunit I	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0
arCOG01545	COG0650	C	Formate hydrogenlyase subunit 4	1	1	1	0	0	0	0	0	2	3	3	1	3	1	4	2	0
arCOG01546	COG1005	C	NADH dehydrogenase subunit H	3	3	5	2	1	1	1	4	0	0	0	1	5	0	0	3	0
arCOG01547	COG3261	C	Ni,Fe-hydrogenase III large subunit and subunit G	1	1	1	0	0	0	0	0	2	3	3	1	3	1	4	2	0
arCOG01548	COG0649	C	NADH dehydrogenase subunit D	3	3	5	2	1	1	1	4	0	0	0	0	5	0	4	3	0
arCOG01549	COG3259	C	Coenzyme F420-reducing hydrogenase, alpha subun	0	0	0	0	1	1	1	0	2	3	3	1	3	1	4	0	0
arCOG01550	COG0374	C	Ni,Fe-hydrogenase I large subunit	1	0	3	0	0	0	1	0	0	0	0	1	3	1	0	0	0
arCOG01551	COG0852	C	NADH dehydrogenase subunit C	3	3	4	2	1	1	0	0	0	0	0	1	4	0	4	3	0
arCOG01552	COG3262	C	Ni,Fe-hydrogenase III component G	0	0	0	0	0	0	0	0	0	0	2	0	0	0	4	0	0
arCOG01553	COG3260	C	Ni,Fe-hydrogenase III small subunit	1	1	1	0	0	0	0	0	2	3	3	1	3	1	4	2	0
arCOG01554	COG0377	C	F420H2 dehydrogenase subunit, related to NADH:u	3	3	5	2	1	1	1	4	0	0	0	0	5	0	4	3	0
arCOG01555	COG0852	C	NADH dehydrogenase subunit C	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG01556	COG3262	C	Ni,Fe-hydrogenase III component G	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG01557	COG0838	C	NADH dehydrogenase subunit A	2	3	5	2	1	1	1	4	0	0	0	0	5	0	0	3	0
arCOG01559	COG0480	J	Translation elongation factor G, EF-G (GTPase)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01560	COG0532	J	Translation initiation factor 2 (IF-2; GTPase)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01561	COG5256	J	Translation elongation factor EF-1alpha (GTPase)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01562	COG5258	R	GTPase	0	3	4	0	1	1	1	4	1	0	0	1	0	0	0	0	0
arCOG01563	COG5257	J	Translation initiation factor 2, gamma subunit (eIF-2	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01564	COG3276	J	Selenocysteine-specific translation elongation factor	0	3	1	2	0	0	0	0	0	3	3	1	5	1	0	3	0
arCOG01565	COG0618	R	Exopolyphosphatase-related protein	3	0	5	0	1	0	0	0	0	3	0	1	5	1	4	0	0
arCOG01566	COG0618	R	Exopolyphosphatase-related protein fused to TrkA-N	0	0	0	0	0	0	1	4	0	3	3	1	4	1	4	0	0
arCOG01567	COG1227	C	Inorganic pyrophosphatase/exopolyphosphatase	0	0	0	0	0	0	1	0	0	3	3	0	1	0	0	0	0
arCOG01568	COG0668	M	Small-conductance mechanosensitive channel	3	3	5	2	1	0	1	4	2	3	3	1	5	1	4	3	1
arCOG01569	COG0668	M	Small-conductance mechanosensitive channel	0	0	0	0	0	0	0	0	0	1	1	1	4	0	0	0	0
arCOG01570	COG0668	M	Small-conductance mechanosensitive channel	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01571	COG0668	M	Small-conductance mechanosensitive channel	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01572		S	Uncharacterized conserved membrane protein	1	3	4	0	0	0	0	0	0	0	1	0	4	0	0	0	0
arCOG01573	COG0668	M	Small-conductance mechanosensitive channel	0	3	5	0	1	1	0	0	0	0	0	0	0	0	0	3	0
arCOG01574	COG2123	J	RNase PH-related exoribonuclease	3	3	5	2	1	1	1	0	2	0	0	1	5	1	4	3	1
arCOG01575	COG0689	J	Ribonuclease PH	3	3	5	2	1	1	1	0	2	0	0	1	4	1	4	3	1
arCOG01576	COG2217	P	Cation transport ATPase	3	3	4	0	1	1	1	4	2	2	3	1	5	0	3	3	0
arCOG01577	COG2216	P	High-affinity K+ transport system, ATPase chain B	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	3	0
arCOG01578	COG0474	P	Cation transport ATPase	0	0	1	0	1	1	0	1	2	3	3	1	5	0	0	2	0
arCOG01579	COG4087	R	Soluble P-type ATPase	0	0	0	0	0	0	0	0	2	3	3	1	5	0	0	0	0
arCOG01580	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	3	3	5	2	1	1	1	4	2	3	3	1	5	0	4	3	1
arCOG01581	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	0
arCOG01582	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01583	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01584	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01585	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	2	3	1	1	0	0	1	4	0	0	0	1	0	0	4	3	0	0
arCOG01586	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	3	0	2	0	0	0	0	0	0	0	1	0	0	0	1	0	0
arCOG01587	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG01588		E	lysine biosynthesis protein LysW	1	3	4	2	1	1	0	3	0	0	0	0	0	0	4	1	0	0
arCOG01589	COG0189	H	Glutathione synthase/glutaminyl transferase/alpha-L	3	3	4	2	1	1	1	4	0	3	3	1	5	0	4	1	0	0
arCOG01590	COG0439	I	Biotin carboxylase	2	3	1	2	0	0	1	0	2	3	3	1	5	0	0	0	0	0
arCOG01591	COG4770	I	Acetyl/propionyl-CoA carboxylase, alpha subunit	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG01592	COG1821	R	Predicted ATP-utilizing enzyme (ATP-grasp superfa	0	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG01593	COG0458	E	Carbamoylphosphate synthase large subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG01594	COG0458	E	Carbamoylphosphate synthase large subunit	1	3	4	2	0	0	1	4	2	3	3	1	5	1	1	3	0	0
arCOG01595	COG2232	R	Predicted ATP-dependent carboligase related to bioti	0	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG01596	COG0458	E	Carbamoylphosphate synthase large subunit	0	0	0	0	0	0	0	0	0	2	0	0	0	4	1	0	0	0
arCOG01597	COG0026	F	Phosphoribosylaminoimidazole carboxylase (NCAIl	0	3	4	2	0	0	0	4	0	0	0	0	0	0	2	3	0	0
arCOG01598	COG0027	F	Formate-dependent phosphoribosylglycinamide forr	0	3	1	0	0	0	0	1	0	3	0	0	1	0	0	4	0	0
arCOG01599	COG1013	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	3	3	5	2	1	1	1	4	2	3	3	0	4	1	4	3	0	0
arCOG01600	COG1014	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	0	0	0	0	0	0	0	0	1	2	0	0	5	0	0	0	0	0
arCOG01601	COG1013	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	2	3	5	0	1	1	1	0	2	3	3	1	5	1	4	2	0	0
arCOG01602	COG1014	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	2	3	5	0	0	1	1	0	2	3	3	1	5	1	4	2	0	0
arCOG01603	COG1014	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	2	3	5	0	1	1	1	0	1	3	3	1	5	1	4	2	0	0
arCOG01604	COG1144	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	1	2	2	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG01605	COG1144	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	2	2	5	0	1	1	1	0	1	3	3	1	5	1	4	2	0	0
arCOG01606	COG0674	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	2	3	5	2	1	0	1	4	1	2	2	0	4	0	2	3	0	0
arCOG01607	COG0674	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	0	0	0	0	0	1	1	0	2	3	3	0	5	1	4	0	0	0

arCOG01608	COG0674	C	Pyruvate:ferredoxin oxidoreductase or related 2-oxo	2	3	5	0	1	1	1	0	2	3	3	1	5	1	4	2	0
arCOG01609	COG4231	C	Indolepyruvate ferredoxin oxidoreductase, alpha and	2	3	5	0	0	1	1	0	2	3	3	1	5	0	4	2	0
arCOG01610	COG1145	C	Ferredoxin	0	0	0	0	0	0	1	0	1	2	1	0	5	0	0	0	0
arCOG01611	COG1145	C	Ferredoxin	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG01612	COG4231	C	Indolepyruvate ferredoxin oxidoreductase, alpha and	0	0	0	0	0	0	0	0	0	0	3	1	5	0	0	0	0
arCOG01613	COG4032	R	Predicted thiamine-pyrophosphate-binding protein	0	0	0	0	0	0	0	0	2	3	0	0	2	1	0	0	0
arCOG01614	COG0028	E	Sulfopyruvate decarboxylase alpha chain	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG01615	COG2431	S	Predicted membrane protein	1	3	5	0	0	1	0	0	0	2	0	1	0	0	4	0	0
arCOG01616	COG1650	S	Uncharacterized protein conserved in archaea	3	3	4	2	1	1	1	4	0	3	3	0	5	1	4	3	0
arCOG01617	COG0667	C	Predicted oxidoreductase (related to aryl-alcohol del	1	3	3	2	0	0	0	4	0	0	0	0	0	0	0	3	0
arCOG01618	COG0656	R	Aldo/keto reductase, related to diketogulonate reduc	3	1	4	0	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01619	COG0656	R	Aldo/keto reductase, related to diketogulonate reduc	3	3	5	0	1	1	0	4	0	0	0	0	0	0	4	3	0
arCOG01620	COG0673	R	Predicted dehydrogenase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01621	COG1063	E	Threonine dehydrogenase or related Zn-dependent d	0	0	0	0	0	0	0	4	0	0	1	0	1	0	0	0	0
arCOG01622	COG0673	R	Predicted dehydrogenase	1	1	5	2	1	1	0	2	2	1	2	1	5	1	4	3	0
arCOG01623	COG0667	C	Predicted oxidoreductase (related to aryl-alcohol del	0	0	0	2	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01624	COG1453	R	Predicted oxidoreductase of the aldo/keto reductase	0	0	0	0	0	0	0	0	1	1	1	1	4	0	0	0	0
arCOG01625	COG1453	R	Predicted oxidoreductase of the aldo/keto reductase	0	0	0	0	0	0	0	0	1	1	2	1	3	0	0	0	0
arCOG01626	COG1453	R	Predicted oxidoreductase of the aldo/keto reductase	0	0	0	0	0	0	0	0	2	0	1	0	2	0	0	0	0
arCOG01627	COG1453	R	Predicted oxidoreductase of the aldo/keto reductase	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0
arCOG01628	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	2	3	4	2	0	0	1	4	0	0	1	0	5	0	0	0	0
arCOG01629	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	0	0	0	0	0	0	0	0	0	1	0	5	0	0	0	0
arCOG01630	COG0251	J	Putative translation initiation inhibitor, yjgF family	2	3	5	2	1	1	0	4	0	0	2	0	1	0	3	0	0
arCOG01631	COG0500	Q	SAM-dependent methyltransferase	3	3	5	2	1	0	0	0	0	0	0	0	0	1	0	0	0
arCOG01632	COG0500	Q	SAM-dependent methyltransferase	0	0	1	0	0	0	0	0	0	2	3	0	5	0	0	0	0
arCOG01633	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	3	1	3	0	0	0	0
arCOG01634	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG01635	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG01636	COG2230	M	Cyclopropane fatty acid synthase or related methyltr	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG01637	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0
arCOG01638	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
arCOG01639	COG0500	Q	SAM-dependent methyltransferase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01640	COG1601	J	Translation initiation factor 2, beta subunit (eIF-2bet	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01641	COG3269	R	Predicted RNA-binding protein, contains TRAM do	1	0	4	0	0	0	1	4	1	3	0	0	5	1	4	0	0
arCOG01643	COG3269	R	Predicted RNA-binding protein, contains TRAM do	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01644	COG2245	S	Predicted membrane protein	1	0	3	0	1	0	0	0	0	1	0	0	0	0	4	1	0
arCOG01645		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01646	COG1506	E	Dipeptidyl aminopeptidase/acylaminoacyl-peptidase	3	3	4	0	0	1	0	4	0	0	1	0	0	0	4	3	0
arCOG01647	COG1505	E	Serine protease of the peptidase family S9A	0	1	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01648	COG0596	R	Alpha/beta superfamily hydrolase	2	3	4	2	1	0	1	4	0	0	3	1	4	0	0	3	0
arCOG01649	COG1073	R	alpha/beta superfamily hydrolase	1	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG01650	COG2267	I	Lysophospholipase, alpha-beta hydrolase superfamil	0	0	1	0	0	0	1	0	0	0	0	0	0	0	3	0	0
arCOG01651	COG1073	R	alpha/beta superfamily hydrolase	1	0	1	0	0	0	1	0	1	0	0	0	0	0	3	0	0
arCOG01652	COG2945	R	Predicted hydrolase of the alpha/beta superfamily	0	0	0	0	0	0	1	4	0	0	0	0	0	0	0	0	0
arCOG01653	COG0596	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01654	COG1073	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	0	0	0	2	1	4	0	0	0	0
arCOG01655	COG0596	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG01656	COG1073	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	0	0	1	2	0	2	0	0	0	0
arCOG01657	COG0596	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0
arCOG01658	COG1073	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG01659	COG0412	Q	Dienelactone hydrolase or related enzyme	0	3	1	0	0	0	0	0	0	0	1	0	2	0	0	2	0
arCOG01660	COG0596	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG01661	COG1073	R	alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	1	1	0	1	1	4	0	0	0	0
arCOG01662	COG1073	R	alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG01663	COG2026	K	Cytotoxic translational repressor of toxin-antitoxin s	1	0	0	0	1	0	0	2	0	1	2	0	2	0	1	0	0
arCOG01664	COG2026	K	Cytotoxic translational repressor of toxin-antitoxin s	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01665	COG2026	K	Cytotoxic translational repressor of toxin-antitoxin s	0	0	0	0	1	0	1	0	0	1	2	0	3	0	2	0	0
arCOG01666	COG2026	K	Cytotoxic translational repressor of toxin-antitoxin s	0	1	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0
arCOG01667	COG3369	S	Zinc finger domain containing protein (CDGSH-type	1	0	2	0	0	0	0	1	0	0	0	0	0	0	0	2	0
arCOG01668	COG3370	S	Uncharacterized protein conserved in archaea	1	3	2	0	0	0	1	0	0	0	0	0	0	0	1	3	0
arCOG01669	COG3370	S	Uncharacterized protein conserved in archaea	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01670	COG2044	R	Predicted peroxiredoxin	0	3	1	0	0	0	0	2	0	3	0	0	0	0	0	0	0
arCOG01671	COG0043	H	3-polyprenyl-4-hydroxybenzoate decarboxylase or r	3	3	5	2	1	1	1	2	2	3	3	1	5	1	4	3	0
arCOG01672	COG3889	R	Predicted solute binding protein	3	1	5	2	1	1	0	0	0	0	0	0	0	0	4	0	0
arCOG01673	COG0747	E	ABC-type dipeptide transport system, periplasmic co	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01674	COG1254	C	Acylphosphatase	2	3	5	1	1	1	1	3	0	1	3	1	5	0	4	3	0
arCOG01676	COG0476	H	Dinucleotide-utilizing enzyme involved in molybdop	3	3	5	2	1	1	1	4	2	2	3	1	5	0	4	3	1
arCOG01677	COG4015	R	Predicted dinucleotide-utilizing enzyme of the ThiF/	0	0	0	0	0	0	0	0	1	3	2	0	0	1	0	0	0
arCOG01678	COG1812	E	Archaeal S-adenosylmethionine synthetase	3	3	5	0	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01679	COG0640	K	Transcriptional regulator containing HTH domain, A	3	3	1	0	1	0	0	0	0	1	1	1	4	0	1	0	0
arCOG01680	COG0640	K	Transcriptional regulator containing HTH domain, A	1	0	4	1	1	0	1	3	0	3	3	1	5	1	4	0	0
arCOG01681	COG0640	K	Transcriptional regulator containing HTH domain, A	0	3	1	1	0	0	0	1	2	1	1	1	5	0	2	2	0
arCOG01682	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	0	0	0	2	1	2	0	0	0	0
arCOG01683	COG0640	K	Transcriptional regulator containing HTH domain, A	1	0	0	0	0	0	1	0	0	1	1	0	2	0	4	0	0
arCOG01684	COG1777	K	Predicted transcriptional regulator	0	0	0	0	0	1	1	4	2	0	3	1	4	0	4	3	0
arCOG01685	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	1	1	1	3	0	0	0	0	4	0	0	0	0
arCOG01686	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	1	0	3	0	2	3	1	4	0	0	0	0
arCOG01687	COG0640	K	Transcriptional regulator containing HTH domain, A	1	0	1	2	0	0	0	1	0	0	0	1	0	0	4	3	0
arCOG01688	COG1719	R	Predicted hydrocarbon binding protein, contains V4I	1	0	1	0	1	1	0	0	2	1	3	1	4	1	0	0	1
arCOG01690	COG1719	R	Predicted hydrocarbon binding protein, contains V4I	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01691	COG2345	K	Transcriptional regulator ArsR family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01692	COG2345	K	Transcriptional regulator ArsR family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG01693	COG0467	T	RecA-superfamily ATPase implicated in signal trans	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2	0
arCOG01694	COG1716	T	FHA domain and HTH domain	0	0	3	0	0	1	0	0	0	0	2	0	0	0	0	0	0
arCOG01695	COG1293	K	Predicted RNA-binding protein homologous to euka	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01696	COG3635	G	Predicted phosphoglycerate mutase, AP superfamily	3	3	5	2	1	1	1	0	2	3	3	1	5	1	4	3	0
arCOG01697	COG1048	C	Aconitase A	1	3	4	2	1	0	0	4	0	0	0	0	4	0	1	3	0
arCOG01698	COG0065	E	3-isopropylmalate dehydratase large subunit	0	3	4	2	1	1	1	4	2	3	3	1	5	1	4	1	0
arCOG01699	COG4353	S	Uncharacterized conserved protein	2	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01700	COG0010	E	Arginase family enzyme	3	3	5	2	1	1	1	4	2	3	2	1	4	1	4	3	1
arCOG01701	COG1676	J	tRNA splicing endonuclease	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01702	COG1676	J	tRNA splicing endonuclease	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01703	COG0163	H	3-polyprenyl-4-hydroxybenzoate decarboxylase	3	3	4	2	1	0	1	0	2	3	3	1	5	1	4	3	0
arCOG01704	COG0452	H	Phosphopantothenoylcysteine synthetase/decarboxyl	3	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG01705	COG1036	C	Archaeal flavoprotein	0	0	0	0	0	0	1	0	2	3	0	1	5	1	0	0	0
arCOG01706	COG0508	C	Pyruvate/2-oxoglutarate dehydrogenase complex, di	1	1	2	0	1	0	0	3	0	0	0	1	0	0	0	3	0
arCOG01707	COG1960	I	Acyl-CoA dehydrogenase	1	3	4	0	1	0	1	4	0	0	0	0	0	0	0	3	0
arCOG01708	COG1960	I	Acyl-CoA dehydrogenase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	3	0
arCOG01709	COG1960	I	Acyl-CoA dehydrogenase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01710	COG2185	I	Methylmalonyl-CoA mutase, C-terminal domain/sut	1	3	0	2	0	0	1	4	0	0	0	0	0	0	4	3	0
arCOG01711	COG0221	C	Inorganic pyrophosphatase	3	3	2	1	0	0	0	4	2	0	0	0	3	1	4	3	1
arCOG01712	COG0221	C	Inorganic pyrophosphatase	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG01713	COG5440	S	Uncharacterized conserved protein	2	3	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
arCOG01714	COG5440	S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01715	COG0719	O	Cysteine desulfurase activator SufB	3	3	5	2	1	1	1	4	2	2	3	1	5	0	4	3	0
arCOG01716	COG0719	O	Cysteine desulfurase activator SufB	0	0	0	0	0	0	0	0	0	1	0	0	3	1	1	0	1
arCOG01717	COG0154	J	Asp-tRNAAsn/Glu-tRNAGln amidotransferase A su	1	3	3	2	1	0	1	4	2	3	3	1	5	1	0	0	1
arCOG01718	COG0064	J	Asp-tRNAAsn/Glu-tRNAGln amidotransferase B su	2	3	0	2	0	0	1	4	2	3	3	1	5	1	0	0	1
arCOG01719	COG2511	J	Archaeal Glu-tRNAGln amidotransferase subunit E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01720	COG0723	C	Rieske Fe-S protein	1	3	2	2	1	1	0	1	0	0	0	0	0	0	0	3	0
arCOG01721	COG1290	C	Cytochrome b subunit of the bc complex	1	3	3	2	1	1	0	3	0	0	0	0	0	0	0	3	0
arCOG01722	COG0099	J	Ribosomal protein S13	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01723	COG1437	F	Adenylate cyclase, class 2 (thermophilic)	3	3	5	0	0	1	1	4	2	3	3	1	5	1	4	0	0
arCOG01724	COG4072	S	Uncharacterized protein conserved in archaea	3	0	0	0	0	0	0	0	0	3	0	0	0	1	4	0	0
arCOG01726	COG0142	H	Geranylgeranyl pyrophosphate synthase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01727	COG0142	H	Geranylgeranyl pyrophosphate synthase	1	3	5	2	0	1	1	0	0	0	1	1	5	0	0	0	0
arCOG01728	COG1355	R	Predicted dioxygenase	3	3	5	2	1	1	1	0	2	3	3	1	5	1	4	3	1
arCOG01729	COG3885	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	4	3	0
arCOG01730	COG3384	E	Aromatic ring-opening dioxygenase, catalytic LigB	0	3	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0
arCOG01731	COG0534	V	Na+-driven multidrug efflux pump	3	0	0	0	0	1	1	4	2	3	3	0	3	0	4	0	0
arCOG01732	COG0534	V	Na+-driven multidrug efflux pump	0	0	0	0	0	0	0	0	0	2	0	0	4	0	0	0	0
arCOG01733	COG0534	V	Na+-driven multidrug efflux pump	0	0	0	0	0	0	0	0	0	2	0	0	3	0	0	0	0
arCOG01734	COG4933	S	Uncharacterized conserved protein	3	0	4	0	0	0	0	0	0	1	0	0	0	1	4	0	0
arCOG01736	COG1514	J	2'-5' RNA ligase	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	1
arCOG01737	COG1514	J	2'-5' RNA ligase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01738		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01739	COG0681	U	Signal peptidase I	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01740	COG0681	U	Signal peptidase I	0	2	0	0	0	0	1	2	0	0	0	0	0	0	4	0	0

arCOG01741	COG1537	R	Predicted RNA-binding protein	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01742	COG1503	J	Peptide chain release factor 1 (eRF1)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01743	COG1503	J	Peptide chain release factor 1 (eRF1)	0	0	0	0	0	0	0	4	0	0	0	0	5	0	0	0	0
arCOG01744	COG1988	R	Membrane-bound metal-dependent hydrolase	3	0	0	0	0	1	1	3	1	0	1	1	0	0	0	0	1
arCOG01745		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0
arCOG01746	COG3044	R	Predicted ATPase of the ABC class	3	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
arCOG01747	COG0015	F	Adenylosuccinate lyase	0	3	4	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01748	COG0165	E	Argininosuccinate lyase	1	3	4	2	1	1	1	4	2	3	3	1	5	1	1	3	0
arCOG01749	COG0114	C	Fumarase	1	3	2	0	1	0	0	4	0	0	0	0	3	0	0	0	0
arCOG01750	COG1027	E	Aspartate ammonia-lyase	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01751	COG1358	J	Ribosomal protein HS6-type (S12/L30/L7a)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01752	COG1911	J	Ribosomal protein L30E	3	3	5	2	1	1	1	0	2	3	3	1	5	1	4	0	1
arCOG01753	COG1581	K	Archaeal DNA-binding protein	3	3	5	2	1	1	1	0	2	3	3	1	1	1	4	3	1
arCOG01754	COG0111	H	Phosphoglycerate dehydrogenase or related dehydro	2	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01755	COG1052	C	Lactate dehydrogenase or related 2-hydroxyacid deh	2	0	3	2	0	1	0	0	0	2	0	0	0	0	4	1	0
arCOG01756	COG1052	C	Lactate dehydrogenase or related 2-hydroxyacid deh	0	3	4	0	1	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01757	COG0111	H	Phosphoglycerate dehydrogenase or related dehydro	0	0	1	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01758	COG0051	J	Ribosomal protein S10	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01759	COG1259	S	Uncharacterized conserved protein	3	3	5	2	0	0	1	4	0	0	1	1	4	0	0	0	0
arCOG01760	COG0195	K	Transcription elongation factor	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01761	COG0195	K	Transcription elongation factor	2	3	4	1	1	0	0	0	1	0	0	0	0	1	4	0	0
arCOG01762	COG0085	K	DNA-directed RNA polymerase subunit B	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01764	COG2101	K	TATA-box binding protein (TBP), component of TF	3	3	5	2	1	1	1	4	2	3	3	1	4	1	4	3	1
arCOG01765	COG2101	K	TATA-box binding protein (TBP), component of TF	0	0	0	0	0	0	0	0	0	0	3	0	4	0	0	0	0
arCOG01766	COG2430	S	Uncharacterized conserved protein	3	0	1	1	0	0	1	0	0	2	2	0	4	0	4	0	0
arCOG01767	COG3425	I	3-hydroxy-3-methylglutaryl CoA synthase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01768	COG0705	E	Membrane associated serine protease	3	3	4	2	1	1	1	4	0	0	0	1	5	1	4	0	0
arCOG01769	COG3582	R	Predicted nucleic acid binding protein containing the	0	0	0	2	1	0	0	1	0	0	1	1	0	0	0	0	0
arCOG01770	COG0076	E	Rhomboid family membrane associated serine proteas	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
arCOG01771	COG0705	E	Membrane associated serine protease	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01772	COG2407	G	L-fucose isomerase or related protein	3	0	5	0	0	0	0	0	0	0	0	0	0	1	4	0	0
arCOG01773	COG0500	Q	SAM-dependent methyltransferase	3	3	5	2	0	0	1	2	0	1	2	1	4	0	4	3	0
arCOG01774	COG0500	Q	SAM-dependent methyltransferase	0	0	3	0	1	0	0	0	0	1	1	1	1	0	0	0	0
arCOG01775	COG0500	Q	SAM-dependent methyltransferase	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01776	COG0500	Q	SAM-dependent methyltransferase	0	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
arCOG01778	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	2	0	3	1	0	0	0
arCOG01779	COG2226	H	Methylase involved in ubiquinone/menaquinone bio	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG01780	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	3	0	0	0	0	1	0	2	0	0
arCOG01781	COG0500	Q	SAM-dependent methyltransferase	0	0	0	2	0	0	0	4	0	0	0	0	1	0	0	0	0
arCOG01782	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01783	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	1	0	0	2	0	3	0	0	0	0
arCOG01784	COG2226	H	Methylase involved in ubiquinone/menaquinone bio	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG01786	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	1	2	0	3	0	0	0	0
arCOG01787	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	1	0	1	1	4	0	0	0	0
arCOG01788	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01789	COG0500	Q	SAM-dependent methyltransferase	1	0	0	0	0	0	0	0	0	3	1	1	3	0	0	0	0
arCOG01790	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	1	0	0	0	0	3	0	4	0	0
arCOG01791	COG0500	Q	SAM-dependent methyltransferase	0	3	5	0	1	1	0	0	0	0	2	1	4	1	3	0	0
arCOG01792	COG0500	Q	SAM-dependent methyltransferase	0	0	0	1	1	1	0	2	0	2	1	1	5	0	0	0	0
arCOG01793	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01794	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01795	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01796	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG01797	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG01798	COG0765	E	ABC-type amino acid transport system, permease cc	3	0	4	0	0	1	1	3	1	2	3	1	2	0	0	0	0
arCOG01799	COG0834	E	ABC-type amino acid transport/signal transduction s	2	0	4	1	0	1	1	3	1	2	3	1	2	0	1	0	0
arCOG01801	COG2358	R	TRAP-type uncharacterized transport system, peripl	1	0	1	0	0	1	1	4	0	0	0	1	0	0	1	0	0
arCOG01802	COG2358	R	TRAP-type uncharacterized transport system, peripl	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0
arCOG01803	COG0715	P	ABC-type nitrate/sulfonate/bicarbonate transport sy	2	0	1	2	1	1	1	1	1	3	3	1	5	1	0	0	0
arCOG01804	COG3888	K	Predicted transcriptional regulator	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	3	0
arCOG01805	COG3221	P	ABC-type phosphate/phosphonate transport system,	0	0	1	2	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01806		S	Uncharacterized conserved protein	2	0	1	2	0	0	0	0	0	0	0	0	0	0	1	3	0
arCOG01807		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01808	COG2064	N	Flp pilus assembly protein TadC	2	3	5	1	1	0	1	3	0	1	2	1	4	0	0	0	0
arCOG01809	COG1955	N	Archaeal flagella assembly protein J	1	3	0	0	1	0	1	3	0	3	2	1	4	0	4	2	0
arCOG01810	COG1955	N	Archaeal flagella assembly protein J	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01811	COG2064	N	Flp pilus assembly protein TadC	1	0	4	0	0	0	0	0	2	3	2	1	1	1	4	2	1
arCOG01812	COG2064	N	Flp pilus assembly protein TadC	2	0	5	0	0	0	0	0	0	3	2	0	1	1	4	2	1
arCOG01814		S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	3	0	0	0	1	4	0	0	0	1
arCOG01815	COG2064	N	Flp pilus assembly protein TadC	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01816	COG2064	N	Flp pilus assembly protein TadC	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG01817	COG0630	N	Type IV secretory pathway, VirB11 component, or r	3	3	5	1	1	0	1	3	0	3	3	1	4	0	4	2	1
arCOG01818	COG0630	N	Type IV secretory pathway, VirB11 component, or r	0	0	3	0	0	1	0	4	0	1	0	1	4	0	3	0	1
arCOG01819	COG4962	U	Flp pilus assembly protein, ATPase CpaF	0	0	0	0	0	0	0	0	2	3	0	0	0	1	1	0	0
arCOG01822	COG3354	N	Putative archaeal flagellar protein G	1	2	0	0	1	0	1	3	0	3	2	1	4	0	4	2	0
arCOG01824	COG3353	N	Putative archaeal flagellar protein F	1	3	0	0	0	0	1	3	0	3	2	1	4	0	4	2	0
arCOG01829	COG1681	N	Archaeal flagellins	1	3	0	0	1	0	1	3	0	3	2	1	4	0	4	2	0
arCOG01830	COG1665	R	Predicted nucleotidyltransferase	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01831	COG1665	R	Predicted nucleotidyltransferase	1	3	0	0	1	0	1	0	2	3	3	1	5	1	0	0	0
arCOG01832	COG0071	O	Molecular chaperone (HSP20 family)	1	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01833	COG0071	O	Molecular chaperone (HSP20 family)	3	3	4	2	1	1	1	0	0	0	0	1	5	0	0	1	0
arCOG01834	COG0071	O	Molecular chaperone (HSP20 family)	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01835	COG0071	O	Molecular chaperone (HSP20 family)	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01836	COG0071	O	Molecular chaperone (HSP20 family)	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01837	COG0071	O	Molecular chaperone (HSP20 family)	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01838	COG0071	O	Molecular chaperone (HSP20 family)	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG01839	COG0071	O	Molecular chaperone (HSP20 family)	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG01840	COG0071	O	Molecular chaperone (HSP20 family)	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01841	COG0071	O	Molecular chaperone (HSP20 family)	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG01842	COG3255	I	Putative sterol carrier protein	1	2	2	0	0	0	1	2	0	0	0	0	0	0	0	2	0
arCOG01843	COG3255	I	Putative sterol carrier protein	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	2	0
arCOG01844	COG3255	I	Putative sterol carrier protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG01845	COG2151	R	Predicted metal-sulfur cluster biosynthetic enzyme	3	3	5	2	1	1	0	1	2	3	0	0	2	1	4	3	1
arCOG01846	COG2151	R	PaaD-like, metal-sulfur cluster biosynthetic enzyme	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG01847	COG1045	E	Serine acetyltransferase	0	0	0	0	0	0	0	4	1	0	2	0	3	0	0	0	0
arCOG01848	COG0110	R	Acetyltransferase (isoleucine patch superfamily)	1	0	5	2	1	1	0	3	2	2	3	1	5	1	2	0	0
arCOG01849	COG0663	R	Isoleucine patch superfamily protein	0	3	1	0	0	0	0	2	2	3	3	1	5	1	4	3	0
arCOG01850	COG0110	R	Acetyltransferase (isoleucine patch superfamily)	0	0	0	0	0	0	0	4	0	0	0	1	3	0	0	0	0
arCOG01851	COG1045	E	Serine acetyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG01852	COG2151	R	Predicted metal-sulfur cluster biosynthetic enzyme	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01853	COG2151	R	PaaD-like, metal-sulfur cluster biosynthetic enzyme	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG01854	COG0110	R	Acetyltransferase (isoleucine patch superfamily)	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0
arCOG01855	COG2151	R	PaaD-like, metal-sulfur cluster biosynthetic enzyme	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01856	COG2151	R	Predicted metal-sulfur cluster biosynthetic enzyme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG01857	COG1303	R	SpoU rRNA Methylase family enzyme	3	3	1	2	1	0	1	4	2	3	3	1	5	1	4	3	0
arCOG01858	COG1418	R	Predicted HD superfamily hydrolase	0	0	0	0	0	0	1	0	2	3	3	1	4	1	0	0	0
arCOG01859	COG2316	R	Predicted hydrolase (HD superfamily)	0	0	0	0	0	0	1	0	0	2	1	0	0	0	0	0	0
arCOG01860	COG1418	R	Predicted HD superfamily hydrolase	2	0	1	1	0	0	1	4	0	0	2	0	4	1	4	0	0
arCOG01861	COG3481	R	Predicted HD-superfamily hydrolase fused to OB-fo	1	0	0	1	0	0	0	1	1	3	2	0	1	1	0	0	0
arCOG01862	COG1418	R	Predicted HD superfamily hydrolase	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
arCOG01863	COG1813	K	Predicted transcription factor, homolog of eukaryoti	3	3	5	0	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01864	COG1476	K	Predicted transcriptional regulator, xre family	0	0	0	0	0	0	1	1	2	3	3	1	4	0	2	0	0
arCOG01865	COG1396	K	Predicted transcriptional regulator, xre family	0	0	0	0	0	0	0	0	1	2	0	0	4	0	0	0	0
arCOG01866	COG1396	K	Predicted transcriptional regulator, xre family	0	0	0	0	0	0	0	0	2	2	0	1	5	0	0	0	0
arCOG01867	COG1396	K	Predicted transcriptional regulator, xre family	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG01868	COG0735	P	Fe2+/Zn2+ uptake regulation protein, fur/PerR	2	3	4	0	0	0	1	0	0	0	0	0	2	0	2	2	0
arCOG01869	COG1267	I	Phosphatidylglycerophosphatase A fused to adenosy	1	0	3	0	0	0	0	0	2	3	1	0	5	1	4	0	0
arCOG01870	COG1865	H	Adenosylcobinamide amidohydrolase	0	2	1	0	0	0	1	4	1	1	3	1	4	1	4	3	0
arCOG01871	COG2266	H	GTP:adenosylcobinamide-phosphate guanylyltransfe	1	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG01872	COG0746	H	Molybdopterin-guanine dinucleotide biosynthesis pr	2	3	4	0	1	1	1	4	1	3	3	1	4	1	4	3	0
arCOG01873	COG2068	R	Uncharacterized MobA-related protein	2	3	3	0	1	0	0	2	2	0	0	0	0	1	0	1	0
arCOG01874	COG0746	H	Molybdopterin-guanine dinucleotide biosynthesis pr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01875	COG1475	K	ParB-like nuclease domain	3	3	1	2	1	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01876	COG0620	E	Methionine synthase II (cobalamin-independent)	3	3	5	0	1	1	0	3	2	3	3	1	0	1	4	3	0
arCOG01877	COG0620	E	Methionine synthase II (cobalamin-independent)	2	3	0	0	1	0	0	4	0	0	0	0	0	0	4	3	0
arCOG01878	COG0620	E	Methionine synthase II (cobalamin-independent)	0	0	0	0	0	0	1	0	0	0	0	0	5	0	0	0	0
arCOG01879		S	Dolichol kinase family protein	3	3	3	0	1	1	0	0	0	0	0	0	1	0	3	0	0
arCOG01880	COG0170	I	Dolichol kinase	0	0	1	0	0	0	1	0	1	1	2	1	5	1	4	3	0

arCOG01881	COG0170	I	Dolichol kinase	0	0	0	0	0	0	1	4	0	0	0	0	0	0	0	0	0
arCOG01882	COG0170	I	Dolichol kinase	0	0	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG01883	COG1351	F	Alternative thymidylate synthase	3	3	4	0	1	1	0	2	0	0	0	0	0	0	4	0	1
arCOG01884	COG1351	F	Alternative thymidylate synthase	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01885	COG1383	J	Ribosomal protein S17E	3	3	5	1	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01886	COG0162	J	Tyrosyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01887	COG0180	J	Tryptophanyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01888	COG2309	E	Leucyl aminopeptidase (aminopeptidase T)	3	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG01889	COG2309	E	Leucyl aminopeptidase (aminopeptidase T)	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01890	COG2309	E	Leucyl aminopeptidase (aminopeptidase T)	0	0	0	0	0	1	0	4	0	0	0	1	1	1	1	0	0
arCOG01891	COG0125	F	Thymidylate kinase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01893	COG0125	F	Thymidylate kinase	0	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	0
arCOG01894	COG0648	L	Endonuclease IV	3	3	5	2	1	1	0	4	2	3	3	1	5	0	4	3	1
arCOG01895	COG1082	G	Sugar phosphate isomerase/epimerase	2	0	2	0	1	1	1	2	2	3	3	1	5	1	4	0	0
arCOG01896	COG1082	G	Sugar phosphate isomerase/epimerase	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01897	COG1082	G	Sugar phosphate isomerase/epimerase	0	0	0	0	0	1	1	0	0	3	3	0	0	0	0	0	0
arCOG01898	COG4294	L	UV damage repair endonuclease	0	1	0	0	0	0	0	2	0	0	1	1	0	0	0	0	0
arCOG01899	COG1082	G	Sugar phosphate isomerase/epimerase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG01900	COG1082	G	Sugar phosphate isomerase/epimerase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01901	COG1082	G	Sugar phosphate isomerase/epimerase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01902	COG1082	G	Sugar phosphate isomerase/epimerase	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG01903	COG1082	G	Sugar phosphate isomerase/epimerase	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01904	COG1339	K	Transcriptional regulator of a riboflavin/FAD biosyn	3	3	5	2	1	1	1	4	2	3	3	1	4	1	4	3	0
arCOG01905	COG4189	K	Predicted transcriptional regulator	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01906	COG4666	R	TRAP-type uncharacterized transport system, fused	1	0	1	0	0	1	1	4	0	0	0	1	0	0	1	0	0
arCOG01907	COG2013	S	Uncharacterized conserved protein	2	3	1	0	1	1	1	3	1	2	2	1	5	0	3	3	0
arCOG01908	COG2013	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	1	3	1	0	0	0
arCOG01909	COG0174	E	Glutamine synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01910	COG1030	O	Short-chain alcohol dehydrogenase	3	0	5	0	1	1	1	0	0	0	0	0	5	0	4	3	0
arCOG01911	COG0616	O	Periplasmic serine protease (ClpP class)	3	0	1	1	0	1	1	0	0	3	1	1	4	0	4	0	0
arCOG01912	COG1585	O	Membrane protein implicated in regulation of membr	1	3	0	0	0	0	0	4	1	3	3	1	0	1	3	0	0
arCOG01913	COG1585	O	Membrane protein implicated in regulation of membr	0	0	3	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG01914	COG1585	O	Membrane protein implicated in regulation of membr	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01915	COG0330	O	Membrane protease subunit, stomatin/prohibitin hon	3	3	5	1	1	1	1	4	1	3	3	1	5	1	4	3	0
arCOG01916		R	RHH-fold DNA-binding protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG01917		S	Zn-ribbon domain containing protein	1	1	4	0	0	0	0	1	1	3	2	1	1	0	1	0	0
arCOG01918	COG0330	O	Membrane protease subunit, stomatin/prohibitin hon	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01919	COG0805	U	Sec-independent protein secretion pathway compone	2	3	5	2	1	1	1	4	0	0	0	1	3	0	0	3	0
arCOG01920	COG0250	K	Transcription antiterminator NusG	3	3	5	2	0	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01921	COG2083	S	Uncharacterized protein conserved in archaea	1	0	0	0	1	0	1	0	1	3	1	0	1	1	4	0	0
arCOG01922		S	Uncharacterized conserved protein	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01923	COG1498	J	Protein implicated in ribosomal biogenesis, Nop56p	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01924	COG0252	E	L-asparaginase/archaeal Glu-tRNAGln amidotransfe	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01925	COG2080	C	Aerobic-type carbon monoxide dehydrogenase, sma	2	3	3	0	1	0	0	2	0	0	0	0	0	0	0	1	0
arCOG01926	COG1319	C	Aerobic-type carbon monoxide dehydrogenase, mid	2	3	3	0	1	0	0	1	0	0	0	0	0	0	0	1	0
arCOG01927	COG3427	C	Carbon monoxide dehydrogenase subunit G, CoxG	1	3	4	0	1	0	0	4	0	0	0	0	0	0	0	3	0
arCOG01928	COG3427	C	Carbon monoxide dehydrogenase subunit G, CoxG	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01929	COG1975	O	Xanthine and CO dehydrogenase maturation factor,	2	3	2	0	1	0	0	2	0	0	1	0	0	0	0	1	0
arCOG01930	COG2159	R	Predicted metal-dependent hydrolase of the TIM-bar	1	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG01931	COG2159	R	Predicted metal-dependent hydrolase of the TIM-bar	1	3	1	0	0	0	0	3	0	0	0	0	0	1	3	0	0
arCOG01932	COG2159	R	Predicted metal-dependent hydrolase of the TIM-bar	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01933	COG2159	R	Predicted metal-dependent hydrolase of the TIM-bar	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01934	COG2159	R	Predicted metal-dependent hydrolase of the TIM-bar	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01935	COG4006	V	CRISPR system related protein	2	2	4	0	1	0	0	0	0	0	0	0	0	1	0	0	0
arCOG01936		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01937	COG1750	R	Archaeal serine protease	3	0	5	0	0	1	1	0	0	3	0	0	0	4	0	1	0
arCOG01938	COG1750	R	Archaeal serine protease	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01939	COG0095	H	Lipoate-protein ligase A	3	3	0	0	0	1	0	3	0	0	0	1	0	0	4	2	0
arCOG01940	COG0340	H	Biotin-(acetyl-CoA carboxylase) ligase	2	3	1	2	1	0	1	4	2	3	3	1	5	0	4	0	0
arCOG01941	COG0095	H	Lipoate-protein ligase A	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG01942	COG0321	H	Lipoate-protein ligase B	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	1	0
arCOG01943	COG1335	Q	Amidase related to nicotinamidase	3	3	5	0	1	1	1	4	0	0	2	1	3	1	4	3	0
arCOG01944	COG1335	Q	Amidase related to nicotinamidase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01945	COG1335	Q	Amidase related to nicotinamidase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG01946	COG2125	J	Ribosomal protein S6E (S10)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01947	COG1280	E	Putative threonine efflux protein	2	3	4	1	0	1	1	3	1	0	2	1	5	1	0	3	0
arCOG01948	COG1280	E	Putative threonine efflux protein	0	0	0	0	0	0	0	1	0	2	0	0	3	0	0	0	0
arCOG01949	COG1279	R	Lysine efflux permease	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
arCOG01950	COG2075	J	Ribosomal protein L24E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01951	COG1444	R	Predicted P-loop ATPase fused to an acetyltransfera	3	3	5	0	0	1	1	3	0	0	0	0	0	1	4	0	1
arCOG01952	COG0009	J	Putative translation factor (SUA5)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01953	COG0475	P	Kef-type K+ transport system, membrane componen	2	3	1	2	0	1	1	1	1	3	3	1	4	0	4	2	0
arCOG01954	COG0475	P	Kef-type K+ transport system, membrane componen	0	0	0	0	0	0	0	0	0	2	0	0	0	0	4	0	0
arCOG01955	COG0475	P	Kef-type K+ transport system, membrane componen	0	0	0	2	0	0	1	1	2	2	2	1	5	0	0	0	0
arCOG01956	COG0475	P	Kef-type K+ transport system, membrane componen	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG01957	COG0569	P	K+ transport system, NAD-binding component	3	0	4	0	0	0	1	4	2	3	3	1	4	1	4	0	0
arCOG01958	COG1226	P	Kef-type K+ transport system, predicted NAD-bindi	2	3	1	0	0	0	1	3	1	3	1	0	3	1	1	3	0
arCOG01959	COG0569	P	K+ transport system, NAD-binding component	0	0	0	0	0	0	1	3	0	0	0	0	5	0	0	0	0
arCOG01960	COG1226	P	K+ transport system, NAD-binding component fuse	0	0	0	0	0	0	1	4	0	0	1	0	1	0	0	0	0
arCOG01961	COG0025	P	NhaP-type Na+/H+ and K+/H+ antiporter	0	0	1	0	0	0	1	4	1	3	1	0	4	1	1	3	0
arCOG01962	COG3263	P	NhaP-type Na+/H+ and K+/H+ antiporter with a uni	0	0	0	2	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG01963	COG3273	S	PhoU-like domain fused to TrkA-C domain	2	0	0	0	0	1	1	4	1	0	2	0	4	1	4	0	0
arCOG01964	COG1226	P	Kef-type K+ transport system, predicted NAD-bindi	1	0	0	1	1	0	0	1	2	1	1	1	4	1	0	0	0
arCOG01966	COG1226	P	Ion channel	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0
arCOG01967	COG2074	G	2-phosphoglycerate kinase	0	0	0	0	0	0	0	0	2	3	0	0	0	1	4	3	0
arCOG01968	COG1827	R	2-phosphoglycerate kinase fused to 3H domain	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
arCOG01969	COG0475	P	Kef-type K+ transport system, membrane componen	0	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG01970	COG0490	P	Putative regulatory, ligand-binding protein related to	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG01971	COG1226	P	Ion channel	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG01972	COG0526	O	Thiol-disulfide isomerase or thioredoxin	3	3	4	2	1	1	1	4	2	3	3	1	5	0	2	3	0
arCOG01974	COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG01975	COG0526	O	Thiol-disulfide isomerase or thioredoxin	2	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG01976	COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	0	0	0	0	0	2	1	0	1	1	0	0	0	0	0
arCOG01977	COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG01978	COG0294	H	Dihydropteroate synthase or related enzyme	3	3	4	2	0	1	1	4	2	3	3	1	5	1	4	3	0
arCOG01979	COG1456	C	CO dehydrogenase/acetyl-CoA synthase gamma sub	0	0	0	0	0	0	1	0	1	3	1	1	5	1	0	0	0
arCOG01980	COG2069	C	CO dehydrogenase/acetyl-CoA synthase delta subun	0	0	0	0	0	0	1	0	1	3	1	1	5	1	0	0	0
arCOG01981	COG1405	K	Transcription initiation factor TFIIIB, Brf1 subunit/T	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01982	COG0434	R	Predicted TIM-barrel enzyme	3	1	3	0	1	0	1	2	0	1	0	0	0	1	4	0	0
arCOG01983	COG0135	E	Phosphoribosylanthranilate isomerase	1	3	4	0	1	0	1	4	2	3	3	1	5	1	3	3	0
arCOG01984	COG2440	C	Ferredoxin-like protein	1	3	4	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01985	COG2440	C	Ferredoxin-like protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG01986	COG4670	I	Acyl CoA:acetate/3-ketoacid CoA transferase	1	0	3	0	0	1	0	1	0	0	0	0	0	0	0	1	0
arCOG01987	COG1788	I	Acyl CoA:acetate/3-ketoacid CoA transferase, alpha	0	3	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG01988	COG2092	J	Translation elongation factor EF-1beta	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01989	COG2888	J	Predicted Zn-ribbon RNA-binding protein with a fus	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG01991	COG0406	R	Broad specificity phosphatase PhoE or related phosp	0	3	1	2	0	0	0	3	0	0	1	1	1	0	0	3	0
arCOG01992	COG2062	T	Phosphohistidine phosphatase SixA	2	3	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG01993	COG0588	G	Phosphoglycerate mutase 1	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG01994	COG1300	S	Uncharacterized membrane protein	2	0	1	0	0	1	1	3	2	3	2	1	5	1	4	0	0
arCOG01995		S	Oligoketide cyclase/lipid transport protein family	1	3	1	2	1	0	0	0	0	0	0	0	0	0	0	3	0
arCOG01996	COG1300	S	Uncharacterized membrane protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0
arCOG01997	COG2095	U	Multiple antibiotic transporter	3	3	5	0	1	1	1	0	0	3	3	1	5	1	4	3	0
arCOG01998	COG0028	E	Acetolactate synthase large subunit or other thiamin	1	3	4	2	1	1	1	3	2	3	3	1	5	1	2	1	0
arCOG01999	COG0028	E	Pyruvate oxidase	0	2	0	0	0	0	0	0	1	0	2	1	0	0	0	2	0
arCOG02000	COG0028	E	Acetolactate synthase large subunit or other thiamin	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG02001	COG0028	E	Acetolactate synthase large subunit or other thiamin	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02002	COG0028	E	Acetolactate synthase large subunit or other thiamin	0	0	1	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02003	COG0028	E	Acetolactate synthase large subunit or other thiamin	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG02004	COG3473	Q	Maleate cis-trans isomerase	1	2	1	0	1	0	0	0	0	0	0	0	0	0	4	1	0
arCOG02005	COG1794	M	Aspartate racemase	0	0	0	0	0	0	1	0	0	1	0	0	0	0	4	1	0
arCOG02006	COG1794	M	Aspartate racemase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG02007	COG1331	O	Highly conserved protein containing a thioredoxin d	1	3	2	2	1	0	1	4	1	0	2	1	5	0	0	3	0
arCOG02008	COG3371	S	Predicted membrane protein	3	3	5	0	1	1	0	1	0	0	1	1	0	0	4	3	0
arCOG02009	COG1757	C	Na+/H+ antiporter	2	0	0	0	0	0	0	3	0	2	1	0	0	0	4	0	0
arCOG02010	COG1757	C	Na+/H+ antiporter	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02011	COG1757	C	Na+/H+ antiporter	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02012	COG0547	E	Anthranilate phosphoribosyltransferase	1	3	4	2	1	0	1	4	2	3	3	1	5	1	3	3	0

arCOG02013	COG0213	F	Thymidine phosphorylase	1	0	1	0	0	0	1	1	0	3	3	1	5	0	4	0	0
arCOG02014	COG0147	E	Anthranilate/para-aminobenzoate synthase compone	1	3	4	2	0	0	1	4	2	3	3	1	5	1	3	3	0
arCOG02015	COG1169	H	Menaquinone-specific isochorismate synthase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02016	COG1853	R	Conserved protein/domain typically associated with	1	0	3	0	1	0	0	0	0	0	0	1	3	0	0	0	0
arCOG02017	COG1853	R	Conserved protein/domain typically associated with	2	3	5	0	1	1	1	1	2	0	2	1	4	0	4	1	0
arCOG02018	COG1853	R	Conserved protein/domain typically associated with	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02019	COG2897	P	Rhodanese-related sulfurtransferase	1	3	3	2	1	0	0	4	1	0	1	0	1	0	0	0	0
arCOG02020	COG2603	R	Predicted ATPase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG02021	COG0607	P	Rhodanese-related sulfurtransferase	0	3	1	1	0	0	0	4	1	0	2	1	4	0	0	3	0
arCOG02022	COG0491	R	Rhodanese-related sulfurtransferase	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02023	COG0301	H	Rhodanese Homology Domain	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG02024	COG4881	S	Predicted membrane protein	1	0	2	0	1	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02025	COG5557	C	Polysulphide reductase	1	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG02026	COG5557	C	Polysulphide reductase	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02027	COG3301	P	Formate-dependent nitrite reductase, membrane com	0	3	3	0	1	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02028	COG5012	R	Predicted cobalamin binding protein	1	0	1	0	0	1	1	0	0	2	0	1	4	0	0	0	0
arCOG02029	COG1410	E	Methionine synthase I, cobalamin-binding domain	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG02030	COG5012	R	Predicted cobalamin binding protein	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02031	COG5012	R	Predicted cobalamin binding protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02032	COG5012	R	Predicted cobalamin binding protein	0	0	0	0	0	0	0	0	1	0	0	0	4	0	0	0	0
arCOG02033	COG5012	R	Predicted cobalamin binding protein	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG02034	COG5012	R	Predicted cobalamin binding protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02035	COG3894	R	Uncharacterized metal-binding protein	1	0	1	0	0	1	1	0	1	2	1	1	4	0	0	0	0
arCOG02036	COG3894	C	Methyltransferase activation protein; predicted flavo	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02037	COG1378	K	Sugar-specific transcriptional regulator TrmB	0	3	4	2	1	1	1	4	2	1	2	1	3	0	4	3	1
arCOG02038	COG1378	K	Sugar-specific transcriptional regulator TrmB	2	1	2	0	0	0	0	3	0	0	0	0	1	1	3	3	0
arCOG02039	COG1502	I	Phosphatidylserine/phosphatidylglycerophosphate/c	0	0	0	1	0	1	1	3	0	0	3	0	1	0	0	0	0
arCOG02041	COG1502	I	Phosphatidylserine/phosphatidylglycerophosphate/c	0	0	4	0	0	1	0	0	0	2	0	0	0	0	1	3	0
arCOG02042	COG1378	K	Predicted transcriptional regulator	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02043	COG1287	R	Uncharacterized membrane protein, required for N-l	0	0	0	2	0	0	1	4	0	0	3	1	5	0	0	1	0
arCOG02044	COG1287	R	Uncharacterized membrane protein, required for N-l	2	3	5	0	1	1	0	0	2	3	0	0	0	0	4	0	1
arCOG02046	COG3875	S	Uncharacterized conserved protein	0	0	0	2	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG02047	COG3875	S	Uncharacterized conserved protein	0	0	0	0	0	1	0	0	0	0	0	1	5	0	0	0	0
arCOG02048	COG1587	H	Uroporphyrinogen-III synthase	1	3	4	2	0	0	1	4	2	3	3	1	4	1	0	3	0
arCOG02049	COG1587	H	Uroporphyrinogen-III synthase	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02050	COG0730	R	Predicted permease	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	0
arCOG02052	COG0730	R	Predicted permease	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02053	COG0589	T	Nucleotide-binding protein, UspA family	2	3	5	2	1	1	1	4	2	3	3	1	5	1	3	3	0
arCOG02054	COG2881	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	2	0	1	3	1	4	0	0	0	0
arCOG02055	COG0155	P	Sulfite reductase, beta subunit (hemoprotein)	0	3	2	2	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG02056	COG1251	C	Sulfite or nitrite reductase, assimilatory-type, 4Fe-4S	0	0	0	0	0	0	0	0	0	0	2	1	5	0	0	0	0
arCOG02057	COG2221	C	Dissimilatory sulfite reductase (desulfoviridin), alph	0	0	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02058	COG2221	C	Dissimilatory sulfite reductase (desulfoviridin), alph	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02059	COG2221	C	Dissimilatory sulfite reductase (desulfoviridin), alph	0	0	4	0	0	0	1	0	1	2	3	0	4	1	0	0	0
arCOG02060	COG1145	C	Ferredoxin	0	0	0	0	0	0	0	0	0	1	0	0	4	0	0	0	0
arCOG02061	COG1035	C	Coenzyme F420-reducing hydrogenase, beta subunit	0	0	0	0	0	0	0	0	1	1	0	0	1	1	0	0	0
arCOG02062	COG0425	O	Predicted redox protein, regulator of disulfide bond	0	3	4	2	1	1	1	3	0	3	1	0	4	1	0	2	0
arCOG02064	COG2210	R	Peroxiredoxin family protein	0	3	4	0	1	1	1	3	0	0	0	0	4	0	0	2	0
arCOG02065	COG2210	R	Peroxiredoxin family protein	0	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02066	COG2044	R	Predicted peroxiredoxins	0	3	3	0	0	0	1	0	1	3	0	0	0	1	0	0	0
arCOG02067	COG2044	R	Predicted peroxiredoxins	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02068	COG1553	P	Uncharacterized conserved protein involved in intra	0	0	0	0	0	0	0	1	1	3	0	0	4	1	0	0	0
arCOG02069	COG2923	P	Uncharacterized protein involved in the oxidation of	0	0	0	0	0	0	1	1	1	0	0	0	4	0	0	0	0
arCOG02070	COG2044	R	Predicted peroxiredoxins	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02071	COG0425	O	Predicted redox protein, regulator of disulfide bond	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02072	COG0425	O	Predicted redox protein, regulator of disulfide bond	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02073		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02074	COG0425	O	Predicted redox protein, regulator of disulfide bond	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02075		S	Uncharacterized conserved protein	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
arCOG02076	COG2044	R	Predicted peroxiredoxins	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02077	COG0822	C	NifU homolog involved in Fe-S cluster formation	0	0	0	2	1	1	1	4	1	0	3	1	5	0	0	0	0
arCOG02078	COG1852	S	Uncharacterized conserved protein	0	0	0	0	0	1	1	0	2	3	3	1	5	0	1	0	0
arCOG02079	COG1361	M	S-layer domain	0	0	0	2	0	1	1	4	0	2	1	0	5	0	3	0	1
arCOG02080	COG1361	M	S-layer domain	0	0	0	2	0	1	1	0	0	2	2	1	4	0	0	0	0
arCOG02081	COG1470	S	Predicted membrane protein	0	0	1	0	0	1	1	0	0	0	0	1	4	0	1	0	0
arCOG02082		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0
arCOG02083	COG1361	M	S-layer domain	0	0	0	0	0	0	1	0	0	0	0	1	5	0	0	0	0
arCOG02085		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0
arCOG02086	COG1361	M	S-layer domain	0	0	1	0	0	0	1	0	0	0	2	1	5	0	1	0	0
arCOG02087	COG1470	S	Predicted membrane protein	0	0	1	0	0	1	0	1	0	0	1	0	0	4	0	0	0
arCOG02088		S	Uncharacterized conserved protein	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
arCOG02089	COG1361	M	S-layer domain	0	3	3	0	1	0	0	0	0	0	0	0	0	0	0	3	0
arCOG02090		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02091	COG1361	M	S-layer domain	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02092	COG0119	E	Isopropylmalate/homocitrate/citramalate synthase	0	3	4	2	1	1	1	3	2	3	3	1	5	1	4	2	0
arCOG02093	COG0119	E	Isopropylmalate/homocitrate/citramalate synthase	0	0	1	0	0	1	0	0	0	0	0	1	5	0	0	0	0
arCOG02094	COG0119	E	Isopropylmalate/homocitrate/citramalate synthase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02095	COG5016	C	Pyruvate/oxaloacetate carboxyltransferase	1	0	1	2	0	0	1	0	2	3	3	1	5	0	2	0	0
arCOG02096	COG0119	E	Isopropylmalate/homocitrate/citramalate synthase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02097	COG0710	E	3-dehydroquinate dehydratase	1	3	4	2	1	1	1	4	2	3	2	1	5	1	3	3	0
arCOG02098	COG1605	E	Chorismate mutase	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG02099	COG1321	K	Mn-dependent transcriptional regulator (DtxR famil	1	3	1	0	0	0	1	4	2	2	3	1	4	0	0	3	0
arCOG02100	COG1321	K	Mn-dependent transcriptional regulator (DtxR famil	2	3	3	2	1	1	1	4	1	1	3	1	4	1	4	3	0
arCOG02101	COG1321	K	Mn-dependent transcriptional regulator (DtxR famil	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02102	COG1918	P	Fe2+ transport system protein A	2	0	1	0	0	1	1	0	2	1	3	0	5	1	4	0	0
arCOG02103		S	Uncharacterized conserved protein	1	3	5	2	1	1	0	0	0	0	0	0	0	4	0	0	0
arCOG02104		S	Transcriptional regulator, ArsR family	0	0	0	0	0	0	1	0	0	0	0	0	4	0	0	0	0
arCOG02105	COG1708	R	Predicted nucleotidyltransferase	1	0	2	0	0	0	1	0	1	0	2	1	3	0	3	0	0
arCOG02106	COG1708	R	Predicted nucleotidyltransferase	0	0	3	0	1	0	0	0	0	0	1	0	0	0	0	0	0
arCOG02107	COG1708	R	Predicted nucleotidyltransferase	0	0	0	0	0	0	1	0	1	1	2	0	0	0	2	1	0
arCOG02108	COG2445	S	HEPN domain containing protein	1	1	3	0	0	0	1	0	1	0	2	0	2	0	3	0	0
arCOG02109	COG2445	S	HEPN domain containing protein	1	0	3	0	1	0	1	0	0	1	2	0	2	0	1	0	0
arCOG02110	COG1708	R	Predicted nucleotidyltransferase	0	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02111		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02112	COG1708	R	Predicted nucleotidyltransferase fused to HEPN don	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02113	COG2427	S	Uncharacterized conserved protein	0	3	4	0	0	1	1	1	0	0	0	0	0	0	0	1	0
arCOG02114	COG2427	S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02115	COG2427	S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG02116	COG2427	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG02117	COG2427	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02118	COG2427	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02119	COG1885	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	4	0	3	3	1	5	1	4	0	0
arCOG02120	COG1569	V	PIN domain containing protein	0	0	0	0	0	0	1	0	0	1	1	0	0	0	3	0	0
arCOG02121	COG5378	V	PIN domain containing protein	1	0	0	0	0	0	0	1	0	1	0	0	0	0	2	0	0
arCOG02122	COG5378	V	PIN domain containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG02123	COG1895	S	HEPN domain containing protein	0	0	0	0	0	0	1	0	0	1	2	1	1	0	2	0	0
arCOG02124	COG1895	S	HEPN domain containing protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG02125	COG2801	L	Transposase	0	0	0	1	0	0	1	0	0	0	0	0	1	0	0	2	0
arCOG02126	COG4584	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02127	COG3335	L	Transposase	0	1	0	0	0	0	0	0	0	0	0	0	4	0	0	1	0
arCOG02128	COG3415	L	Transposase	0	0	0	0	0	0	1	3	0	0	0	1	3	0	0	1	0
arCOG02129	COG3335	L	Transposase	0	1	0	0	0	0	1	1	0	0	0	1	2	0	0	0	0
arCOG02130	COG3335	L	Transposase	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02132	COG3677	L	Transposase	0	0	0	0	1	0	0	3	0	0	0	0	3	0	0	0	0
arCOG02133	COG1662	L	Transposase and inactivated derivatives, IS1 family	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02134	COG3316	L	Transposase	0	2	0	1	1	0	1	3	0	1	0	0	2	0	1	0	0
arCOG02137	COG3677	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0
arCOG02138	COG3677	L	Transposase	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG02139	COG1662	L	Transposase and inactivated derivatives, IS1 family	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02140		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG02141	COG3335	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02142	COG1916	S	Uncharacterized homolog of PrgY (pheromone shut	0	0	0	0	0	0	1	4	2	3	3	1	5	1	4	0	0
arCOG02143	COG2368	Q	Aromatic ring hydroxylase	0	3	3	2	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02144	COG2036	L	Histones H3 and H4	0	0	2	2	1	1	1	4	2	3	3	1	5	1	4	0	1
arCOG02145	COG2036	L	Histones H3 and H4	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG02146	COG2033	C	Desulfoferrodoxin	2	0	1	0	0	1	1	0	2	3	2	1	3	0	4	0	1
arCOG02147	COG2033	C	Desulfoferrodoxin	0	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0
arCOG02148	COG0599	S	Uncharacterized homolog of gamma-carboxymucon	1	0	0	0	0	0	1	0	1	3	3	1	5	0	1	3	0

arCOG02149	COG0599	S	Uncharacterized homolog of gamma-carboxymucon	0	2	1	0	0	0	0	0	1	1	0	1	2	0	0	0	0
arCOG02150	COG0599	S	Uncharacterized homolog of gamma-carboxymucon	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02151	COG0599	S	Uncharacterized homolog of gamma-carboxymucon	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02152	COG0599	S	Uncharacterized homolog of gamma-carboxymucon	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG02153	COG0599	S	Uncharacterized homolog of gamma-carboxymucon	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02154	COG0599	S	Uncharacterized homolog of gamma-carboxymucon	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02155	COG1873	R	Protein implicated in RNA metabolism, contains PR	0	0	0	0	0	1	1	4	2	3	3	1	5	1	4	2	1
arCOG02156	COG1873	R	Protein implicated in RNA metabolism, contains PR	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG02157	COG1873	R	Protein implicated in RNA metabolism, contains PR	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02158	COG1873	R	Protein implicated in RNA metabolism, contains PR	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG02159	COG4089	S	Predicted membrane protein	1	3	4	0	0	0	1	0	0	0	2	1	5	1	2	0	0
arCOG02160	COG1067	O	Predicted ATP-dependent protease	0	0	0	0	0	0	1	4	2	3	3	1	5	0	4	3	1
arCOG02161	COG0466	O	ATP-dependent Lon protease, bacterial type	0	0	0	0	0	0	0	0	1	0	2	0	3	0	0	0	0
arCOG02162	COG1067	O	Predicted ATP-dependent protease	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	3	0
arCOG02163	COG4930	O	Predicted ATP-dependent Lon-type protease	0	0	3	0	0	1	0	1	0	0	1	0	2	0	0	0	0
arCOG02164	COG1800	R	Predicted transglutaminase-like protease	1	0	0	0	0	0	1	0	0	3	0	0	0	0	3	0	0
arCOG02165	COG1305	E	Transglutaminase-like enzyme, putative cysteine prc	1	2	1	0	0	0	0	0	1	0	2	1	4	1	0	0	0
arCOG02167	COG1305	E	Transglutaminase-like enzyme, putative cysteine prc	0	0	1	0	0	1	0	0	0	0	2	0	0	0	0	0	0
arCOG02168	COG1305	E	Transglutaminase-like enzyme, putative cysteine prc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG02169	COG1305	E	Transglutaminase-like enzyme, putative cysteine prc	0	0	3	0	0	0	0	2	0	0	0	0	0	0	1	0	0
arCOG02170		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02171	COG1305	E	Transglutaminase-like enzyme, putative cysteine prc	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG02172	COG0720	H	6-pyruvoyl-tetrahydropterin synthase	1	3	3	2	1	0	1	4	2	3	3	1	5	1	4	3	0
arCOG02173	COG0602	O	Organic radical activating enzyme	1	3	3	2	0	0	1	2	2	3	3	1	4	1	4	3	0
arCOG02174	COG1033	R	Predicted exporter of the RND superfamily	0	0	0	0	0	0	1	4	0	3	3	1	5	1	4	0	0
arCOG02175	COG2409	R	Predicted transporter of the RND superfamily	2	3	4	0	0	0	0	0	0	0	0	1	0	0	1	3	0
arCOG02177	COG1967	S	Predicted membrane protein	0	0	0	0	0	0	1	4	1	3	3	1	5	0	4	0	1
arCOG02178	COG1967	S	Predicted membrane protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02179	COG1145	C	Polyferredoxin	0	0	0	0	0	0	1	0	1	3	0	0	0	1	0	0	0
arCOG02180	COG1145	C	Polyferredoxin	0	0	1	0	0	0	1	0	1	3	3	1	5	1	0	0	0
arCOG02181	COG1145	C	Polyferredoxin	0	1	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG02182	COG1145	C	Polyferredoxin	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG02183	COG1145	C	Polyferredoxin	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG02184	COG1145	C	Polyferredoxin	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG02185	COG1145	C	Polyferredoxin	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG02186	COG2878	C	Predicted NADH:ubiquinone oxidoreductase, subun	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02187	COG1145	C	Ferredoxin domain containing protein	1	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02189	COG1145	C	HTH containing ranscriptional regulator fused to fer	0	0	0	0	0	0	1	0	2	0	1	1	0	1	0	0	0
arCOG02190	COG0798	P	Arsenite efflux pump ACR3 or related permease	1	0	0	0	0	1	1	2	2	1	2	1	4	0	3	0	0
arCOG02191	COG0385	R	Predicted Na+-dependent transporter	0	0	0	0	0	0	0	2	0	2	0	0	3	0	0	0	0
arCOG02192	COG4031	R	Predicted metal-binding protein	0	0	0	0	0	0	1	4	0	0	0	0	4	1	0	0	0
arCOG02193	COG4031	R	Predicted metal-binding protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG02194	COG2181	C	Nitrate reductase gamma subunit	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02195	COG2181	C	Nitrate reductase gamma subunit	0	0	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02196	COG2181	C	Nitrate reductase gamma subunit	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02197	COG1617	S	Uncharacterized conserved protein	0	0	0	1	0	1	1	3	2	3	3	1	5	1	4	0	0
arCOG02198	COG1617	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG02199	COG0543	H	2-polyprenylphenol hydroxylase or related flavodox	2	3	1	2	1	1	1	0	2	3	3	1	5	1	4	3	0
arCOG02200	COG1018	C	Flavodoxin reductase (ferredoxin-NADPH reductase	0	0	0	2	0	0	0	4	0	0	0	1	2	0	0	0	1
arCOG02201	COG0206	D	Cell division GTPase	0	0	0	2	1	1	1	4	2	3	3	1	5	1	4	2	1
arCOG02202	COG0206	D	Cell division GTPase	0	0	0	0	0	0	1	4	0	0	3	0	3	0	4	0	0
arCOG02203	COG0206	D	Cell division GTPase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG02204	COG2443	U	Preprotein translocase subunit Sss1	2	3	0	0	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG02206		S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	1	4	0	0	2	1	5	0	0	3	0
arCOG02207	COG0708	L	Exonuclease III	0	3	1	0	0	0	1	0	1	2	2	1	4	0	0	3	0
arCOG02208	COG0040	E	ATP phosphoribosyltransferase	0	3	4	2	1	0	1	4	2	3	3	1	5	1	2	1	0
arCOG02209	COG2244	R	Polysaccharide biosynthesis protein, Mvin family	0	3	1	0	0	1	1	4	2	3	3	1	5	1	4	3	1
arCOG02210	COG2244	R	Polysaccharide biosynthesis protein, Mvin family	1	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG02211	COG2244	R	Polysaccharide biosynthesis protein, Mvin family	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG02212	COG2244	R	Polysaccharide biosynthesis protein, Mvin family	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG02213	COG2244	R	Polysaccharide biosynthesis protein, Mvin family	0	0	0	0	0	0	0	0	0	0	1	1	1	0	2	0	0
arCOG02214	COG2244	R	Polysaccharide biosynthesis protein, Mvin family	3	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02215		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02216		S	Uncharacterized conserved protein	1	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02217		K	Predicted antitoxin associated with PIN domain	2	3	2	0	1	0	1	0	0	0	1	0	0	0	4	0	0
arCOG02218		S	Uncharacterized conserved protein	2	3	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02219	COG1487	V	Predicted nucleic acid-binding protein, contains PIN	1	3	2	0	1	1	1	3	1	1	2	0	2	0	4	0	0
arCOG02221	COG1848	V	PIN domain containing protein	0	3	2	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG02222	COG1848	V	PIN domain containing protein	1	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG02223	COG1487	V	PIN domain containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG02224	COG1487	V	PIN domain containing protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG02225	COG1487	V	PIN domain containing protein	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
arCOG02226	COG1487	V	PIN domain containing protein	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
arCOG02227	COG1487	V	PIN domain containing protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02228	COG2246	S	Predicted membrane protein	1	3	0	0	1	0	1	4	0	0	0	1	0	1	0	3	0
arCOG02230	COG0066	E	3-isopropylmalate dehydratase small subunit	0	3	4	2	1	1	1	3	2	3	3	1	5	1	4	1	0
arCOG02231	COG2509	R	Uncharacterized FAD-dependent dehydrogenase	0	3	4	0	0	1	1	0	0	2	0	1	4	1	4	0	0
arCOG02232	COG2303	E	Choline dehydrogenase or related flavoprotein	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG02233	COG2303	E	Choline dehydrogenase or related flavoprotein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02234	COG1148	C	Heterodisulfide reductase, subunit A, polyferredoxin	0	3	0	0	0	0	1	0	0	0	3	0	0	0	0	0	0
arCOG02235	COG1148	C	Heterodisulfide reductase, subunit A or related polyf	0	0	0	0	0	1	1	0	2	3	3	1	5	1	0	0	0
arCOG02236	COG1148	C	Heterodisulfide reductase, subunit A or related polyf	0	3	0	0	0	0	0	0	1	0	0	1	3	0	0	0	0
arCOG02237	COG1145	C	Polyferredoxin	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02238	COG1342	R	Predicted DNA-binding protein	2	0	2	0	0	1	1	0	1	3	3	1	5	0	4	0	0
arCOG02239	COG1342	R	Predicted DNA-binding protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02240	COG1942	R	4-oxalocrotonate tautomerase related protein	0	0	0	2	0	1	1	0	2	2	2	1	0	0	1	0	0
arCOG02241	COG3355	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	3	0	2	0	0	0	0	0	0	0
arCOG02242	COG3355	K	Predicted transcriptional regulator	1	3	1	0	0	0	1	4	0	3	0	0	4	1	0	0	1
arCOG02243	COG5625	K	Predicted transcripton regulator containing HTH do	0	0	0	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG02244	COG2009	C	Succinate dehydrogenase/fumarate reductase, cytocl	2	0	5	2	1	1	1	4	0	0	0	0	0	0	0	2	0
arCOG02245	COG1836	S	Predicted membrane protein	0	0	5	0	1	1	1	4	2	3	3	1	5	0	4	3	0
arCOG02246	COG2138	P	Sirohydrochlorin ferrochelatase	0	3	0	2	0	0	1	4	2	3	3	1	5	1	0	0	0
arCOG02247	COG2082	H	Precorrin isomerase	0	3	2	2	0	0	1	4	2	3	3	0	5	1	0	3	0
arCOG02248	COG0310	P	ABC-type Co2+ transport system, permease compor	2	0	3	0	0	1	1	3	2	3	3	1	5	1	2	0	0
arCOG02249	COG0619	P	ABC-type cobalt transport system, permease compo	0	0	0	0	0	0	1	2	2	3	3	0	5	1	0	0	0
arCOG02250	COG0619	P	ABC-type cobalt transport system, permease compo	2	3	2	0	1	1	1	3	2	3	3	1	5	0	4	0	0
arCOG02252	COG0619	P	ABC-type cobalt transport system, permease compo	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02254	COG1745	R	Predicted metal-binding protein	0	0	0	0	0	0	1	4	1	3	3	1	3	1	0	0	0
arCOG02255	COG0253	E	Diaminopimelate epimerase	0	0	0	0	0	1	1	2	2	3	3	1	1	0	0	0	0
arCOG02256	COG0384	R	Predicted epimerase, PhzC/PhzF homolog	0	0	0	0	0	0	0	4	0	0	1	1	1	0	0	0	0
arCOG02257	COG3390	R	RPA family protein, a subunit of RPA complex in P.	0	0	0	0	0	0	1	4	0	0	3	1	5	0	0	0	0
arCOG02258	COG3390	R	RPA family protein, a subunit of RPA complex in P.	0	0	0	0	0	1	0	4	0	0	3	1	4	1	4	3	0
arCOG02259	COG1241	R	Zn-finger domain containing protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG02260		S	Zn-finger domain containing protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02261		R	Protein containing OB-fold-like and PCI domains	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	1
arCOG02262	COG3390	R	RPA family protein, a subunit of RPA complex in P.	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG02263	COG2450	S	Uncharacterized conserved protein	0	0	0	2	0	1	1	4	0	3	3	1	5	1	4	2	1
arCOG02264	COG1808	S	Predicted membrane protein	1	0	0	0	0	1	1	4	0	3	2	0	4	0	0	0	0
arCOG02265	COG0598	P	Mg2+ and Co2+ transporter	1	0	1	2	0	1	1	0	0	3	3	1	5	0	3	0	1
arCOG02266	COG0598	P	Mg2+ and Co2+ transporter	0	2	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG02267	COG0306	P	Phosphate/sulphate permease	1	3	2	0	0	0	1	4	1	1	3	1	3	1	4	3	0
arCOG02268	COG0019	E	Diaminopimelate decarboxylase	0	0	1	0	0	1	1	3	2	3	3	1	5	1	0	3	0
arCOG02269	COG1166	E	Arginine decarboxylase (spermidine biosynthesis)	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG02270	COG5428	S	Uncharacterized conserved small protein	1	0	1	0	1	1	1	0	0	0	1	0	0	0	2	0	0
arCOG02271	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	1	3	3	0	1	1	1	0	0	0	0	1	0	0	1	3	0
arCOG02272	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	1	3	2	0	0	0	0	4	0	0	1	0	0	0	0	3	0
arCOG02273	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02274	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	2	0
arCOG02276	COG2202	T	Signal transduction regulator, containsPAS and HTH	0	0	0	0	0	0	1	4	1	0	1	0	0	0	0	0	0
arCOG02278	COG2203	T	Putative light- and oxygen-sensing transcription reg	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02279	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	0	0	0	0	1	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02280	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02281	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02282	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02283	COG3413	K	Predicted transcriptional regulator, c-terminal HTH-	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG02284	COG4880	R	Secreted protein containing C-terminal beta-propelle	2	0	3	1	0	0	1	0	0	3	2	1	0	0	0	0	0
arCOG02285	COG3270	S	Uncharacterized conserved protein	0	0	0	0	1	1	1	0	0	0	0	0	0	0	4	0	1
arCOG02286	COG3270	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	1	0	0	0	0

arCOG02287	COG0393	S	Uncharacterized conserved protein	2	2	2	0	0	0	1	2	2	3	1	1	1	0	4	3	0
arCOG02288	COG0393	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG02289	COG2043	R	3-hydroxy-3-methylglutaryl CoA synthase family en	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG02290	COG2043	R	3-hydroxy-3-methylglutaryl CoA synthase family en	0	0	0	0	0	0	0	0	0	0	2	1	4	0	0	0	0
arCOG02291	COG1011	R	HAD superfamily hydrolase	2	3	5	0	1	1	0	4	2	3	3	1	5	1	4	0	0
arCOG02292	COG0546	R	Predicted phosphatase	1	0	0	0	1	1	1	4	2	0	2	1	4	0	4	0	1
arCOG02293	COG0637	R	Phosphatase/phosphohexomutase HAD superfamily	1	3	4	0	0	0	0	1	0	0	0	1	4	0	0	3	0
arCOG02294	COG1011	R	HAD superfamily hydrolase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02295	COG1011	R	HAD superfamily hydrolase	1	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG02296	COG0546	R	Predicted phosphatase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02297	COG0115	E	Branched-chain amino acid aminotransferase/4-amir	0	0	2	2	1	0	1	4	2	3	3	1	5	1	0	0	1
arCOG02298	COG1989	N	Type II secretory pathway, prepilin signal peptidase	0	0	0	0	1	0	1	0	0	3	3	1	4	0	0	0	0
arCOG02299		N	Peptidase A24A, prepilin type IV	3	3	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG02300	COG1989	N	Type II secretory pathway, prepilin signal peptidase	0	0	0	0	0	0	0	0	2	0	0	0	0	1	4	0	0
arCOG02301	COG1627	S	Archaeal Peptidase A24	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG02302	COG1989	N	Type II secretory pathway, prepilin signal peptidase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02303	COG0496	R	Predicted acid phosphatase	2	0	5	0	1	1	1	4	2	3	3	1	5	1	1	1	0
arCOG02304	COG1804	C	Predicted acyl-CoA transferase/carnitine dehydratas	0	3	4	0	1	0	1	3	0	0	0	0	0	0	0	2	0
arCOG02305	COG0347	E	Nitrogen regulatory protein PII	0	0	1	2	0	0	1	2	2	3	3	1	5	1	1	0	0
arCOG02306	COG0347	E	Nitrogen regulatory protein PII	0	0	0	1	0	0	0	0	1	2	0	1	2	0	0	0	0
arCOG02307	COG0347	E	Nitrogen regulatory protein PII	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02308	COG0347	E	Nitrogen regulatory protein PII	0	0	0	0	0	0	0	0	1	2	0	1	3	0	0	0	0
arCOG02309	COG0347	E	Nitrogen regulatory protein PII	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG02310	COG2113	E	ABC-type proline/glycine betaine transport system,	0	0	0	0	0	0	0	0	0	2	2	0	4	0	0	0	0
arCOG02311	COG1732	M	Periplasmic glycine betaine/choline-binding (lipo)pr	0	0	0	0	0	0	1	1	0	0	0	0	2	0	0	0	0
arCOG02312	COG0577	V	ABC-type antimicrobial peptide transport system, pe	2	2	5	0	1	1	1	4	1	3	3	1	5	1	1	0	1
arCOG02313	COG4591	M	ABC-type transport system, involved in lipoprotein	0	0	0	2	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02314	COG4591	M	ABC-type transport system, involved in lipoprotein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02315	COG0577	V	ABC-type antimicrobial peptide transport system, pe	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG02316	COG2150	R	Predicted regulator of amino acid metabolism, conta	0	0	1	0	0	0	1	4	2	0	3	1	5	0	4	3	0
arCOG02317	COG2150	R	Predicted regulator of amino acid metabolism, conta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	0
arCOG02318	COG0840	N	Sensory protein; contains PAS, HAMP and Methyl-a	0	0	0	0	0	0	1	3	0	0	2	1	3	0	0	0	0
arCOG02320	COG0840	N	Methyl-accepting chemotaxis protein	0	0	0	2	0	0	0	3	0	2	2	1	0	0	3	0	0
arCOG02322	COG2770	T	HAMP domain	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG02325	COG0840	N	Methyl-accepting chemotaxis protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	2	0	0
arCOG02326	COG0840	N	Methyl-accepting chemotaxis protein	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0
arCOG02327	COG0642	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	3	0	0	1	0	3	0	0	0	0
arCOG02329	COG0642	T	Signal transduction histidine kinase with PAS and R	0	0	0	0	0	0	1	4	0	0	2	0	1	0	0	0	0
arCOG02330	COG2202	T	Bacterio-opsin activator protein (contains PAS, GAI	0	0	0	0	0	0	1	3	0	0	2	1	1	0	0	0	0
arCOG02331	COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	0	3	0	0	0	0	1	0	0	0	0
arCOG02332	COG0642	T	Signal transduction histidine kinase, contains REC a	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0	0	0
arCOG02333	COG0642	T	Signal transduction histidine kinase, contains REC a	0	0	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02334	COG2202	T	Signal transduction histidine kinase with PAS domai	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02335	COG3920	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	0	1	0	2	1	3	0	0	0	0
arCOG02336	COG2202	T	Signal transduction histidine kinase with PAS domai	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0
arCOG02338	COG2202	T	Sensory protein, contains PAS and GAF domains	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0	0	0
arCOG02339	COG2202	T	Sensory protein, contains PAS domain	0	0	0	0	0	0	0	1	0	0	0	0	4	0	0	0	0
arCOG02340	COG0642	T	GAF and PAS domains	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0
arCOG02341	COG2202	T	Sensory protein, contains PAS and GAF domains	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG02342	COG3920	T	Signal transduction histidine kinase, contains Cache	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG02343	COG0642	T	Sensory protein, contains PAS and HAMP domains	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG02344	COG0840	N	Methyl-accepting chemotaxis protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02346	COG2202	T	PAS/PAC domain containing protein	0	0	0	0	0	0	0	0	0	0	2	1	4	0	0	0	0
arCOG02347	COG3920	T	PAS domain	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG02348	COG3920	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG02349	COG3920	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0
arCOG02350	COG3920	T	PAS domain	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG02351	COG2202	T	PAS domain	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG02352	COG2202	T	Signal transduction histidine kinase with PAS and PA	0	0	0	0	0	0	0	2	0	0	2	1	3	0	0	0	0
arCOG02353	COG3920	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG02354	COG0642	T	GAF and PAS domains	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0
arCOG02356	COG2203	T	GAF domain	0	0	0	0	0	0	0	1	0	0	1	0	3	0	0	0	0
arCOG02357	COG2203	T	GAF domain	0	0	0	0	0	0	0	0	1	0	0	1	2	0	0	0	0
arCOG02358	COG0642	T	Signal transduction histidine kinase and HAMP dom	0	0	0	1	0	0	0	3	0	0	1	1	5	0	0	0	0
arCOG02359	COG2202	T	GAF and PAS domains	0	0	0	0	0	0	0	2	0	0	1	0	1	0	0	0	0
arCOG02360	COG2202	T	Signal transduction histidine kinase, contains GAF a	0	0	0	0	0	0	0	2	0	0	0	0	3	0	0	0	0
arCOG02361	COG3920	T	Signal transduction histidine kinase, contains GAF a	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02362	COG0840	N	Methyl-accepting chemotaxis protein	0	0	0	0	0	0	0	0	0	0	2	1	3	0	3	0	0
arCOG02363	COG0642	T	Cache and HAMP domains	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG02364	COG0642	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	4	0	0	1	0	0	0	0	0	0
arCOG02365	COG2202	T	Signal transduction histidine kinase with PAS domai	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02366	COG2202	T	Signal transduction histidine kinase with PAS domai	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG02367	COG2202	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	1	2	0	0	2	0	0	0	0	0	0
arCOG02369	COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG02371	COG0784	T	Rec, PAS, GAF domain containing sensory protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02372	COG0840	N	Methyl-accepting chemotaxis protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG02374	COG0642	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02376	COG0642	T	Signal transduction histidine kinase, contains REC a	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02377	COG2202	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG02378	COG0642	T	Signal transduction histidine kinase, contains REC d	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG02380	COG1871	N	Chemotaxis protein; stimulates methylation of MCP	0	0	0	0	0	0	1	3	0	2	2	1	4	0	3	0	0
arCOG02381	COG1776	N	Chemotaxis protein CheC, inhibitor of MCP methyla	0	0	0	0	0	0	1	3	0	2	2	1	3	0	3	0	0
arCOG02382	COG2201	N	Chemotaxis response regulator containing a CheY-li	0	0	0	0	0	0	1	3	0	2	2	1	4	0	3	0	0
arCOG02383	COG0784	T	Rec domain	0	0	0	0	0	0	0	1	1	0	2	0	3	0	0	0	0
arCOG02384	COG2202	T	REC and PAS domains	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG02385	COG0784	T	Rec domain	0	0	0	0	0	0	0	1	0	0	2	1	1	0	0	0	0
arCOG02386	COG3920	T	REC domain	0	0	0	0	0	0	0	0	1	0	1	0	2	0	0	0	0
arCOG02387	COG0784	T	Signal transduction regulator, contains Rec and HTH	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02388	COG2202	T	REC domain	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02389	COG0784	T	Rec domain	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02390	COG0642	T	REC domain	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02391	COG0784	T	Rec domain	0	0	0	1	0	0	1	4	0	2	2	1	5	0	3	0	0
arCOG02392	COG0784	T	Rec domain	0	0	0	0	0	0	0	0	1	0	1	0	4	0	0	0	0
arCOG02393	COG0784	T	Rec domain	0	0	0	0	0	0	0	0	1	0	1	1	3	0	0	0	0
arCOG02394	COG2469	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	3	0	3	2	1	3	0	3	0	0
arCOG02395	COG0835	N	Chemotaxis signal transduction protein	0	0	0	0	0	0	1	3	0	2	2	1	4	0	3	0	0
arCOG02396		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	2	1	3	0	0	0	0
arCOG02397		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02398	COG0785	O	Cytochrome c biogenesis protein	0	0	0	2	0	0	1	2	1	1	1	1	4	0	0	0	0
arCOG02399	COG0785	O	Cytochrome c biogenesis protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG02400	COG0785	O	Cytochrome c biogenesis protein	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG02402	COG4232	O	Thiol:disulfide interchange protein	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG02403	COG0785	O	Cytochrome c biogenesis protein	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG02404	COG0785	O	Cytochrome c biogenesis protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	1
arCOG02405	COG0785	O	Cytochrome c biogenesis protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG02406	COG0785	O	Cytochrome c biogenesis protein	2	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG02407	COG0526	O	Thioredoxin fused to Cytochrome c biogenesis prote	2	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG02408	COG1432	S	Uncharacterized conserved protein	0	0	0	0	0	1	1	4	1	3	0	1	5	1	4	0	0
arCOG02409	COG1432	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0
arCOG02410	COG2141	C	Coenzyme F420-dependent N5,N10-methylene tetra	0	1	0	2	1	0	1	4	2	3	3	1	5	1	0	0	0
arCOG02411	COG1598	R	Predicted nuclease of the RNAse H fold, HicB famil	0	0	0	0	0	0	1	0	1	0	2	1	4	0	2	1	0
arCOG02412	COG1598	R	Predicted nuclease of the RNAse H fold, HicB famil	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG02413	COG1598	R	Predicted nuclease of the RNAse H fold, HicB famil	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0
arCOG02414	COG2026	K	Cytotoxic translational repressor of toxin-antitoxin s	0	0	0	0	0	0	1	0	0	3	0	0	2	0	0	0	0
arCOG02415	COG2026	K	Cytotoxic translational repressor of toxin-antitoxin s	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02416	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	4	0	0	2	1	4	0	0	0	0
arCOG02417	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	2	1	0	0	0	0	0
arCOG02418	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02419	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02420	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG02421	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG02422	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0	0	0
arCOG02423	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2	0
arCOG02424	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG02425	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02426	COG3430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02427	COG0836	M	Mannose-1-phosphate guanylyltransferase fused to c	0	0	0	0	0	1	1	3	0	1	2	0	4	0	4	0	0
arCOG02428	COG1152	C	CO dehydrogenase/acetyl-CoA synthase alpha subun	0	0	0	0	0	0	1	0	1	3	1	1	5	1	0	0	0

arCOG02429	COG1151	C	6Fe-6S prismane cluster-containing protein	0	0	0	0	0	1	1	0	0	1	1	0	4	1	0	0	0
arCOG02430	COG1151	C	6Fe-6S prismane cluster-containing protein	0	0	0	0	0	0	0	0	2	2	2	1	2	0	2	0	0
arCOG02431	COG1611	R	Predicted Rossmann fold nucleotide-binding protein	2	3	5	2	1	0	1	3	1	0	3	1	3	1	3	3	0
arCOG02432	COG0758	L	Predicted Rossmann fold nucleotide-binding protein	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
arCOG02433	COG5418	S	Predicted secreted protein	0	0	0	0	0	0	0	0	0	2	3	0	5	0	4	0	0
arCOG02434	COG3613	F	Nucleoside 2-deoxyribosyltransferase	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG02435	COG3613	F	Nucleoside 2-deoxyribosyltransferase	0	0	1	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02436	COG1277	R	ABC-type transport system involved in multi-copper	0	0	1	0	0	0	1	3	0	0	1	1	3	0	4	1	0
arCOG02438	COG1277	R	ABC-type transport system involved in multi-copper	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG02440	COG1277	R	ABC-type transport system involved in multi-copper	0	0	1	0	1	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02441	COG1277	R	ABC-type transport system involved in multi-copper	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02442	COG1277	R	ABC-type transport system involved in multi-copper	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02443	COG1277	R	ABC-type transport system involved in multi-copper	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG02444	COG3368	R	Predicted permease	0	0	0	0	0	1	1	0	0	0	0	0	0	0	4	3	0
arCOG02445	COG1145	C	Ferredoxin	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG02446	COG2006	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	3	0	0	0	0
arCOG02447	COG2006	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	1	0	2	1	4	0	0	0	0
arCOG02448	COG2768	R	Uncharacterized Fe-S center protein	0	0	0	0	0	0	1	0	2	1	3	1	4	1	0	0	0
arCOG02449	COG1145	C	Flavodoxin fused to ferredoxin domain	0	0	0	0	0	0	0	0	1	0	3	1	2	0	0	0	0
arCOG02451	COG1145	C	Ferredoxin fused to a conserved domain of DUF362	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02452		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	3	0	0	1	0	1	0	0	0	0
arCOG02453	COG0467	T	Predicted RecA-superfamily ATPase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02454		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02455	COG0636	C	Archaeal/vacuolar-type Na+/H+-ATPase, subunit K	3	3	5	1	0	1	1	4	2	3	3	1	5	1	4	3	1
arCOG02459	COG1527	C	Archaeal/vacuolar-type H+-ATPase subunit C	0	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG02460	COG1145	C	Ferredoxin	0	0	0	0	0	0	1	0	1	3	3	1	5	1	0	0	0
arCOG02461	COG1146	C	Ferredoxin	0	0	0	0	0	0	0	0	1	1	1	1	1	0	1	0	0
arCOG02462	COG1878	E	Kynurenine formamidase	1	2	3	2	1	0	1	3	1	3	2	1	5	0	2	3	0
arCOG02464	COG0041	F	Phosphoribosylcarboxyaminoimidazole (NCAIR) m	0	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG02465	COG1691	R	NCAIR mutase (PurE)-related protein	0	0	0	2	0	1	1	2	2	3	3	1	5	1	0	0	0
arCOG02466	COG3277	J	RNA-binding protein involved in rRNA processing	1	1	5	2	1	0	1	4	2	3	1	1	5	1	4	3	0
arCOG02467	COG3277	J	RNA-binding protein involved in rRNA processing	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02468	COG1810	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	1	2	0	0	5	1	0	0	0
arCOG02469	COG1810	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	1	3	1	0	5	1	0	0	0
arCOG02470	COG2834	M	Outer membrane lipoprotein-sorting protein	0	0	0	0	0	0	1	3	0	1	1	0	4	0	1	0	0
arCOG02471	COG4801	R	Predicted acyltransferase	0	0	0	0	0	0	1	4	0	0	2	0	4	1	0	0	0
arCOG02472	COG1941	C	Coenzyme F420-reducing hydrogenase, gamma subu	0	0	0	0	1	1	1	0	2	3	1	1	0	1	4	0	0
arCOG02473	COG1941	C	Coenzyme F420-reducing hydrogenase, gamma subu	0	0	0	0	0	0	0	0	2	3	3	1	3	1	0	0	0
arCOG02474	COG1740	C	Ni,Fe-hydrogenase I small subunit	1	0	3	0	0	0	1	0	0	0	0	1	3	0	0	0	0
arCOG02475	COG1908	C	Coenzyme F420-reducing hydrogenase, delta subuni	0	0	0	0	0	1	1	0	2	3	3	1	0	1	0	0	0
arCOG02476	COG1148	C	Heterodisulfide reductase, subunit A; ferredoxin don	0	0	0	0	0	0	1	0	0	0	0	0	5	0	0	0	0
arCOG02477	COG2864	C	Cytochrome b subunit of formate dehydrogenase	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG02478	COG2864	C	Cytochrome b subunit of formate dehydrogenase	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG02479	COG1520	S	WD40-like repeat	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG02480	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	1	1	0	0	0	3	0	0	0	0
arCOG02481	COG1520	S	WD40-like repeat	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02482	COG1520	S	WD40-like repeat	0	0	0	0	0	0	0	0	2	0	1	1	3	0	0	0	0
arCOG02483	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0
arCOG02485	COG1520	S	WD40-like repeat	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02486	COG1305	E	Transglutaminase-like enzyme, putative cysteine prc	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3	0	0
arCOG02487		S	Cell suface protein	1	0	2	0	0	1	1	0	1	2	3	1	1	0	3	0	0
arCOG02488		S	Cell suface protein	0	0	0	0	0	0	0	2	1	0	0	1	0	0	0	0	0
arCOG02489	COG2319	S	WD40 repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02490	COG1520	S	WD40-like repeat	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0
arCOG02491	COG2319	S	WD40 repeats containing protein	1	0	0	0	0	0	0	0	0	0	1	1	3	0	1	0	0
arCOG02492	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02493	COG1520	S	WD40-like repeat	0	0	0	0	0	0	0	1	0	2	0	1	1	0	0	0	0
arCOG02495	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	1	1	0	0	0	2	0	0	0	0
arCOG02496	COG1520	S	WD40-like repeat	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02497		S	S-layer protein	0	0	0	0	0	1	1	0	2	2	1	0	5	0	0	0	0
arCOG02498		S	S-layer protein	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0	0	0
arCOG02499	COG3420	S	NosD-like periplasmic protein	0	0	0	0	0	1	1	0	0	1	1	0	4	0	0	0	0
arCOG02500	COG3420	R	NosD-like periplasmic protein	0	0	0	0	0	0	0	0	2	1	0	0	5	0	0	0	0
arCOG02501	COG4870	O	C1 Peptidase family protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG02502	COG3420	S	NosD-like periplasmic protein	0	0	0	0	0	0	0	0	1	1	0	0	2	0	0	0	0
arCOG02503	COG3391	S	beta-propeller repeat protein	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG02505	COG3391	S	beta-propeller repeat protein	0	0	0	1	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG02506	COG3391	S	beta-propeller repeat protein	0	0	0	1	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG02507	COG3391	S	beta-propeller repeat protein	0	0	0	1	0	0	0	1	0	0	0	1	1	0	0	0	0
arCOG02508	COG3291	S	PKD repeats containing protein	0	0	0	0	0	1	1	0	1	1	1	0	3	0	0	0	0
arCOG02510	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	2	1	3	0	0	0	0
arCOG02511	COG5563	S	Predicted integral membrane protein containing PKI	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG02512	COG1404	S	WD40 and PKD repeats	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG02514	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02515	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	1	0	2	0	2	0	0	0	0
arCOG02516	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG02517	COG3420	S	NosD-like periplasmic protein fused to PKD repeat	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0
arCOG02519	COG3420	P	Lipoprotein involved in nitrous oxide reduction Nos	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	1	0
arCOG02521	COG3420	S	NosD-like periplasmic protein	0	0	0	0	0	0	0	0	1	0	1	1	4	0	0	0	0
arCOG02522	COG3420	S	NosD-like periplasmic protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02523	COG0526	O	NosD-like periplasmic protein fused to thioredoxin	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02524	COG3420	S	NosD-like periplasmic protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02525	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02526	COG3420	S	NosD-like periplasmic protein	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02527	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG02531	COG3291	S	beta-propeller repeat protein fused to CARDB-like a	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG02532	COG3291	S	beta-propeller repeat protein fused to CARDB-like a	0	0	0	0	0	0	1	0	0	0	1	0	3	0	1	0	0
arCOG02533	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG02534	COG3391	S	beta-propeller repeat protein	0	0	0	0	0	0	0	0	1	0	1	0	3	0	0	0	0
arCOG02536	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG02537		S	beta-propeller repeat protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02538	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02539	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG02540	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	1	0	0	1	0	3	0	0	0	0
arCOG02541		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02542		R	Diverged archaeal ATPase	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02543	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02544	COG3291	S	NosD-like periplasmic protein fused to PKD repeat	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02545	COG3291	S	NosD-like periplasmic protein fused to PKD repeat	0	0	0	0	0	0	0	1	0	0	1	0	3	0	0	0	0
arCOG02546	COG3291	S	PKD repeats containing protein	0	0	0	0	0	1	0	0	0	0	1	0	3	0	0	0	0
arCOG02547		S	Surface protein, enriched in asn/thr	0	0	0	0	0	0	1	0	1	0	1	0	1	0	0	0	0
arCOG02549		S	Cell suface protein	0	0	0	0	0	0	0	1	0	0	0	0	4	0	0	0	0
arCOG02550	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02552	COG3291	S	NosD-like periplasmic protein fused to PKD repeat	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG02553	COG1404	O	Subtilisin-like serine protease	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02554	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02555	COG3420	S	NosD-like periplasmic protein	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
arCOG02556	COG1520	S	WD40-like repeat	0	1	1	0	0	1	0	4	0	1	0	1	2	1	0	1	0
arCOG02558		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02559		S	Cell suface protein	1	0	1	0	0	1	0	0	1	0	3	1	3	0	3	0	0
arCOG02560	COG3391	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	2	0
arCOG02561	COG2319	S	WD40 repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02562	COG3391	S	Uncharacterized conserved protein	0	2	0	1	0	0	0	1	0	0	0	1	3	0	0	0	0
arCOG02563	COG3291	S	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02565	COG5276	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	3	0	0	0	0
arCOG02566		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0
arCOG02567	COG3420	P	NosD-like periplasmic protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02568		S	beta-propeller repeat periplasmic protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02569	COG0038	P	Chloride channel protein EriC	3	3	2	0	0	0	1	1	0	1	2	0	5	1	3	3	0
arCOG02570	COG4855	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	2	2	3	0	5	0	0	0	0
arCOG02571	COG4855	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02572	COG0655	R	Multimeric flavodoxin WrbA	1	0	0	0	0	0	1	0	1	2	3	1	5	0	0	0	0
arCOG02573	COG0655	R	Multimeric flavodoxin WrbA	1	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG02574	COG0655	R	Multimeric flavodoxin WrbA	0	0	0	0	0	0	0	0	0	0	3	0	2	0	0	0	0
arCOG02575	COG0655	R	Multimeric flavodoxin WrbA	0	0	0	0	0	0	0	0	1	0	3	1	3	0	0	0	0
arCOG02576	COG0655	R	Multimeric flavodoxin WrbA	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02577	COG2249	R	Putative NADPH-quinone reductase (modulator of d	0	0	0	1	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG02578	COG0655	R	Multimeric flavodoxin WrbA	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0

arCOG02579	COG0727	R	Predicted Fe-S-cluster oxidoreductase	2	0	5	2	0	1	1	4	0	3	3	1	5	0	4	0	0
arCOG02581	COG0727	R	Predicted Fe-S-cluster oxidoreductase	0	0	0	0	0	0	0	1	0	0	3	1	4	0	0	0	0
arCOG02582	COG0727	R	Predicted Fe-S-cluster oxidoreductase	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02583	COG0727	R	Predicted Fe-S-cluster oxidoreductase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02584	COG0727	R	Predicted Fe-S-cluster oxidoreductase	2	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02585	COG0727	R	Predicted Fe-S-cluster oxidoreductase	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02586	COG0727	R	Predicted Fe-S-cluster oxidoreductase	0	3	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG02587	COG1146	C	Ferredoxin	0	0	1	0	0	0	1	0	1	3	0	0	0	0	0	0	0
arCOG02588	COG1145	C	Ferredoxin	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02589	COG0784	T	Rec domain	0	0	0	0	0	0	1	2	1	0	1	0	5	0	0	0	0
arCOG02590	COG0643	N	Rec domain	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG02591	COG0784	T	Rec domain	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG02592	COG0784	T	Rec domain	0	0	0	0	0	0	0	0	1	0	2	0	4	0	0	0	0
arCOG02594	COG0784	T	Rec domain	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG02595	COG0745	T	REC domain	0	0	0	0	0	0	0	0	0	2	2	1	1	0	0	0	0
arCOG02597	COG0784	T	Rec domain	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0
arCOG02598	COG0745	T	REC domain containing protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG02599	COG0784	T	Rec domain	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02600	COG0784	T	Signal transduction regulator, contains Rec and HTF	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02601	COG0784	T	Rec domain	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02602	COG2140	G	Thermophilic glucose-6-phosphate isomerase or rela	0	0	0	0	0	1	1	0	0	0	3	1	5	0	4	0	0
arCOG02603	COG2018	R	Roadblock/LC7 domain	1	0	2	0	0	0	1	0	1	3	2	1	0	1	0	0	0
arCOG02605	COG2018	R	Roadblock/LC7 domain	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG02606	COG0695	O	Glutaredoxin	0	0	0	0	0	0	1	1	1	0	2	1	4	0	0	0	0
arCOG02607	COG0695	O	Glutaredoxin	0	0	0	0	0	0	0	0	0	0	2	1	4	0	0	0	0
arCOG02608	COG0695	O	Glutaredoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02609	COG0695	O	Glutaredoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02610	COG1354	L	Rec8/ScpA/Scc1-like protein (kleisin family)	0	0	0	2	1	1	1	4	0	3	3	1	5	0	4	3	0
arCOG02611	COG3398	S	Predicted transcriptional regulator, containd two HT	0	0	2	2	0	1	1	4	0	2	3	1	4	0	0	0	0
arCOG02613	COG1386	K	Chromosome segregation and condensation protein I	0	0	0	2	1	1	1	0	0	0	0	1	5	0	4	3	0
arCOG02614		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG02615		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG02616	COG0535	R	Radical SAM superfamily enzyme	0	0	3	0	0	0	1	0	0	1	0	0	1	0	0	0	0
arCOG02617		S	Uncharacterized conserved protein	0	3	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02618	COG1146	C	Ferredoxin	0	0	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG02619	COG1145	C	Ferredoxin	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG02620	COG1541	H	Coenzyme F390 synthetase	0	3	0	0	1	0	1	1	2	2	3	1	5	0	0	0	0
arCOG02622	COG1541	H	Coenzyme F390 synthetase	0	0	0	0	0	0	0	0	1	0	2	0	4	0	0	0	0
arCOG02623	COG1541	H	Coenzyme F390 synthetase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02624	COG1541	H	Coenzyme F390 synthetase	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG02625	COG1451	R	Predicted metal-dependent hydrolase	1	0	0	1	0	0	1	1	2	3	3	1	5	0	4	1	0
arCOG02626	COG0732	V	Restriction endonuclease S subunit	1	0	0	1	0	0	1	1	2	2	3	1	3	0	1	2	0
arCOG02627	COG0732	V	Restriction endonuclease S subunit	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG02628	COG0732	V	Restriction endonuclease S subunit	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG02629	COG0732	V	Restriction endonuclease S subunit	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG02630	COG0732	V	Restriction endonuclease S subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02631	COG0732	V	Type I restriction modification DNA specificity dom	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
arCOG02632	COG0286	V	Type I restriction-modification system methyltransfe	1	0	1	1	0	1	1	1	2	2	2	1	5	0	1	1	0
arCOG02633	COG1002	V	Type II restriction enzyme, methylase subunit	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0
arCOG02634	COG1002	V	Type II restriction enzyme, methylase subunit	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG02635	COG1002	V	Type II restriction enzyme, methylase subunit	0	0	0	0	1	0	0	3	0	1	1	0	2	0	1	2	0
arCOG02636	COG0827	L	Adenine-specific DNA methylase	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0
arCOG02638	COG0657	I	Esterase/lipase	0	3	2	1	0	0	1	2	0	0	0	1	1	0	0	2	0
arCOG02639	COG5561	S	Predicted metal-binding protein	0	0	0	0	0	0	1	0	0	2	2	0	4	0	0	0	0
arCOG02640	COG1392	P	Phosphate transport regulator (distant homolog of PI	1	3	0	2	1	0	1	0	1	1	3	1	3	0	4	0	0
arCOG02641	COG1392	P	Phosphate transport regulator (distant homolog of PI	2	3	5	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG02642	COG0628	R	Predicted permease, member of the PurR regulon	0	0	0	0	0	0	1	4	1	3	3	1	5	0	4	0	1
arCOG02643	COG1309	K	Transcriptional regulator, TetR/AcrR family	0	0	0	0	0	0	1	1	1	2	3	1	2	0	0	0	0
arCOG02644	COG1309	K	Transcriptional regulator, TetR/AcrR family	0	0	0	0	0	0	0	0	1	0	0	1	3	0	0	0	0
arCOG02645	COG1309	K	Transcriptional regulator, TetR/AcrR family	0	0	0	0	0	0	0	0	0	1	0	1	3	0	0	0	0
arCOG02646	COG1309	K	Transcriptional regulator, TetR/AcrR family	0	0	0	0	0	0	0	2	1	0	0	0	3	0	0	0	0
arCOG02647	COG1309	K	Transcriptional regulator, TetR/AcrR family	0	3	0	0	0	0	0	1	0	0	2	1	2	0	0	0	0
arCOG02648	COG1309	K	Transcriptional regulator, TetR/AcrR family	0	0	0	0	0	0	0	1	1	0	0	1	3	0	0	0	0
arCOG02649	COG1309	K	Transcriptional regulator, TetR/AcrR family	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0
arCOG02650	COG1035	C	Coenzyme F420-reducing hydrogenase, beta subunit	0	0	0	0	1	0	1	1	2	3	2	1	5	0	0	0	0
arCOG02651	COG1035	C	Coenzyme F420-reducing hydrogenase, beta subunit	0	0	0	0	1	0	0	0	2	3	3	1	3	1	0	0	0
arCOG02652	COG1035	C	Coenzyme F420-reducing hydrogenase, beta subunit	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0
arCOG02653	COG1035	C	Coenzyme F420-reducing hydrogenase, beta subunit	0	0	0	0	0	0	0	0	2	3	3	1	1	0	0	0	0
arCOG02654	COG3337	V	CRISPR system related protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0
arCOG02655	COG3337	V	CRISPR system related protein	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02656	COG3337	V	CRISPR system related protein	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG02657	COG1336	V	CRISPR system related protein, RAMP superfamily	1	2	3	0	0	1	1	0	1	0	0	0	3	1	1	0	0
arCOG02658	COG1337	V	CRISPR system related protein, RAMP superfamily	1	3	3	0	1	0	0	0	1	1	1	0	1	1	1	2	0
arCOG02659	COG1337	V	CRISPR system related protein, RAMP superfamily	0	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02660	COG1337	V	CRISPR system related protein, RAMP superfamily	0	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02661	COG1604	V	CRISPR system related protein, RAMP superfamily	1	2	3	0	0	1	1	0	0	0	0	0	1	1	1	0	0
arCOG02662	COG1604	V	CRISPR system related protein, RAMP superfamily	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG02663	COG1769	V	CRISPR system related protein, RAMP superfamily	0	0	0	0	0	0	1	0	0	0	0	0	1	1	1	0	0
arCOG02664	COG1517	V	CRISPR system related protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02665	COG1769	V	CRISPR system related protein, RAMP superfamily	1	2	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG02666	COG1353	V	Predicted CRISPR-associated polymerase	1	2	3	0	0	1	1	0	0	0	0	0	1	1	1	0	0
arCOG02667	COG1353	V	Predicted CRISPR-associated polymerase	1	0	1	0	0	0	0	0	1	1	0	0	1	1	1	2	0
arCOG02668	COG1353	V	Predicted CRISPR-associated polymerase	0	3	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0
arCOG02669	COG1353	V	Predicted CRISPR-associated polymerase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02670	COG1688	V	CRISPR system related protein, RAMP superfamily	2	2	0	0	1	1	1	0	0	0	0	0	0	0	3	0	0
arCOG02671	COG1688	V	CRISPR system related protein, RAMP superfamily	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02672	COG1688	V	CRISPR system related protein, RAMP superfamily	1	0	1	0	0	0	1	0	0	1	0	0	0	0	1	0	0
arCOG02673	COG1422	S	Predicted membrane protein	0	0	0	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG02674	COG1153	C	Formylmethanofuran dehydrogenase subunit D	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG02675	COG3252	H	Methenyltetrahydromethanopterin cyclohydrolase	0	0	0	0	0	0	1	4	2	3	3	1	5	1	0	0	0
arCOG02676	COG0139	E	Phosphoribosyl-AMP cyclohydrolase	0	3	4	2	1	0	1	4	2	3	3	1	5	1	2	1	0
arCOG02677	COG0140	E	Phosphoribosyl-ATP pyrophosphohydrolase	0	3	4	0	0	0	0	4	2	3	3	1	4	1	0	0	0
arCOG02678	COG1924	I	Activator of 2-hydroxyglutaryl-CoA dehydratase (H	0	0	0	0	1	0	1	0	0	3	0	1	0	1	0	0	0
arCOG02679	COG1924	I	Activator of 2-hydroxyglutaryl-CoA dehydratase (H	0	0	0	0	0	1	0	0	2	3	3	1	5	1	0	0	0
arCOG02680	COG1326	R	Uncharacterized archaeal Zn-finger protein	0	0	0	0	0	0	1	4	2	3	3	1	5	1	4	0	0
arCOG02681	COG1753	K	Predicted antotoxin, copG family	0	2	0	0	1	0	1	0	0	1	1	0	2	0	4	0	0
arCOG02682	COG0477	G	permease of the major facilitator superfamily	1	3	5	0	0	1	0	1	0	0	1	0	0	0	3	0	0
arCOG02683	COG0477	G	permease of the major facilitator superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG02684	COG0477	G	permease of the major facilitator superfamily	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG02685	COG0477	G	permease of the major facilitator superfamily	0	2	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG02686	COG0477	G	permease of the major facilitator superfamily	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG02687	COG0477	G	permease of the major facilitator superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG02688	COG0477	G	permease of the major facilitator superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG02689	COG0477	G	permease of the major facilitator superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG02690	COG0477	G	permease of the major facilitator superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG02691	COG0477	G	permease of the major facilitator superfamily	0	3	4	0	0	0	1	0	0	0	0	0	0	0	3	0	0
arCOG02692	COG0477	G	permease of the major facilitator superfamily	0	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
arCOG02693	COG0477	G	permease of the major facilitator superfamily	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02694	COG1826	U	Sec-independent protein secretion pathway compone	2	3	5	2	1	1	1	4	0	0	0	1	4	1	0	3	0
arCOG02695	COG2037	C	Formylmethanofuran:tetrahydromethanopterin form	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG02696		S	Uncharacterized conserved protein, DUF1102 family	0	0	0	0	0	0	1	1	0	0	0	0	0	0	4	0	0
arCOG02697		S	Uncharacterized conserved protein, DUF1102 family	0	0	0	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG02698		S	Uncharacterized conserved protein, DUF1102 family	0	0	0	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG02699	COG0511	I	Biotin carboxyl carrier protein	2	3	0	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG02700	COG0508	C	Pyruvate/2-oxoglutarate dehydrogenase complex, di	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02701	COG1641	S	Uncharacterized conserved protein	0	0	0	2	0	1	1	2	2	3	3	1	5	1	0	0	0
arCOG02702	COG0500	Q	SAM-dependent methyltransferase	0	3	1	0	0	0	1	3	1	0	1	1	3	0	2	3	0
arCOG02703	COG0500	Q	SAM-dependent methyltransferase	0	2	0	0	1	0	0	0	0	0	2	0	2	0	0	0	0
arCOG02704	COG2226	H	Methylase involved in ubiquinone/menaquinone bio	0	0	0	0	0	0	0	0	0	0	1	0	2	0	1	0	0
arCOG02705	COG4799	I	Acetyl-CoA carboxylase, carboxyltransferase compo	2	3	1	2	1	0	1	4	0	0	0	0	0	0	4	0	0
arCOG02706	COG0346	E	Lactoylglutathione lyase or related enzyme	0	3	1	2	0	0	1	4	0	0	1	1	0	0	4	1	0
arCOG02708	COG0346	E	Lactoylglutathione lyase or related enzyme	0	0	0	2	0	0	0	4	1	0	1	1	1	0	0	0	0
arCOG02709	COG0346	E	Lactoylglutathione lyase or related enzyme	0	0	0	2	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02710	COG1693	K	Repressor of nif and glnA expression	0	0	0	0	0	0	1	0	2	3	2	1	5	1	0	0	0
arCOG02711	COG1693	K	Repressor of nif and glnA expression	0	0	0	0	0	0	0	0	0	0	2	1	5	0	0	0	0
arCOG02712	COG0701	R	Predicted permease	0	0	0	0	0	0	1	3	1	3	3	1	5	1	0	0	0
arCOG02713	COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	1	0	0	0	1	0	1	3	3	1	5	0	0	0	0
arCOG02714	COG1478	H	GTP and metal dependent enzyme involved F420 co	0	0	0	2	1	1	1	4	2	3	3	1	5	1	0	0	0

arCOG02715	COG4071	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG02716		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	4	0	0	0	0
arCOG02717	COG2034	S	Predicted membrane protein	0	0	0	0	0	1	1	0	1	1	0	0	3	1	4	2	0
arCOG02718	COG2034	S	Predicted membrane protein	2	2	2	0	0	0	0	0	0	0	0	0	4	0	0	1	0
arCOG02719	COG2034	S	Predicted membrane protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02720	COG1271	C	Cytochrome bd-type quinol oxidase, subunit 1	1	0	3	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG02721	COG1271	C	Cytochrome bd-type quinol oxidase, subunit 1	1	0	3	0	0	1	1	1	0	0	0	0	2	0	0	3	0
arCOG02722	COG2170	H	Glutamate-cysteine ligase family 2(GCS2)	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02723	COG2170	S	Glutamate-cysteine ligase family 2	0	0	0	0	0	0	1	1	0	2	0	0	1	0	0	0	0
arCOG02724	COG0350	L	Methylated DNA-protein cysteine methyltransferase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG02726	COG0721	J	Asp-tRNAAsn/Glu-tRNAGln amidotransferase C su	1	3	0	1	0	0	1	4	0	0	3	1	5	0	0	0	1
arCOG02727	COG1673	S	Uncharacterized protein conserved in archaea	0	3	0	0	1	1	1	0	1	2	2	0	0	0	2	0	0
arCOG02728		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
arCOG02729	COG1673	S	Uncharacterized protein conserved in archaea	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02730	COG1848	V	PIN domain containing protein	1	3	2	0	0	1	1	0	0	0	0	0	0	0	4	0	0
arCOG02731	COG1487	V	PIN domain containing protein	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG02732	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	1	0	0	0	0	1	0	0	4	0	0
arCOG02733	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG02734	COG1433	S	NifX family protein	2	1	5	0	0	1	1	0	1	3	3	1	5	1	4	2	0
arCOG02736	COG1433	S	NifX family protein	0	0	0	0	0	1	0	0	2	2	0	0	2	0	0	0	0
arCOG02737	COG1433	S	NifX family protein	1	0	2	0	0	0	0	0	0	0	0	0	0	0	3	0	1
arCOG02738	COG1433	S	NifX family protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG02739	COG1433	S	NifX family protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02740	COG1600	C	Uncharacterized Fe-S protein	0	0	0	0	0	1	1	0	2	2	3	1	4	0	2	0	0
arCOG02741	COG0422	H	Thiamine biosynthesis protein ThiC	1	3	2	2	0	0	1	3	2	3	3	1	5	1	3	0	0
arCOG02742	COG1721	R	Uncharacterized conserved protein, DUF58 family,	2	0	2	0	1	0	1	4	0	0	0	0	0	0	4	2	1
arCOG02743	COG1721	R	Uncharacterized conserved protein, DUF58 family,	0	0	0	0	0	0	0	0	0	2	0	0	0	0	3	0	0
arCOG02744	COG1721	R	Uncharacterized conserved protein, DUF58 family,	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02745	COG1721	R	Uncharacterized conserved protein, DUF58 family,	1	0	0	2	0	0	0	2	0	0	2	1	5	0	0	0	0
arCOG02746	COG1721	R	Uncharacterized conserved protein, DUF58 family,	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02747	COG1721	R	Uncharacterized conserved protein, DUF58 family,	2	0	0	0	0	0	0	2	0	0	3	0	0	0	0	0	0
arCOG02748	COG1721	R	Uncharacterized conserved protein, DUF58 family,	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02749	COG1378	K	Predicted transcriptional regulator	1	0	0	0	0	0	0	4	0	0	0	0	0	0	0	1	0
arCOG02750		K	Predicted transcriptional regulator, HTH	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02751	COG3039	L	Transposase, IS5 family	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02752	COG3039	L	Transposase, IS5 family	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02753	COG3039	L	Transposase, IS5 family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02754	COG3039	L	Transposase, IS5 family	0	1	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0
arCOG02755	COG3039	L	Transposase, IS5 family	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02756	COG4190	K	Predicted transcriptional regulator	0	0	1	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02757	COG3649	V	CRISPR system related protein	0	0	0	0	0	0	0	1	1	1	0	0	3	0	0	0	0
arCOG02758	COG1688	V	CRISPR system related protein, RAMP superfamily	0	0	0	0	0	0	0	1	2	1	0	0	3	0	1	0	1
arCOG02759	COG1943	L	Transposase	0	2	0	0	0	0	0	4	0	0	0	0	3	0	1	2	0
arCOG02761	COG3439	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	1	0	1	3	0
arCOG02762	COG3439	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG02763	COG2217	P	Heavy-metal-associated domain (HMA)	1	1	5	0	0	0	1	4	2	0	3	1	5	0	2	0	0
arCOG02764	COG2608	P	Copper-ion-binding protein	1	1	0	0	0	0	1	3	0	2	0	1	4	0	1	2	0
arCOG02765	COG2608	P	Copper-ion-binding protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02766	COG1266	R	Metal-dependent membrane protease, CAAX family	0	0	0	0	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02767	COG1266	R	Metal-dependent membrane protease, CAAX family	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02768	COG1266	R	Metal-dependent membrane protease, CAAX family	1	0	3	0	0	1	0	1	1	1	2	1	3	0	0	0	0
arCOG02769	COG1266	R	Metal-dependent membrane protease, CAAX family	0	0	1	0	0	0	0	2	1	0	0	1	4	0	1	0	0
arCOG02770	COG1266	R	Metal-dependent membrane protease, CAAX family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02771		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02772	COG0348	C	Polyferredoxin	1	1	1	0	0	0	1	0	0	3	3	0	4	1	0	0	0
arCOG02773		K	HTH-domain containg transcriptional regulator	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02774		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02775	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02776	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02777	COG1715	V	Restriction endonuclease	0	0	0	0	0	0	0	4	0	1	1	0	1	0	0	0	0
arCOG02780		V	Endonuclease, HJR/Mrr/RecB family	0	0	0	0	0	0	0	0	0	0	3	1	4	0	0	0	0
arCOG02781	COG1715	V	Endonuclease, HJR/Mrr/RecB family	0	0	0	0	0	0	0	0	1	0	2	0	3	0	0	0	0
arCOG02782	COG1787	V	Endonuclease, HJR/Mrr/RecB family	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0
arCOG02783	COG2135	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0
arCOG02784	COG2135	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02785	COG3119	P	Arylsulfatase A or related enzyme	0	0	1	1	0	0	0	3	0	0	1	0	0	0	1	0	0
arCOG02787	COG3119	P	Arylsulfatase A or related enzyme	0	0	1	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02788	COG3119	P	Arylsulfatase A or related enzyme	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02789	COG3119	P	Arylsulfatase A or related enzyme	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02790	COG3119	P	Arylsulfatase A or related enzyme	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02791	COG3119	P	Arylsulfatase A or related enzyme	0	0	0	0	0	0	0	1	0	0	0	1	3	0	0	0	0
arCOG02792	COG0477	G	permease of the major facilitator superfamily	0	3	4	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG02793	COG0477	G	permease of the major facilitator superfamily	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG02794	COG0477	G	permease of the major facilitator superfamily	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02795	COG1510	K	Predicted transcriptional regulator	0	0	1	0	0	0	0	1	0	1	0	1	1	0	4	0	0
arCOG02796	COG2133	G	Glucose/sorbosone dehydrogenase	0	0	1	2	1	0	0	3	0	0	1	1	2	0	0	0	0
arCOG02797	COG4746	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	4	1	3	2	1	3	0	0	0	0
arCOG02798	COG1414	K	Transcriptional regulator (IclR family)	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02799	COG1414	K	Transcriptional regulator (IclR family)	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02800	COG1414	K	Transcriptional regulator (IclR family)	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02801		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02802		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02803		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02804		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02805	COG2233	F	Xanthine/uracil permease	0	0	0	0	0	0	0	2	0	2	3	0	0	0	3	0	0
arCOG02806	COG0659	P	Sulfate permease or related transporter (MFS superfa	0	0	0	0	0	0	0	2	0	2	2	1	3	0	0	0	0
arCOG02807	COG2252	F	Xanthine/uracil/vitamin C permease	0	1	1	0	0	0	0	3	0	3	0	1	0	0	4	0	0
arCOG02808	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02809		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02810	COG5524	R	Bacteriorhodopsin	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02811	COG5524	R	Bacteriorhodopsin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02812	COG5524	R	Bacteriorhodopsin	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02813	COG5524	R	Bacteriorhodopsin	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02814	COG2124	Q	Cytochrome P450	0	2	0	0	0	0	0	4	0	0	0	0	1	0	0	1	0
arCOG02815	COG0229	O	Conserved domain frequently associated with peptid	0	0	0	2	0	0	0	4	2	0	3	1	4	0	1	0	0
arCOG02816	COG0225	O	Peptide methionine sulfoxide reductase	0	2	0	2	0	0	0	4	1	2	2	1	4	0	0	1	0
arCOG02817	COG0285	H	Folylpolyglutamate synthase and Dihydropteroate sy	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	3	0
arCOG02818	COG0771	M	UDP-N-acetylmuramoylalanine-D-glutamate ligase	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG02819	COG0771	M	UDP-N-acetylmuramoylalanine-D-glutamate ligase	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG02820	COG0769	M	UDP-N-acetylmuramyl tripeptide synthase	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG02821	COG0771	M	UDP-N-acetylmuramoylalanine-D-glutamate ligase	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG02822	COG0770	M	UDP-N-acetylmuramyl pentapeptide synthase	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG02823	COG0769	M	UDP-N-acetylmuramyl tripeptide synthase	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
arCOG02824	COG0138	F	AICAR transformylase/IMP cyclohydrolase PurH	0	0	0	0	0	0	1	4	0	0	3	0	5	0	0	3	0
arCOG02825	COG0299	F	Folate-dependent phosphoribosylglycinamide formy	0	0	3	2	0	0	0	0	0	0	3	0	5	0	0	3	0
arCOG02826	COG0788	F	Formyltetrahydrofolate hydrolase	0	0	0	2	0	0	0	4	0	0	1	0	0	0	0	0	0
arCOG02827		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	1	0	0	0
arCOG02828	COG3367	R	NAD dependent epimerase/dehydratase family	1	0	1	0	0	1	0	4	2	2	0	0	0	1	1	3	0
arCOG02829		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02830		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02831	COG0380	G	Trehalose-6-phosphate synthase	0	0	3	0	0	0	0	1	1	0	1	0	1	0	0	3	0
arCOG02832	COG0737	F	5'-nucleotidase/2',3'-cyclic phosphodiesterase or rela	0	0	0	0	0	0	1	4	1	0	2	0	0	0	0	0	0
arCOG02833	COG0265	O	Serine protease Do (heat-shock protein)	0	3	5	2	1	1	0	4	1	0	1	1	2	0	0	0	0
arCOG02834	COG0750	M	Predicted membrane-associated Zn-dependent prote	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0
arCOG02835	COG2324	S	Uncharacterized conserved membrane protein	0	0	1	0	0	1	0	4	1	0	1	1	0	0	0	0	0
arCOG02836	COG0864	K	Transcriptional regulator, CopG/Arc/MetJ family (D	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02837		K	CopG-family DNA-binding protein	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG02838	COG3287	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	3	0	0	1	1	0	0	0
arCOG02839	COG3046	R	Uncharacterized protein related to deoxyribodipyrim	0	0	0	0	0	0	0	4	1	0	0	0	0	0	0	0	0
arCOG02840	COG0415	L	Deoxyribodipyrimidine photolyase	0	3	0	0	1	0	0	4	1	0	1	0	5	0	0	1	0
arCOG02841	COG1132	V	ABC-type multidrug transport system, ATPase and p	0	3	3	0	0	0	0	4	0	0	3	1	3	0	4	1	0
arCOG02842	COG0633	C	Ferredoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02843	COG0633	C	Ferredoxin	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02844	COG0633	C	Ferredoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02845	COG0633	C	DnaJ-like chaperone fused to ferredoxin	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02846	COG0484	O	DnaJ-class molecular chaperone	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
arCOG02847	COG2214	O	DnaJ-class molecular chaperone	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02848	COG2214	O	DnaJ-class molecular chaperone	0	0	0	0	0	0	0	3	0	0	0	0	1	0	0	0	0

arCOG02849	COG0003	P	Oxyanion-translocating ATPase	3	0	3	0	1	1	0	4	2	3	0	0	0	1	2	3	0
arCOG02850	COG0003	P	Oxyanion-translocating ATPase	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02851	COG2146	P	Ferredoxin subunit of nitrite reductase or ring-hydro	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02852	COG2146	P	Ferredoxin subunit of nitrite reductase or ring-hydro	0	3	1	2	1	0	0	1	0	0	0	1	2	0	0	2	0
arCOG02853	COG2146	P	Ferredoxin subunit of nitrite reductase or ring-hydro	0	3	2	1	1	0	0	0	0	0	0	1	0	0	0	0	0
arCOG02854	COG2146	P	Ferredoxin subunit of nitrite reductase or ring-hydro	0	3	2	2	0	0	0	0	0	0	0	1	0	0	0	3	0
arCOG02855	COG2146	P	Ferredoxin subunit of nitrite reductase or ring-hydro	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02856		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02857		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02858		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02859		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02860	COG0288	P	Carbonic anhydrase	0	3	2	0	0	0	0	3	2	2	3	1	0	0	0	1	0
arCOG02861	COG2259	S	Predicted membrane protein, DoxD family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02862	COG2259	S	Predicted membrane protein, DoxD family	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG02863	COG2259	S	Predicted membrane protein, DoxD family	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02864	COG2322	S	Predicted membrane protein	0	0	0	0	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02865	COG2322	S	Predicted membrane protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02866		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	3	1	0	0	0	0	0
arCOG02867		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02868	COG1651	O	Protein-disulfide isomerase	0	0	0	2	0	0	1	4	0	0	0	1	0	0	0	0	0
arCOG02869	COG2761	Q	Predicted dithiol-disulfide isomerase involved in pol	0	3	0	0	1	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02870	COG1651	O	Protein-disulfide isomerase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02871	COG1651	O	Protein-disulfide isomerase	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02872	COG1651	O	Protein-disulfide isomerase	1	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02874		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	5	0	0	0	0
arCOG02875		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG02876	COG0726	G	Predicted xylanase/chitin deacetylase	1	0	0	0	0	0	0	1	0	0	0	1	3	1	2	0	0
arCOG02877	COG0726	G	Predicted xylanase/chitin deacetylase	2	0	0	0	0	0	0	0	0	0	2	1	3	0	0	1	0
arCOG02878	COG0726	G	Predicted xylanase/chitin deacetylase	0	0	1	0	0	0	0	0	0	1	0	0	2	0	0	0	0
arCOG02879		S	Uncharacterized conserved protein	0	0	2	0	0	1	0	2	2	2	3	1	0	0	0	0	0
arCOG02880		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG02881	COG0530	P	Ca2+/Na+ antiporter	0	3	4	2	0	0	1	4	1	3	1	1	4	1	4	3	1
arCOG02882	COG1944	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	2	3	3	1	5	1	0	0	0
arCOG02883	COG1944	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG02884	COG4743	S	Predicted membrane protein	0	0	1	0	0	0	0	2	2	1	3	1	5	0	3	0	0
arCOG02886	COG4743	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	1	0	0	2	0	0	0	0
arCOG02887	COG4743	S	Predicted membrane protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02888	COG2988	E	Succinylglutamate desuccinylase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02889	COG3608	R	Predicted deacylase	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
arCOG02890	COG3608	R	Predicted deacylase	0	0	0	0	0	0	0	4	0	0	0	0	2	0	0	0	0
arCOG02891	COG2766	T	Predicted Ser/Thr protein kinase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02892	COG2766	T	Predicted Ser/Thr protein kinase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02893		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02894		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02895	COG1193	L	DNA structure-specific ATPase involved in suppress	0	0	0	0	0	0	0	4	2	0	0	1	5	0	4	0	0
arCOG02896	COG0249	L	Mismatch repair ATPase (MutS family)	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	1	0
arCOG02897	COG0249	L	Mismatch repair ATPase (MutS family)	0	0	0	0	0	0	0	4	0	0	3	0	5	0	0	1	0
arCOG02898		R	Polyketide cyclase/dehydrase family protein involve	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02899		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02900	COG2304	R	Uncharacterized protein containing a von Willebran	1	3	1	2	0	0	1	1	0	0	1	0	1	0	0	1	1
arCOG02902	COG2304	R	Uncharacterized protein containing a von Willebran	1	0	0	2	0	1	0	0	0	0	2	0	5	0	0	0	0
arCOG02903		R	Protein comtaining Bacterial Ig-like domain and vW	0	0	0	0	0	0	1	1	0	0	2	1	0	0	0	0	0
arCOG02904	COG2304	R	Uncharacterized protein containing a von Willebran	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02905	COG2304	R	Uncharacterized protein containing a von Willebran	0	0	0	0	0	0	0	2	0	0	0	0	5	0	0	0	0
arCOG02906	COG2304	R	Uncharacterized protein containing a von Willebran	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02907	COG2304	R	Uncharacterized protein containing a von Willebran	0	0	0	0	0	0	0	2	0	0	0	0	5	0	0	0	0
arCOG02908	COG2304	R	Uncharacterized protein containing a von Willebran	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02909	COG4250	T	Predicted sensor protein/domain	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02910	COG4250	T	Predicted sensor protein/domain	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02911		S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	1	4	0	0	2	1	1	0	0	0	0
arCOG02912		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG02913		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02914		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02915		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG02916		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0
arCOG02917	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02918	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02919	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG02920	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02921	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02922	COG4892	R	Predicted heme/steroid binding protein	0	0	0	0	0	0	0	0	1	0	0	0	4	0	0	0	0
arCOG02923	COG4892	R	Predicted heme/steroid binding protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02924		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02926	COG3794	C	Plastocyanin	0	0	0	2	1	0	0	0	0	2	1	1	0	0	0	0	0
arCOG02929	COG3794	C	Plastocyanin	0	0	0	2	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02930	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG02931	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02932	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02933	COG3794	C	Plastocyanin	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02934	COG3794	C	Plastocyanin	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02935	COG1741	R	Pirin-related protein	0	2	3	0	0	0	0	1	0	0	2	1	2	0	0	3	0
arCOG02936	COG1562	I	Phytoene/squalene synthetase	0	2	0	0	1	0	0	4	1	0	1	0	0	0	0	1	0
arCOG02937	COG3407	I	Mevalonate pyrophosphate decarboxylase	0	3	0	0	1	0	0	4	0	0	0	0	0	0	0	3	0
arCOG02938	COG3407	I	Mevalonate pyrophosphate decarboxylase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG02939	COG2154	H	Pterin-4a-carbinolamine dehydratase	0	3	2	2	1	0	0	4	0	0	1	0	0	0	0	0	0
arCOG02940	COG4347	S	Predicted membrane protein	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG02941	COG0328	L	Ribonuclease HI	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02942	COG0328	L	Ribonuclease HI	0	2	2	2	1	0	0	4	0	0	2	1	1	0	0	0	0
arCOG02943	COG0640	K	Transcriptional regulator containing HTH domain, A	0	2	0	0	0	0	0	4	0	0	2	1	1	0	2	3	0
arCOG02944		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02945		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	1	3	0	0	0	0
arCOG02946		R	Bacteriorhodopsin related protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02947		R	Bacteriorhodopsin related protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02948	COG0366	G	Glycosidase	1	0	4	0	0	0	0	2	0	0	1	0	1	0	2	3	0
arCOG02949	COG1523	G	Type II secretory pathway, pullulanase PulA or relat	0	3	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02950	COG0296	G	1,4-alpha-glucan branching enzyme	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
arCOG02951	COG0296	G	1,4-alpha-glucan branching enzyme	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02952	COG0366	G	Glycosidase	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG02953	COG0296	G	1,4-alpha-glucan branching enzyme	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02954	COG0366	G	Glycosidase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG02955	COG3280	G	Maltooligosyl trehalose synthase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG02956	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	4	0	0	0	0	2	0	0	0	0
arCOG02957	COG4023	U	Preprotein translocase subunit Sec61beta	1	1	1	0	0	0	0	4	0	0	0	0	1	4	3	0	0
arCOG02958	COG4023	U	Preprotein translocase subunit Sec61beta	0	1	0	1	1	0	1	0	1	2	0	1	4	0	0	0	0
arCOG02959	COG2234	R	Predicted aminopeptidase	2	0	1	0	0	0	0	3	0	0	0	1	0	1	4	0	0
arCOG02960	COG4882	R	Predicted aminopeptidase, Iap family	3	2	4	0	0	1	0	0	0	0	0	0	0	0	0	0	1
arCOG02962	COG2234	R	Predicted aminopeptidase	0	0	0	0	0	0	1	0	1	0	1	0	3	0	0	0	0
arCOG02963	COG3351	N	Putative archaeal flagellar protein D/E	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02964	COG3351	N	Putative archaeal flagellar protein D/E	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02965	COG3351	N	Putative archaeal flagellar protein D/E	0	0	0	0	0	0	0	0	0	3	0	0	1	0	4	2	0
arCOG02966	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	3	1	0	2	1	4	0	0	0	0
arCOG02967	COG5635	T	NACHT family NTPase fused to HEAT repeats dom	0	0	0	0	0	0	0	0	0	0	2	1	2	0	0	0	0
arCOG02968	COG5635	T	NACHT family domain	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG02969	COG0308	E	Aminopeptidase N	0	3	5	2	1	0	0	0	0	0	2	0	4	0	3	3	0
arCOG02970	COG1413	S	HEAT repeats containing protein	0	0	0	1	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG02971	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG02972	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG02973	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02974	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02975	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02976		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	3	1	1	0	0	0	0
arCOG02977		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG02978		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG02979		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	3	0	0	0	0	0	0	3	0	0
arCOG02980		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	4	0	0
arCOG02981		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	1	3	0	0	0	0
arCOG02982		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG02983	COG1278	K	Cold shock protein, CspA family	0	0	0	2	0	0	0	4	0	0	0	0	0	0	0	0	0

arCOG02984	COG1278	K	Cold shock protein, CspA family	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG02985	COG2339	S	Membrane proteinase, regulator of anti-sigma factor	0	0	0	0	0	0	0	4	0	0	1	1	2	0	4	0	0	0
arCOG02986	COG1268	R	Uncharacterized conserved protein	0	0	1	0	0	0	1	4	2	0	3	1	4	0	4	0	0	0
arCOG02987	COG0633	C	Ferredoxin	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG02988	COG0633	C	Ferredoxin	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG02989		S	Uncharacterized conserved protein	0	0	0	0	1	0	0	4	0	0	0	0	0	0	2	0	0	0
arCOG02990	COG4729	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	4	0	0	0	1	0	0	0	0	0	0
arCOG02991	COG4729	S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG02992	COG0662	G	Cupin domain	0	0	0	0	0	0	0	0	0	0	3	0	4	0	1	0	0	0
arCOG02993	COG1917	S	Cupin domain containing protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG02994	COG1917	S	Cupin domain containing protein	2	2	1	0	1	1	0	3	0	0	1	0	1	0	4	3	0	0
arCOG02996	COG2140	G	Cupin domain	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG02998	COG1917	S	Uncharacterized conserved protein, contains double-	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG02999	COG1917	S	Uncharacterized conserved protein, contains double-	0	0	3	0	1	1	0	1	0	0	0	1	0	0	0	0	0	0
arCOG03000	COG3435	Q	Gentisate 1,2-dioxygenase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03001	COG0662	G	Cupin domain	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0
arCOG03002	COG1917	S	Cupin domain fused to uncharacterized domain of C	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG03003	COG0662	G	Protein containing cupin domain	0	1	0	1	1	1	0	1	1	1	2	1	4	1	0	0	0	0
arCOG03004	COG1917	S	Cupin domain containing protein	0	0	0	0	0	0	0	0	2	0	3	1	2	0	0	0	0	0
arCOG03005	COG4997	S	Uncharacterized conserved protein, contains double-	1	0	0	0	0	0	0	0	0	1	0	1	3	0	0	0	0	0
arCOG03006	COG4997	S	Uncharacterized conserved protein, contains double-	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0
arCOG03007	COG0840	N	Sensory protein; Cache domain	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG03008	COG0662	G	Cupin domain	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03009	COG2333	R	Predicted hydrolase (metallo-beta-lactamase superfa	0	0	0	0	0	0	0	2	0	0	3	1	1	0	0	0	0	0
arCOG03011		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG03012		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG03013	COG2219	L	Eukaryotic-type DNA primase, large subunit	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	0
arCOG03015	COG0702	M	Predicted nucleoside-diphosphate-sugar epimerase	0	0	0	2	0	0	0	4	0	0	0	0	1	0	0	0	0	0
arCOG03016	COG0451	M	Nucleoside-diphosphate-sugar epimerase	1	3	4	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03017	COG0702	M	Predicted nucleoside-diphosphate-sugar epimerase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG03018	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG03019	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03020		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG03021		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03022	COG1429	H	Cobalamin biosynthesis protein CobN or related Mg	0	0	1	0	0	0	0	4	2	3	2	0	5	1	0	1	0	0
arCOG03024	COG1429	H	Cobalamin biosynthesis protein CobN or related Mg	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0	0
arCOG03025	COG1429	H	Cobalamin biosynthesis protein CobN or related Mg	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0	0
arCOG03026	COG0694	O	Thioredoxin-like protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03027	COG0694	O	Thioredoxin-like protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03028	COG0694	O	Thioredoxin-like protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0
arCOG03029		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03030		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03031	COG3253	R	Chlorite dismutase	1	3	0	2	0	0	0	4	0	0	0	0	0	0	0	3	0	0
arCOG03032	COG0457	R	TPR repeats containing protein	0	2	0	2	0	0	0	4	1	3	3	1	5	0	0	3	0	0
arCOG03034	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	2	0	1	0	4	0	0	0	0	0
arCOG03035	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0
arCOG03036	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0
arCOG03037	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03038	COG0457	R	TPR repeats containing protein	1	3	0	1	0	0	0	0	0	3	3	1	5	0	0	0	0	0
arCOG03039	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03040	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG03041	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03042	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	1	0	2	1	4	0	0	2	0	0
arCOG03043	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	1	0	0	4	0	0	0
arCOG03044	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG03045	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	1	0	1	0	0	1	3	0	0	0	0	0
arCOG03046	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0	0
arCOG03047	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	1	3	0	1	0	0	0
arCOG03048	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG03049	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03050	COG0589	T	Nucleotide-binding protein, UspA family	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03051	COG0589	T	Nucleotide-binding protein, UspA family	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0
arCOG03052		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03053		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03054	COG0341	U	Preprotein translocase subunit SecF	0	0	0	0	0	0	0	4	2	3	3	1	5	1	4	0	1	0
arCOG03055	COG0342	U	Preprotein translocase subunit SecD	0	0	0	0	0	0	0	4	2	3	3	1	5	1	4	0	1	0
arCOG03056	COG0671	I	Membrane-associated phospholipid phosphatase	0	3	1	2	0	0	0	2	2	2	1	1	4	1	0	0	0	0
arCOG03057	COG0671	I	Membrane-associated phospholipid phosphatase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG03058	COG0671	I	Membrane-associated phospholipid phosphatase	2	0	1	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03059	COG3030	R	Protein affecting phage T7 exclusion by the F plasm	0	0	0	0	0	0	0	4	0	0	0	0	3	0	0	0	0	0
arCOG03060	COG0443	O	Chaperone DnaK (HSP70)	0	0	0	2	1	0	0	4	2	0	3	1	5	0	0	3	0	0
arCOG03061	COG1077	D	Actin-like ATPase involved in cell morphogenesis	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	0	0	0
arCOG03062	COG1077	D	Actin-like ATPase involved in cell morphogenesis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03063		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03064		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03065	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03066	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03067	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	2	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03068	COG0696	G	Phosphoglyceromutase	0	0	0	0	0	0	0	4	0	0	0	0	5	0	0	0	0	0
arCOG03069	COG1524	R	Uncharacterized protein of the AP superfamily	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG03070	COG2259	S	Predicted membrane protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG03072	COG1006	P	Multisubunit Na+/H+ antiporter, MnhC subunit	1	0	0	0	1	0	0	4	2	3	2	0	2	0	4	0	0	0
arCOG03073	COG0713	C	NADH dehydrogenase subunit 4L (K,kappa)	1	2	2	2	0	1	1	4	0	0	0	0	5	0	0	3	0	0
arCOG03076	COG1563	P	Predicted subunit of the Multisubunit Na+/H+ antip	1	0	0	0	0	0	0	0	2	3	0	0	0	0	4	0	0	0
arCOG03077	COG2111	P	Multisubunit Na+/H+ antiporter, MnhB subunit	0	0	0	0	0	0	0	4	0	0	0	0	0	0	4	0	0	0
arCOG03078	COG1563	P	Predicted subunit of the Multisubunit Na+/H+ antip	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG03079	COG2111	P	Multisubunit Na+/H+ antiporter, MnhB subunit	1	0	0	0	0	0	0	4	2	3	2	0	0	0	4	0	0	0
arCOG03080	COG2111	P	Multisubunit Na+/H+ antiporter, MnhB subunit	0	0	0	0	0	0	0	0	2	0	2	0	0	0	4	0	0	0
arCOG03081	COG2111	P	Multisubunit Na+/H+ antiporter, MnhB subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG03082	COG1320	P	Multisubunit Na+/H+ antiporter, MnhG subunit	1	0	0	0	0	0	0	4	0	0	2	0	2	0	4	0	0	0
arCOG03083	COG1320	P	Multisubunit Na+/H+ antiporter, MnhG subunit	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG03085		T	Histidine kinase, HisKA_3 family	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0
arCOG03086	COG1724	R	Predicted RNA binding protein (dsRBD-like fold), I	0	0	0	0	0	0	0	0	0	0	2	0	2	0	2	0	0	0
arCOG03087	COG1724	R	Predicted RNA binding protein (dsRBD-like fold), I	0	0	0	0	0	0	0	4	0	0	1	0	0	0	0	0	0	0
arCOG03088	COG1724	R	Predicted RNA binding protein (dsRBD-like fold), I	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0	0
arCOG03089	COG1724	R	Predicted RNA binding protein (dsRBD-like fold), I	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
arCOG03090		Q	Gas vesicle synthesis protein GvpL/GvpF.	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0
arCOG03091		Q	Gas vesicle synthesis protein GvpL/GvpF.	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0
arCOG03092		Q	Gas vesicle synthesis protein GvpA	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0
arCOG03093		Q	Gas vesicle synthesis protein GvpA	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0
arCOG03094		Q	Gas vesicle synthesis protein GvpA	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0
arCOG03095	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03096	COG1090	R	NAD dependent epimerase/dehydratase family enzy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03097		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	1	4	0	0	0	0	0
arCOG03098		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03099	COG1863	P	Multisubunit Na+/H+ antiporter, MnhE subunit	1	0	0	0	0	0	0	4	0	0	2	0	2	0	4	0	0	0
arCOG03100	COG1863	P	Multisubunit Na+/H+ antiporter, MnhE subunit	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0	0
arCOG03101	COG0346	E	Lactoylglutathione lyase or related enzyme	1	0	0	0	1	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03102	COG2514	R	Predicted ring-cleavage extradiol dioxygenase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03103	COG1612	O	Uncharacterized protein required for cytochrome ox	1	0	0	2	1	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03104		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03105		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03106	COG3631	R	Ketosteroid isomerase-related protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	1	0	0
arCOG03107	COG1739	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	1	2	2	0	4	0	1	0	0	0
arCOG03108	COG2235	E	Arginine deiminase	0	3	1	0	0	1	0	1	0	0	1	0	0	0	0	3	0	0
arCOG03109	COG1834	E	N-Dimethylarginine dimethylaminohydrolase	1	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0
arCOG03110	COG3177	K	Predicted transciptional regulator, contains Fic and I	0	0	0	0	0	0	0	1	0	2	2	1	2	0	0	0	0	0
arCOG03111	COG3177	S	Predicted transciptional regulator, contains Fic and I	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0
arCOG03112	COG3177	S	Fic family protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0
arCOG03113	COG1430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	3	0	1	1	1	4	0	0	0
arCOG03114	COG1430	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG03115	COG1430	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03116	COG1430	S	Uncharacterized conserved protein	0	0	0	2	1	0	0	4	0	0	0	1	0	0	0	0	0	0
arCOG03117	COG0586	S	Uncharacterized membrane-associated protein, Ded	0	3	1	2	0	1	0	2	0	0	1	1	1	0	0	3	0	0
arCOG03118	COG1238	S	Membrane protein DegA family	0	0	0	0	0	0	0	1	0	3	0	0	4	1	0	0	0	0
arCOG03119		S	DedA family membrane protein	3	3	5	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03120	COG2212	P	Multisubunit Na+/H+ antiporter, MnhF subunit	0	0	0	0	0	0	0	2	0	0	0	0	0	0	4	0	0	0
arCOG03121	COG2212	P	Multisubunit Na+/H+ antiporter, MnhF subunit	1	0	0	0	0	0	0	0	0	0	2	0	2	0	4	0	0	0

arCOG03122	COG2212	P	Multisubunit Na+/H+ antiporter, MnhF subunit	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03123	COG1357	S	Pentapeptide repeats containing protein	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0
arCOG03124	COG1357	S	Pentapeptide repeats containing protein	0	0	0	0	0	0	0	1	0	0	2	0	3	0	0	0	0	0
arCOG03125	COG1357	S	Pentapeptide repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0
arCOG03126	COG1357	S	Pentapeptide repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0
arCOG03127	COG1226	P	Ion channel fused to ion transporting domain	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG03128	COG1357	S	Pentapeptide repeats containing protein	0	0	0	0	0	0	0	3	0	1	0	0	2	0	0	0	0	0
arCOG03129		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0
arCOG03130	COG3359	L	Predicted exonuclease	0	0	0	0	0	0	0	4	1	1	3	1	4	0	0	0	0	0
arCOG03131	COG0468	L	Predicted DNA repair protein, contains HHH and en	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG03132	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03133	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03134	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0
arCOG03135	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03136	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03137	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03138	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG03139	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG03140	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG03141	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG03142		S	Uncharacterized conserved protein	3	3	0	2	0	0	0	3	0	0	0	1	0	0	4	3	0	
arCOG03143		R	An uncharacterized C-terminal domain of COG1202	0	0	0	0	0	0	0	2	0	0	3	0	0	0	0	0	0	
arCOG03144		R	An uncharacterized C-terminal domain of COG1202	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	
arCOG03145	COG1318	F	Intein/homing endonuclease	1	0	0	0	0	0	0	0	0	1	0	0	0	1	3	0	0	
arCOG03146	COG1241	L	Intein/homing endonuclease	0	0	0	0	0	0	0	4	0	0	0	1	0	0	1	0	0	
arCOG03147	COG1372	L	Intein/homing endonuclease	0	0	0	0	0	0	0	2	0	0	1	0	0	0	1	0	0	
arCOG03148	COG1372	L	Intein/homing endonuclease	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	
arCOG03149	COG1372	L	Intein/homing endonuclease	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	
arCOG03151	COG1372	L	Intein/homing endonuclease	0	0	0	0	0	0	0	1	0	1	0	0	0	1	4	0	0	
arCOG03154	COG1372	L	Intein/homing endonuclease	0	0	0	0	0	0	0	1	0	1	0	0	0	1	4	0	0	
arCOG03155	COG1241	L	Cdc46/Mcm family protein (inactivated)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	
arCOG03156	COG3780	L	DNA endonuclease related to intein-encoded endon	1	0	1	0	1	0	0	0	0	1	0	0	0	1	4	0	0	
arCOG03157	COG1372	L	Intein/homing endonuclease	0	0	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	
arCOG03158	COG1372	L	Intein/homing endonuclease	0	0	0	0	1	0	0	0	0	1	0	0	0	1	4	0	0	
arCOG03159	COG0310	P	ABC-type Co2+ transport system, permease compor	2	0	3	0	0	1	0	2	0	0	0	0	0	0	0	0	0	
arCOG03160	COG0310	P	ABC-type Co2+ transport system, permease compor	0	0	0	0	0	0	0	0	2	1	1	0	3	0	2	0	0	
arCOG03161		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	
arCOG03162	COG1961	L	Site-specific recombinase, DNA invertase Pin homo	1	1	4	0	0	0	0	2	0	1	1	0	2	0	1	1	0	
arCOG03164	COG2452	L	Predicted site-specific integrase-resolvase	1	3	1	0	0	1	0	1	0	1	1	0	0	0	3	2	0	
arCOG03165		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	3	3	1	1	0	0	0	0	
arCOG03166	COG1672	R	Predicted ATPase (AAA+ superfamily)	0	3	3	0	0	1	0	1	1	1	2	0	2	0	4	0	0	
arCOG03167	COG1373	R	Predicted ATPase (AAA+ superfamily)	0	3	4	0	0	1	0	0	1	2	3	1	3	0	4	1	0	
arCOG03168	COG1373	R	Predicted ATPase (AAA+ superfamily)	0	1	2	0	0	0	0	0	0	0	1	0	3	0	1	0	0	
arCOG03169	COG1672	R	Predicted ATPase (AAA+ superfamily)	0	3	5	0	1	1	0	0	1	0	0	1	1	0	4	1	0	
arCOG03171	COG1672	R	Predicted ATPase (AAA+ superfamily)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	4	0	0	
arCOG03172	COG1672	R	Predicted ATPase (AAA+ superfamily)	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	
arCOG03173	COG1672	R	Predicted ATPase (AAA+ superfamily)	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
arCOG03174	COG3369	S	Zinc finger domain containing protein (CDGSH-type	0	0	0	0	0	0	0	0	1	0	0	1	3	0	0	0	0	
arCOG03175	COG3592	S	CDGSH-type zinc finger	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	
arCOG03176	COG1584	S	Predicted membrane protein	0	3	1	0	0	0	0	0	1	2	1	1	5	0	0	3	0	
arCOG03177	COG1846	K	Transcriptional regulator, MarR family	0	0	0	0	0	0	0	0	2	0	2	1	2	0	0	1	0	
arCOG03178	COG1846	K	Transcriptional regulator, MarR family	0	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	
arCOG03179	COG1846	K	Transcriptional regulator, MarR family	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	1	0	
arCOG03180	COG1846	K	Transcriptional regulator, MarR family	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03181	COG1846	K	Transcriptional regulator, MarR family	0	3	0	0	0	0	0	0	0	1	0	0	3	0	0	1	0	
arCOG03182	COG1846	K	Transcriptional regulator, MarR family	0	2	0	0	0	0	0	0	0	2	1	1	3	0	0	3	0	
arCOG03183	COG1846	K	Transcriptional regulator, MarR family	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	
arCOG03184	COG4906	S	Predicted membrane protein	0	0	0	0	0	0	0	0	2	1	1	1	2	0	1	0	0	
arCOG03185		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03186		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	
arCOG03187		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	
arCOG03188		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	4	0	2	0	0	
arCOG03189		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	
arCOG03190	COG4039	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0	
arCOG03191	COG4040	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	0	1	0	0	1	0	0	0	
arCOG03192	COG1525	L	Micrococcal nuclease (thermonuclease)	0	0	0	1	0	0	0	3	2	3	0	0	2	1	3	0	1	
arCOG03193	COG1525	L	Micrococcal nuclease (thermonuclease)	0	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG03194		S	Uncharacterized conserved protein	0	0	0	1	0	0	0	1	1	0	1	0	1	0	0	0	0	
arCOG03195	COG4007	R	Predicted dehydrogenase related to H2-forming N5,I	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0	
arCOG03196	COG4074	C	H2-forming N5,N10-methylenetetrahydromethanopt	0	0	0	0	0	0	0	0	1	3	1	0	0	1	0	0	0	
arCOG03197		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	3	1	4	0	0	0	0	
arCOG03198	COG1771	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	0	0	0	4	0	0	
arCOG03199	COG0472	M	UDP-N-acetylmuramyl pentapeptide phosphotransfe	3	3	5	2	1	1	0	0	2	3	0	0	3	1	4	0	1	
arCOG03200	COG4978	K	Transcriptional regulator, effector-binding domain/c	0	0	3	0	0	0	0	0	2	0	3	1	4	0	0	0	0	
arCOG03201	COG4832	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	
arCOG03202	COG0826	O	Collagenase family protease	0	0	0	0	0	0	0	0	2	3	0	0	4	0	0	0	0	
arCOG03203	COG0826	O	Collagenase family protease	0	0	0	0	0	0	0	0	2	0	3	0	5	0	0	0	0	
arCOG03204	COG0826	O	Collagenase family protease	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	
arCOG03205	COG0826	O	Collagenase family protease	0	2	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	
arCOG03206	COG1822	S	Predicted archaeal membrane protein	0	0	0	0	0	1	0	0	2	3	0	0	0	0	3	0	0	
arCOG03207	COG1822	S	Predicted archaeal membrane protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	
arCOG03208	COG4744	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	2	1	0	5	1	0	0	0	
arCOG03209	COG0811	U	Biopolymer transport protein	0	0	0	0	0	0	0	0	2	2	1	0	5	1	0	0	0	
arCOG03210	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0	
arCOG03211	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03212	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03213	COG4079	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	1	0	4	1	0	0	0	
arCOG03214	COG0207	F	Thymidylate synthase	0	0	1	0	0	0	1	2	2	3	3	1	5	1	0	0	0	
arCOG03215	COG4066	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	3	1	1	1	0	0	0	
arCOG03216	COG2014	S	Uncharacterized conserved protein	0	1	3	0	0	0	0	0	1	2	3	0	3	0	3	0	0	
arCOG03217	COG2014	S	Uncharacterized conserved protein	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG03218	COG4021	S	Uncharacterized conserved protein	0	0	0	0	0	1	0	0	2	0	3	1	5	1	0	0	0	
arCOG03219	COG4021	S	Uncharacterized conserved protein	1	0	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	
arCOG03220	COG4063	H	Tetrahydromethanopterin S-methyltransferase, subu	0	0	0	2	0	0	0	0	0	0	0	0	4	0	0	0	0	
arCOG03221	COG4063	H	Tetrahydromethanopterin S-methyltransferase, subu	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0	
arCOG03222	COG1567	V	CRISPR system related protein, RAMP superfamily	1	0	0	0	0	0	0	0	1	1	0	0	1	0	1	2	0	
arCOG03223	COG1567	V	CRISPR system related protein, RAMP superfamily	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG03224	COG1323	R	Predicted nucleotidyltransferase	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0	
arCOG03225	COG4056	H	Methyl coenzyme M reductase, subunit C	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0	
arCOG03226	COG4052	R	Uncharacterized protein related to methyl coenzyme	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0	
arCOG03228	COG1136	V	ABC-type antimicrobial peptide transport system, A	0	0	0	0	0	0	0	0	1	3	3	1	4	0	0	0	0	
arCOG03229	COG2454	S	Uncharacterized conserved protein	1	3	1	0	0	1	0	0	1	3	0	0	4	1	4	0	0	
arCOG03230		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	2	0	1	1	0	0	0	
arCOG03231	COG4069	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	1	0	4	1	0	0	0	
arCOG03232	COG5652	S	VanZ like family protein	0	0	0	0	0	0	0	3	0	0	0	0	3	0	0	0	0	
arCOG03233	COG4938	R	Predicted ATPase	0	2	5	0	1	0	0	0	0	0	1	0	1	0	0	0	0	
arCOG03234	COG4938	R	Predicted ATPase	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG03235	COG3593	L	Predicted ATP-dependent endonuclease of the OLD	0	0	0	2	0	0	0	0	0	2	0	0	4	0	1	0	0	
arCOG03237	COG1106	R	Predicted ATPase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG03238	COG3593	L	Predicted ATP-dependent endonuclease of the OLD	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	
arCOG03239	COG1106	R	Predicted ATPase	0	3	2	0	0	0	0	0	0	1	1	0	0	0	3	0	0	
arCOG03240	COG1195	L	Recombinational DNA repair ATPase RecF	0	1	2	0	0	0	0	0	0	1	0	0	2	0	0	0	0	
arCOG03241	COG4637	R	Predicted ATPase	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	
arCOG03242	COG1195	L	Recombinational DNA repair ATPase RecF	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG03245	COG1106	R	Predicted ATPase, fragment	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
arCOG03246	COG1509	E	Lysine 2,3-aminomutase	1	0	0	2	0	0	0	0	0	3	2	1	5	0	0	0	0	
arCOG03247	COG2136	J	Predicted exosome subunit/U3 small nucleolar ribon	3	3	5	0	0	1	1	0	2	3	3	0	4	1	4	0	0	
arCOG03249		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	
arCOG03250		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	
arCOG03251		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03252		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03253		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03254		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03255		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	
arCOG03256		S	Cell suface protein	0	0	0	0	0	0	0	2	0	0	0	0	5	0	1	0	0	
arCOG03257		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	
arCOG03259		S	Cell suface protein	0	0	0	0	0	0	1	0	0	0	0	1	5	0	0	0	0	
arCOG03260		S	Uncharacterized conserved protein	0	0	5	0	0	0	0	1	0	0	3	1	0	0	0	0	0	

arCOG03264		S	Cell suface protein	0	0	0	0	0	0	0	1	0	0	3	1	2	0	1	0	0
arCOG03265		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03266		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03267		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03268		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03269		S	Uncharacterized conserved protein, contains DUF11	0	0	0	0	0	0	0	0	0	0	0	0	5	0	4	0	0
arCOG03270		S	Uncharacterized conserved protein, contains DUF11	0	0	0	0	0	1	0	0	0	0	0	0	3	0	4	0	0
arCOG03271	COG2105	S	Uncharacterized conserved protein	0	3	1	0	1	0	0	0	0	1	0	0	4	0	3	0	0
arCOG03272		S	Uncharacterized conserved protein	0	0	0	1	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG03273		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03274		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03275		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03276		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03277		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03278	COG1449	G	Glycosyl hydrolase family 57	1	3	5	0	0	0	0	0	0	3	2	1	5	0	0	3	0
arCOG03279	COG1449	G	Glycosyl hydrolase family 57	0	0	3	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG03280	COG1449	G	Glycosyl hydrolase family 57	1	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03281	COG1543	G	Glycosyl hydrolase family 57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03282	COG1543	G	Glycosyl hydrolase family 57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03283	COG1543	G	Glycosyl hydrolase family 57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03284	COG1449	G	Glycosyl hydrolase family 57	1	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03285	COG3387	G	Glycosyl hydrolase family 15	0	3	1	0	0	0	0	2	0	3	0	1	5	0	0	3	0
arCOG03286	COG3387	G	Glycosyl hydrolase family 15	0	3	1	0	0	0	0	0	0	0	0	1	1	0	0	3	0
arCOG03287	COG3408	G	Glycogen debranching enzyme	0	3	1	0	0	0	0	0	0	0	0	1	5	0	3	3	0
arCOG03288	COG3408	G	Glycogen debranching enzyme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03289	COG3408	G	Glycogen debranching enzyme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03290		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03291		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03292		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03293	COG2314	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	2	2	1	2	0	0	0	0
arCOG03294		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	4	0	0	0	0
arCOG03295		S	Membrane protein containing Zn-ribbon domain	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0
arCOG03296	COG2865	K	Predicted transcriptional regulator containing an HT	0	0	0	0	0	0	0	2	0	2	3	0	4	0	1	1	0
arCOG03298	COG2865	K	Predicted transcriptional regulator containing an HT	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03299	COG2865	K	Predicted transcriptional regulator containing an HT	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG03300	COG4828	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	1	1	4	0	0	0	0
arCOG03301	COG4828	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03302	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG03303	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	2	0	0	0	1	0	0	3	3	0	5	0	4	0	0
arCOG03304	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03305	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03306	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03307	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03308	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03309	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03310	COG0753	P	Catalase	0	0	0	0	0	0	0	0	0	0	2	1	3	0	0	0	0
arCOG03311		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	1	0	0
arCOG03312		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03313		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03314		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03315		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG03316		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03317	COG3344	L	Retron-type reverse transcriptase	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0	0	0
arCOG03318	COG3344	L	Retron-type reverse transcriptase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03319	COG2348	M	Peptidoglycan interpeptide bridge formation enzyme	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	0	0
arCOG03320	COG2349	M	Peptidoglycan interpeptide bridge formation enzyme	0	0	0	0	0	0	0	0	0	1	1	1	3	0	0	0	0
arCOG03321		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG03322		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03323	COG0407	H	Uroporphyrinogen-III decarboxylase	0	0	0	0	0	0	1	0	1	2	0	0	4	0	0	3	0
arCOG03324	COG0407	H	Uroporphyrinogen-III decarboxylase	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03325	COG0407	H	Uroporphyrinogen-III decarboxylase	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03326	COG0407	H	Uroporphyrinogen-III decarboxylase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03327	COG0407	H	Uroporphyrinogen-III decarboxylase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03328	COG0407	H	Uroporphyrinogen-III decarboxylase	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG03330		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	1	4	0	0	0	0
arCOG03331		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03332		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03333	COG4273	S	Uncharacterized conserved protein	0	0	0	0	0	1	0	0	0	1	3	0	5	1	1	0	0
arCOG03334	COG4273	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG03335	COG2335	M	Secreted and surface protein containing fasciclin-like	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG03336	COG2335	M	Secreted and surface protein containing fasciclin-like	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG03337	COG2335	M	Secreted and surface protein containing fasciclin-like	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG03338		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03339		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03340	COG3527	Q	Alpha-acetolactate decarboxylase	0	0	0	0	0	0	0	0	0	2	2	1	5	0	0	0	0
arCOG03341		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03342		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03343		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03344		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03345		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03346		E	Zinc-dependent metalloprotease, M12B family	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG03347		R	Predicted metallohydrolase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03348		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03349	COG1633	S	Uncharacterized conserved protein	2	0	1	0	0	0	0	0	0	2	2	1	5	0	4	0	0
arCOG03350	COG3461	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03351	COG1710	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	0	0	0	4	0	0
arCOG03352		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG03353		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03354		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03355		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03356		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03357		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03358	COG3355	K	Predicted transcriptional regulator	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03359		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG03360		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG03361	COG4804	R	Predicted nuclease of restriction endonuclease-like f	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG03362	COG4804	R	Predicted nuclease of restriction endonuclease-like f	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG03363	COG2811	C	Archaeal/vacuolar-type H+-ATPase subunit H	0	0	0	0	0	1	1	4	2	3	3	1	5	0	4	3	0
arCOG03365		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	1	4	0	0	0	0
arCOG03366		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	2	0	5	0	0	0	0
arCOG03367		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03368		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03369	COG4809	G	Archaeal ADP-dependent phosphofructokinase/gluco	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG03370	COG4809	G	Archaeal ADP-dependent phosphofructokinase/gluco	0	0	0	0	0	0	0	0	0	3	0	0	4	0	4	0	0
arCOG03371	COG4809	G	Archaeal ADP-dependent phosphofructokinase/gluco	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03372		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03373		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03374		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03375	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	1	0	1	0	3	0	0	0	0
arCOG03377		E	Serine protease	1	0	1	1	0	0	0	0	0	0	0	0	3	0	1	0	0
arCOG03378		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03379		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	3	0
arCOG03380	COG4064	H	Tetrahydromethanopterin S-methyltransferase, subu	0	0	0	0	0	0	0	0	2	3	0	1	5	1	0	0	0
arCOG03381	COG4218	H	Tetrahydromethanopterin S-methyltransferase, subu	0	0	0	0	0	0	0	0	2	1	3	0	5	0	0	0	0
arCOG03382	COG0823	U	Periplasmic component of the Tol biopolymer transp	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03383	COG0823	U	Periplasmic component of the Tol biopolymer transp	0	0	0	0	0	0	1	0	0	0	1	0	3	0	0	0	0
arCOG03384	COG4946	S	Uncharacterized protein related to the periplasmic c	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03385	COG0823	U	Periplasmic component of the Tol biopolymer transp	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03386		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03387		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03388		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG03389		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03390		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	1	3	0	0	0	0
arCOG03391	COG1988	R	Predicted membrane-bound metal-dependent hydrol	0	0	0	0	0	0	0	0	0	0	2	1	4	0	0	0	0
arCOG03392	COG1988	R	Predicted membrane-bound metal-dependent hydrol	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG03393	COG1988	R	Predicted membrane-bound metal-dependent hydrol	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG03394		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	5	0	0	0	0
arCOG03396	COG1657	I	Squalene cyclase	0	0	0	0	0	0	0	0	0	2	0	1	4	1	4	0	0

arCOG03397	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG03398	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03399	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03400	COG4085	R	Predicted RNA-binding protein, contains TRAM do	0	0	0	0	0	0	0	0	2	0	1	0	0	1	0	0	0
arCOG03401	COG4085	R	Predicted RNA-binding protein, contains TRAM do	0	0	0	0	0	0	0	0	0	0	2	1	5	0	1	0	0
arCOG03402	COG5012	R	Predicted cobalamin binding protein	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG03403		V	PemK/MazF family toxin	0	0	0	0	0	0	0	0	0	0	2	0	1	0	2	0	0
arCOG03404		V	PemK/MazF family toxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG03405	COG5598	H	Trimethylamine:corrinoid methyltransferase	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03406	COG5598	H	Trimethylamine:corrinoid methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03407	COG1672	R	Predicted ATPase (AAA+ superfamily)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0
arCOG03408	COG1672	R	Predicted ATPase (AAA+ superfamily)	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03409		R	Predicted ATPase	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03410		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03411	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	1	0	0	3	2	0	3	0	0	0	0
arCOG03412		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	3	1	1	0	0	0	0	0
arCOG03413	COG2453	T	Predicted protein-tyrosine phosphatase	2	3	5	2	1	1	0	1	0	1	1	0	3	0	4	0	0
arCOG03414		S	Uncharacterized conserved protein	0	0	0	0	0	1	0	0	0	3	0	0	0	0	3	0	0
arCOG03415		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	4	0	0
arCOG03416	COG0338	L	Site-specific DNA methylase	0	0	0	2	0	0	0	0	1	3	2	1	0	0	1	3	0
arCOG03417	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	3	0	1	0	0	0	0	1	1	0	0	0	0	0	0
arCOG03418		R	S-layer-like protein	0	0	0	0	0	1	0	0	0	3	0	0	0	0	4	0	0
arCOG03419	COG1800	R	Predicted transglutaminase-like protease	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG03420		R	S-layer-like protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG03421	COG1627	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	0	0	1	4	0	0
arCOG03422	COG3373	S	Uncharacterized protein conserved in archaea	0	0	1	0	0	0	0	0	0	3	0	1	0	0	4	2	0
arCOG03423	COG1846	K	Transcriptional regulator, MarR family	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03424	COG4075	S	Uncharacterized conserved protein, homolog of nitr	0	0	0	0	0	0	0	0	1	3	0	0	1	1	0	0	0
arCOG03425	COG0697	G	permease of the drug/metabolite transporter (DMT)	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0
arCOG03426	COG2510	S	Predicted membrane protein	1	0	0	0	1	0	0	0	0	3	0	0	0	0	0	0	0
arCOG03427	COG2510	S	Predicted membrane protein	1	0	1	0	1	0	0	0	1	0	0	0	0	1	3	0	0
arCOG03428	COG0457	R	TPR repeats containing protein	0	3	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG03429	COG4715	R	SWIM zinc finger containing protein	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0
arCOG03430	COG4279	R	SWIM zinc finger containing protein	0	1	0	0	0	0	0	0	0	3	0	1	0	0	1	0	0
arCOG03431	COG4279	R	SWIM zinc finger containing protein	0	1	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG03432	COG4907	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	1	2	0	3	0	0	0	0
arCOG03433	COG1517	V	CRISPR system related protein	2	2	4	0	0	1	0	0	0	1	0	0	0	0	2	2	0
arCOG03435	COG1517	V	CRISPR system related protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03436	COG1517	V	CRISPR system related protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03437		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03439		S	vWFa domain containing protein	0	0	0	0	0	0	0	1	1	2	1	0	0	0	0	0	0
arCOG03441		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	1	1	0	0	0	0	0
arCOG03442		S	Uncharacterized conserved membrane protein	0	0	1	0	0	0	0	2	0	2	3	1	0	0	3	0	0
arCOG03443		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	2	0	1	1	0	0	0	0
arCOG03444	COG1917	S	Cupin domain containing protein	0	0	1	2	0	0	0	0	0	1	0	0	2	0	0	0	0
arCOG03445		S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	1	3	3	0	0	0	0	0	0
arCOG03446	COG2862	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	2	1	0	3	0	0	0	0
arCOG03447	COG1457	F	Purine-cytosine permease or related protein	0	2	1	0	1	1	0	0	0	1	1	0	0	0	3	3	0
arCOG03448	COG1953	F	Cytosine/uracil/thiamine/allantoin permease	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03449	COG3582	R	Predicted nucleic acid binding protein containing the	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG03450		R	Predicted surface protease of transglutaminase famil	0	0	0	0	0	1	0	0	0	2	2	0	4	0	0	0	1
arCOG03451		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG03452		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03453		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03454	COG2116	P	Formate/nitrite family of transporter	0	0	1	0	0	0	0	3	0	2	3	1	0	0	1	0	0
arCOG03455	COG1983	K	Phage shock protein C	0	0	0	0	0	0	0	0	0	2	3	0	3	0	0	0	0
arCOG03456	COG1983	K	Phage shock protein C	0	0	0	0	1	0	0	0	0	0	0	0	3	0	3	0	0
arCOG03457	COG0571	K	dsRNA-specific ribonuclease	0	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0
arCOG03458	COG2119	S	Predicted membrane protein	0	0	0	0	0	0	0	3	0	1	0	0	1	0	3	0	0
arCOG03459		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	1	0	0	0
arCOG03460	COG2120	S	Uncharacterized protein, LmbE homolog	1	2	2	0	0	0	0	0	0	0	0	1	3	1	4	0	0
arCOG03461	COG4049	R	Uncharacterized protein containing archaeal-type C2	0	0	0	0	0	0	0	0	0	1	0	0	0	1	4	0	0
arCOG03462	COG0531	E	Amino acid transporter	0	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG03463	COG0531	E	Amino acid transporter	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03464	COG0531	E	Amino acid transporter	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03465	COG0531	E	Amino acid transporter	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03466	COG0531	E	Amino acid transporter	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03467		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03468		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03469	COG5421	L	Transposase	0	0	0	0	0	0	0	0	0	0	1	1	4	0	0	0	0
arCOG03470	COG5421	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03472	COG5421	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03473	COG5421	L	Transposase	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	1	0
arCOG03474	COG5421	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03477		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03478		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03479		R	Predicted methyltransferase	0	0	0	0	0	0	0	0	0	0	3	1	4	0	0	0	0
arCOG03480		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	0
arCOG03481		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG03482		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	1	0	0	1	0	1	0	0	1	0
arCOG03483	COG1205	R	Distinct helicase family with a unique C-terminal do	0	1	1	0	0	0	0	1	0	0	1	0	1	0	0	1	0
arCOG03484		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03485		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03486		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03487		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03488		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03489		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03490		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03491		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03492		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03494	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03495		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03496		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03497		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03498		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03499		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03500		S	Disaggregatase-like cell surface protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03501		S	Disaggregatase-like cell surface protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03502		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03504		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03505		S	Cell suface protein, containing metal-binding domai	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG03506	COG3293	L	Transposase	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG03507	COG3293	L	Transposase	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03508	COG5306	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	3	0	0	0	0
arCOG03509	COG3291	R	Cell suface protein, containing PKD repeats	0	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG03511	COG5306	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG03512	COG5306	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03513	COG3666	L	Transposase	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03514	COG3666	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03515	COG3666	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03516	COG1262	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03517	COG1262	S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03518		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	1	1	3	0	0	0	0
arCOG03519		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03520		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03521	COG1002	V	Type II restriction enzyme, methylase subunit	0	0	2	0	0	0	0	0	0	1	0	0	0	0	1	1	0
arCOG03522		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03523		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03524	COG5316	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03525	COG5316	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03526	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG03527	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03528	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03529	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	2	1	2	0	0	0	0
arCOG03530	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03531	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03532	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03533	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0

arCOG03534	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03535		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03536		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03537		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03538		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03539		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03540		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03541	COG1988	R	Membrane-bound metal-dependent hydrolase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03542	COG1988	R	Membrane-bound metal-dependent hydrolase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03543	COG1988	R	Membrane-bound metal-dependent hydrolase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03544	COG5513	S	Predicted secreted protein	0	0	0	0	0	0	0	0	0	0	3	1	4	0	0	0	0
arCOG03545	COG4880	R	Secreted protein containing C-terminal beta-propelle	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG03546	COG5513	S	Predicted secreted protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03547	COG5513	S	Predicted secreted protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03548		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03549	COG1572	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03550		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03551		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03552		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03553	COG1572	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	0	0
arCOG03555	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03557		S	Cell suface protein	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0
arCOG03558	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03559	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03560		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG03561	COG3391	S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG03562	COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	0	2	1	0	0	0	0	0	1	0	1	0	0	0	0
arCOG03563	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03564	COG4257	V	Streptogramin lyase	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0
arCOG03565		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03566		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03567	COG2202	T	PAS domain	0	0	0	0	0	0	0	0	0	0	2	1	3	0	0	0	0
arCOG03569	COG3920	T	PAS domain	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03570	COG0500	Q	SAM-dependent methyltransferase	1	0	0	0	0	0	0	0	1	0	1	0	2	0	0	0	0
arCOG03571		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0
arCOG03572		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG03573	COG4198	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3	0
arCOG03574	COG4198	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03575	COG2326	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG03576	COG2326	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03577		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03578		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03579		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03580	COG2020	O	Putative protein-S-isoprenylcysteine methyltransfera	1	1	0	0	0	0	1	1	0	1	1	1	3	0	3	0	0
arCOG03581	COG2020	O	Putative protein-S-isoprenylcysteine methyltransfera	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03582	COG3247	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	3	0	0	0	0
arCOG03583	COG3247	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG03584		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG03585	COG3547	L	Transposase	0	0	0	0	1	0	0	1	0	0	1	0	3	0	0	0	0
arCOG03586	COG3547	L	Transposase	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG03587	COG3547	L	Transposase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03588	COG3315	Q	O-Methyltransferase involved in polyketide biosyntl	0	0	0	0	0	0	0	0	0	1	1	0	3	0	0	0	0
arCOG03589	COG3315	Q	O-Methyltransferase involved in polyketide biosyntl	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG03590		S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03591	COG2334	R	Putative homoserine kinase type II (protein kinase fe	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG03592		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03593		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03594		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03595		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03596		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03597		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0
arCOG03598		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03599		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03600	COG1305	E	Transglutaminase-like enzyme, putative cysteine pro	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03601	COG1305	E	Transglutaminase-like enzyme, putative cysteine pro	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG03602	COG4690	E	Dipeptidase	1	0	1	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG03606		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	2	1	0	3	0	0	0	0
arCOG03607	COG4870	O	Cysteine protease	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG03610	COG1404	O	Subtilisin-like serine protease	0	0	0	0	0	0	0	1	1	0	0	0	0	0	4	0	0
arCOG03611	COG1404	O	Uncharacterized domain associated with subtilisin-li	0	0	0	0	0	0	1	3	0	0	1	0	0	0	0	0	0
arCOG03612	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG03613		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0
arCOG03614	COG4870	O	Cysteine protease	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03615		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03616		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03617	COG1857	V	CRISPR system related protein	0	0	1	0	0	0	0	0	1	0	0	0	2	0	3	0	1
arCOG03618	COG2230	M	Cyclopropane fatty acid synthase or related methyltr	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03619	COG2230	M	Cyclopropane fatty acid synthase or related methyltr	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03620	COG2155	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	3	0	0	0	0
arCOG03621	COG2155	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG03622		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	1	1	4	0	0	0	0
arCOG03623		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03624		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03625		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03626	COG4237	C	Hydrogenase 4 membrane component (E)	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	2	0
arCOG03627	COG4237	C	Hydrogenase 4 membrane component (E)	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03628		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03629		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0
arCOG03630	COG2881	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	3	0	0	0	0	3	0	0	0	0
arCOG03631		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03632		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03633	COG1714	S	Predicted membrane protein/domain	0	0	0	0	0	0	0	1	2	0	2	1	2	1	0	0	0
arCOG03634	COG3274	R	Predicted O-acyltransferase	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG03635	COG1835	I	Predicted acyltransferase	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03636	COG1380	R	Putative effector of murein hydrolase LrgA	0	0	0	0	0	0	0	0	0	0	0	0	3	0	4	0	0
arCOG03637		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG03638		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG03639	COG0121	R	Predicted glutamine amidotransferase	2	3	5	0	0	1	0	0	2	1	0	1	0	0	4	2	0
arCOG03640	COG0205	G	6-phosphofructokinase	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
arCOG03641	COG0205	G	6-phosphofructokinase	0	0	1	0	0	0	0	0	0	0	2	1	0	0	0	0	0
arCOG03642	COG0840	N	Methyl-accepting chemotaxis protein	0	0	0	0	0	0	0	0	0	0	3	0	1	0	0	0	0
arCOG03643	COG0834	E	Periplasmic domain fused to Cache domains	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG03644		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG03645		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	1	0	0	0	0
arCOG03646	COG1722	L	Exonuclease VII small subunit	0	0	0	0	0	0	0	0	0	0	3	0	2	0	0	0	0
arCOG03647	COG2388	R	Predicted acetyltransferase	2	0	1	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG03648		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1
arCOG03649	COG0531	E	Amino acid transporter	0	3	1	0	0	0	0	1	0	0	0	0	0	0	0	3	0
arCOG03650	COG0531	E	Amino acid transporter	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03651	COG0531	E	Amino acid transporter	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03652	COG0531	E	Amino acid transporter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG03653	COG0531	E	Amino acid transporter	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03654	COG0531	E	Amino acid transporter	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03655		S	Uncharacterized conserved protein	3	0	1	0	1	0	0	2	0	0	0	0	0	0	2	0	0
arCOG03656	COG0028	E	Thiamine pyrophosphate-requiring enzyme, carboxy	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0
arCOG03657	COG0028	E	Acetolactate synthase large subunit or other thiamin	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03658	COG0208	F	Ribonucleotide reductase, beta subunit	0	3	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG03659	COG2971	G	Predicted N-acetylglucosamine kinase	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03660	COG0477	G	permease of the major facilitator superfamily	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03661	COG0383	G	Alpha-mannosidase	1	2	2	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03662	COG0383	G	Alpha-mannosidase	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG03663	COG1501	G	Alpha-glucosidase, family 31 of glycosyl hydrolase	0	3	4	0	0	0	0	1	0	0	0	0	0	0	0	3	0
arCOG03664	COG1215	G	Glycosyltransferase	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03665	COG4934	O	Subtilase family protease	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03666	COG4934	O	Subtilase family protease	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03667	COG4934	O	Subtilase family protease	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03668	COG4934	O	Subtilase family protease	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03669	COG4934	O	Subtilase family protease	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0

arCOG03670	E	Thermopsin-like protease	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG03671	E	Thermopsin-like protease	0	3	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
arCOG03672	E	Thermopsin-like protease	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG03673	E	Thermopsin-like protease	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03674	E	Thermopsin-like protease	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03675	E	Thermopsin-like protease	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03676 COG4934	O	Subtilase family protease	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03677	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03678	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03681	S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	0	0	1	0	0	3	0
arCOG03682 COG0515	R	Membrane associated serine/threonine protein kinas	1	3	4	0	0	0	0	0	0	0	1	0	0	0	0	1	0
arCOG03683 COG0515	R	Serine/threonine protein kinase fused to HEAT repe	0	0	1	0	0	1	0	3	0	0	3	1	0	0	1	1	0
arCOG03685 COG1765	O	Predicted redox protein, regulator of disulfide bond	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	0
arCOG03686 COG1765	O	Predicted redox protein, regulator of disulfide bond	1	3	1	0	1	1	0	0	0	1	2	0	1	1	3	0	0
arCOG03687 COG1765	O	Predicted redox protein, regulator of disulfide bond	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG03688 COG1764	Q	Organic hydroperoxide reductase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03689 COG1277	R	ABC-type transport system involved in multi-copper	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03690 COG1277	R	ABC-type transport system involved in multi-copper	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03691	S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	3	0
arCOG03692	S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03693	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03694	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG03695	S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03696 COG0348	C	Polyferredoxin	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03697 COG0348	C	Polyferredoxin	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03698 COG4344	S	Uncharacterized protein conserved in archaea	0	3	1	0	0	0	0	1	0	0	0	0	0	0	2	3	0
arCOG03699	S	Uncharacterized conserved protein	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG03700	S	Uncharacterized conserved protein	0	3	1	1	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03701 COG5650	S	Predicted integral membrane protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03702 COG5650	S	Predicted integral membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03703 COG5650	S	Predicted integral membrane protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03704	S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03705 COG1547	R	Predicted metal-dependent hydrolase	1	3	4	2	1	0	0	0	0	0	0	0	0	0	0	3	0
arCOG03706	S	Uncharacterized conserved protein	0	3	2	1	0	1	0	0	0	0	0	0	0	0	0	1	0
arCOG03707	R	HEPN domain	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03708	R	HEPN domain	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03709	R	HEPN domain	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03710	R	HEPN domain	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03711	R	HEPN domain	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03712	R	HEPN domain	0	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03713 COG0209	F	Ribonucleotide reductase associated ATP-cone doma	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	2	0
arCOG03714 COG1328	F	ATP cone domain	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0
arCOG03715	R	ATP-cone domain	0	0	5	0	0	1	0	0	0	0	1	0	0	0	0	0	0
arCOG03716	R	ATP-cone domain	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0
arCOG03717	R	ATP-cone domain	0	0	2	0	0	1	0	0	0	0	1	0	0	0	0	0	0
arCOG03718 COG1332	V	CRISPR system related protein, RAMP superfamily	1	0	1	0	0	0	0	0	1	1	0	0	1	0	1	0	0
arCOG03719 COG1332	V	CRISPR system related protein, RAMP superfamily	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG03720 COG1332	V	CRISPR system related protein, RAMP superfamily	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03721	R	HEPN domain	1	3	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG03722	R	HEPN domain	2	1	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG03723	R	HEPN domain	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03724	S	Uncharacterized conserved protein	0	1	5	1	0	1	0	0	0	0	1	0	0	0	0	0	0
arCOG03725	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03726	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03727	S	Restriction endonuclease family enzyme	1	0	5	2	1	1	1	0	0	0	0	1	0	0	0	0	0
arCOG03729	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0
arCOG03730	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	3	1	0	0	1	0	0	0	0	0
arCOG03732	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG03733	S	Uncharacterized conserved protein	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03734	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03735 COG1266	R	Predicted metal-dependent membrane protease	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03736 COG1266	R	Predicted metal-dependent membrane protease	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03737	S	Uncharacterized conserved protein	0	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03738	S	Uncharacterized conserved protein	0	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03739	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03740	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03741 COG5550	O	Predicted aspartyl protease	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03742 COG5550	O	Predicted aspartyl protease	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03743 COG5550	O	Predicted aspartyl protease	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03744 COG5550	O	Predicted aspartyl protease	0	0	5	0	0	1	0	0	0	0	0	0	1	0	0	0	0
arCOG03745 COG5550	O	Predicted aspartyl protease	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03746	S	Uncharacterized conserved protein	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03747	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03748 COG1846	K	Transcriptional regulator, MarR family	1	2	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03749 COG4243	S	Predicted membrane protein	1	3	4	0	1	0	0	1	0	0	0	0	0	0	0	0	0
arCOG03750	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03751	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03752	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03753	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03754	S	Uncharacterized conserved protein	2	0	3	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03755	S	Uncharacterized conserved protein	0	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG03756	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03757	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03758	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03759	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03760	S	Uncharacterized conserved protein	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03761	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03762	R	Predicted methyltransferase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03763	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03764	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03765	S	Uncharacterized conserved membrane protein	1	3	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03766	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03767	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03768	S	Uncharacterized conserved protein	0	3	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG03769	S	Uncharacterized conserved protein	0	3	4	0	0	1	0	0	0	0	0	0	0	0	0	2	0
arCOG03770	S	Uncharacterized conserved protein	3	1	5	2	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG03771 COG4945	G	Alpha-amylase/alpha-mannosidase	1	0	3	0	0	0	0	0	0	0	0	0	0	0	3	1	0
arCOG03772 COG4345	S	Uncharacterized protein conserved in archaea	3	3	3	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03773 COG0500	Q	SAM-dependent methyltransferase	3	0	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03774	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03775	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03776	S	Zn finger protein	0	0	4	0	0	0	0	0	0	0	1	1	0	0	1	0	0
arCOG03777	S	Zn finger protein	0	0	4	0	1	0	0	0	0	0	1	0	0	0	1	0	0
arCOG03778	S	Uncharacterized conserved protein	0	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03779 COG1401	V	GTPase subunit of restriction endonuclease	1	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03780 COG1401	V	GTPase subunit of restriction endonuclease	0	0	0	0	0	0	0	1	0	1	1	0	2	0	1	1	0
arCOG03782	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03783	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03784	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03785	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03786	S	Uncharacterized conserved protein, containing C-ter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03787 COG5608	V	LEA14-like dessication related protein	0	0	0	0	0	0	1	1	0	0	0	0	0	0	4	0	0
arCOG03788 COG5608	V	LEA14-like dessication related protein	0	0	1	2	0	1	0	0	0	0	0	0	0	0	2	0	0
arCOG03789	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03790	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03791	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03792	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03793	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03794 COG3601	S	Predicted membrane protein	0	0	2	0	1	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03795	S	Uncharacterized conserved protein, DUF835 family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03796	S	Uncharacterized conserved protein, DUF835 family	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0
arCOG03797 COG1633	S	Ferritin-like domain	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03798	S	Uncharacterized conserved protein, DUF835 family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03799 COG2202	T	GAF, PAS/PAC domains containing signal transduct	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
arCOG03801	S	Uncharacterized conserved protein, DUF835 family	0	0	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0
arCOG03802	S	Uncharacterized conserved protein, DUF835 family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03803	S	Uncharacterized conserved protein, DUF835 family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03804	S	Uncharacterized conserved protein, DUF835 family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0

arCOG03805		S	Uncharacterized conserved protein, DUF835 family	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03806		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03807		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03808		R	KaiC-like ATPase	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03809		R	KaiC-like ATPase	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03810		R	KaiC-like ATPase	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03811		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0
arCOG03812	COG3463	S	Predicted membrane protein	0	1	0	0	0	0	0	0	0	0	0	0	0	3	3	0
arCOG03813		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03814		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03815		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03816		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03817		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03818		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03819		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03820		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03821		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	4	0	0
arCOG03822	COG1991	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03823		V	CRISPR-associated protein	1	2	0	0	1	0	0	0	0	0	0	0	0	3	0	0
arCOG03824		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03825	COG3595	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0
arCOG03826		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
arCOG03827	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	1	0	0	0	4	0	0
arCOG03828		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	4	0	0
arCOG03829		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03830		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03831		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03832		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0
arCOG03833	COG4043	R	ProFAR isomerase family protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG03834	COG4043	R	ProFAR isomerase family protein	0	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0
arCOG03835		S	Uncharacterized conserved membrane protein	0	0	2	0	0	0	1	0	0	0	0	0	0	3	0	0
arCOG03836		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03837	COG0095	H	Lipoate-protein ligase A associated domain	2	0	0	0	0	1	0	1	0	0	0	1	0	4	2	0
arCOG03838		S	Uncharacterized conserved protein	1	3	0	0	0	0	0	1	0	0	0	1	0	2	0	0
arCOG03839	COG2253	S	Uncharacterized conserved protein	0	0	0	1	0	1	0	2	0	0	1	1	0	2	1	0
arCOG03840	COG3535	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG03841	COG3535	S	Uncharacterized conserved protein	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03842		R	TlpA/TrxA-like family protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03843		R	TlpA/TrxA-like family protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG03844		R	TlpA/TrxA-like family protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG03845	COG3609	K	Predicted antitoxin, copG family	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03846	COG3609	K	Predicted antitoxin, copG family	3	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG03847		S	Uncharacterized conserved protein	0	3	0	0	1	1	0	0	0	1	0	0	0	0	2	0
arCOG03848		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	0	2	0	0
arCOG03849		S	Uncharacterized conserved protein	0	2	2	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03850	COG4122	R	Predicted O-methyltransferase	0	2	1	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG03851		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03852		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG03853		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG03854		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03855		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03856		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03857		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03858		S	Uncharacterized conserved protein	0	2	2	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG03859	COG0640	K	Transcriptional regulator containing HTH domain, A	2	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03860		S	Predicted transcriptional regulator, contains HTH do	0	2	1	0	0	0	1	2	0	0	0	0	0	0	0	0
arCOG03861		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03862		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03863	COG4354	G	Predicted bile acid beta-glucosidase	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03864	COG4354	G	Predicted bile acid beta-glucosidase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03865	COG4354	G	Predicted bile acid beta-glucosidase	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03867	COG4354	G	Predicted bile acid beta-glucosidase	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03868		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03869		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG03870		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03871		S	Uncharacterized conserved membrane protein	2	3	4	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG03872		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03873	COG2855	S	Predicted membrane protein	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0
arCOG03874	COG2855	S	Predicted membrane protein	0	0	3	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG03875		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	2	1	0	0	0	0
arCOG03876		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG03877		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03878		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03879	COG3682	K	Predicted transcriptional regulator	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03880	COG2880	S	Uncharacterized protein conserved in archaea	2	0	0	0	0	0	1	0	0	0	1	0	0	2	0	0
arCOG03881		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG03882		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03883	COG3466	S	Putative transposon-encoded protein	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0
arCOG03884	COG3466	S	Putative transposon-encoded protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG03885	COG5559	S	Uncharacterized conserved small protein	0	0	0	0	0	0	1	0	0	0	0	0	0	3	0	0
arCOG03886		K	CopG family DNA-binding protein	0	0	1	0	0	1	1	0	0	0	2	0	0	4	0	0
arCOG03887	COG4711	S	Predicted membrane protein	0	0	0	0	0	0	1	3	0	0	0	0	0	1	0	0
arCOG03888		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0	0
arCOG03889	COG3465	S	Uncharacterized conserved protein	0	0	2	1	0	0	1	0	0	0	2	0	0	0	1	0
arCOG03890	COG1431	J	Argonaute homolog, implicated in RNA metabolism	0	1	0	0	0	0	1	0	0	1	0	0	0	1	0	0
arCOG03891	COG1367	V	CRISPR system related protein, RAMP superfamily	0	0	2	0	0	1	1	0	0	0	0	0	1	0	1	0
arCOG03892	COG1367	V	CRISPR system related protein, RAMP superfamily	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0
arCOG03893	COG1367	V	CRISPR system related protein, RAMP superfamily	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03894		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	3	0	0	0
arCOG03895		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	1	2	0	0	0
arCOG03896		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0
arCOG03897		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG03898	COG1403	V	Restriction endonuclease, McrA/HNH family	0	0	0	0	0	0	0	3	0	0	2	1	1	0	0	0
arCOG03899	COG3183	V	Predicted restriction endonuclease	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0
arCOG03900	COG3385	L	Transposase	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0
arCOG03902	COG3385	L	Transposase	0	2	0	0	0	0	0	1	0	0	1	1	4	0	0	0
arCOG03904	COG3385	L	Transposase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG03906		S	Cell surface protein	0	0	0	0	0	0	0	3	0	0	3	0	0	0	0	0
arCOG03909	COG3462	S	Predicted membrane protein	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0
arCOG03910	COG3462	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG03911	COG3462	S	Predicted membrane protein	0	0	0	0	0	0	0	3	0	0	0	0	1	0	0	2
arCOG03912	COG3462	S	Predicted membrane protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
arCOG03913	COG3019	R	Predicted metal-binding protein	0	0	2	0	1	0	0	2	0	0	0	0	0	0	0	0
arCOG03914	COG2132	Q	Multicopper oxidase	0	0	1	2	1	0	0	3	0	0	0	0	0	0	0	0
arCOG03915		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
arCOG03916		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
arCOG03917		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
arCOG03918	COG2215	R	ABC-type uncharacterized transport system, permea	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG03919	COG2215	R	ABC-type uncharacterized transport system, permea	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG03920		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
arCOG03921		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG03922		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
arCOG03923		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
arCOG03924	COG1846	K	Transcriptional regulator, MarR family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
arCOG03925		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	3	0	0	0
arCOG03926		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	1	0	1	0	0
arCOG03927		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
arCOG03928	COG4309	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG03929		R	SirA-like two-layered alpha/beta sandwich domain	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG03931	COG2202	K	ArsR-like HTH and PAS domain	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG03932	COG2202	K	Icl-like HTH and PAS domain	0	0	0	2	0	0	0	0	1	0	2	0	1	0	0	0
arCOG03933		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
arCOG03934		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG03935		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG03936	COG2002	K	Transcriptional regulator AbrB	0	0	2	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG03937	COG2002	K	Transcriptional regulator AbrB	0	0	0	2	0	0	0	3	0	0	0	0	0	0	0	0
arCOG03938		Q	Gas vesicle protein gvpG	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0
arCOG03939		K	RHH-fold DNA-binding ptotein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0

arCOG03940	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0
arCOG03941	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG03942	S	Uncharacterized conserved protein	1	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0
arCOG03943	COG2337	V	Toxin-antitoxin addiction module toxin component !	0	0	0	0	0	0	0	1	0	1	2	0	0	0	0	0	0
arCOG03944		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG03946		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	1	1	0	0	0
arCOG03947	COG0542	O	ATP-binding subunits of Clp protease and DnaK/Dn	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0
arCOG03948	COG1061	K	DNA or RNA helicase of superfamily II	0	0	0	1	0	0	0	1	1	0	1	0	1	0	0	0	0
arCOG03949	COG3815	S	Predicted membrane protein	0	0	0	0	0	0	0	1	2	1	0	1	0	0	0	0	0
arCOG03950		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG03951	COG0671	I	Membrane-associated phospholipid phosphatase	0	0	0	0	0	0	0	1	0	1	0	0	2	0	1	0	0
arCOG03952	COG3187	O	Heat shock protein	0	0	0	0	0	0	0	0	0	0	3	0	3	0	0	0	0
arCOG03953		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03954	COG4657	C	Predicted NADH:ubiquinone oxidoreductase, subun	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03955	COG4660	C	Predicted NADH:ubiquinone oxidoreductase, subun	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03956	COG0068	O	Hydrogenase maturation factor	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG03957	COG4902	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	0	3	1	0	2	0	1	0	0
arCOG03958	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03961		S	Cell suface protein	0	0	0	0	0	0	0	0	0	2	0	1	4	0	0	0	0
arCOG03962	COG2340	S	Uncharacterized protein with SCP/PR1 domains	0	0	2	1	0	0	1	3	0	2	1	0	0	1	0	0	0
arCOG03964	COG3335	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0
arCOG03965		R	Transposase related protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03966		K	CopG family DNA-binding protein	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG03967		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03968		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03969		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03970		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03971		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03972		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03973		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG03974		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG03975		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03976		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03977		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03978		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03979	COG0236	I	Acyl carrier protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03980	COG1807	M	Glycosyltransferase of PMT family	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03981	COG1807	M	Glycosyltransferase of PMT family	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG03982		C	Vanadium/alternative nitrogenase delta subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03983		C	Vanadium/alternative nitrogenase delta subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03984	COG1840	P	ABC-type Fe3+ transport system, periplasmic comp	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03985	COG1840	P	ABC-type Fe3+ transport system, periplasmic comp	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03986		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03987		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03988		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03989	COG0582	L	Integrase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03990	COG0582	L	Integrase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03991	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	1	1	0	2	0	0	0	0
arCOG03993	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	1	0	0
arCOG03994	COG3291	R	PKD domain containing protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG03995	COG4894	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03996		S	Zn finger protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03997		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG03998		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG03999		E	Clostripain family peptidase, C11	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG04000	COG2202	T	PAS domain	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG04001	COG2202	T	PAS domain	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG04002		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG04003		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG04004	COG0666	R	Ankyrin repeats containing protein	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	2	0
arCOG04005		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0	0	0
arCOG04006	COG1413	S	HEAT repeats containing protein	0	0	0	2	1	0	0	0	0	0	3	0	0	0	0	0	0
arCOG04007		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG04008		S	Uncharacterized conserved protein	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04009		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04010		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04011	COG4314	R	NosL family protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04012		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG04013		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04014		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04015		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04016		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04017		S	Uncharacterized conserved protein	0	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG04018		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04019		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04020		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG04021		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG04022		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG04023		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG04024		S	Uncharacterized conserved protein	2	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0
arCOG04025		S	Uncharacterized conserved protein	1	2	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG04026		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG04027	COG1725	K	Transcriptional regulator (GntR family)	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
arCOG04028	COG5550	O	Predicted aspartyl protease	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04029		S	Uncharacterized conserved protein	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG04030		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04031		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04032		S	Uncharacterized conserved protein	2	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG04033		S	Uncharacterized conserved protein	1	2	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG04034	COG3451	L	Type IV secretory pathway, VirB4 component	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG04035	COG3451	U	Type IV secretory pathway, VirB4 component	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG04036		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04037		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04038		S	Uncharacterized conserved protein	0	0	1	2	1	0	0	0	0	0	0	1	2	0	0	0	0
arCOG04039		S	Uncharacterized conserved protein	2	2	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG04040		Q	Gas vesicle synthesis protein GvpO	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0
arCOG04041		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	2	0	2	0	0
arCOG04044	COG1830	G	DhnA-type fructose-1,6-bisphosphate aldolase or rel	2	2	2	2	1	1	1	4	2	3	3	1	5	1	4	0	0
arCOG04045	COG0129	E	Dihydroxyacid dehydratase/phosphogluconate dehy	1	3	4	2	1	1	1	3	2	3	3	1	5	1	2	1	0
arCOG04046	COG4996	R	Predicted phosphatase	1	3	2	0	0	1	0	0	0	0	0	0	0	0	1	1	0
arCOG04047		S	Uncharacterized conserved protein	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04048	COG0717	F	Deoxycytidine deaminase	3	3	5	0	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04049	COG1552	J	Ribosomal protein L40E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04050	COG0258	L	5'-3' exonuclease (including N-terminal domain of P	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04051	COG2412	S	Uncharacterized conserved protein	3	3	1	2	1	0	1	4	0	0	3	1	5	1	4	3	0
arCOG04052	COG4756	R	Predicted cation transporter	2	0	3	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG04053	COG0405	E	Gamma-glutamyltransferase	2	3	4	1	0	1	0	2	0	0	0	0	0	0	0	3	0
arCOG04054		S	Uncharacterized conserved protein	3	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04055	COG1371	R	SHS2 domain protein implicated in nucleic acid met	3	3	5	2	1	1	1	2	2	3	3	1	5	1	4	3	1
arCOG04056	COG0640	K	Transcriptional regulator containing HTH domain, A	2	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG04057		J	Ribosomal L38E	3	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04058	COG1872	S	Uncharacterized conserved protein	3	0	0	0	0	1	1	0	1	3	2	1	5	1	4	0	0
arCOG04059		S	Uncharacterized conserved protein	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04060	COG1709	K	Predicted transcriptional regulator	3	3	5	0	1	1	1	4	0	3	3	1	5	1	4	3	0
arCOG04061	COG1308	K	Transcription factor homologous to NACalpha-BTF	3	2	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04062		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04063	COG1859	J	RNA:NAD 2'-phosphotransferase	3	0	3	0	0	0	1	1	0	0	0	1	5	1	4	2	0
arCOG04064	COG0750	M	Predicted membrane-associated Zn-dependent prote	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04065	COG0612	R	Predicted Zn-dependent peptidase	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	1
arCOG04066	COG2413	R	Predicted nucleotidyltransferase	3	3	1	0	1	1	1	0	0	0	0	1	0	1	4	0	0
arCOG04067	COG0090	J	Ribosomal protein L2	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04068		S	Uncharacterized conserved protein	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04069	COG2106	S	Uncharacterized conserved protein	3	3	5	2	1	0	1	4	2	0	0	0	1	1	4	0	0
arCOG04070	COG0087	J	Ribosomal protein L3	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04071	COG0088	J	Ribosomal protein L4	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04072	COG0089	J	Ribosomal protein L23	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04073	COG1149	C	MinD superfamily P-loop ATPase containing an inse	1	0	2	0	0	0	1	0	1	3	3	0	5	1	4	0	0
arCOG04074	COG1145	C	Ferredoxin	0	0	1	0	0	0	0	0	1	0	1	0	0	1	0	0	0

arCOG04075	COG0214	H	Pyridoxine biosynthesis enzyme	3	3	4	2	0	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04076	COG1909	S	Uncharacterized protein conserved in archaea	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	0
arCOG04077	COG2093	K	DNA-directed RNA polymerase, subunit E"	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04078	COG2346	T	Globin-like domain	1	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0
arCOG04079		S	Uncharacterized conserved protein	2	0	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0
arCOG04080	COG2362	E	D-aminopeptidase	3	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG04081	COG1224	K	DNA helicase TIP49, TBP-interacting protein	3	3	5	0	0	1	1	0	0	0	0	0	0	1	4	0	0
arCOG04082	COG2366	R	Protein related to penicillin acylase	1	2	2	0	0	0	1	2	0	0	0	0	0	0	3	0	0
arCOG04083	COG2355	E	Zn-dependent dipeptidase, microsomal dipeptidase h	1	3	4	0	1	0	0	0	0	0	0	0	0	0	4	1	0
arCOG04084	COG2152	G	Predicted glycosylase	3	0	2	0	0	0	0	0	0	0	0	0	3	0	3	0	0
arCOG04085	COG1649	S	Uncharacterized protein conserved in bacteria	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04086	COG1841	J	Ribosomal protein L30	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04087	COG0098	J	Ribosomal protein S5	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04088	COG0256	J	Ribosomal protein L18	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04089	COG2147	J	Ribosomal protein L19E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04090	COG0097	J	Ribosomal protein L6P	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04091	COG0096	J	Ribosomal protein S8	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04092	COG0094	J	Ribosomal protein L5	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04093	COG1471	J	Ribosomal protein S4E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04094	COG0198	J	Ribosomal protein L24	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04095	COG0093	J	Ribosomal protein L14	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04096	COG0186	J	Ribosomal protein S17	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04097	COG0092	J	Ribosomal protein S3	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04098	COG0091	J	Ribosomal protein L22	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04099	COG0185	J	Ribosomal protein S19	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04100	COG1960	I	Acyl-CoA dehydrogenase	1	2	1	0	0	0	0	1	0	0	0	0	0	0	0	2	0
arCOG04101	COG1394	C	Archaeal/vacuolar-type H+-ATPase subunit D	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04102	COG1436	C	Archaeal/vacuolar-type H+-ATPase subunit F	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04103		S	Uncharacterized conserved protein	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04104		S	Uncharacterized conserved protein	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04105		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04106	COG0575	I	CDP-diglyceride synthetase	3	3	5	0	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04107	COG1093	J	Translation initiation factor 2, alpha subunit (eIF-2al	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04108	COG2051	J	Ribosomal protein S27E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04109	COG1631	J	Ribosomal protein L44E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04110	COG1467	L	Eukaryotic-type DNA primase, catalytic (small) sub	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04111	COG1761	K	DNA-directed RNA polymerase, subunit L	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04112	COG1736	J	Diphthamide synthase subunit DPH2	3	3	5	2	1	0	1	4	2	3	3	1	5	1	4	3	1
arCOG04113	COG0197	J	Ribosomal protein L16	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04114		S	Uncharacterized conserved protein	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04115	COG1489	R	DNA-binding protein, stimulates sugar fermentation	3	3	5	0	1	0	1	1	2	0	0	0	1	0	2	3	0
arCOG04116	COG1855	R	ATPase (PilT family)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04117	COG1148	C	Ferredoxin	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG04118		S	Mn2+/Fe2+ transporter, NRAMP family	1	0	2	0	0	1	0	1	0	0	0	0	0	0	0	0	0
arCOG04119	COG4914	R	Predicted nucleotidyltransferase	3	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04120	COG0469	G	Pyruvate kinase	3	3	5	0	1	1	0	4	0	3	2	1	4	0	4	3	0
arCOG04121	COG0164	L	Ribonuclease HII	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04122	COG1756	S	Uncharacterized conserved protein	3	3	5	2	1	1	1	0	0	1	0	0	1	1	4	3	0
arCOG04123	COG4755	S	Uncharacterized protein conserved in archaea	3	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04124	COG2835	S	Uncharacterized conserved protein	3	3	5	2	1	1	0	4	0	1	3	1	5	0	0	0	0
arCOG04125	COG0430	J	RNA 3'-terminal phosphate cyclase	3	3	5	2	1	1	1	2	1	3	1	1	5	1	4	0	0
arCOG04126	COG2126	J	Ribosomal protein L37E	3	3	4	2	1	1	1	3	2	3	2	0	5	1	4	2	0
arCOG04127	COG1341	R	Predicted GTPase or GTP-binding protein	3	3	5	0	1	1	1	0	0	1	1	1	0	1	4	0	0
arCOG04128	COG0035	F	Uracil phosphoribosyltransferase	3	3	5	0	1	0	0	4	1	2	0	0	0	0	3	0	0
arCOG04129	COG2139	J	Ribosomal protein L21E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04130	COG1491	J	Predicted RNA-binding protein	3	3	5	2	1	1	1	4	1	3	3	1	5	1	4	3	1
arCOG04131	COG0030	J	Dimethyladenosine transferase (rRNA methylation)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04132	COG4697	S	Uncharacterized protein conserved in archaea	3	1	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG04133	COG0082	E	Chorismate synthase	1	3	4	2	1	1	1	4	2	3	3	1	5	1	3	3	0
arCOG04134	COG0128	E	5-enolpyruvylshikimate-3-phosphate synthase	2	3	4	2	1	1	1	4	2	3	3	1	5	1	3	3	0
arCOG04135		R	Zn-finger protein	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04136	COG4888	R	Uncharacterized Zn ribbon-containing protein	3	3	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04137	COG0499	H	S-adenosylhomocysteine hydrolase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04138	COG1269	C	Archaeal/vacuolar-type H+-ATPase subunit I	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04139	COG1893	H	Ketopantoate reductase	3	0	4	0	0	0	1	3	1	1	2	1	0	0	4	0	0
arCOG04140	COG1888	S	Uncharacterized protein conserved in archaea	3	3	4	0	1	1	1	1	2	3	0	0	2	1	4	3	0
arCOG04141		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04142	COG1899	O	Deoxyhypusine synthase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04143	COG1697	L	DNA topoisomerase VI, subunit A	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	0	1
arCOG04144	COG4047	L	8-oxoguanine DNA glycosylase	3	0	5	0	0	0	0	0	0	2	0	0	0	1	4	0	1
arCOG04145	COG0168	P	Trk-type K+ transport system, membrane componen	3	0	0	2	0	0	1	4	2	3	2	1	5	1	4	0	0
arCOG04146		S	Uncharacterized conserved protein	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04147	COG0605	P	Superoxide dismutase	1	3	4	2	1	0	0	4	1	0	2	0	4	0	0	3	0
arCOG04148	COG2874	N	Predicted ATPase involved in biogenesis of archaeal	1	3	0	0	1	0	1	3	0	3	2	1	4	0	4	2	0
arCOG04149	COG1499	J	NMD protein affecting ribosome stability and mRN.	3	3	5	0	0	0	1	4	2	3	3	1	5	1	4	3	1
arCOG04150	COG1094	R	Predicted RNA-binding protein (contains KH domai	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04151	COG2237	R	ABC-type multidrug transport system, permease cor	3	3	5	2	1	1	1	4	0	3	3	1	5	0	4	3	0
arCOG04152	COG1395	K	Predicted transcriptional regulator	3	3	5	0	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG04153	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	3	3	5	1	1	0	1	4	0	0	3	1	5	0	0	0	0
arCOG04154	COG2007	J	Ribosomal protein S8E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04155		S	HhH-GPD superfamily base excision DNA repair pr	3	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04156	COG1590	J	Wybutosine (yW) biosynthesis enzyme	3	3	5	0	0	1	1	0	0	3	0	0	0	1	4	0	1
arCOG04157	COG0270	L	Site-specific DNA methylase	3	3	5	2	0	0	0	0	1	3	1	1	2	1	3	0	0
arCOG04158		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG04159	COG0714	R	MoxR-like ATPase	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04160		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04161	COG1798	J	Diphthamide biosynthesis methyltransferase	3	3	5	2	1	0	1	4	2	3	3	1	5	1	4	3	1
arCOG04162	COG2142	C	Succinate dehydrogenase, hydrophobic anchor subu	2	0	1	2	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG04163	COG1223	R	Predicted ATPase (AAA+ superfamily)	0	0	0	0	0	0	1	0	2	3	0	0	5	1	0	0	0
arCOG04164	COG4034	S	Uncharacterized protein conserved in archaea	3	3	3	0	0	0	1	0	0	0	0	0	0	1	0	0	0
arCOG04165		S	Uncharacterized conserved protein	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04166	COG4879	S	Uncharacterized protein conserved in archaea	3	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04167	COG2163	J	Ribosomal protein L14E/L6E/L27E	3	3	5	0	1	1	0	0	2	3	0	0	0	1	4	0	1
arCOG04168	COG2174	J	Ribosomal protein L34E	3	3	4	0	0	1	0	0	2	3	0	0	0	1	4	0	1
arCOG04169	COG0201	U	Preprotein translocase subunit SecY	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04170	COG2379	G	Putative glycerate kinase	3	3	4	2	1	1	0	3	0	0	0	1	0	0	4	3	0
arCOG04171	COG2090	S	Uncharacterized protein conserved in archaea	3	3	4	2	0	1	1	4	2	3	3	1	0	1	4	0	0
arCOG04172	COG0329	E	Dihydrodipicolinate synthase/N-acetylneuraminate l	1	3	5	0	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04173	COG0295	F	Cytidine deaminase	3	0	4	1	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04174	COG0731	C	Wybutosine (yW) biosynthesis enzyme, Fe-S oxidor	3	3	5	1	1	1	1	3	2	3	3	1	5	1	4	3	1
arCOG04175	COG2157	J	Ribosomal protein L20A (L18A)	3	3	5	0	0	0	1	2	2	3	1	1	5	1	4	0	1
arCOG04176	COG1976	J	Translation initiation factor 6 (eIF-6)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04177	COG2167	J	Ribosomal protein L39E	3	3	4	2	0	0	1	4	1	3	3	0	5	1	4	3	0
arCOG04179	COG2118	R	DNA-binding protein	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04180	COG1980	G	Archaeal fructose 1,6-bisphosphatase	3	3	5	2	1	1	1	0	2	3	2	0	1	1	4	3	0
arCOG04181	COG4046	S	Uncharacterized protein conserved in archaea	2	3	5	2	1	1	0	0	1	0	0	0	0	1	0	0	0
arCOG04182	COG2004	J	Ribosomal protein S24E	3	3	5	0	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04183	COG1998	J	Ribosomal protein S27AE	3	3	5	2	1	1	1	3	2	3	3	1	5	1	4	3	1
arCOG04184	COG0127	F	Xanthosine triphosphate pyrophosphatase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04185	COG0184	J	Ribosomal protein S15P	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04186	COG1890	J	Ribosomal protein S3AE	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04187	COG1500	J	Predicted exosome subunit	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04188	COG1898	M	dTDP-4-dehydrorhamnose 3,5-epimerase or related	1	3	2	1	0	1	1	0	2	1	3	1	5	0	2	2	0
arCOG04189	COG5625	K	Predicted transcription regulator containing HTH do	2	0	5	2	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG04190		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04191	COG2046	P	ATP sulfurylase (sulfate adenylyltransferase)	3	3	4	2	0	0	1	0	0	0	0	1	0	0	2	0	0
arCOG04192	COG1857	V	CRISPR system related protein	3	2	4	0	1	1	1	0	0	1	0	0	0	0	4	0	0
arCOG04193		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04194	COG1343	V	CRISPR-associated protein Cas2	3	3	2	0	1	1	1	2	2	2	2	0	5	0	3	2	1
arCOG04195	COG4343	V	CRISPR-associated protein, RecB family exonuclea	3	2	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG04196	COG3033	E	Tryptophanase	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG04197		R	Transposase related protein	2	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG04198		S	Uncharacterized conserved protein	1	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG04199	COG1022	I	Long-chain acyl-CoA synthetase (AMP-forming)	1	0	1	0	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG04200		L	CC1 family DNA binding protein	2	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG04201	COG0365	I	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligas	1	3	5	1	1	0	1	4	2	2	3	1	5	0	0	3	0
arCOG04202	COG2429	F	Archaeal GTP cyclohydrolase III	2	3	3	2	0	0	0	4	2	3	0	0	0	0	0	0	0
arCOG04203	COG3174	S	Predicted membrane protein	2	0	0	0	0	0	0	4	1	0	0	1	5	1	0	0	0

arCOG04204	COG3342	S	Uncharacterized conserved protein	3	3	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG04206	COG1948	L	ERCC4-type nuclease	3	3	5	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG04207	COG0322	L	Excinuclease-associated helix-hairpin-helix domain	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG04208	COG1997	J	Ribosomal protein L37AE/L43A	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04209	COG1632	J	Ribosomal protein L15E	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04210	COG0780	R	Enzyme related to GTP cyclohydrolase I	2	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04211		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04212	COG1661	R	Predicted DNA-binding protein with PD1-like DNA	3	0	0	0	0	1	1	4	1	0	2	0	5	1	4	3	0	
arCOG04213	COG1260	I	Myo-inositol-1-phosphate synthase	3	3	5	2	1	1	1	0	2	0	1	0	5	0	4	0	0	
arCOG04214	COG0432	S	Uncharacterized conserved protein	3	3	5	2	1	1	1	3	2	3	2	1	4	1	4	0	1	
arCOG04215	COG3375	R	NH2-acetyltransferase	2	0	1	0	0	1	0	0	0	0	0	0	0	0	0	3	0	
arCOG04216		S	Uncharacterized conserved protein	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04217	COG4900	R	Predicted metallopeptidase	3	3	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04218	COG1423	L	ATP-dependent DNA ligase, homolog of eukaryotic	3	0	0	0	0	0	1	1	1	3	0	0	5	1	4	0	0	
arCOG04219	COG2433	R	Possible nuclease of RNase H fold, RuvC/YqgF fam	3	3	5	0	0	1	1	4	1	0	3	1	4	1	4	0	1	
arCOG04220		S	Uncharacterized conserved protein	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	
arCOG04221	COG0647	G	Phosphatase of the HAD superfamily	2	3	0	0	1	1	1	4	0	0	2	0	1	0	4	0	0	
arCOG04222		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0		
arCOG04223	COG0023	J	Translation initiation factor 1 (eIF-1/SUI1)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04224		S	Uncharacterized conserved protein	3	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04225	COG2110	R	Predicted phosphatase homologous to the C-termina	3	3	5	0	1	1	1	2	0	0	1	0	4	1	4	2	0	
arCOG04226	COG0235	G	Ribulose-5-phosphate 4-epimerase or related epimer	3	0	5	0	0	1	1	2	2	3	3	1	5	1	4	2	0	
arCOG04227	COG1832	R	Predicted CoA-binding protein	1	3	2	2	1	1	0	4	0	2	0	0	1	0	4	3	0	
arCOG04228	COG1990	J	Peptidyl-tRNA hydrolase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04229	COG1781	F	Aspartate carbamoyltransferase, regulatory subunit	3	3	5	2	0	1	1	4	2	3	3	1	5	1	4	3	0	
arCOG04230	COG3294	R	HD supefamily hydrolase	2	0	4	0	0	1	0	4	0	1	1	0	0	0	2	0	0	
arCOG04231	COG1324	P	Uncharacterized protein involved in tolerance to div	3	2	3	2	1	1	1	2	1	2	2	1	5	1	4	2	0	
arCOG04232	COG1884	I	Methylmalonyl-CoA mutase	1	3	0	2	0	0	1	4	0	0	0	0	0	0	4	3	0	
arCOG04233	COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	3	3	4	2	1	0	1	4	0	0	1	3	1	4	0	4	3	0
arCOG04234		S	Uncharacterized conserved protein	3	1	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04235	COG5494	O	Predicted thioredoxin/glutaredoxin	3	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04236	COG0396	O	Cysteine desulfurase activator ATPase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04237	COG0372	C	Citrate synthase	1	3	4	2	1	0	1	4	1	0	0	0	3	0	1	3	0	
arCOG04238	COG1767	H	Triphosphoribosyl-dephospho-CoA synthetase	3	3	0	0	1	0	1	3	2	3	3	1	5	1	4	0	0	
arCOG04239	COG0522	J	Ribosomal protein S4 or related protein	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04240	COG0100	J	Ribosomal protein S11	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04241	COG0202	K	DNA-directed RNA polymerase subunit D	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04242	COG0102	J	Ribosomal protein L13	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04243	COG0103	J	Ribosomal protein S9	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04244	COG1644	K	DNA-directed RNA polymerase, subunit N (RpoN/R	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04245	COG0052	J	Ribosomal protein S2	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04246	COG1690	R	RtcB family protein, predicted to be implicated in R	3	3	5	2	0	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04247	COG2317	E	Zn-dependent carboxypeptidase	3	3	4	0	0	1	0	4	0	0	0	1	0	0	4	0	1	
arCOG04248	COG0846	K	NAD-dependent protein deacetylase, SIR2 family	3	3	4	1	0	1	1	2	0	0	0	0	1	1	4	0	0	
arCOG04249	COG1746	J	tRNA nucleotidyltransferase (CCA-adding enzyme)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04250	COG3382	R	Solo B3/4 domain (OB-fold DNA/RNA-binding) of	2	3	4	0	1	1	0	0	0	0	2	1	0	1	0	0	0	
arCOG04251	COG5399	S	Uncharacterized protein conserved in archaea	2	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04252	COG0585	J	tRNA pseudouridine synthase D	3	3	5	2	0	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04253	COG1415	S	Uncharacterized conserved protein	3	3	5	0	1	1	1	0	2	0	0	0	1	1	4	3	0	
arCOG04254	COG0049	J	Ribosomal protein S7	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04255	COG0048	J	Ribosomal protein S12	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04256	COG0086	K	DNA-directed RNA polymerase subunit A"	3	3	5	1	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04257	COG0086	K	DNA-directed RNA polymerase subunit A'	3	3	5	2	1	0	1	4	2	3	3	1	5	1	4	3	1	
arCOG04258	COG2012	K	DNA-directed RNA polymerase, subunit H, RpoH/R	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04259		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		
arCOG04260	COG1257	I	Hydroxymethylglutaryl-CoA reductase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	0	
arCOG04261		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04262	COG1701	S	Uncharacterized protein conserved in archaea	3	3	4	2	0	0	1	4	2	3	3	1	5	1	4	0	0	
arCOG04263	COG1829	R	Predicted archaeal kinase (sugar kinase superfamily)	3	3	5	2	1	0	1	4	2	3	3	1	5	1	4	0	0	
arCOG04264		S	Uncharacterized conserved protein	3	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04265	COG1779	R	C4-type Zn-finger protein	3	3	5	0	0	0	1	0	2	3	3	1	5	1	4	3	1	
arCOG04266		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04267		S	Uncharacterized conserved protein	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04268		S	Uncharacterized conserved protein	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04269	COG1602	S	Uncharacterized conserved protein	3	3	5	2	1	1	1	4	2	2	3	1	5	1	4	3	0	
arCOG04270	COG1675	K	Transcription initiation factor IIE, alpha subunit	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	0	1	
arCOG04271		K	DNA-directed RNA polymerase, subunit RPB8	3	3	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	
arCOG04272	COG2038	H	NaMN:DMB phosphoribosyltransferase	1	3	3	2	0	0	1	4	2	3	3	1	5	1	4	3	0	
arCOG04273	COG0079	E	Histidinol-phosphate/aromatic aminotransferase or c	2	3	4	2	1	0	1	4	2	3	3	1	5	1	4	3	0	
arCOG04274	COG1270	H	Cobalamin biosynthesis protein CobD/CbiB	1	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0	
arCOG04275		S	Uncharacterized conserved protein	3	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	
arCOG04276	COG0209	F	Ribonucleotide reductase, alpha subunit	2	3	4	2	1	0	1	4	1	0	2	0	4	0	4	3	0	
arCOG04277	COG0231	J	Translation elongation factor P (EF-P)/translation in	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04278	COG1679	R	Predicted aconitase	3	0	5	2	0	1	1	0	2	3	3	1	5	1	4	0	0	
arCOG04279	COG1786	C	Swiveling domain associated with predicted aconita	3	0	5	2	0	0	1	0	2	3	3	1	5	1	4	0	0	
arCOG04280	COG1940	K	Transcriptional regulator/sugar kinase	2	0	5	2	1	0	1	3	0	0	3	0	0	0	0	3	0	
arCOG04281	COG0358	L	DNA primase (bacterial type)	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04283		S	Uncharacterized conserved protein	3	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04284	COG1738	R	Uncharacterized member of the PurR regulon	2	0	4	0	0	0	1	3	1	1	0	0	3	0	0	0	0	
arCOG04285	COG2079	R	Uncharacterized protein involved in propionate catal	1	3	4	0	1	0	0	1	1	0	0	0	0	0	0	3	0	
arCOG04286	COG1966	T	Carbon starvation protein, predicted membrane prot	3	0	2	0	1	0	0	3	0	0	0	0	1	0	2	0	0	
arCOG04287	COG2058	J	Ribosomal protein L12E/L44/L45/RPP1/RPP2	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04288	COG0244	J	Ribosomal protein L10	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04289	COG0081	J	Ribosomal protein L1	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04290	COG1656	R	PIN-domain and Zn ribbon	3	3	5	0	1	1	1	3	0	0	2	1	1	1	4	3	0	
arCOG04291	COG1801	S	Uncharacterized conserved protein	3	3	5	0	1	1	1	0	0	0	1	1	3	0	4	3	0	
arCOG04292		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04293	COG4919	J	Ribosomal protein S30	3	3	5	2	1	1	0	0	0	0	0	0	0	0	0	0	0	
arCOG04294	COG0468	L	RecA/RadA recombinase	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04295	COG2094	L	3-methyladenine DNA glycosylase	1	0	1	2	1	1	0	0	0	0	1	1	0	0	0	0	0	
arCOG04296	COG0477	G	permease of the major facilitator superfamily	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
arCOG04297	COG2401	R	ABC-type ATPase fused to a predicted acetyltransfe	1	0	0	0	0	0	1	0	0	0	0	0	1	4	0	0	0	
arCOG04298	COG1839	S	Uncharacterized conserved protein	3	3	5	0	1	1	1	0	1	0	0	0	1	0	4	3	0	
arCOG04299	COG0181	H	Porphobilinogen deaminase	2	3	4	2	0	0	1	4	2	3	3	1	5	1	0	3	0	
arCOG04300	COG0113	H	Delta-aminolevulinic acid dehydratase	2	3	4	2	0	0	1	4	2	3	3	1	5	1	0	3	0	
arCOG04301	COG1469	S	Uncharacterized conserved protein	1	0	0	0	1	1	1	4	2	3	3	1	5	1	4	3	0	
arCOG04302	COG0008	J	Glutamyl- or glutaminyl-tRNA synthetase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04303	COG1634	R	Uncharacterized Rossmann fold enzyme	2	3	4	2	1	1	1	4	2	3	3	1	5	1	4	3	0	
arCOG04304	COG2451	J	Ribosomal protein L35AE/L33A	3	0	1	0	0	0	0	0	0	0	0	0	1	4	0	1		
arCOG04305	COG4830	J	Ribosomal protein S26	3	3	5	2	1	1	0	0	0	0	0	0	0	0	0	0	1	
arCOG04306	COG4998	L	Predicted endonuclease (RecB family)	3	0	5	0	0	1	0	0	0	0	0	0	1	0	0	0		
arCOG04307	COG1530	J	Ribonuclease G and E	3	3	5	0	0	0	0	4	0	0	0	0	0	1	4	0	0	
arCOG04308	COG1698	S	Uncharacterized protein conserved in archaea	3	3	2	2	1	1	1	0	2	3	3	1	5	1	4	3	0	
arCOG04309	COG1912	S	Uncharacterized conserved protein	3	3	5	0	1	1	1	4	0	1	0	1	4	1	4	0	0	
arCOG04310	COG1960	I	Acyl-CoA dehydrogenase	1	0	4	0	1	1	0	0	0	0	0	0	0	0	0	3	0	
arCOG04311	COG1896	R	Predicted hydrolase of HD superfamily	3	3	4	2	1	1	1	2	0	0	0	1	0	1	4	0	0	
arCOG04312	COG1412	R	Uncharacterized protein of PilT N-term./Vapc superf	3	3	5	2	1	1	1	4	2	3	2	1	5	1	4	3	1	
arCOG04313	COG0105	F	Nucleoside diphosphate kinase	3	3	4	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04314	COG2053	J	Ribosomal protein S28E/S33	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1	
arCOG04315	COG2031	I	Short chain fatty acids transporter	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	
arCOG04316		S	Uncharacterized conserved protein	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	
arCOG04317	COG4732	S	Predicted membrane protein	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	
arCOG04318	COG2178	J	Predicted RNA-binding protein of the translin famil	3	3	5	2	0	1	1	0	0	3	0	1	4	1	4	0	1	
arCOG04319	COG4920	S	Predicted membrane protein	3	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04320	COG0274	F	Deoxyribose-phosphate aldolase	3	0	4	0	1	0	0	4	1	0	0	1	0	0	1	2	0	
arCOG04321	COG2848	S	Uncharacterized conserved protein	3	3	5	0	0	1	0	0	0	3	3	1	4	1	0	0	0	
arCOG04322	COG0260	E	Leucyl aminopeptidase	3	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	
arCOG04323		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04324		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04325	COG1702	T	Phosphate starvation-inducible protein PhoH, predic	3	1	5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	
arCOG04326		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
arCOG04327	COG4901	J	Ribosomal protein S25	3	3	5	1	1	1	0	0	0	0	0	0	0	0	0	0	0	
arCOG04328	COG4028	R	Predicted P-loop ATPase/GTPase	3	3	0	0	0	0	0	2	0	0	0	0	0	1	2	0	0	
arCOG04329	COG2441	C	Predicted butyrate kinase	2	3	0	0	1	0	1	0	0	0	0	0	0	4	0	0	0	
arCOG04330	COG0672	P	High-affinity Fe2+/Pb2+ permease	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	
arCOG04331	COG5496	R	Predicted thioesterase	3	2	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	
arCOG04332	COG2606	S	Uncharacterized conserved protein	1	1	4	0	1	1	0	1	0	0	0	0	0	0	0	0	0	
arCOG04333	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	1	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	

arCOG04334	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	0	0	3	0	0	0	0	1	0	0	0	0	0	0	0	3	0
arCOG04335	COG1301	C	Na+/H+-dicarboxylate symporter	2	0	0	1	0	0	0	2	0	0	1	0	3	0	4	0	0
arCOG04336	COG1962	H	Tetrahydromethanopterin S-methyltransferase, subu	1	0	0	0	0	1	1	0	2	3	3	1	5	1	0	0	0
arCOG04337	COG1504	S	Uncharacterized conserved protein	1	0	1	0	0	1	1	0	1	0	0	0	3	1	4	0	0
arCOG04338	COG0368	H	Cobalamin-5-phosphate synthase	1	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG04339	COG1682	G	ABC-type polysaccharide/polyol phosphate export s	0	0	0	0	0	0	1	0	1	0	2	1	4	0	0	0	0
arCOG04340	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	1	1	0	0	1	1	3	0	0	0	0
arCOG04341	COG1996	K	DNA-directed RNA polymerase, subunit RPC10 (co	3	3	5	2	1	0	1	4	2	3	3	1	5	1	4	3	0
arCOG04342	COG1583	V	CRISPR system related protein, RAMP superfamily	0	0	0	0	0	0	1	1	2	1	0	0	3	0	4	2	1
arCOG04343	COG1751	S	Uncharacterized conserved protein	0	0	0	0	0	1	1	0	1	3	3	1	4	0	0	0	0
arCOG04344	COG4818	S	Predicted membrane protein	1	0	0	0	0	0	1	1	0	2	0	1	2	0	2	0	0
arCOG04345	COG2023	J	RNase P subunit RPR2	2	3	1	1	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04346	COG1759	F	5-formaminoimidazole-4-carboxamide-1-beta-D-rib	1	3	4	2	1	1	1	0	2	3	0	1	5	1	4	0	0
arCOG04347	COG0500	Q	SAM-dependent methyltransferase	0	0	1	2	0	0	1	4	0	0	0	0	4	1	3	0	1
arCOG04348	COG2226	H	Methylase involved in ubiquinone/menaquinone bio	1	3	4	2	1	1	0	0	0	0	0	0	0	0	0	2	0
arCOG04349	COG3374	S	Predicted membrane protein	0	3	3	0	0	0	1	0	0	0	0	0	0	0	0	2	0
arCOG04350	COG1960	I	Acyl-CoA dehydrogenase	0	3	0	0	1	0	1	2	0	0	0	0	0	0	0	0	0
arCOG04351	COG3356	S	Predicted membrane protein	1	3	5	2	1	1	1	4	2	0	3	1	0	1	0	3	0
arCOG04352	COG0141	E	Histidinol dehydrogenase	0	3	4	2	1	0	1	4	2	3	3	1	5	1	2	1	0
arCOG04353	COG1465	E	3-dehydroquinate synthase	0	0	0	2	1	1	1	4	2	3	3	1	5	1	0	0	0
arCOG04354	COG1906	S	Uncharacterized conserved protein	1	0	3	0	0	1	1	0	0	0	0	0	0	0	3	0	0
arCOG04355	COG1275	P	Tellurite resistance protein or related permease	0	1	0	0	0	0	1	0	0	1	0	0	0	0	3	2	1
arCOG04356	COG3372	R	Predicted nuclease of restriction endonuclease-like f	0	3	4	0	0	1	1	4	0	0	0	1	3	0	3	3	0
arCOG04357	COG1059	L	Thermostable 8-oxoguanine DNA glycosylase	0	3	0	0	1	1	1	0	0	1	0	0	1	0	0	3	0
arCOG04358	COG1526	C	Uncharacterized protein required for formate dehydr	1	3	4	0	1	0	1	0	1	3	3	1	5	0	0	3	0
arCOG04359	COG2517	R	Predicted RNA-binding protein containing a C-term	2	0	0	0	0	1	1	0	2	0	0	0	0	1	4	0	0
arCOG04360	COG1614	C	CO dehydrogenase/acetyl-CoA synthase beta subuni	0	0	0	0	0	0	1	0	1	3	1	1	5	1	0	0	0
arCOG04361	COG5423	S	Predicted metal-binding protein	0	0	0	0	0	0	1	0	1	0	2	1	4	0	4	0	0
arCOG04362	COG4742	K	Predicted transcriptional regulator	1	1	1	1	0	0	1	1	2	0	1	1	5	0	0	0	0
arCOG04364	COG1772	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	0	1	0	1	4	1	4	0	0
arCOG04365	COG4012	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	1	2	1	1	4	1	0	0	0
arCOG04366	COG4860	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	0	0	2	1	5	0	0	3	0
arCOG04367	COG0188	L	Type IIA topoisomerase (DNA gyrase/topo II, topois	0	0	0	0	0	0	1	4	0	0	3	1	5	0	0	3	0
arCOG04368	COG0464	O	ATPase of the AAA+ class	0	0	0	0	0	0	1	4	0	0	3	1	5	0	0	0	0
arCOG04369	COG1548	K	Predicted transcriptional regulator/sugar kinase	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG04370	COG3503	S	Predicted membrane protein	0	0	0	0	0	0	1	0	1	2	3	0	4	0	1	0	0
arCOG04371	COG0187	L	Type IIA topoisomerase (DNA gyrase/topo II, topois	0	0	0	0	0	0	1	4	0	0	3	1	5	0	0	3	0
arCOG04372	COG0080	J	Ribosomal protein L11	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04373	COG0011	S	Uncharacterized conserved protein	1	1	4	2	0	1	1	4	2	1	0	0	1	1	4	2	0
arCOG04374	COG3804	S	Uncharacterized conserved protein related to dihydr	2	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG04375	COG4800	K	Predicted transcriptional regulator with an HTH don	0	0	0	0	0	0	1	0	0	3	3	1	5	0	0	0	0
arCOG04376	COG2122	R	Nucleoside-diphosphate-sugar pyrophosphorylase	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG04377	COG4738	K	Predicted transcriptional regulator	0	0	0	0	0	0	1	0	0	0	2	1	5	0	0	3	0
arCOG04378	COG2142	C	Succinate dehydrogenase, hydrophobic anchor subu	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04379	COG2142	C	Succinate dehydrogenase, hydrophobic anchor subu	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	2	0
arCOG04380		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2	0	0
arCOG04381		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	2	1	4	0	0	0	0
arCOG04382	COG1927	C	Coenzyme F420-dependent N(5),N(10)-methenyltet	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG04383	COG1903	H	Cobalamin biosynthesis protein CbiD	0	3	2	2	0	0	1	0	2	3	3	0	5	1	0	3	0
arCOG04384	COG1930	P	ABC-type cobalt transport system, periplasmic comp	0	0	0	0	0	0	1	2	2	3	3	0	5	0	0	0	0
arCOG04385	COG1255	S	Predicted small methyltransferase	0	0	0	0	0	0	1	3	2	3	3	1	1	0	4	0	0
arCOG04386	COG1620	C	L-lactate permease	0	1	2	0	0	0	1	3	0	0	0	1	0	1	0	0	0
arCOG04387	COG0104	F	Adenylosuccinate synthase	0	3	4	2	1	1	1	4	2	3	3	1	5	1	4	3	0
arCOG04388		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	5	0	0	0	0
arCOG04389		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	5	0	0	0	0
arCOG04390	COG4068	S	Uncharacterized protein containing a Zn-ribbon	0	0	0	0	0	0	1	0	2	2	0	0	1	1	0	0	0
arCOG04391	COG1773	C	Rubredoxin	0	0	1	0	0	1	1	0	2	3	3	1	3	0	3	0	0
arCOG04392	COG0028	E	Rubredoxin	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG04393	COG0289	E	Dihydrodipicolinate reductase	0	0	0	0	0	0	1	3	2	3	3	1	5	1	0	0	0
arCOG04394	COG1416	S	Uncharacterized conserved protein	0	1	3	0	0	0	1	1	1	0	1	0	0	0	2	0	0
arCOG04395	COG0391	S	Uncharacterized conserved protein, YbhK/UPF0052	0	0	0	2	1	0	1	4	2	3	3	1	5	1	0	0	0
arCOG04396	COG2061	E	ACT-domain-containing protein, predicted allosteric	0	0	0	0	0	0	1	3	2	3	3	1	5	1	0	0	0
arCOG04397	COG0004	P	Ammonia permease	0	3	2	2	0	0	1	3	2	3	3	1	5	1	0	3	0
arCOG04398	COG0131	E	Imidazoleglycerol-phosphate dehydratase	0	3	4	2	1	0	1	4	2	3	3	1	5	1	2	1	0
arCOG04399	COG1497	K	Predicted transcriptional regulator	0	0	0	0	0	0	1	4	2	3	3	1	5	1	0	3	0
arCOG04400	COG1361	M	S-layer domain	0	0	0	0	1	1	1	4	0	1	3	0	1	0	0	0	0
arCOG04402	COG1352	N	Methylase of chemotaxis methyl-accepting protein	0	0	0	0	0	0	1	3	0	2	2	1	4	0	3	0	0
arCOG04403	COG0643	N	Chemotaxis protein histidine kinase or related kinas	0	0	0	0	0	0	1	3	0	2	2	1	4	0	3	0	0
arCOG04404	COG3679	L	Regulatory protein involved in competence develop	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG04405	COG2411	S	Uncharacterized conserved protein	0	0	0	1	0	0	1	0	0	0	0	0	1	0	4	0	0
arCOG04406	COG1838	C	Tartrate dehydratase beta subunit/Fumarate hydratas	1	0	4	0	0	1	1	0	2	3	3	1	5	1	4	0	0
arCOG04407	COG1951	C	Tartrate dehydratase alpha subunit/Fumarate hydrata	1	0	4	0	0	1	1	0	2	3	3	1	5	1	4	0	0
arCOG04408	COG1880	C	CO dehydrogenase/acetyl-CoA synthase epsilon sub	0	0	0	0	0	0	1	0	1	3	1	1	5	1	0	0	0
arCOG04409	COG2410	R	Predicted nuclease (RNAse H fold)	3	3	5	0	1	1	1	0	1	0	0	1	0	1	0	0	0
arCOG04410	COG1578	R	Predicted ATP-grasp domain fused to redox center	2	0	5	0	0	1	1	0	2	3	3	1	5	1	4	0	0
arCOG04411	COG4749	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	4	0	0	3	1	5	0	0	0	0
arCOG04412	COG4004	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	0	0	3	1	5	0	0	3	0
arCOG04413	COG1364	E	N-acetylglutamate synthase (N-acetylornithine amin	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG04414	COG2892	S	Uncharacterized protein conserved in archaea	2	0	1	0	1	0	1	3	2	3	3	1	5	1	4	1	0
arCOG04415	COG0151	F	Phosphoribosylamine-glycine ligase	0	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG04416	COG3365	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	4	1	0	3	1	5	1	0	0	0
arCOG04417	COG3364	R	Zn-ribbon containing protein	0	0	0	0	0	1	1	4	1	0	3	1	5	1	0	0	0
arCOG04418	COG3612	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	4	0	0	3	1	5	0	0	3	0
arCOG04419		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	3	1	5	0	0	0	0
arCOG04420	COG1935	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	3	2	1	5	1	4	0	0
arCOG04421	COG0152	F	Phosphoribosylaminoimidazolesuccinocarboxamide	0	3	4	2	0	0	1	4	2	3	3	1	5	1	4	3	0
arCOG04422	COG1915	S	Uncharacterized conserved protein	0	0	0	2	0	0	1	1	2	3	3	1	1	1	0	0	0
arCOG04423		R	Pyridine nucleotide-disulphide oxidoreductase	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG04424	COG3377	S	Uncharacterized conserved protein	1	0	0	0	0	0	1	0	0	0	3	0	5	0	0	3	0
arCOG04425	COG0394	T	Protein-tyrosine-phosphatase	0	0	0	1	0	0	1	4	1	2	3	0	3	0	2	0	0
arCOG04426	COG0375	R	Zn finger protein HypA/HybF (possibly regulating h	2	1	3	0	1	1	1	0	2	3	3	1	3	1	4	0	0
arCOG04427	COG0298	O	Hydrogenase maturation factor	2	0	3	0	1	1	1	0	2	3	3	1	3	1	4	0	0
arCOG04428	COG0409	O	Hydrogenase maturation factor	2	0	3	0	1	1	1	0	2	3	3	1	3	1	4	0	0
arCOG04429	COG0680	C	Ni,Fe-hydrogenase maturation factor	2	1	3	0	1	1	1	0	2	3	3	1	3	1	4	0	0
arCOG04430	COG1078	R	HD superfamily phosphohydrolase	3	3	5	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04431	COG0580	G	Glycerol uptake facilitator or related permease (Maj	0	2	0	2	0	0	1	0	2	2	3	1	2	0	0	0	0
arCOG04432	COG4883	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	1	2	3	1	3	0	0	0	0
arCOG04433		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0
arCOG04434	COG3476	T	Tryptophan-rich sensory protein (mitochondrial ben	0	0	0	0	0	0	1	1	0	0	3	0	3	0	0	0	0
arCOG04435	COG1892	G	Phosphoenolpyruvate carboxylase	0	3	5	0	1	0	1	1	1	0	1	0	3	1	3	1	0
arCOG04436		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	1	0	0	1	1	0	0	1	0	0
arCOG04437	COG3863	S	Uncharacterized distant relative of cell wall-associat	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG04438	COG1689	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	1	0	1	0	1	0	4	0	0
arCOG04439	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	1	0	0	0	0	0	5	0	0	0	0
arCOG04440	COG4854	S	Predicted membrane protein	0	0	0	0	0	0	1	0	0	1	3	0	3	0	2	0	0
arCOG04442		L	Transposase	0	0	0	0	0	0	1	0	0	0	1	0	2	0	0	0	0
arCOG04443	COG1850	G	Ribulose 1,5-bisphosphate carboxylase, large subuni	2	0	1	0	0	0	1	1	0	1	3	1	5	0	4	0	0
arCOG04444	COG4747	R	ACT domain-containing protein	0	0	0	0	0	0	1	0	2	2	3	1	5	0	0	0	0
arCOG04445	COG0440	E	Acetolactate synthase, small subunit	0	0	0	2	0	0	1	3	2	3	3	1	5	1	0	0	0
arCOG04446	COG0642	T	CHASE and HAMP domains	0	0	0	0	0	0	1	0	0	0	1	0	2	0	0	0	0
arCOG04447	COG1933	L	Archaeal DNA polymerase II, large subunit	0	0	0	2	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04448	COG1397	O	ADP-ribosylglycohydrolase	1	0	1	0	0	0	1	1	1	3	3	0	4	0	0	0	0
arCOG04449	COG0101	J	Pseudouridylate synthase	0	0	3	0	0	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04450	COG1668	C	ABC-type Na+ efflux pump, permease component	0	0	0	0	0	0	1	3	0	0	2	1	0	0	0	0	0
arCOG04451	COG1753	K	Predicted antotoxin, copG family	0	0	0	0	0	0	1	2	0	0	0	1	1	0	0	0	0
arCOG04452	COG1296	E	Predicted branched-chain amino acid permease (azal	0	0	1	0	0	0	1	3	0	2	0	0	3	0	0	0	0
arCOG04453	COG1624	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	4	0	3	3	1	4	1	4	0	0
arCOG04454	COG0327	S	Uncharacterized conserved protein, NIF3 homolog	0	0	1	0	0	0	1	4	1	3	3	1	4	1	4	0	0
arCOG04455	COG1311	L	Archaeal DNA polymerase II, small subunit/DNA po	0	0	0	2	1	1	1	4	2	3	3	1	4	1	4	3	1
arCOG04456	COG3543	S	Uncharacterized conserved predicted metal-binding	0	0	0	0	0	0	1	0	1	0	0	1	3	0	0	0	0
arCOG04457		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3	0	0
arCOG04458	COG2457	R	Uncharacterized protein of DIM6/NTAB family	0	3	0	0	1	0	1	3	2	3	3	1	5	1	4	0	0
arCOG04459	COG0379	H	Quinolinate synthase	1	3	2	2	0	0	1	4	2	3	3	1	5	1	4	0	0
arCOG04460		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	2	0	0	0	0
arCOG04461	COG1229	C	Formylmethanofuran dehydrogenase subunit A	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG04462	COG1828	F	Phosphoribosylformylglycinamidine (FGAM) synth	0	3	4	2	0	0	1	4	2	1	1	0	4	1	4	3	0
arCOG04463	COG3389	S	Uncharacterized conserved membrane protein	0	0	0	0	0	1	1	4	0	0	3	1	5	0	0	3	0
arCOG04464	COG1775	E	Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA deh	0	0	0	0	1	0	1	0	0	3	0	1	0	1	0	0	0

arCOG04465	COG0059	E	Ketol-acid reductoisomerase	0	3	4	2	1	1	1	3	2	3	3	1	5	1	2	1	0
arCOG04466	COG0733	R	Na+–dependent transporter of the SNF family	2	0	0	0	0	0	1	3	1	3	1	0	1	0	4	0	0
arCOG04467		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG04468	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	1	0	1	1	1	1	0	0	0	0	0	0	0	2	0
arCOG04469	COG1784	S	Predicted membrane protein	0	0	0	0	0	0	1	4	2	3	3	1	5	1	4	0	1
arCOG04470	COG0688	I	Phosphatidylserine decarboxylase	0	0	0	0	0	0	1	3	1	1	0	0	5	1	0	0	0
arCOG04471	COG4083	S	Predicted membrane protein	0	0	0	0	0	0	1	4	0	0	3	1	5	0	0	0	0
arCOG04472	COG1920	R	Predicted nucleotidyltransferase, CobY/MobA/RfbA	0	0	0	2	1	0	1	4	2	3	3	1	5	1	0	0	0
arCOG04473	COG2097	J	Ribosomal protein L31E	3	3	5	1	1	1	1	4	2	3	3	1	5	1	4	3	1
arCOG04474		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG04475	COG1883	C	Na+–transporting methylmalonyl-CoA/oxaloacetate	1	0	0	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG04476	COG1145	C	Ferredoxin	0	0	0	0	0	0	1	0	0	0	0	0	4	0	0	0	0
arCOG04477	COG1860	S	Uncharacterized protein conserved in archaea	0	0	4	0	0	1	1	4	2	3	2	1	5	0	4	3	0
arCOG04478	COG4885	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	2	0	0	1	0	4	0	0	0	0
arCOG04479	COG3357	K	Predicted transcriptional regulator containing an HT	2	3	4	0	0	1	1	4	0	0	0	0	0	1	4	0	1
arCOG04480	COG2002	K	Transcriptional regulator AbrB	0	1	0	0	0	0	1	0	0	0	0	0	0	0	3	0	0
arCOG04481		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG04482	COG1891	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	2	3	3	1	5	1	0	0	0
arCOG04483	COG4739	S	Uncharacterized protein containing a ferredoxin don	0	0	0	0	0	1	1	0	0	0	2	1	4	1	0	0	0
arCOG04484	COG5658	S	Predicted integral membrane protein	0	0	0	0	0	0	1	0	0	0	2	0	3	0	1	0	0
arCOG04485		S	Uncharacterized conserved protein	0	0	0	1	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG04486	COG2920	P	Dissimilatory sulfite reductase (desulfoviridin), gam	0	0	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG04487	COG0376	P	Catalase (peroxidase I)	0	0	0	0	0	0	1	3	0	0	1	0	1	0	0	0	0
arCOG04488	COG2164	S	Uncharacterized conserved protein	0	0	1	1	1	1	1	0	1	0	0	0	1	0	0	0	0
arCOG04489	COG4689	Q	Acetoacetate decarboxylase related enzyme	0	3	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG04490	COG1945	E	Pyruvoyl-dependent arginine decarboxylase (PvlArg	0	0	1	2	0	0	1	4	2	3	3	1	4	1	4	3	0
arCOG04492	COG2028	S	Uncharacterized conserved protein	0	0	0	0	0	1	1	0	1	1	1	0	0	0	3	0	0
arCOG04493	COG2405	V	PIN domain containing protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04494		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04495		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04496	COG3385	L	Transposase	0	0	0	0	0	0	0	3	0	0	1	0	2	0	0	1	0
arCOG04497		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04498		K	Predicted transcriptional regulator related to sugar-s	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04499		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0
arCOG04500		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04501	COG2002	K	SpoVT / AbrB like domain	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04502	COG2402	V	PIN domain containing protein	1	1	0	0	0	0	1	4	0	0	1	0	0	0	2	0	0
arCOG04505		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04506	COG0582	L	Integrase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04507	COG3350	S	Uncharacterized conserved protein	1	3	4	0	1	0	0	0	0	0	1	0	5	0	0	2	0
arCOG04508	COG2217	P	TRASH, metallochaperone	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG04509		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04510		S	Metal-binding domain	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04511	COG3470	P	Uncharacterized protein probably involved in high-a	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04512	COG2838	P	Predicted iron-dependent peroxidase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04513	COG1570	L	Exonuclease VII, large subunit	0	0	0	0	0	0	0	2	0	2	3	0	2	0	0	0	0
arCOG04514		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04515		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04516		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04517		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04518		K	Predicted transcriptional regulator, contains HTH do	0	0	0	0	0	0	0	2	0	0	0	0	2	0	1	0	0
arCOG04519	COG1556	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04520	COG3002	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04521		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	2	1	3	0	0	0	0
arCOG04522	COG0785	O	Cytochrome c biogenesis protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04523	COG3011	S	Protein-disulfide isomerase family protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04524		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04525		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04526		R	Predicted SAM-dependent methyltransferase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04527	COG0832	E	Urea amidohydrolase (urease) beta subunit	0	1	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04528	COG0831	E	Urea amidohydrolase (urease) gamma subunit	0	1	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04529	COG0829	O	Urease accessory protein UreH	0	0	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04530	COG0830	O	Urease accessory protein UreF	0	1	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04531	COG1914	P	Mn2+ and Fe2+ transporter of the NRAMP family	0	3	2	2	0	0	0	3	1	0	1	1	0	0	0	3	0
arCOG04532	COG1914	P	Mn2+ and Fe2+ transporter of the NRAMP family	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG04533		S	Zn finger domain containing protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04534		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04535	COG0855	P	Polyphosphate kinase	0	0	0	0	0	0	0	2	1	0	2	0	3	0	0	0	0
arCOG04536	COG1402	R	Uncharacterized protein, putative amidase	3	3	5	2	1	1	0	4	2	3	0	0	1	1	0	0	0
arCOG04537	COG1894	C	NADH:ubiquinone oxidoreductase, NADH-binding	0	0	0	0	0	0	0	2	1	0	1	0	0	0	1	0	0
arCOG04538	COG0190	H	5,10-methylene-tetrahydrofolate dehydrogenase/Met	0	0	3	2	0	0	0	4	0	0	2	0	5	0	0	3	0
arCOG04539	COG0262	H	Dihydrofolate reductase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04540	COG1292	M	Choline-glycine betaine transporter	0	0	0	0	0	0	0	4	0	0	1	0	0	0	0	0	0
arCOG04541	COG2759	F	Formyltetrahydrofolate synthetase	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	3	0
arCOG04542	COG0302	H	GTP cyclohydrolase I	1	3	4	2	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG04543	COG1925	G	Phosphotransferase system HPr-related protein	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG04544		S	Uncharacterized conserved protein in acc operon	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04545		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04546		G	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04547		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04548	COG1146	C	Ferredoxin	0	3	0	2	1	0	0	4	0	0	0	0	0	0	0	3	0
arCOG04549		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04550		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04551		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04552	COG1028	I	Short-chain alcohol dehydrogenase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04553	COG0069	E	Glutamate synthase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04554	COG1356	K	Transcriptional regulator	2	0	0	0	0	0	0	4	1	3	3	1	1	0	4	0	0
arCOG04555		S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	1	0	0	2	0	5	0	0	0	0
arCOG04556	COG2171	E	Tetrahydrodipicolinate N-succinyltransferase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04557		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04558	COG1957	F	Inosine-uridine nucleoside N-ribohydrolase	0	3	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0
arCOG04559	COG2076	P	Membrane transporter of cations and cationic drugs	0	0	0	0	0	0	0	3	0	0	1	0	4	0	0	0	0
arCOG04560	COG0316	O	Fe-S cluster assembly scaffold protein	0	0	0	2	1	0	0	3	0	0	0	1	5	0	0	0	0
arCOG04561	COG3360	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04562		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04563		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04564	COG2259	S	Predicted membrane protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04565	COG2035	S	Predicted membrane protein	0	0	0	0	0	0	0	4	2	0	3	0	0	0	0	0	0
arCOG04566		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04567		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04568		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04569		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04570	COG3358	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04571		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04572		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04573		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04574	COG1704	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	1	1	2	0	2	0	0	0	0
arCOG04575		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04576		S	Zn finger domain containing protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04577		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04578		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04579	COG3361	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04580	COG5459	R	Predicted rRNA methylase	0	0	0	0	0	0	0	4	0	0	3	1	1	0	0	0	0
arCOG04581		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04582	COG0389	L	Nucleotidyltransferase/DNA polymerase involved in	0	3	0	2	1	0	0	4	0	0	2	0	4	0	0	1	0
arCOG04583	COG0500	Q	SAM-dependent methyltransferase	0	3	5	0	0	1	0	4	0	0	0	0	0	0	0	0	0
arCOG04584		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04585	COG3075	E	Anaerobic glycerol-3-phosphate dehydrogenase	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0
arCOG04586	COG0175	E	3'-phosphoadenosine 5'-phosphosulfate sulfotransfer	0	1	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04587		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04588		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04589	COG1546	R	Uncharacterized protein (competence- and mitomyc	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04590		S	Predicted membrane-bound metal-dependent hydrol	0	0	0	0	0	0	0	3	0	0	0	0	0	1	0	0	0
arCOG04591		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04592		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04593		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04594	COG1290	C	Cytochrome b subunit of the bc complex	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04595	COG0723	C	Rieske Fe-S protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0

arCOG04596		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04597		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04598		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04599		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04600		S	Zn finger domain containing protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04601	COG1605	E	Chorismate mutase	1	0	0	0	0	0	0	4	2	3	2	1	5	1	0	0	1
arCOG04602		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04603	COG0158	G	Fructose-1,6-bisphosphatase	0	0	0	0	0	0	0	4	0	0	2	0	0	0	0	0	0
arCOG04604	COG4276	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04605		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04606		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04607	COG5282	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04608		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04609		S	Predicted lipoprotein	0	0	1	0	0	1	0	1	0	0	1	1	1	0	0	0	0
arCOG04610		K	CopG-family DNA-binding protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04611	COG1165	H	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxy	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04612	COG4044	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	1	0	4	0	0	0	0	4	1	4	0	0
arCOG04613	COG1405	K	Transcription initiation factor TFIIIB, Brf1 subunit/T	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04614	COG1545	R	Predicted nucleic-acid-binding protein containing a Z	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04615		R	Predicted glycosyltransferase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	1	0	0
arCOG04616		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04617		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04618	COG3651	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04619	COG3428	S	Predicted membrane protein	0	0	0	0	0	0	0	4	0	0	2	1	0	0	0	0	0
arCOG04622	COG3402	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG04623	COG3380	R	Predicted NAD/FAD-dependent oxidoreductase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04624	COG0431	R	Predicted flavoprotein	0	1	0	2	0	0	0	2	0	0	0	1	0	0	1	1	0
arCOG04625		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04626		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG04627	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0
arCOG04628	COG1547	R	Predicted metal-dependent hydrolase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04629		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04630		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04631	COG2718	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04632	COG2719	R	Uncharacterized membrane protein, required for deh	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04633	COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04634	COG1472	G	Beta-glucosidase-related glycosidase	0	1	2	0	0	0	0	1	0	0	0	1	0	0	0	1	0
arCOG04635		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04636		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04637		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04638	COG2836	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04639		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04640		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04641	COG2860	S	Predicted membrane protein	0	3	4	1	0	0	0	2	0	2	1	1	0	0	0	0	0
arCOG04642		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	3	0	0	0	0	0	0
arCOG04643		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04644		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04645		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04646	COG3011	R	Thioredoxin superfamily protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04647	COG0271	T	Stress-induced morphogen (activity unknown)	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04648	COG0278	O	Glutaredoxin-related protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04649		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04650	COG1845	C	Heme/copper-type cytochrome/quinol oxidase, subu	0	0	0	0	1	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04651		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04652		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	2	0	0	1	1	1	0	0	0	0
arCOG04653	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04654	COG0839	C	NADH dehydrogenase subunit J	2	3	1	2	0	1	0	4	0	0	0	0	4	0	0	3	0
arCOG04655	COG3269	R	Predicted RNA-binding protein, contains TRAM do	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04656	COG1077	D	MreB/Mbl protein, ATPase	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0
arCOG04657		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04658	COG3470	P	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04659	COG0398	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG04660		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04661		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04662		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	1	0	1	0	2	0	0	0	0
arCOG04663		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04664		R	Predicted membrane-bound metal-dependent hydrol	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04665		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04666		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04667		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04668		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG04669		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04670	COG2987	E	Urocanate hydratase	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	3	0
arCOG04671	COG2986	E	Histidine ammonia-lyase	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	3	0
arCOG04672		S	Transcriptional regulator, HTH domain	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04673		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04674		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04675		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	1	0	0	0	0
arCOG04676	COG1619	V	Uncharacterized protein, homolog of microcin C7 re	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	3	0
arCOG04677	COG1884	I	Methylmalonyl-CoA mutase, N-terminal domain/sul	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG04678	COG2109	H	ATP:corrinoid adenosyltransferase	0	0	4	2	0	1	0	4	0	0	1	0	3	0	4	2	0
arCOG04679		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0
arCOG04680		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04681	COG1640	G	4-alpha-glucanotransferase	0	0	3	0	0	0	0	2	0	0	2	0	0	0	0	0	0
arCOG04682	COG3173	R	Predicted aminoglycoside phosphotransferase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04683		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04684	COG0662	G	Cupin domain	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04685		H	Lycopene cyclase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04686	COG0557	K	Exoribonuclease R	0	0	0	0	0	0	0	4	0	0	2	1	1	0	0	0	0
arCOG04687		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04688		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04689		S	Zn-finger domains containing protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04690		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04691	COG3403	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04692	COG0546	R	Predicted phosphatase	0	0	0	2	1	0	0	4	0	0	0	0	0	0	2	0	0
arCOG04693		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0
arCOG04694	COG0178	L	Excinuclease ABC (subunit A, ATPase)	0	0	0	2	0	0	0	4	2	2	3	1	4	0	0	0	0
arCOG04695		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04696		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04697		S	Selenium binding protein SBP56 homolog	0	3	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG04698		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04699		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04700		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04701	COG0239	D	Integral membrane protein possibly involved in chrc	0	0	0	1	0	0	0	4	0	3	1	1	4	1	4	0	0
arCOG04702	COG1881	R	Phospholipid-binding protein	2	3	2	2	0	1	1	3	1	0	3	1	4	0	3	3	1
arCOG04703	COG3256	P	Nitric oxide reductase large subunit	0	1	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG04704	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04705	COG2098	S	Uncharacterized protein conserved in archaea	0	0	0	0	1	0	1	4	2	3	3	1	5	1	0	3	0
arCOG04706		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	2	1	4	0	0	0	0
arCOG04707		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04708	COG3410	S	Uncharacterized conserved protein	0	1	1	0	0	0	0	2	0	0	0	0	0	0	0	2	0
arCOG04710		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04711	COG4923	R	Predicted nuclease (RNAse H fold)	0	0	0	0	0	0	0	2	0	0	0	0	4	0	0	0	0
arCOG04712	COG0435	O	Predicted glutathione S-transferase	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04713	COG0307	H	Riboflavin synthase alpha chain	0	0	0	2	0	0	0	4	0	0	1	0	0	0	2	0	0
arCOG04714		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04715	COG2968	S	Uncharacterized conserved protein	0	0	0	2	1	0	0	3	0	0	3	1	4	0	0	0	0
arCOG04716	COG2968	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG04717		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04718		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04719		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04720	COG0561	R	HAD superfamily hydrolase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04721	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04722	COG2827	L	Predicted endonuclease containing a URI domain	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04723		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04724		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04725		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	3	0	1	0	0	0	0
arCOG04726		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0

arCOG04727	COG3363	F	Archaeal IMP cyclohydrolase	0	0	0	0	0	0	0	4	2	3	0	1	1	1	1	0	0
arCOG04728		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04729		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04730		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04731		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04732		Q	Glutamate-cysteine ligase, GCS2	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04733	COG2042	S	Uncharacterized conserved protein	2	3	0	2	0	1	0	4	2	3	3	1	5	1	0	3	0
arCOG04734	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0
arCOG04735	COG3609	K	Predicted transcriptional regulators containing the C	0	0	0	0	0	0	0	3	0	0	0	1	5	0	0	0	0
arCOG04736	COG0805	U	Sec-independent protein secretion pathway compone	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04737		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04738		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04739		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04740		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	1	5	0	0	0	0
arCOG04741		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04742		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04743	COG1205	R	Helicase associated uncharacterized terminal domai	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04744		L	Chromosomal protein MC1	0	0	0	0	0	0	0	4	0	0	0	1	5	0	0	0	0
arCOG04745		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04746		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04747		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04748	COG0556	L	Excinuclease ABC (subunit B, helicase)	0	0	0	2	0	0	0	4	2	2	3	0	4	0	0	0	0
arCOG04749		S	Uncharacterized conserved protein in cobalamin ope	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04750	COG2138	C	Sirohydrochlorin iron chelatase fused to [2Fe-2S] Fe	0	0	0	0	0	0	0	4	0	0	0	1	1	0	0	0	0
arCOG04752		S	Uncharacterized conserved protein in cobalamin ope	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04753	COG0322	L	Excinuclease ABC subunit C	0	0	0	2	0	0	0	4	2	2	3	0	4	0	0	0	0
arCOG04754	COG0272	L	NAD-dependent DNA ligase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04755	COG2928	S	Uncharacterized membrane protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04756	COG0679	R	Predicted permease	1	0	1	0	0	1	0	3	2	3	3	1	1	1	2	0	0
arCOG04757		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04758	COG1164	E	Oligoendopeptidase F	0	0	0	2	0	0	0	4	0	0	0	0	3	0	0	0	0
arCOG04759		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04760		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04761	COG1968	I	Undecaprenyl pyrophosphate phosphatase	0	2	4	0	1	1	0	1	2	2	0	0	2	1	1	0	0
arCOG04762	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	3	1	0	0	0	0	2	0	0	0	0	0	0	0	3	0
arCOG04763		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04764		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04765		C	Ferredoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04766	COG3217	R	Uncharacterized Fe-S protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04767	COG0652	O	Peptidyl-prolyl cis-trans isomerase (rotamase) - cycl	0	0	0	2	0	0	0	4	2	2	3	1	5	0	0	1	0
arCOG04769		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04770	COG0318	I	Acyl-CoA synthetase (AMP-forming)/AMP-acid lig	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04771	COG0484	O	DnaJ-like domain containing protein	0	0	0	2	1	0	0	4	2	0	3	1	5	0	0	3	0
arCOG04772	COG0576	O	Molecular chaperone GrpE (heat shock protein)	0	0	0	2	1	0	0	4	2	0	3	1	5	0	0	3	0
arCOG04773		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04774		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04775		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04776		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04777		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04779	COG1446	E	Asparaginase	2	3	5	1	0	1	0	4	0	0	0	0	0	0	4	3	0
arCOG04780	COG0589	T	Universal stress protein UspA	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04781		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04782	COG1842	K	Phage shock protein A	0	0	0	0	0	1	0	3	0	0	0	1	5	0	0	0	0
arCOG04783	COG0569	P	TrkA, K+ transport system, NAD-binding componer	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04784		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04785	COG1477	H	Membrane-associated lipoprotein involved in thiami	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0
arCOG04786	COG3396	S	Phenylacetic acid catabolic protein	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG04787	COG2391	R	Predicted transporter component	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0	0	0
arCOG04788	COG2391	R	Predicted transporter component	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04789		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04790	COG2320	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	1	0	3	0	0	0	0
arCOG04791	COG1294	C	Cytochrome bd-type quinol oxidase, subunit 2	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0
arCOG04792	COG3436	L	Transposase	0	0	0	1	0	0	0	1	0	0	1	0	3	0	0	1	0
arCOG04793	COG5340	K	Predicted transcriptional regulator	0	0	0	1	0	1	0	1	0	0	0	1	0	0	2	1	0
arCOG04794	COG0463	M	Glycosyltransferase	0	0	0	0	0	0	0	3	0	0	0	0	1	0	0	0	0
arCOG04795		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04796	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG04797		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0
arCOG04798	COG1435	F	Thymidine kinase	0	0	1	0	0	0	0	2	0	0	0	0	0	0	1	1	0
arCOG04799		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	1	0	0	0	0
arCOG04800		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04801		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04802	COG0589	T	Nucleotide-binding protein, UspA family	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG04803		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04804	COG2060	P	K+-transporting ATPase, A chain	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	3	0
arCOG04805	COG2156	P	K+-transporting ATPase, c chain	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3	0
arCOG04806	COG1359	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	1	0	1	0	3	0	0	0	0
arCOG04807	COG1297	S	Predicted membrane protein	1	0	0	0	0	0	0	1	0	0	0	1	0	0	2	0	0
arCOG04808	COG1785	P	Alkaline phosphatase	0	0	0	0	0	0	0	1	0	0	0	0	3	0	2	0	0
arCOG04809	COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	0	1	0	0	2	0	2	0	0	0	0
arCOG04811	COG2383	S	Uncharacterized conserved membrane protein	1	0	0	0	0	0	0	1	0	3	0	0	0	4	0	0	0
arCOG04812	COG2383	S	Uncharacterized conserved membrane protein	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG04813	COG0853	H	Aspartate 1-decarboxylase	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG04814	COG1002	V	Type II restriction enzyme, methylase subunit	0	0	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG04816	COG3505	L	TraG/TraD/VirD4 family enzyme, ATPase	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	2	0
arCOG04817	COG1083	M	CMP-N-acetylneuraminic acid synthetase	0	0	0	1	0	0	0	1	0	2	1	0	2	0	0	0	0
arCOG04818	COG0553	K	Superfamily II DNA/RNA helicase, SNF2 family	0	0	0	1	1	0	0	1	1	0	1	0	1	0	0	1	0
arCOG04820		T	SOUL heme-binding protein	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0
arCOG04821	COG4740	R	Predicted metalloprotease	0	0	0	0	0	0	0	0	1	0	0	0	3	1	0	0	0
arCOG04822	COG1790	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	1	3	0	0	0	1	0	0	0
arCOG04823		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	4	0	0	0
arCOG04824		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG04825		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG04826	COG2327	M	Polysaccharide pyruvyl transferase family protein	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0
arCOG04827	COG1887	M	Putative glycosyl/glycerophosphate transferase invo	0	0	0	0	0	0	0	1	1	0	1	0	0	2	0	0	0
arCOG04828	COG4041	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	3	3	0	0	1	0	0	0
arCOG04829	COG4039	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG04830	COG4038	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	3	3	0	0	1	0	0	0
arCOG04831	COG4037	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	3	3	0	0	1	0	0	0
arCOG04832	COG4036	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	3	3	0	0	1	0	0	0
arCOG04833	COG4078	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	3	3	0	0	1	0	0	0
arCOG04834	COG4035	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG04835	COG4084	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0
arCOG04836	COG0721	J	Asp-tRNAAsn/Glu-tRNAGln amidotransferase C su	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG04838		S	Zn-ribbon containing protein	0	0	0	0	0	0	0	0	1	0	2	0	2	0	0	0	0
arCOG04839	COG4053	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG04840	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG04841	COG4827	R	Predicted transporter	0	0	0	0	0	0	0	0	2	2	1	0	5	1	0	0	0
arCOG04842	COG1844	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	1	4	1	4	0	0
arCOG04843	COG4076	R	Predicted RNA methylase	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG04844	COG4033	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	3	1	5	1	0	0	0
arCOG04845	COG4081	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	3	0	4	1	0	0	0
arCOG04846	COG4014	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04847	COG4090	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	2	1	5	1	0	0	0
arCOG04848	COG3272	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	0	1	2	2	0	4	0	0	0	0
arCOG04849		S	Uncharacterized conserved protein	0	0	0	0	0	1	0	0	1	0	0	0	0	4	0	0	0
arCOG04850	COG1417	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	1	3	0	0	1	1	0	0	0
arCOG04851		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG04852	COG2099	H	Precorrin-6x reductase	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	1	0
arCOG04853	COG4008	K	Predicted metal-binding transcription factor	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG04854		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG04855	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	1	1	0	0	2	0	0	0	0
arCOG04856	COG1532	R	Predicted RNA-binding protein	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG04857	COG4058	H	Methyl coenzyme M reductase, alpha subunit	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04858	COG4057	H	Methyl coenzyme M reductase, gamma subunit	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04859	COG4055	H	Methyl coenzyme M reductase, subunit D	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04860	COG4054	H	Methyl coenzyme M reductase, beta subunit	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04861	COG4018	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	2	0	0	1	0	0	0

arCOG04862	COG0243	C	Formate dehydrogenase alpha subunit	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0	0
arCOG04863	COG4019	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	1	0	0	1	0	0	0
arCOG04864	COG4017	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	2	0	0	1	0	0	0
arCOG04865	COG4016	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	2	0	0	1	0	0	0
arCOG04866	COG4065	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04867	COG4062	H	Tetrahydromethanopterin S-methyltransferase, subu	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04868	COG4061	H	Tetrahydromethanopterin S-methyltransferase, subu	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04869	COG4060	H	Tetrahydromethanopterin S-methyltransferase, subu	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04870	COG4059	H	Tetrahydromethanopterin S-methyltransferase, subu	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04871	COG2045	H	Phosphosulfolactate phosphohydrolase or related en	0	0	0	0	0	0	0	0	2	3	0	1	0	1	0	3	0
arCOG04872	COG4024	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG04873	COG4077	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG04874	COG2055	C	Malate/L-lactate dehydrogenase	1	1	0	0	0	1	0	0	2	3	0	0	0	1	2	0	0
arCOG04875	COG2029	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	3	0	1	4	1	4	0	0
arCOG04876		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG04877	COG1320	P	Multisubunit Na+/H+ antiporter, MnhG subunit	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG04878	COG2212	P	Multisubunit Na+/H+ antiporter, MnhF subunit	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG04879		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG04880	COG1988	R	Membrane-bound metal-dependent hydrolase	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG04881	COG1379	R	PHP family phosphoesterase with a Zn ribbon	0	0	0	0	0	0	0	0	2	3	2	0	5	1	4	0	0
arCOG04882		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
arCOG04883		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	2	0	1	0	0
arCOG04884		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0
arCOG04885	COG4020	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	3	1	4	1	0	0	0
arCOG04886		S	Uncharacterized conserved protein	0	3	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0
arCOG04887	COG3548	S	Predicted integral membrane protein	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0
arCOG04888	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04889	COG1328	F	Oxygen-sensitive ribonucleoside-triphosphate reduc	2	0	2	2	0	1	0	0	2	3	2	1	5	1	4	0	1
arCOG04890	COG1905	C	NADH:ubiquinone oxidoreductase 24 kD subunit	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0
arCOG04891	COG1146	C	Ferredoxin fused to HTH-domain transcriptional regu	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG04892		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0
arCOG04893	COG4022	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	1	0	0	2	3	3	1	5	1	0	0	0
arCOG04894	COG4073	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	0	0	4	1	0	0	0
arCOG04895		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG04896	COG1809	H	(2R)-phospho-3-sulfolactate synthase (PSL synthase	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG04897	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG04898	COG1971	S	Uncharacterized conserved membrane protein	0	0	0	0	0	1	0	0	2	0	3	0	3	0	0	0	0
arCOG04899		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	2	0	0	3	0	0	0	0
arCOG04900	COG4070	O	Predicted peptidyl-prolyl cis-trans isomerase (rotam	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04901	COG4029	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04902	COG4048	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	2	1	5	1	0	0	0
arCOG04903	COG4050	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04904	COG4051	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	3	1	5	1	0	0	0
arCOG04905	COG4009	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG04906	COG4010	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	2	3	0	0	0	1	0	0	0
arCOG04907		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04908		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04909		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	4	0	0	0	0
arCOG04910		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0	0	0
arCOG04911		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG04912		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	0
arCOG04913	COG3464	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	1	0
arCOG04915		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	4	0	1	0	0
arCOG04916	COG3393	R	Predicted acetyltransferase	0	0	0	0	0	0	0	0	0	2	2	1	4	0	0	0	0
arCOG04917		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04918	COG3328	L	Transposase	0	1	0	0	0	0	0	0	0	0	0	0	4	0	0	2	0
arCOG04919	COG2003	L	DNA repair protein	0	0	0	0	0	0	0	0	0	0	3	0	4	0	0	0	0
arCOG04920	COG4895	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	0	0	2	3	1	4	0	0	0	0
arCOG04921	COG1352	N	Methylase of chemotaxis methyl-accepting protein,	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04922	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG04923	COG2610	G	H+/gluconate symporter or related permease	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG04924	COG3431	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	4	1	0	0	0
arCOG04925		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG04926	COG0417	L	DNA polymerase elongation subunit (family B)	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG04927	COG0417	L	DNA polymerase elongation subunit (family B)	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG04928		V	CRISPR-associated protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG04929	COG1857	V	CRISPR-associated protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG04930	COG1343	V	CRISPR-associated protein Cas2	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG04931		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	4	0	0	0	0
arCOG04932		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG04933	COG4826	O	Serine protease inhibitor	0	0	3	1	0	1	0	0	0	0	1	0	3	0	1	0	0
arCOG04934	COG0726	G	Polysaccharide deacetylase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG04935	COG0726	G	Polysaccharide deacetylase	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG04936	COG0463	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04937		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	4	0	0	0	0
arCOG04938		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	1	0	0	4	0	1	0	0
arCOG04939		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	3	0	0
arCOG04940	COG0696	G	Phosphoglyceromutase	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	0
arCOG04941	COG3830	T	ACT domain-containing protein	0	0	3	0	0	1	0	0	0	3	3	1	4	1	0	0	0
arCOG04942	COG0841	V	Cation/multidrug efflux pump	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04943		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04944		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04945		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04946	COG3324	R	Predicted enzyme related to lactoylglutathione lyase	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04947	COG3663	L	G:T/U mismatch-specific DNA glycosylase	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0	0	0
arCOG04948	COG1418	R	HD superfamily phosphohydrolases	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04949	COG3808	C	Inorganic pyrophosphatase	0	0	4	2	1	1	0	0	0	0	3	1	4	0	0	0	0
arCOG04950	COG0325	R	Predicted enzyme with a TIM-barrel fold	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04951		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04952		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG04953	COG0390	R	ABC-type uncharacterized transport system, permea	0	0	0	0	0	0	0	0	0	3	0	1	4	0	0	0	0
arCOG04954		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04955		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04956	COG3943	R	Virulence protein	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG04957	COG2332	O	Cytochrome c-type biogenesis protein CcmE	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04958		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	0
arCOG04959		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04960		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	0
arCOG04961	COG1494	G	Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisp	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04962		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04963	COG0697	G	permease of the drug/metabolite transporter (DMT)	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04964		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	4	0	0	0	0
arCOG04965	COG1295	L	Ribonuclease BN family enzyme	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04966		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG04967	COG1993	T	PII-like signaling protein	0	0	0	0	0	0	0	0	0	3	1	1	3	1	4	0	0
arCOG04968	COG1546	F	CinA-like domain fused to cytidylyltransferase-like	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04969		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	1	1	0	0	0	0
arCOG04970		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	5	0	0	0	0
arCOG04971	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04972	COG3874	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	2	0	4	0	0	0	0
arCOG04973		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	1	5	0	0	0	0
arCOG04974	COG3836	G	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	0	0	2	0	1	0	0	0	0	0	0	0	1	0	0	0	0
arCOG04975		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04976		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04977		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04978	COG3937	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04979		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04980		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG04981		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG04982		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	2	0	1	0	0	0	0
arCOG04983	COG3326	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG04984	COG1032	C	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	1	3	1	5	0	0	0	0
arCOG04985		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG04986		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04987		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	2	1	4	0	0	0	0
arCOG04988		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04989	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	2	0	0	3	1	5	0	0	0	0
arCOG04990		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	4	0	0	0	0

arCOG04991	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04992	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG04993	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	0
arCOG04994	COG5549	O	Predicted Zn-dependent protease	0	0	0	1	0	0	0	1	0	0	0	0	4	0	0	0	0
arCOG04995	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG04996	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04997	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG04998	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	1	5	0	0	0	0
arCOG04999	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05000	COG1277	R	ABC-type transport system involved in multi-copper	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05001	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05002	COG3482	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	2	3	1	5	0	0	0	0
arCOG05003	COG4887	R	Uncharacterized metal-binding protein conserved in	0	0	0	0	0	0	0	0	0	3	0	0	4	1	0	0	0
arCOG05004	COG2084	I	3-hydroxyisobutyrate dehydrogenase related enzyme	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05005	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05006	COG1115	E	Na+/alanine symporter	0	0	0	0	0	0	0	0	0	2	1	1	4	0	3	0	0
arCOG05007	COG0424	D	Nucleotide-binding protein implicated in inhibition	1	0	0	0	0	0	0	0	0	0	0	0	4	0	4	0	0
arCOG05008	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05009	C	Membrane-bound multiheme cytochrome c subunit	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05010	COG4921	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	0	1	0	0	4	1	0	0	0
arCOG05011	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	5	0	0	0	0
arCOG05012	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG05013	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05014	COG2181	C	CoB--CoM heterodisulfide reductase subunit E	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
arCOG05015	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	4	1	4	3	0
arCOG05016	COG2848	S	Uncharacterized conserved protein, DUF711	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05017	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG05018	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05019	COG2603	R	Predicted ATPase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05020	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05021	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05022	COG4095	S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	1	1	1	2	0	0	0	0
arCOG05023	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05024	COG2361	S	HEPN domain containing protein	0	0	0	0	0	0	0	0	0	1	3	0	3	0	0	0	0
arCOG05025	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05026	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05028	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05029	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05030	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05031	S	Zn finger protein	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG05032	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05033	COG3233	R	Predicted deacetylase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3	0	0
arCOG05034	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05035	COG4042	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG05036	COG3620	K	Predicted transcriptional regulator with C-terminal C	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05037	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	4	0	0
arCOG05038	COG4013	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0
arCOG05039	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05040	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05041	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05042	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG05043	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05044	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05045	COG0551	L	Zn-finger domain associated with topoisomerase typ	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05046	COG0036	G	Pentose-5-phosphate-3-epimerase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	3	0
arCOG05047	COG1773	C	Rubredoxin	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05048	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0
arCOG05049	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05050	S	Transcriptional regulator, HTH domain	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05051	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	2	0	0	0	0
arCOG05052	COG4085	R	Predicted RNA-binding protein, contains TRAM do	0	0	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0
arCOG05053	COG1991	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05054	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05055	COG1627	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05056	COG2158	R	Uncharacterized protein containing a Zn-finger-like	0	0	0	0	0	0	1	0	0	3	0	0	4	1	0	0	0
arCOG05057	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05058	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	4	0	0
arCOG05059	COG0727	R	Predicted Fe-S-cluster oxidoreductase	0	0	0	0	0	0	1	0	0	3	0	0	0	0	0	0	0
arCOG05060	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	4	0	0
arCOG05061	COG0176	G	Transaldolase	0	0	0	2	0	0	0	0	0	3	0	0	0	0	0	3	0
arCOG05062	K	Predicted transcriptional regulator, HTH domain	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG05063	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05064	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05065	COG3681	E	L-cysteine desulfidase	0	0	0	0	0	0	0	0	0	3	0	1	0	0	0	0	0
arCOG05066	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05067	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05068	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05069	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05070	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	1	1	0	0	0	0	0
arCOG05071	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	3	0	0	0	0
arCOG05072	COG2414	C	Aldehyde:ferredoxin oxidoreductase	1	0	4	0	0	0	0	0	0	3	0	0	0	4	0	0	0
arCOG05073	COG3478	R	Predicted nucleic-acid-binding protein containing a	0	0	0	0	0	0	0	1	0	1	0	0	2	0	0	0	0
arCOG05074	S	Uncharacterized conserved protein	0	0	0	0	1	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05075	COG1424	H	Pimeloyl-CoA synthetase	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05076	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG05077	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05078	COG0063	G	Predicted sugar kinase	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0
arCOG05079	COG1542	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0
arCOG05080	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05081	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05082	COG1991	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05083	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05084	COG1851	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	4	0	0
arCOG05085	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05086	COG0436	E	Predicted Fe-S cluster containing protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05087	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0
arCOG05088	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05089	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05090	COG0310	P	ABC-type Co2+ transport system, permease compor	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0
arCOG05091	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG05092	COG2456	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	3	0	0	0	0	4	0	0
arCOG05093	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0
arCOG05094	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	1	0	0	0	0	2	0	0
arCOG05095	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	4	0	0
arCOG05096	S	Uncharacterized conserved membrane protein	0	0	0	1	0	0	0	0	0	3	0	0	2	0	1	0	0
arCOG05097	COG0517	R	CBS domain	1	0	0	0	0	0	0	0	0	2	0	0	0	4	0	0	0
arCOG05098	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	3	0	0
arCOG05099	COG2105	S	AIG2-like family protein	0	0	0	0	0	0	0	0	0	2	0	1	0	1	0	0	0
arCOG05100	COG2364	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	2	1	0	1	0	0	0	0
arCOG05101	COG2607	R	Predicted ATPase (AAA+ superfamily)	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
arCOG05102	COG4268	V	McrBC 5-methylcytosine restriction system compon	0	0	0	0	0	0	0	1	0	1	1	0	2	0	1	1	0
arCOG05103	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0
arCOG05104	R	Predicted ATPase	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0
arCOG05105	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0
arCOG05106	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0
arCOG05107	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0
arCOG05108	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0
arCOG05109	COG0847	L	DNA polymerase III, epsilon subunit or related 3'-5'	0	0	0	0	0	0	1	0	1	2	2	1	0	0	1	0	0
arCOG05110	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	2	1	3	0	0	0	0	0
arCOG05111	COG1576	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	2	0	1	0	0	0	0
arCOG05112	COG3774	M	Mannosyltransferase OCH1 or related enzyme	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0
arCOG05113	COG2183	K	Transcriptional accessory protein Tex, contains RNA	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
arCOG05114	COG4087	R	Soluble P-type ATPase, fragment	0	0	0	0	0	0	0	0	0	3	0	0	0	1	1	0	0
arCOG05115	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0
arCOG05116	J	OB-fold nucleic acid binding domain	0	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0
arCOG05117	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0
arCOG05118	COG2391	R	Predicted transporter component	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0
arCOG05119	COG3352	N	Putative archaeal flagellar protein C	0	0	0	1	0	0	0	0	0	3	0	0	0	0	4	2	0

arCOG05120	COG5014	R	Radical SAM superfamily enzyme	2	0	4	0	0	1	0	0	0	0	0	0	0	1	0	0	0
arCOG05121	COG2755	E	Lysophospholipase L1 or related esterase	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG05122	COG4912	L	Predicted DNA alkylation repair enzyme	0	0	0	0	0	0	0	0	0	0	2	0	5	0	0	0	0
arCOG05123		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05124		V	CRISPR-associated protein	0	0	0	0	0	0	0	1	1	1	0	0	2	0	0	0	0
arCOG05125		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	4	0	0	0	0
arCOG05126		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05127		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG05128	COG1145	C	Ferredoxin	0	0	0	0	1	1	0	0	0	0	0	0	1	0	4	2	0
arCOG05129	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05130		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05131	COG2168	P	DsrH like protein	0	0	0	0	0	0	0	0	1	0	0	0	4	0	0	0	0
arCOG05132		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	4	0	0	0	0
arCOG05133	COG0572	F	Uridine kinase	0	0	0	0	0	0	0	1	0	0	2	0	1	0	0	0	0
arCOG05134		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0
arCOG05135	COG5551	V	CRISPR system related protein, RAMP superfamily	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0
arCOG05136		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	1	4	0	0	0	0
arCOG05137	COG0457	R	TPR repeats containing protein	0	0	0	2	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG05138	COG0248	F	Exopolyphosphatase	0	3	0	0	0	0	0	0	1	0	2	0	3	0	0	0	0
arCOG05139	COG3025	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05141	COG0346	E	Lactoylglutathione lyase or related enzyme	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG05142		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05143		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05144		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG05145		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05146		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05147	COG4715	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	3	0	0	0	0
arCOG05148		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG05149		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05150		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05151		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05152		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05153	COG0234	O	Co-chaperonin GroES (HSP10)	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05154	COG0459	O	Chaperonin GroEL (HSP60 family)	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05155		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG05156		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05157		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05158		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05159	COG1750	R	Archaeal serine protease	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05160	COG3339	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG05161	COG0454	K	Acetyltransferase (GNAT) family	0	1	0	0	0	0	0	0	0	0	2	0	3	0	2	0	0
arCOG05162		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05163		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05164		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05165		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05166		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG05167		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG05168		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05169		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05170	COG1497	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05171	COG3409	M	Putative peptidoglycan-binding domain-containing p	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05173		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG05174	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG05175	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05176	COG4908	R	Uncharacterized protein containing a NRPS condens	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG05177	COG3619	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05178		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05179		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05180		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG05181	COG0839	C	NADH dehydrogenase subunit J	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	3	0
arCOG05182	COG5310	Q	Homospermidine synthase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05183	COG3920	T	Signal transduction histidine kinase, contains PocR-l	0	0	0	0	0	0	0	0	0	0	1	1	4	0	0	0	0
arCOG05185		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05186	COG2940	R	Protein containing SET domain	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05187		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05188	COG4845	V	Chloramphenicol O-acetyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05189	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG05190		S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05191	COG4866	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	1	3	0	0	0	0
arCOG05192	COG1124	E	ABC-type dipeptide/oligopeptide/nickel transport sy	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0	0
arCOG05193		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05194	COG4127	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05195	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05197	COG2815	T	PASTA domain	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05198		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05199		R	ATP-grasp domain	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05200	COG3590	O	Predicted metalloendopeptidase	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	1	0
arCOG05201		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	2	0	4	0	0	0	0
arCOG05202	COG2710	C	Nitrogenase molybdenum-iron protein, alpha or beta	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG05203		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	0
arCOG05204		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05205		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05206		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05207	COG1598	R	Predicted nuclease of the RNAse H fold, HicB famil	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG05208	COG1835	I	Predicted acyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05209		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05210		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05211	COG4831	S	Roadblock/LC7 domain	0	3	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG05212		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05213	COG1970	M	Large-conductance mechanosensitive channel	0	0	0	0	0	0	0	0	0	0	1	1	4	0	0	0	0
arCOG05214		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05215		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05216		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05217		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05218		R	Alkaline phosphatase superfamily enzyme	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05219		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG05220		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG05221		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05222		R	HD superfamily phosphohydrolase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05223	COG1479	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	1	0	1	1	0	1	0	0	1	0
arCOG05224	COG2032	P	Cu/Zn superoxide dismutase	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG05225		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05226		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05227	COG4803	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05228		S	Nonspecific acid phosphatase, NapD-like	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG05229	COG2195	E	Di- or tripeptidase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05230		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05231	COG2898	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05232		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0
arCOG05233	COG3603	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	1	2	0	0	0	0
arCOG05234		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05235		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05236		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG05237		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05238		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	3	0
arCOG05239	COG3173	R	Predicted aminoglycoside phosphotransferase	0	0	0	0	0	0	0	0	0	1	2	0	3	0	0	0	0
arCOG05240	COG5295	U	Autotransporter adhesin	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05241		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05242	COG3158	P	K+ transporter	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG05243		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05244		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05245		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05246		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05247	COG1346	M	Putative effector of murein hydrolase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	4	0	0
arCOG05248	COG0477	G	Predicted permease of the major facilitator superfam	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05249		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG05250		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05251		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	3	0	0	0	0

arCOG05252	COG4741	F	Predicted secreted endonuclease distantly related to	0	1	1	0	0	0	0	0	0	0	2	0	2	0	0	2	0
arCOG05253		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05254	COG1848	V	PIN domain containing protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05255		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05256	COG1793	L	ATP-dependent DNA ligase, N-terminal domain	0	0	0	0	0	1	0	0	0	0	1	1	3	0	0	0	0
arCOG05257	COG1687	E	Predicted branched-chain amino acid permease (azal	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05258		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05259	COG0662	G	Cupin domain	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG05260	COG0282	C	Acetate kinase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05261	COG3832	S	Aha1 domain, activator of Hsp90 ATPase homolog	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG05262	COG0708	L	Exonuclease III	0	0	0	0	0	0	0	0	2	0	1	0	2	0	0	0	0
arCOG05263		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05264	COG4891	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05265		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05266	COG1835	I	Predicted acyltransferase	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0
arCOG05267		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05268	COG1688	V	CRISPR system related protein, RAMP superfamily	0	0	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0
arCOG05269		V	CRISPR-associated protein, MTH1090 family	0	0	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0
arCOG05270	COG1119	P	ABC-type molybdenum transport system, ATPase co	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG05271	COG2091	H	Phosphopantetheinyl transferase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05272		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05273	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG05274	COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05275		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05276		S	Uncharacterized conserved protein	0	0	0	1	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05277		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05278	COG5466	S	Predicted small metal-binding protein	0	3	0	1	0	0	0	0	0	0	0	0	3	0	0	3	0
arCOG05279		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
arCOG05280		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05281	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG05282	COG0286	V	Type I restriction-modification system methyltransfe	0	0	0	0	0	0	0	0	0	1	1	0	3	0	0	0	0
arCOG05283		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG05284		S	Hemerythrin HHE cation binding domain	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG05285	COG5361	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	1	2	0	0	0	0
arCOG05286		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	2	0	0
arCOG05287	COG0457	R	TPR repeats containing protein	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG05288		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG05289		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG05290		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05291		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05292		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05293		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0
arCOG05294		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05295		S	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05296		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05297	COG2402	V	PIN domain containing protein	0	0	1	0	1	0	1	0	0	0	1	0	0	0	2	0	0
arCOG05298		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05299	COG2899	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05300		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05301		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05302	COG0631	T	Serine/threonine protein phosphatase	0	0	0	1	0	0	0	1	0	0	2	0	0	0	0	1	0
arCOG05303	COG0190	H	Muconolactone delta-isomerase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05304		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05305		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05306	COG4039	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05307		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05308		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	4	0	0
arCOG05309		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05310		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05311		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05312		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05313		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05314		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05315		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG05316	COG2057	I	Acyl CoA:acetate/3-ketoacid CoA transferase, beta s	0	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG05317	COG2721	G	Altronate dehydratase	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG05318	COG2721	G	SAF domain, altronate dehydratase related	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG05319	COG0500	Q	SAM-dependent methyltransferase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05320		S	Predicted membrane-bound metal-dependent hydrol	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05321		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG05322	COG0500	Q	SAM-dependent methyltransferase	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG05323		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05324	COG1312	G	D-mannonate dehydratase	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05325		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05326	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05327		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05328		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG05329		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05330		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05331	COG2391	R	Predicted transporter component	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05332	COG1716	T	FHA domain containing protein	1	3	4	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05334		R	Predicted DEAD/DEAH box helicase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05335	COG0451	M	Nucleoside-diphosphate-sugar epimerase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05336	COG0776	L	Bacterial nucleoid DNA-binding protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05337		S	Transcriptional regulator, HTH domain	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05338		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05339		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05340		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05341	COG0477	G	permease of the major facilitator superfamily	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG05342		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05343	COG1100	R	GTPase SAR1 or related small G protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05344	COG0477	G	permease of the major facilitator superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05345		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05346		S	PP-loop superfamily ATPase fused to Zn-finger dom	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	3	0
arCOG05347		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05348	COG0446	R	NAD(FAD)-dependent dehydrogenase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05349	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05350		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05351		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05352		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05353		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05354		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05355	COG0279	G	Phosphoheptose isomerase	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3	0
arCOG05356	COG2382	P	Enterochelin esterase or related enzyme	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05357		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05358		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05359		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05360		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05361	COG2017	G	Galactose mutarotase or related enzyme	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05362		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05363		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05365		I	Oligosaccharyl transferase STT3 subunit related pro	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05366		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05367	COG5592	S	Hemerythrin HHE cation binding domain containing	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05368		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05369		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05370	COG3386	G	Gluconolactonase	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05371		S	Uncharacterized conserved protein	1	3	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0
arCOG05372	COG1121	P	ABC-type Mn/Zn transport system, ATPase compon	1	3	2	0	0	1	0	0	0	0	0	0	0	0	1	1	0
arCOG05373	COG0276	H	Protoheme ferro-lyase (ferrochelatase)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05374	COG1956	T	GAF domain-containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05375		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05376		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05377	COG1814	S	Uncharacterized membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05378		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05379	COG4754	S	Uncharacterized conserved protein	0	3	5	0	1	1	0	0	0	0	0	0	0	0	0	3	0
arCOG05380	COG2149	S	Predicted membrane protein	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0
arCOG05381		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0

arCOG05382	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05383	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05384	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05385	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05386 COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	3	0
arCOG05387	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05388	S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05389	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05390	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05391	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05392 COG5615	S	Predicted integral membrane protein	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05393	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05394 COG3643	E	Glutamate formiminotransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05395 COG3404	E	Methenyl tetrahydrofolate cyclohydrolase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05396 COG4272	S	Predicted membrane protein	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05397	S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05398	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05399	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05400	S	Uncharacterized conserved protein	0	3	1	2	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05401	S	Uncharacterized conserved protein	1	3	2	0	0	1	0	0	0	0	0	0	0	0	0	3	0
arCOG05402	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05403 COG2329	R	Uncharacterized enzyme involved in biosynthesis of	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05404	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05405	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05406	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05407	S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
arCOG05408	S	Zn-ribbon protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG05410 COG0444	E	ABC-type dipeptide/oligopeptide/nickel transport sy	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0
arCOG05411 COG3934	G	Endo-beta-mannanase	0	1	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG05412 COG2723	G	Beta-glucosidase/6-phospho-beta-glucosidase/beta-g	1	3	5	0	0	0	0	0	0	0	0	0	0	4	3	0	0
arCOG05413	S	Uncharacterized conserved protein	0	0	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05414	S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG05415	H	Carotene hydroxylase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG05416	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG05417	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05418	S	Uncharacterized conserved protein	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05419	S	Uncharacterized conserved protein	0	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05420	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05421	S	paREP9 family	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05422	R	Predicted ATPase	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05423	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05424	S	Zn-ribbon protein	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05425	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05426	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05427	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05428	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05429	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05430	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05431 COG0438	M	Glycosyltransferase	0	2	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG05432	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05433	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05434	R	Transposase related protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05435	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05436	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05437	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05438	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05439	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05440	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05441	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05442	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05443	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05444	S	Zn finger protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05445	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05446	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05447	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05448	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05449	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05450 COG1321	K	Mn-dependent transcriptional regulator (DtxR famil	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05451	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05452	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05453	S	Zn finger protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05454	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05455	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05456	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05457	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05458	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05459	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05460 COG1326	R	Uncharacterized archaeal Zn-finger protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05461	S	Uncharacterized conserved protein	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05462	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05463	S	Uncharacterized conserved protein	0	0	5	2	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05464	S	Uncharacterized conserved protein	2	3	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05465	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05466 COG1145	C	Ferredoxin domain containing protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05467	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05468 COG0467	T	RecA-superfamily ATPase implicated in signal trans	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05469	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05470	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05471	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05472	S	Uncharacterized conserved protein	1	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05473	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05474	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05475	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0
arCOG05476	S	Uncharacterized conserved protein	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05477 COG0454	K	Acetyltransferase (GNAT) family	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05478	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05479	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05480	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05481 COG0675	L	Transposase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05482 COG0467	T	RecA-superfamily ATPase implicated in signal trans	0	1	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05483	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05484	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05485	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05486	H	Molybdopterin-Binding domain of the MopB superf	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05487	S	Uncharacterized conserved protein	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05488	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05489	S	Uncharacterized conserved protein	2	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05490	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05491	S	Uncharacterized conserved protein	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05492	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05493	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05494	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05495 COG4911	S	Uncharacterized conserved protein	0	3	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05496	S	SWIM Zn-finger	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05497 COG0438	M	Glycosyltransferase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05498 COG2225	C	Malate synthase	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05499	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05500	S	SWIM Zn-finger	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05501	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05502	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05503	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05504	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05505	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05506	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05507	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05508	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05509	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05510	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0

arCOG05511		S	Uncharacterized conserved protein	0	1	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05512		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG05513		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05514		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05515		S	Uncharacterized conserved protein	0	0	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05516		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05517		S	Uncharacterized conserved protein	1	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05518		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05519		S	NADH-quinone oxidoreductase subunit K	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05520		S	NADH-quinone oxidoreductase subunit J	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05521	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05522		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05523		S	Uncharacterized conserved protein	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05524		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05525		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05526		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05527		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05528		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05529		S	DNA-binding TFAR19-related protein	1	0	5	2	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05530		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05531		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05532		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05533		S	Metal-dependent hydrolase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05534		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05535		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05537		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05538		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05539		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05540		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05541		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05542		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05543	COG0446	R	NAD(FAD)-dependent dehydrogenase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05544		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05545		S	PIN domain containing protein	0	2	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05546		S	Uncharacterized conserved protein	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05547		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05548		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05549	COG0436	E	Aspartate/tyrosine/aromatic aminotransferase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG05550		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05551		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05552		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05553		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05554		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05555		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05556		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05557		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05558	COG0630	N	Type IV secretory pathway, VirB11 component, or r	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05559	COG1405	K	Transcription initiation factor TFIIIB, Brf1 subunit/T	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05561		S	Uncharacterized conserved protein	2	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05562		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05563		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05564		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05565		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05566		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05567		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05568		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05569	COG2892	S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05570		R	Predicted DNA binding protein, contains leucin zipp	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05571		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05572		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05573	COG4742	K	Predicted transcriptional regulator	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05574		R	Predicted ATPase with C-terminal metal-binding clu	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05575		L	Uncharacterized ATPase	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05576		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05577		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05578		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05579		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05580		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05581		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05582		S	Uncharacterized conserved protein	0	0	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05583	COG5277	R	Actin related protein	0	0	5	0	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05584		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05585		S	Uncharacterized conserved protein	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05586	COG3830	T	ACT domain-containing protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05587		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05588		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05589		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05590		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05591		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05592		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05593		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05594		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05595		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05596		K	CopG-family DNA-binding protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05597		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05598		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05599	COG1208	M	Nucleoside-diphosphate-sugar pyrophosphorylase in	0	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05600		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05601		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05602		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05603		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05604	COG4023	U	Preprotein translocase subunit Sec61beta	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05605		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05606		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05607		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05608	COG0455	N	Antiactivator of flagellar biosynthesis FleN, an ATPa	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05609	COG0630	N	Type IV secretory pathway, VirB11 component, or r	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05610		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05611		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05612		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05613		R	Predicted DEAD-box helicase/ATPase	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05614		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05615		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05616		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05617		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05618		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05619		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05620		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05621		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05622	COG3431	S	Predicted membrane protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05623		S	Uncharacterized conservedsecreted (or membrane) p	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05624		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05625		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05626		S	Uncharacterized conserved protein	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05627		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05628	COG0730	R	Predicted permease	0	2	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG05629		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05630		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05631		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05632	COG2391	R	Predicted transporter component	0	2	2	0	1	0	0	0	0	0	0	0	0	0	0	2	0
arCOG05633		S	Uncharacterized conserved protein	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05634	COG3058	O	Uncharacterized protein involved in formate dehydr	2	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05635	COG3058	O	Uncharacterized protein involved in formate dehydr	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05636		S	Formate dehydrogenase, cytochrome b556 subunit	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05637		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05638		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05639		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05640		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0

arCOG05641		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05642		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05643		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05644	COG1192	D	ATPase involved in chromosome partitioning, ParA	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05645		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05646		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05647		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05648		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05649		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05650		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05651		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05652		S	Uncharacterized conserved membrane protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05653		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05654		S	Uncharacterized conserved protein	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05655		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05656		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05657		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05658		S	SWIM zinc finger	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05659		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05660		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05661		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05662		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05663		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05664		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05665		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05666	COG2908	S	Calcineurin-like phosphoesterase	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05667		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05668		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05669		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05670		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05671	COG2771	K	Transcriptional regulator LuxR family	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05672		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05673		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05674		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05675	COG1396	K	Protein containing xre family HTH domain	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05676		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05677		R	Predicted ATPase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05678		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05679		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05680		S	Uncharacterized conserved protein	0	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05681		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05682		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05683		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05684		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05685		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05686		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05687		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05688		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05689		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05690		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05691		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05692		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05693		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05694		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05695		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05696		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05697		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05698		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05699		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05700		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05701		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05702		R	Predicted ATPase	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05703		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05704	COG0725	P	ABC-type molybdate transport system, periplasmic	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05705	COG3839	G	ABC-type sugar transport system, ATPase componer	0	3	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05706	COG1506	E	Dipeptidyl aminopeptidase/acylaminoacyl-peptidase	0	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05707		S	Uncharacterized conserved protein	0	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05708		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05709		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05710		S	Uncharacterized conserved protein	0	3	5	0	0	0	0	0	0	1	1	0	0	1	0	0	0
arCOG05711		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05712		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05713		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05714		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05715		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05716		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
arCOG05717		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05718		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05719		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05720		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
arCOG05721	COG3191	E	L-aminopeptidase/D-esterase	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05722		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05723	COG1822	S	Predicted archaeal membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05724	COG2810	V	Predicted type IV restriction endonuclease	1	0	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0
arCOG05725		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05726		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05727	COG3949	S	Uncharacterized membrane protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG05728	COG0477	G	permease of the major facilitator superfamily	2	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05729	COG0535	R	Radical SAM superfamily enzyme	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05730	COG1988	R	Membrane-bound metal-dependent hydrolase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05731		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05732		S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05733		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05734		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05735		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05736		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05737		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05738	COG0500	Q	SAM-dependent methyltransferase	0	1	1	0	0	1	0	0	0	0	0	0	0	0	3	0	0
arCOG05739	COG3862	S	Uncharacterized protein with conserved CXXC pair	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05740		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05741		R	Nucleic acid binding, OB-fold	0	0	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0
arCOG05742		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05743		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05744	COG1142	C	Fe-S-cluster-containing hydrogenase component 2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05745	COG0446	C	BFD-like [2Fe-2S] binding domain	1	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05746	COG0578	C	BFD-like [2Fe-2S] binding domain of glycerol-3-ph	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG05747		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05748		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	1	0
arCOG05749		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
arCOG05750	COG1266	R	Predicted metal-dependent membrane protease	0	0	0	0	0	0	0	1	0	0	0	0	0	4	0	0	0
arCOG05751		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
arCOG05752	COG4720	S	Predicted membrane protein	1	0	1	0	1	1	0	0	0	0	0	0	0	4	0	0	0
arCOG05754		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05755		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05756		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
arCOG05757		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	1	0	0	4	2	0	0
arCOG05758		P	TrkA-C domain contaning protein	1	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05759		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05760	COG2306	R	Predicted RNA-binding protein, associated with RN	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05761	COG1241	L	Predicted ATPase involved in replication control, Cd	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
arCOG05762		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05763	COG4003	S	Uncharacterized protein conserved in archaea	1	0	0	0	1	0	0	0	0	0	0	0	1	4	0	0	0
arCOG05764	COG3682	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05765		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05766		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05767		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
arCOG05768		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
arCOG05769		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0

arCOG05770		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05771		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05772		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05773		D	Cell division protein 48 (CDC48), domain 2	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05774		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05775		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05776		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05777		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05778	COG3431	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05779		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05780		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05781		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05782		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05783		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0
arCOG05784		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05785		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05786	COG4025	S	Predicted membrane protein	0	0	0	0	0	0	0	0	1	0	0	0	1	4	0	0
arCOG05787		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05788		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	0	4	0	0
arCOG05789		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05790		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05791		S	Uncharacterized cell suface protein, containing DUF	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05792		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05793	COG0630	N	Type IV secretory pathway, VirB11 component, or r	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05794		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05795		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05796		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05797	COG3630	C	Na+-transporting methylmalonyl-CoA/oxaloacetate	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05798		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05799		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05800		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05801		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05802		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05803		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0
arCOG05804		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05805		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05806		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05807		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05808	COG1984	E	Allophanate hydrolase subunit 2	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05809	COG2049	E	Allophanate hydrolase subunit 1	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05810	COG1540	R	Uncharacterized protein, homolog of lactam utilizati	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05811		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05812		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05813		R	Beta-barrel domain related to domain II of E-FG and	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05814		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05815		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05816	COG2886	S	Uncharacterized small protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05817		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05818		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05819		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05820		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05821		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05822		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05823		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05824		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05825	COG1856	R	Radical SAM superfamily enzyme	2	3	0	0	0	1	0	0	0	0	0	0	0	4	0	0
arCOG05826		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05827		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05828	COG1414	K	Transcriptional regulator (IclR family)	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05829		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05830	COG5305	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05831		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05832	COG1989	N	Type II secretory pathway, prepilin signal peptidase	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05833		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05834		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05835	COG0477	G	permease of the major facilitator superfamily	1	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05836		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05837		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05838		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05839		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05840		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05841		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05842		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05843		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05844		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05845		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05846		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05847		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05848		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05849		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05850	COG2039	O	Pyrrolidone-carboxylate peptidase (N-terminal pyro	2	2	1	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05851		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05852		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05853		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05854		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05855		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05856	COG1874	G	Beta-galactosidase	0	0	1	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05857	COG0195	K	NusA_K homology RNA-binding domain (KH)	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05858		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05859		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05860		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05861		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	4	0	0
arCOG05862		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05863	COG1520	S	WD40-like repeat	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05864		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05865	COG1274	C	Phosphoenolpyruvate carboxykinase (GTP)	1	3	2	0	0	0	0	0	0	0	0	0	0	4	2	0
arCOG05866		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05867		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05868	COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05869		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05870		S	Uncharacterized conserved protein	0	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0
arCOG05871		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05872		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05873	COG0840	N	Methyl-accepting chemotaxis protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05874		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG05875	COG1668	P	ABC-type Na+ efflux pump, permease component	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0
arCOG05876		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0
arCOG05877		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05878		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05879		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG05880		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG05881		S	Uncharacterized conserved protein, DUF1177	0	3	1	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG05882		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0
arCOG05883		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05884		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05885		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05886		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05887		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05888		S	Chromosomal protein Sac7d	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05889		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05890		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05891		S	Terminal oxidase, subunit doxC	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05892		S	Terminal oxidase, subunit doxE	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05893		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05894		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05895	COG2427	S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05896	COG0477	G	permease of the major facilitator superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05897		S	Uncharacterized conserved protein	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0

arCOG05898		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05899		S	Cell suface protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05900	COG3355	K	Predicted transcriptional regulator	2	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05901		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05902	COG0608	L	Protein similar to exonuclease RecJ central domain	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05903		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05904		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05905		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05906		S	Uncharacterized conserved protein	1	3	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05907		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05908	COG1633	S	Uncharacterized conserved protein	0	3	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG05909	COG1659	S	Uncharacterized protein, linocin/CFP29 homolog	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG05910		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05911	COG1826	U	Sec-independent protein secretion pathway compone	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05912		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05913		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05914		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05915		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05916		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05917		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05918		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05919	COG0546	R	Predicted phosphatase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05920		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05921		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05922		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05923		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05924		S	Uncharacterized conserved protein	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05925		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05926		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05927		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05928		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05929		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05930		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05931	COG1405	K	Transcription initiation factor TFIIIB, Brf1 subunit/T	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05932	COG0491	R	Zn-dependent hydrolase, glyoxylase family	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05933		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05934		S	Uncharacterized conserved protein	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05935	COG3451	L	Type IV secretory pathway, VirB4 component	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05936		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05937	COG0028	E	Acetolactate synthase large subunit or other thiamin	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05938		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05939		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05941		S	Uncharacterized conserved protein	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05942		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05943	COG0463	M	Glycosyltransferase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05944		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05945		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05946		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05947		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05948		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05949		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05950		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05951		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05952		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05953		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05954		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05955		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05956		S	Uncharacterized conserved protein	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05957		S	Uncharacterized conserved protein	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05958		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05959	COG0622	R	Predicted ICC-like phosphoesterase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05960		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05961	COG1321	K	Mn-dependent transcriptional regulator (DtxR famil	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05962		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05963		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05964	COG1960	I	Acyl-CoA dehydrogenase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05965	COG1960	I	Acyl-CoA dehydrogenase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05966	COG3511	M	Phospholipase C	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05967		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG05968		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05969	COG3355	K	Predicted transcriptional regulator	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05970		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05971		S	MFS family permease	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05972		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05973	COG2226	H	Methylase involved in ubiquinone/menaquinone bio	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05974		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05975		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05976		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05978		S	Extracellular protein containing Kelch and FN3 dom	1	3	0	2	1	0	0	0	0	0	1	0	2	0	0	0	0
arCOG05979		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05980		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05981		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05982		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05983		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05984		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05985	COG2107	R	Predicted periplasmic solute-binding protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05986		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05987		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
arCOG05988		S	Uncharacterized conserved protein	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05989		S	Transcriptional regulator, xre family	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05990	COG0604	C	NADPH:quinone reductase or related Zn-dependent	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05991		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG05992		S	Uncharacterized conserved protein	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05993		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05994		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05995		S	Uncharacterized conserved protein	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05996		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05997		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05998		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG05999		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06000		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06001	COG3889	R	Predicted periplasmic solute-binding protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06002		S	Cell suface protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06003		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06004	COG3971	Q	2-keto-4-pentenoate hydratase	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06005	COG3975	R	Predicted protease with the C-terminal PDZ domain	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06006		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06007		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06008		S	Predicted metal permease	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06009		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06010	COG4280	S	Predicted membrane protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06011		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0
arCOG06012		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06013		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06014	COG4194	R	Predicted membrane protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06015		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06016		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06017		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06018		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06019		S	Uncharacterized conserved protein	0	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG06020		S	Uncharacterized conserved protein	0	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG06021		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06022		S	Uncharacterized conserved protein	1	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06023	COG3376	P	High-affinity nickel permease	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06024		S	Uncharacterized conserved protein	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06025		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06026	COG1011	R	Predicted hydrolase of HAD superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06027	COG3189	S	Uncharacterized conserved protein	0	3	1	0	1	0	0	0	0	0	1	1	0	0	0	2	0

arCOG06028	COG1487	V	PIN domain containing protein	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06029		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06030		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06031	COG5424	H	Pyrroloquinoline quinone (Coenzyme PQQ) biosynt	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06032		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06033		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06034		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06035		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06036		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06037	COG0346	E	Lactoylglutathione lyase or related enzyme	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06038		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06039		S	Cell suface protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06040		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06041		S	Uncharacterized conserved protein	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06042	COG0130	J	DKCLD domain, TruB/PUA associated	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06043		S	Uncharacterized conserved protein	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06044	COG1802	K	Transcriptional regulators	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06045	COG3589	S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06046	COG5592	S	Hemerythrin HHE cation binding domain containing	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06047	COG0477	G	permease of the major facilitator superfamily	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06048		S	Uncharacterized conserved protein	0	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG06049	COG3345	G	Alpha-galactosidase	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06050	COG3431	S	Predicted membrane protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06051	COG1960	I	Acyl-CoA dehydrogenase	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06052		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06053		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG06054		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG06055		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06056	COG0680	C	Ni,Fe-hydrogenase maturation factor	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06057		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06058		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06059	COG1007	C	NADH dehydrogenase subunit N	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06060	COG0365	I	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligas	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06061		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06062		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06063		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06064		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06065		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06066		S	Uncharacterized conserved membrane protein, DUF	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06067	COG3431	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
arCOG06068		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06069		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	2	1	0	0	0	0	0
arCOG06070	COG1486	G	Alpha-galactosidase/6-phospho-beta-glucosidase, fa	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06071		S	Uncharacterized conserved protein	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06072		S	Uncharacterized conserved protein	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06073	COG1866	C	Phosphoenolpyruvate carboxykinase (ATP)	1	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG06074	COG1493	T	Serine kinase of the HPr protein, regulates carbohyd	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG06075	COG0526	O	Thiol-disulfide isomerase or thioredoxin	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06076		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06077	COG1846	K	Transcriptional regulator, MarR family	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06078		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06079		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06080		S	vWFA domain containing protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06081		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06082		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06083		R	Imidazolonepropionase family metallohydrolase	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06084		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06085		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06086		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06087		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06088		S	Uncharacterized conserved protein	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06089		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06090	COG2388	R	Predicted acetyltransferase	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06091		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06092		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06093		S	Uncharacterized conserved protein	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06094		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06095		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06096		S	Uncharacterized conserved protein	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06097		R	Membrane protein, containing cytochrome c-like do	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06098		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06099		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06100		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06101		S	Uncharacterized conserved protein	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06102		S	Uncharacterized conserved protein	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06103		S	Uncharacterized conserved protein	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06104		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06105		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06106	COG2514	R	Predicted ring-cleavage extradiol dioxygenase	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06107		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06108	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG06109		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG06110		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG06111	COG2010	C	Cytochrome c family protein	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG06112	COG0365	I	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligas	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0
arCOG06113		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	2	0	0	0	0
arCOG06114	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG06115		S	Uncharacterized conserved protein	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG06116		S	Uncharacterized conserved protein	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG06117		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	2	0	0	0	1	0	0	0	0	0
arCOG06118		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG06119		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG06120		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG06121	COG0501	O	Zn-dependent protease with chaperone function	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG06122	COG0365	I	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligas	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG06123		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0
arCOG06124	COG0427	C	Acetyl-CoA hydrolase	0	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0	0
arCOG06125	COG3246	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG06126	COG1811	R	Uncharacterized membrane protein, possible Na+ ch	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG06127		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0
arCOG06128	COG1615	S	Uncharacterized conserved protein	0	0	0	2	1	0	1	0	0	0	1	0	0	0	0	0	0
arCOG06129		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG06130	COG1882	C	Pyruvate-formate lyase	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	0	0
arCOG06131	COG2202	T	PAS domain	0	0	0	0	0	0	1	0	0	0	1	0	3	0	0	0	0
arCOG06133		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG06134		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG06135		S	Uncharacterized conserved protein	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG06136		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG06137		S	Uncharacterized conserved protein	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG06138		S	Uncharacterized conserved protein	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
arCOG06139	COG2250	S	HEPN domain containing protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
arCOG06140		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG06141		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG06142		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0
arCOG06143		V	CRISPR-associated protein	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG06144		V	CRISPR-associated protein	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG06145		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG06146		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG06147		S	Uncharacterized conserved protein	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0
arCOG06148		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
arCOG06149	COG1305	E	Transglutaminase-like enzyme, putative cysteine pro	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0
arCOG06150		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	2	0	0	0	0	1	0	0	0	0
arCOG06151	COG2128	R	Alkylhydroperoxidase family enzyme	0	0	0	0	0	0	1	2	0	0	0	0	1	0	0	0	0
arCOG06152		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06153		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06154		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06155		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06156		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0

arCOG06157	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06158	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06159 COG3385	L	Transposase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06160 COG3385	L	Transposase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06161	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06162	S	Cell suface protein	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0
arCOG06163	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06164	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
arCOG06165	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
arCOG06166	S	Transcriptional regulator, ArsR family	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06167	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06168 COG1495	O	Disulfide bond formation protein DsbB	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06169	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06170	S	Exonuclease VII small subunit	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06171	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06172	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06173	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06174	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06175	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06176	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06177	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
arCOG06178	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG06179	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06180 COG0614	P	ABC-type Fe3+-hydroxamate transport system, peri	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06181 COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG06182 COG0459	O	Chaperonin GroEL (HSP60 family)	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06183 COG2226	R	Predicted SAM-dependent methylase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06184	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06185	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06187 COG0849	D	Actin-like ATPase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06188 COG2371	O	Urease accessory protein UreE	0	1	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06189 COG5502	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0
arCOG06190	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06191 COG4314	C	Predicted lipoprotein involved in nitrous oxide reduc	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06192 COG0642	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	1	3	1	0	2	1	3	0	0	0	0	0
arCOG06193 COG0642	T	Signal transduction histidine kinase and PAS domain	0	0	0	0	0	0	1	2	0	0	2	1	4	0	0	0	0	0
arCOG06194 COG3920	T	GAF and PAS domains	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0
arCOG06197 COG2202	T	PAS domain	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06198	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06199	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06200 COG3670	Q	Lignostilbene-alpha,beta-dioxygenase or related enz	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06201 COG2908	S	Calcineurin family phosphoesterase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06202 COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06203	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06204 COG0685	E	5,10-methylenetetrahydrofolate reductase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06205	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06206	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06207 COG3526	O	Uncharacterized protein conserved in bacteria	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG06208	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06209	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06210	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06211	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06212	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06213	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06214	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06215	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06216	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06217 COG4263	C	Nitrous oxide reductase	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
arCOG06218	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06219 COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	1	3	0	0	0	1	0	0	0	0	0	0
arCOG06221	S	Zn-ribbon containing protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06222	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06223	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06224 COG0433	L	HerA helicase	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0
arCOG06225 COG2352	C	Phosphoenolpyruvate carboxylase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06226 COG0410	E	ABC-type branched-chain amino acid transport syste	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06227	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06228	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06229	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0
arCOG06230	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06231 COG4865	E	Glutamate mutase epsilon subunit	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06232 COG3799	E	Methylaspartate ammonia-lyase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06233 COG0550	L	Topoisomerase IA associated Zn-finger domain	0	0	0	0	0	0	0	4	0	0	0	0	5	0	0	0	0	0
arCOG06234 COG3743	R	Predicted nucleic acid binding protein, containing H	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06235 COG0589	T	Nucleotide-binding protein, UspA family	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06236	S	Zn finger protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06237 COG1522	K	Transcriptional regulator (Lrp/AsnC family)	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06238	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06239	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06240	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG06241 COG0334	E	Glutamate dehydrogenase/leucine dehydrogenase fa	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06242	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG06243	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06244	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06245	R	Reversibly glycosylated polypeptide (RGP) family p	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06246	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06247	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06248	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06249	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06250	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06251 COG0769	M	DP-N-acetylmuramyl tripeptide synthase and Folylp	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06252	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06253 COG2202	T	Sensory domain	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0
arCOG06255	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06256 COG0400	R	Predicted esterase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06257	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06258	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06259 COG0455	N	Antiactivator of flagellar biosynthesis FleN, an ATPa	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06260	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06261	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG06262	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06263	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06264	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06265	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06266 COG3460	Q	Uncharacterized enzyme of phenylacetate metabolis	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06267	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0
arCOG06268 COG1858	P	Cytochrome c peroxidase	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0
arCOG06269 COG2332	O	Cytochrome c-type biogenesis protein CcmE	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06270	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06271	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06272	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06273	S	S-layer protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG06274	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06275	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06276 COG4983	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0
arCOG06277	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
arCOG06278	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06279	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06280	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06281	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06282 COG2148	M	Sugar transferase involved in lipopolysaccharide syr	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0
arCOG06283	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06284	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06285	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG06286	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06287	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG06288 COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG06289	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0

arCOG06290		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06291		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06292		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0
arCOG06293		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06294		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06295		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06296		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06297		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06298	COG2746	V	Aminoglycoside N3'-acetyltransferase	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
arCOG06299		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06300	COG0657	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06301		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06302		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06303		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06304		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06305		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06306	COG0667	C	Predicted oxidoreductase (related to aryl-alcohol del	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0
arCOG06307		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06308		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06309		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06310		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06311		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06312		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06313		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06314	COG1803	G	Methylglyoxal synthase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06315	COG0784	T	Rec domain	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06316		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06317		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06318		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06319		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06320		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06321		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06322	COG0506	E	Proline dehydrogenase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06323		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06324		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG06325		S	Predicted lipoprotein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06326		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06327		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06328		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06329		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06330		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06331		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06332		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06333	COG2346	R	Hemoglobin-like protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06334	COG3975	E	Predicted metalloprotease protease	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06335		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06336		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06337	COG4948	M	L-alanine-DL-glutamate epimerase or related enzym	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06338	COG1112	L	Superfamily I DNA/RNA helicase, contains VSR fa	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06339		S	Cell suface protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06340		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06342		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06343		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06344	COG3243	I	Poly(3-hydroxyalkanoate) synthetase	0	0	0	2	0	0	1	2	0	0	0	0	0	0	0	0	0
arCOG06346		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06347		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06348		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06349		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06350		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06351		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06352		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06353		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06354		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06355	COG3216	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06356	COG4317	S	Uncharacterized small membrane protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06357		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06358		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06359		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06360		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06361		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06362	COG4327	S	Uncharacterized small membrane protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06363	COG2203	T	Signal transduction protein, GAF and REC domains	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06364	COG0840	N	Methyl-accepting chemotaxis protein	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06366		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06367		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06368		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06369		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06370		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06371		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06372		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06373		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG06374		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06375		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06376		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06377		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06378		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06379		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06380		S	Transposase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06381	COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
arCOG06382		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06383		S	Predicted transcriptional regulator	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06384		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06385		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06386		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06388	COG0589	T	Nucleotide-binding protein, UspA family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06389		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06390		Q	Gas vesicle protein K	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0
arCOG06391		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06392		Q	Gas vesicle protein C, GVPC	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06393		L	Transposase DDE domain	0	0	0	0	0	0	0	3	0	0	0	1	0	0	0	0	0
arCOG06394		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06395		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06396		P	Arsenical resistance operon trans-acting repressor A	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06397		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06398		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06399		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0
arCOG06400		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06401		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06402		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06403		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06404		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06405		F	HTTM domain containing membrane enzyme	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06406		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06407		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06408	COG0642	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	1	3	0	0	0	0	2	0	0	0	0
arCOG06409	COG0642	T	Signal transduction histidine kinase, contains PAS d	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0
arCOG06410		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06411		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06412		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06413		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0
arCOG06414	COG0464	O	ATPase of the AAA+ class	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06415		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06416		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06417		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	1	0	1	0	0	0	0
arCOG06418	COG2311	S	Predicted membrane protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06419		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06420		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06421		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0

arCOG06422	COG3431	S	Predicted membrane protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06423		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06424		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06425		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06426		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06427		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06428		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06429	COG3332	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06430		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06431		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG06432		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06433		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06434	COG2059	P	Chromate transport protein ChrA	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
arCOG06435		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06436	COG0397	S	Uncharacterized conserved protein, YdiU/UPF0061	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06437		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06438		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06439		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06440		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06441	COG0589	T	Universal stress protein UspA	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06442		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06443		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06444	COG1205	R	Distinct helicase family with a unique C-terminal do	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0
arCOG06445		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06446		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06447		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG06448		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06449		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06450		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06451	COG0582	L	Integrase	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG06453		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06454		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	1	0
arCOG06455		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06456	COG0606	O	Predicted ATPase with chaperone activity	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
arCOG06457		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06458		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06459	COG3339	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG06460		R	Predicted ATPase	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG06461		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG06462		M	Glycosyl transferase family 2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06463		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG06464		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG06465		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06466		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG06467	COG1700	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
arCOG06468		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06469		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06470		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06471		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06472	COG1240	H	Mg-chelatase subunit ChlD	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
arCOG06473		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06474		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06475		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06476	COG2966	S	Uncharacterized membrane domain	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG06477		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06478		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06479		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06480		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06481		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
arCOG06483		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06484		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
arCOG06485	COG4086	S	Predicted secreted protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06486		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG06487	COG1421	V	CRISPR system related protein	0	0	0	0	0	0	0	0	1	0	0	0	1	1	1	0	0
arCOG06488		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06489		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06490		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
arCOG06491		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06492		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06493	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0
arCOG06495		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06496	COG1787	V	Endonuclease, HJR/Mrr/RecB family	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06497	COG0365	I	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligas	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
arCOG06498		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06499		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06500		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06501	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06502	COG3552	R	Protein containing von Willebrand factor type A (vW	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06503		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06504	COG1511	S	Membrane protein related to phage infection protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06505	COG1735	R	Predicted metal-dependent hydrolase with the TIM-l	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
arCOG06506		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG06507	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0
arCOG06508	COG3039	L	Transposase and inactivated derivatives, IS5 family	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	2	0
arCOG06510		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06511	COG3291	R	NosD-like periplasmic protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06512	COG3420	R	NosD-like periplasmic protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06513	COG5485	R	Predicted ester cyclase	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06515	COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06516	COG2202	T	Sensory domain	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG06517		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06518		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06519	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0
arCOG06520		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06521		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG06522		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06523	COG2818	L	3-methyladenine DNA glycosylase	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG06524		V	CRISPR-associated protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06525	COG1688	V	CRISPR-associated protein, RAMP superfamily	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG06526		V	CRISPR-associated protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG06527	COG2389	R	Uncharacterized metal-binding protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06528	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0
arCOG06529		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG06531		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06532		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06533		S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06534		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06535		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06536	COG2202	T	Sensory protein, contains REC and PAS domain	0	0	0	0	0	0	1	0	1	0	2	1	2	0	0	0	0
arCOG06537	COG0784	T	Rec and PAS domains	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0
arCOG06538	COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0
arCOG06542		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06543		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06544	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06545		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06546	COG4659	C	Predicted NADH:ubiquinone oxidoreductase, subun	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06547	COG4658	C	Predicted NADH:ubiquinone oxidoreductase, subun	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06548	COG4656	C	Predicted NADH:ubiquinone oxidoreductase, subun	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06549		C	Membrane-bound multiheme cytochrome c subunit	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06550	COG3422	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0
arCOG06551		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG06552		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	1	1	0	0	0	0
arCOG06553		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06554		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0
arCOG06555	COG3727	L	DNA G:T-mismatch repair endonuclease	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06556		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06557	COG3227	E	Thermolysin metallopeptidase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06558		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0

arCOG06559		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06560	COG0786	E	Na+/glutamate symporter	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06561		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06562		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0
arCOG06563		S	Cell suface protein	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG06564		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06565		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06566		S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	1	2	0	1	0	0	0	0
arCOG06567		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06568		S	Uncharacterized conserved membrane protein	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG06569	COG2343	S	Uncharacterized protein conserved in bacteria	0	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG06570		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06571		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG06572		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
arCOG06573		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0
arCOG06574		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG06575		L	DpmII-like restriction endonuclease	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
arCOG06576		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0
arCOG06577	COG2703	P	Hemerythrin	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
arCOG06578	COG0582	L	Integrase	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
arCOG06579		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG06580		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06581	COG3980	M	Spore coat polysaccharide biosynthesis protein, pred	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
arCOG06582	COG5608	R	Desiccation-related protein, LEA14/Hin1 family	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
arCOG06583	COG0648	L	Endonuclease IV	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
arCOG06584		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG06585		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
arCOG06586		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
arCOG06587		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06588	COG1266	R	Predicted metal-dependent membrane protease	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0
arCOG06589		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06590		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06591		R	Nucleic acid binding protein, OB-fold	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06592		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06593		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06594		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06595		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06596		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06597		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06598		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06599	COG5306	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG06600		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06601	COG3238	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06602		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06603		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06604		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06605		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06606		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06607		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06608		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06609		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06610		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06611		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06612		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06613		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0
arCOG06614		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0
arCOG06615		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06616		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06617		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06618		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06619		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06620		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06621		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06622		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06623		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06624		J	Ribosomal L41E	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06625	COG4392	S	Uncharacterized membrane protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06626		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06627		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06628	COG2892	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06629		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06630		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06631		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06632	COG1722	L	Exonuclease VII small subunit	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06633		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06634		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06635		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0
arCOG06636		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06637	COG0265	O	Serine protease Do (heat-shock protein)	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06638		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0
arCOG06639		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06640	COG4443	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06641		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06642		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06643	COG3341	R	Predicted double-stranded RNA/RNA-DNA hybrid l	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06644		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06645		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06646	COG4760	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06647		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06648		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06649	COG3904	S	Predicted periplasmic protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06650	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0
arCOG06651		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06652	COG3432	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG06653		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06654		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06655		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06656		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06657		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06658	COG1667	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	1	0	1	3	0	0	0	1	0	0	0
arCOG06659		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06660	COG0564	J	Pseudouridylate synthase, 23S RNA-specific	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06661		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0
arCOG06662		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06664		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06665	COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06666		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06667		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06668		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06669		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06670		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06671		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06672		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06673		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06674		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06675		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06676		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06677	COG0787	M	Alanine racemase	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06678	COG0686	E	Alanine dehydrogenase	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06679		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06680		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06681		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06682		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06683		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06684		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06685	COG3259	C	F420-non-reducing hydrogenase vhu subunit U	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06686		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
arCOG06687		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0

arCOG06688	COG5650	S	Predicted integral membrane protein	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG06689		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG06690		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0
arCOG06691		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06692		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06693		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06694	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0
arCOG06696		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06697	COG0640	K	Transcriptional regulator containing HTH domain, A	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0
arCOG06698	COG0457	R	TPR repeats containing protein	0	0	0	2	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG06699	COG1484	L	DNA replication protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06700	COG1672	R	Predicted ATPase (AAA+ superfamily)	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06701	COG0484	O	DnaJ-class molecular chaperone	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06702		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06703	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06704	COG4925	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0
arCOG06705		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06706		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06707		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06708		S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06709		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG06710		H	Dimethylamine methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06711	COG3212	S	Predicted membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06712	COG2202	T	Sensory protein, contains PAS domain	0	0	0	0	0	0	1	0	1	0	2	1	1	0	0	0	0
arCOG06715	COG3961	G	Pyruvate decarboxylase or related thiamine pyropho	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06716		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06717		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0
arCOG06718		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06719		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06720	COG0644	C	Dehydrogenase (flavoprotein)	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06721	COG2202	T	PocR-like and PAS domains	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	0
arCOG06722	COG4301	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06723	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06724	COG3910	R	Predicted ATPase	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06725	COG1131	V	ABC-type multidrug transport system, ATPase comp	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06726		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06727		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06728	COG0730	R	Predicted permease	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06729	COG0398	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06730		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06731		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0
arCOG06732		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06733		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06734		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06735		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06736		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06737	COG2202	T	PAS domain	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06738	COG2335	M	Secreted and surface protein containing fasciclin-lik	0	0	0	0	0	0	0	1	0	0	2	0	4	0	0	0	0
arCOG06742		S	NosD-like cell surface protein	0	0	0	0	0	0	0	0	0	0	2	1	3	0	0	0	0
arCOG06743		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06744		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06745		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	0
arCOG06746		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06747	COG5635	T	SIR2 superfamily domain	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0
arCOG06748	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG06750		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06751		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06752		R	SEC-C motif containing protein	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0
arCOG06753		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06754		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06755		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06756	COG2027	M	D-alanyl-D-alanine carboxypeptidase	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06757		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06758	COG4104	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06759	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06760	COG1988	R	Predicted membrane-bound metal-dependent hydrol	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06761	COG3271	R	Predicted double-glycine peptidase	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG06763	COG1285	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06764		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG06765	COG1573	L	Uracil-DNA glycosylase	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06766		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06767	COG5470	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06768		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06769	COG1100	R	GTPase SAR1 family domain fused to Leucine-rich	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06771		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06772		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06773		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06774	COG0224	C	F0F1-type ATP synthase, gamma subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06775	COG0711	C	F0F1-type ATP synthase, subunit b/b'	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06776	COG0636	C	F0F1-type ATP synthase, subunit c	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06777	COG0356	C	F0F1-type ATP synthase, subunit a	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06778		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06779		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06780	COG0355	C	F0F1-type ATP synthase, epsilon subunit	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06781		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06782	COG4742	K	Predicted transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06783		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06784		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06785		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06786		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06787		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06788		S	Uncharacterized conserved protein, DUF1269 famil	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06789	COG1266	R	Predicted metal-dependent membrane protease	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06790		S	Zn finger protein, UBP-type	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06791		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06792	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG06793		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06794		R	Predicted ATPase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06795		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06796	COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG06797		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06798		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06799		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06800		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06801	COG2334	R	Putative homoserine kinase type II (protein kinase fa	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06802		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06803		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06804		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06805		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06806		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06807	COG1138	O	Cytochrome c biogenesis factor	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06808		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06809		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06810	COG0444	E	ABC-type dipeptide/oligopeptide/nickel transport sy	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06811	COG3183	V	Predicted restriction endonuclease	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06812		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06813	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06814		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06815	COG2866	E	Predicted carboxypeptidase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06816		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0
arCOG06817		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0
arCOG06818		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06819		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06820		R	Acetyltransferase, GNAT family	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06821	COG4584	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06822		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06823	COG1404	O	Subtilisin-like serine protease	0	0	0	0	0	0	0	1	0	0	1	0	2	0	0	0	0
arCOG06824		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0

arCOG06825		S	Cell surface protein, contains CARDB cell adhesion	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06826		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06827		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG06828		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06829		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06830		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06831	COG3654	R	Prophage maintenance system killer protein	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0
arCOG06832		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06833		S	Zn-ribbon protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06834		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06835		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06836	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
arCOG06837	COG3420	S	NosD-like cell surface protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06838	COG0789	K	Transcriptional regulator (MerR family)	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06839		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06840		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06841		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06842		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06843		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06844		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG06845		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06846		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06847	COG1926	R	Predicted phosphoribosyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06848		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06849		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06850		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06851		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06852	COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06853	COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06854		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	0	0	0	2	0	1	0	0	0	0
arCOG06855	COG1835	I	Predicted acyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06856		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06857	COG4119	L	Predicted NTP pyrophosphohydrolase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06858		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06859		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06860		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06861		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06862	COG3291	R	PKD repeats containing protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG06863		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06864		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06865		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06866		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06867		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06868	COG1266	R	Predicted metal-dependent membrane protease	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06869		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG06870	COG0317	T	HD family hydrolase	0	0	0	0	0	0	0	1	0	0	0	1	2	0	0	0	0
arCOG06871		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG06872		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06873		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG06874		S	Uncharacterized conserved protein	1	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0
arCOG06876	COG2865	K	Predicted transcriptional regulator containing an HT	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0
arCOG06877		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0
arCOG06878	COG4572	R	Putative cation transport regulator	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG06879		Q	class II terpene cyclase related protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06880	COG0484	O	DnaJ type Zn finger domain	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG06881		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06883		S	Zn-ribbon domain containing protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
arCOG06884	COG2323	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG06885		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0
arCOG06886		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	2	0	1	0	0	0	0
arCOG06887	COG3587	V	Restriction endonuclease	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG06888		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG06889		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
arCOG06890		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0	0	0
arCOG06891	COG1366	T	Anti-anti-sigma regulatory factor (antagonist of anti-	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG06892	COG2172	T	Anti-sigma regulatory factor (Ser/Thr protein kinase	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG06893	COG2208	T	Serine phosphatase RsbU, regulator of sigma subuni	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG06895	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
arCOG06896	COG0724	R	RNA-binding protein (RRM domain)	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06897	COG3919	R	Predicted ATP-grasp enzyme	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06898		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06899	COG1533	L	DNA repair photolyase	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06900		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
arCOG06901		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG06902	COG4843	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06903	COG3247	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06904		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06905		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06906		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06907		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG06908	COG1145	C	Ferredoxin	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG06909	COG1456	C	CO dehydrogenase/acetyl-CoA synthase gamma sub	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0
arCOG06910	COG0817	L	Holliday junction resolvasome, endonuclease subuni	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG06911	COG0632	L	Holliday junction resolvasome, DNA-binding subun	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG06912		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06913		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0
arCOG06914	COG3378	R	Phage associated DNA primase	0	2	0	0	1	0	0	2	0	0	2	1	1	0	0	0	0
arCOG06915		S	Primase-polymerase (primpol) domain	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0
arCOG06916		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06918	COG2202	T	PAS/PAC domain containing protein	0	0	0	0	0	0	1	0	0	0	2	1	0	0	0	0	0
arCOG06919	COG0784	T	PAS domain	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG06922	COG0457	R	TPR repeats containing protein	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG06923	COG1075	R	Predicted acetyltransferase or hydrolase with the alp	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06924		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG06925		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG06926		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
arCOG06927		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06928		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06929		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06930	COG4689	Q	Acetoacetate decarboxylase	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06931		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06932	COG1328	F	Oxygen-sensitive ribonucleoside-triphosphate reduc	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06933		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG06934		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06935		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06936		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
arCOG06937		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06938		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06939		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG06940	COG2202	T	Signal transduction histidine kinase associate memb	0	0	0	0	0	0	0	0	1	0	2	1	0	0	0	0	0
arCOG06944		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG06945		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
arCOG06946		S	Uncharacterized conserved membrane protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
arCOG06947		S	Zn finger protein	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG06948		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	0	0
arCOG06949		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
arCOG06950	COG3876	S	Uncharacterized protein conserved in bacteria	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06951		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06952		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06953		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06954	COG0531	E	Amino acid transporter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06955		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06956		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06957		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	3	0
arCOG06958		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06959		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06960		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06961		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0

arCOG06962		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06963	COG0477	G	permease of the major facilitator superfamily	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06964		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06965		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06966	COG3609	K	Predicted transcriptional regulators containing the C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06967		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06968		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06969		S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06970		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06971		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06972		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06973	COG1960	I	Acyl-CoA dehydrogenase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06974		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06975		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06976	COG3508	Q	Homogentisate 1,2-dioxygenase	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG06977		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG06978		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG06979		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06980		S	vWFA domain containing protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06981		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06982		R	ABC-type ATPase	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06983		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06984	COG1121	P	ABC-type Mn/Zn transport system, ATPase compon	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06985		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06986		S	Uncharacterized conserved protein	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06987		K	CopG-family DNA-binding protein	0	0	1	0	1	0	0	1	0	0	0	0	0	0	2	0	0
arCOG06988		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06989		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06990	COG4113	V	PIN domain containing protein	1	0	2	0	1	0	0	0	0	0	0	0	0	1	0	0	0
arCOG06991		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06992		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06993		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06994		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06995		S	Predicted ATPase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06996		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06997	COG3809	S	Uncharacterized protein conserved in bacteria	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06998	COG1405	K	Transcription initiation factor TFIIIB, Brf1 subunit/T	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG06999		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07000		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07001		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07002		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07004	COG0425	O	Predicted redox protein, SirA family	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07005		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07006		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07007		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07008		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07009	COG1167	K	Transcriptional regulators containing a DNA-bindin	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07010		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07011	COG3600	S	Uncharacterized phage-associated protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07012		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07013		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07014		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07015		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07016		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07017		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07018	COG2847	P	Copper(I)-binding protein	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07019		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07020		S	Uncharacterized conserved protein	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07021		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG07022	COG0723	C	Rieske Fe-S protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07023		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07024		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07025		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07026	COG3842	E	ABC-type spermidine/putrescine transport system, A	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07027		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07028		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07029		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07030		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07031		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07032		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07033		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07034		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07035		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07036		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07037		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07038		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07039		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07040		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07041		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07042		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07043		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07044		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07045		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07046		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07047		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07048		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07049		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07050		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07051		S	Uncharacterized conserved protein, contains YVTN-	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07052		S	Uncharacterized conserved protein	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07053		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07054	COG3193	R	Uncharacterized protein, possibly involved in utiliza	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07055	COG3546	P	Mn-containing catalase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07056		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07057		S	Uncharacterized conserved protein	0	0	2	0	1	0	0	0	0	0	0	0	1	0	0	0	0
arCOG07058		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07059		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07060		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07061		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07062		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07063		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07064		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07065		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07066		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07067		C	Cytochrome cd1 nitrite reductase, heme region	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07068		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07069		S	Uncharacterized conserved protein	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07070		S	Uncharacterized conserved protein	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07071		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07072		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07073		S	Uncharacterized conserved protein	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07074		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07075		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07076		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07077		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07078		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07079		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07080		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07081		S	Uncharacterized conserved protein	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0
arCOG07082		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07083		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG07084		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07085		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07086		S	Cell suface protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07087		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07088		S	Uncharacterized conserved protein	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07089		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07090		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0

arCOG07091		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07092		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07093		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07094		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07095		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07096		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07097		S	Uncharacterized conserved protein	0	1	0	0	0	1	0	0	0	0	0	1	0	2	0	0
arCOG07098		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07099		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07100		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
arCOG07101		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07102		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07103		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07104		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07105		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07106		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07107		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07108		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07109		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07110	COG5617	S	Predicted integral membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0
arCOG07111		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07112		S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07113		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07114		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07115		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07116		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07117		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07118		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07119		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07120		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07121		S	Uncharacterized conserved protein	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0
arCOG07122		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07123		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07124		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07125	COG0675	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0
arCOG07126		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07127		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07128		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07129		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07130		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07131	COG1131	V	ABC-type multidrug transport system, ATPase comp	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG07132		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG07133		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07134		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07135		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07136		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07137		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07138		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07139	COG2819	R	Predicted hydrolase of the alpha/beta superfamily	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07140	COG1715	V	Restriction endonuclease	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07141		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	1	0	0	2	0	0
arCOG07142	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
arCOG07143		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07144	COG1800	R	Predicted transglutaminase-like protease	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07145		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07146		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07147	COG1657	I	Squalene cyclase	0	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0
arCOG07148		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07149		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07150		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07151		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07152	COG2880	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0
arCOG07154		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07155	COG1211	I	4-diphosphocytidyl-2-methyl-D-erithritol synthase	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07156		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG07157		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07158	COG1554	G	Sugar hydrolase/phosphorylase	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG07159	COG0637	R	Phosphatase/phosphohexomutase HAD superfamily	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG07160		E	AroM protein	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG07161		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07162		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0
arCOG07163		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07164		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	1	0	0	0	2	0	0
arCOG07165		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07166		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07167		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07168		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07169		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07170		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	1	0	0	2	0	0
arCOG07171	COG1131	V	ABC-type multidrug transport system, ATPase comp	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07172		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG07173		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07174		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07175		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07176		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07177		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07178		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07179		S	Uncharacterized conserved protein	0	2	0	0	1	0	0	0	0	0	0	0	0	0	1	0
arCOG07180		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07181	COG3889	R	Predicted solute binding protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07182		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07183	COG2244	R	Polysaccharide biosynthesis protein, Mvin family	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07184		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07185		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07186		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07187		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07188		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07189		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07190		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07191		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07192		S	Uncharacterized conserved protein	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07193		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07194		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07195		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07196		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07197		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07198		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07199		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07200		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07201		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07202		R	Predicted membrane-bound metal-dependent hydrol	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07203	COG0801	H	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokir	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07204	COG2267	I	Lysophospholipase, alpha-beta hydrolase superfamil	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07205		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07206		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07207		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07208		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07209		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07210		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07211		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07212		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07213		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07214		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07215		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07216		S	Uncharacterized conserved protein	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07217		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07218		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07219		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0

arCOG07220		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07221		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07222		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07223		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07224		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07225		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07226		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07227		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07228		P	Heavy-metal-associated domain	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07229		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07230		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07231		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07232		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07233	COG3327	K	Phenylacetic acid-responsive transcriptional repressc	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07234		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07235		S	Uncharacterized conserved protein	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07236	COG0477	G	permease of the major facilitator superfamily	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07237		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07238		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07239		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07240	COG0463	M	Glycosyltransferase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07242		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07243		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07244		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07245		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07246		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07247		S	Uncharacterized conserved protein	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07248		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07249		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07250		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07251		S	Predicted transcriptional regulator	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07252		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07253		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07254	COG5607	S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07255		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07256		S	Uncharacterized conserved protein	0	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07257		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07258		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07259		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07260	COG3191	E	L-aminopeptidase/D-esterase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07262		S	Uncharacterized conserved protein	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07263	COG1735	R	Predicted metal-dependent hydrolase with the TIM-l	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07264		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07265		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07266		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07267	COG3733	Q	Cu2+-containing amine oxidase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07268		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07269		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07270		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07271		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07272		S	Uncharacterized conserved membrane protein	2	3	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
arCOG07273		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07274		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07275		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07276		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07277		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07278		S	Uncharacterized conserved membrane protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07279		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07280		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07281	COG0457	R	TPR repeats containing protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07282		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07283		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07284		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07285		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07286		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07287		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07288		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07289		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07290		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07291		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07292	COG1708	R	Predicted nucleotidyltransferase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07293	COG1192	D	ATPase involved in chromosome partitioning, ParA	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07294	COG2308	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07295	COG2307	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07296		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07297		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07298		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07299		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07300		S	Uncharacterized conserved protein	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07301		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07302	COG1367	V	CRISPR system related protein, RAMP superfamily	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07303	COG0675	L	Transposase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07304		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07305		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07306	COG0675	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07307		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07308		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07309		S	Plasmid regulatory DNA-binding protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07310		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07311		K	Predicted transcriptional regulator, HTH domain	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07312		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07313		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07314		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07315		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07316		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07317		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07318		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07319		S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07320	COG0247	C	Fe-S oxidoreductase	0	3	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07321		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07322		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07323		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07324		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07325		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07326		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07327		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07328		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07329		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07330		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07331		S	Uncharacterized conserved protein	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07332		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07333		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07334		S	Uncharacterized conserved protein	0	2	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG07335	COG0500	Q	SAM-dependent methyltransferase	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07336		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07337	COG3250	G	Beta-galactosidase/beta-glucuronidase	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07338	COG3669	G	Alpha-L-fucosidase	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07339		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07340		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07341		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07342		S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07343		S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07344		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07345	COG0501	O	Zn-dependent protease with chaperone function	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07346		S	Uncharacterized conserved protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07347		S	Uncharacterized conserved protein	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07348		S	Uncharacterized conserved protein	0	1	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07349	COG1670	J	Acetyltransferase, RimL family	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

arCOG07350	R	Predicted ATP/GTPase	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
arCOG07351	S	Uncharacterized conserved membrane protein	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0
arCOG07353	S	Zn-ribbon protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07354	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07355	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07356	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07357 COG2353	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07358 COG0477	G	permease of the major facilitator superfamily	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07359	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07360	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07361	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07362	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07363 COG0477	G	permease of the major facilitator superfamily	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07364	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07365 COG1605	E	Chorismate mutase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07366	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07367	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07368	S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07369	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07370 COG0457	R	TPR repeats containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07371	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07372	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07373	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07374	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07375	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07376	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07377 COG0515	R	Serine/threonine protein kinase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07378	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07379 COG1240	H	Von Willebrand factor type A (vWA) domain	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07380 COG3430	S	Uncharacterized protein conserved in archaea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07381	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07382	S	Predicted ATPase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07383	S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07384 COG0241	E	Histidinol phosphatase or related phosphatase	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0
arCOG07385	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07386	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07387	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07388	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07389 COG1921	E	Selenocysteine synthase [seryl-tRNASer selenium tr	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
arCOG07390 COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07391 COG3254	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07392	S	Restriction-modification system component, N-6 DN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07393	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07394	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07395	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07396	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07397	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07398	S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07399	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07400	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07401	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07402	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07403	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07404	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07405	S	AbrB-like transcriptional regulator	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07406	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07407 COG1024	I	Enoyl-CoA hydratase/carnithine racemase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07408	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07409 COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07410	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07411	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07412	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07413	S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG07414 COG0318	I	Acyl-CoA synthetase (AMP-forming)/AMP-acid lig	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07415	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07416 COG0596	R	Alpha/beta superfamily hydrolase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07417	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07418 COG2512	K	Predicted membrane-associated trancriptional regula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07420	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07421	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07422	S	Uncharacterized conserved protein	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07423	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07424 COG0635	H	Coproporphyrinogen III oxidase or related Fe-S oxic	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07425	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
arCOG07426	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07427	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07428	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07429	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07430	S	Uncharacterized membrane protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07431	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07432	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07433	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07434	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07435	R	HAD superfamily phosphatase	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07436	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07437	R	Transposase related protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07438	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07439	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07440	S	Uncharacterized conserved protein	0	0	1	2	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07441 COG0760	O	Parvulin-like peptidyl-prolyl isomerase	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG07442	S	Uncharacterized conserved protein	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07443 COG0642	T	Signal transduction histidine kinase (ATPase domair	0	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG07444 COG0192	H	S-adenosylmethionine synthetase	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0
arCOG07445 COG0232	F	dGTP triphosphohydrolase	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07446	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07447	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07448 COG1719	R	Predicted hydrocarbon binding protein, contains V4l	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07449	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07450	M	O-Glycosyl hydrolase family 16	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07451 COG4821	R	Uncharacterized protein containing SIS (Sugar ISon	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07452 COG3525	G	N-acetyl-beta-hexosaminidase	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07453	S	Uncharacterized conserved protein	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07454	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07455	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07456	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07457	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07458	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07459	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07460	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07461	S	Uncharacterized conserved protein	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07462	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07463	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07464	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07465	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07466 COG1266	R	Predicted metal-dependent membrane protease	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07467	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07468	K	Predicted transcriptional regulator of MerR family	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07469	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07470	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07471	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07472	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07473	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07474	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07475 COG2856	E	Predicted Zn peptidase fused to xre like transcriptio	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07476 COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
arCOG07477	S	Uncharacterized conserved membrane protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07478	S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07479	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0

arCOG07480		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07481		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07482		S	Uncharacterized conserved protein	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07483		S	Uncharacterized conserved protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07484		S	Predicted solute binding protein	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07485		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07486	COG4721	P	ABC-type cobalt transport system, predicted permea	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07487	COG4708	S	Predicted membrane protein	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07488		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07489		S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07490	COG3281	G	Uncharacterized protein, probably involved in trehal	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG07491		S	Uncharacterized conserved protein	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07492		S	Uncharacterized conserved protein	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07493		S	Uncharacterized conserved protein	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07494		L	DEAD-box helicase, probable R-M system subunit	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0
arCOG07495	COG1497	K	Predicted transcriptional regulator	0	0	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0
arCOG07496	COG3451	U	Type IV secretory pathway, VirB4 component	0	1	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG07497		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG07498		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
arCOG07499		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG07500	COG0191	G	Fructose/tagatose bisphosphate aldolase	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0
arCOG07501	COG1994	R	Zn-dependent protease	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
arCOG07502		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0
arCOG07503	COG2843	M	Putative enzyme of poly-gamma-glutamate biosynth	0	0	0	0	0	0	0	1	1	0	1	0	2	0	0	0	0
arCOG07504		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG07505	COG0450	O	AhpC/TSA family peroxiredoxin	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0
arCOG07506		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	2	0	0	0	0
arCOG07507		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
arCOG07508		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
arCOG07509		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0
arCOG07510		S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07511	COG0500	Q	SAM-dependent methyltransferase, fragment?	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07512	COG4742	K	Predicted transcriptional regulator	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07513	COG0501	O	Zn-dependent protease with chaperone function	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07514		S	Uncharacterized conserved protein	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
arCOG07515		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07516		S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07517		S	Uncharacterized conserved protein	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07518	COG0526	O	Thiol-disulfide isomerase or thioredoxin	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07519	COG2457	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07520	COG2442	S	Uncharacterized conserved protein	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
arCOG07521		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG07522	COG0640	K	Transcriptional regulator containing HTH domain, A	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG07523		S	Uncharacterized conserved protein	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG07524		C	Membrane-bound tetraheme cytochrome c subunit	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG07525		S	Uncharacterized conserved protein	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG07526	COG1715	V	Restriction endonuclease	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG07527		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG07528		V	CRISPR-associated protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG07530		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
arCOG07531		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
arCOG07532		S	Uncharacterized conserved protein	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0
arCOG07533		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG07534		S	Halomucin	0	0	0	0	0	0	1	1	0	1	0	0	0	1	0	0	0
arCOG07535		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0
arCOG07536		S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
arCOG07538		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07539		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07540		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07541		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07542		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG07543	COG3505	L	TraG/TraD/VirD4 family enzyme, ATPase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07544		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07545		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07546		S	Uncharacterized conserved protein	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0
arCOG07547		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07548		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07549		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07550		R	Alpha/beta superfamily hydrolase	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG07551		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07552		S	DnaJ-type Zn-ribbon	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07553		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07554		S	Cell suface protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG07555		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07556		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07557		S	Uncharacterized conserved protein	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG07558		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07560		S	Cell suface protein	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0
arCOG07561		R	Predicted regulatory protein containing HTH domai	0	0	0	2	0	0	0	3	0	0	1	0	1	0	1	0	0
arCOG07562		I	Terpene cyclase related protein	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
arCOG07563		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07564		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG07565		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07566		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07567		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07568		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07569		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG07570	COG0569	P	K+ transport systems, NAD-binding component	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
arCOG07571		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0
arCOG07572		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
arCOG07573		S	Uncharacterized conserved protein	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG07574		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07575		S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07576		S	Transposase related protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07577		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07578		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07579	COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG07580		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07581	COG3325	G	Chitinase	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0
arCOG07582		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07583		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07584		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07585		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07586		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07587		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07588		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
arCOG07589		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
arCOG07590	COG2936	R	Predicted acyl esterase	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
arCOG07591	COG1240	H	Von Willebrand factor type A (vWA) domain	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
arCOG07592		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	0	0	2	0	1	0	0
arCOG07593		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07596		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07597		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07598	COG4357	S	Zinc finger domain containing protein (CHY type)	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07599		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07600	COG1413	S	HEAT repeats containing protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07601		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07602		T	Histidine kinase-like ATPase	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07603		S	Uncharacterized conserved protein	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07604		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07605	COG0642	T	Signal transduction histidine kinase, contains REC d	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0
arCOG07606		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0
arCOG07607		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
arCOG07608		S	Bacterial membrane flanked domain related protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07609		S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
arCOG07610	COG3764	M	Sortase (surface protein transpeptidase)	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG07611		S	Cell surface protein, contains DUF11 domains	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0
arCOG07612	COG0526	O	Thiol-disulfide isomerase or thioredoxin	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0

arCOG07613	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07614 COG0121	R	Predicted glutamine amidotransferase	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2	0	0
arCOG07615 COG0707	M	UDP-N-acetylglucosamine:LPS N-acetylglucosamir	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07616 COG2450	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07617	C	Multiheme cytochrome	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG07618	V	PIN domain containing protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
arCOG07619 COG0642	T	Signal transduction histidine kinase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07622	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07623	E	Predicted peptidase family C39	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07624	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
arCOG07625 COG4185	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0
arCOG07626	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
arCOG07627	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
arCOG07628	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0
arCOG07629	R	DEAD-box helicase	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07630	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07631	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
arCOG07632	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07633	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07634	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07635	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07636 COG1592	C	Rubrerythrin	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07637	S	NosD related cell surface protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07638	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07640	S	beta/gama crystallin family protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07641 COG1517	V	CRISPR-associated protein	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0
arCOG07642	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07643	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07644	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG07645	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07646	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07647	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
arCOG07648	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07649	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07650	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07651 COG0210	L	DNA helicase, fragment?	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07652 COG5519	L	Superfamily II helicase or inactivated derivatives	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07653	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
arCOG07654 COG5337	M	Spore coat assembly protein	0	0	0	0	0	0	0	0	0	3	0	1	0	0	0	0	0
arCOG07655	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07656	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07657	S	Zn-finger protein	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07658	R	Transglutaminase family protease	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG07660	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07661 COG3594	G	Fucose 4-O-acetylase or related acetyltransferase	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07662	R	Transposase related protein	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0
arCOG07663 COG3385	L	Transposase	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07664	R	Transposase related protein	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0
arCOG07665	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
arCOG07666	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07667	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07668	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07669	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07670	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07671	R	Transposase related protein	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG07672	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
arCOG07673	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07674 COG4097	P	Predicted ferric reductase	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
arCOG07675 COG0326	O	Molecular chaperone, HSP90 family	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0
arCOG07676	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG07677	R	Catecholamine-binding domain (DOMON) containi	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0
arCOG07678	S	Uncharacterized conserved protein	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0
arCOG07679 COG3580	S	HSP70-class ATPase fused to uncharacterized protei	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG07680 COG2832	S	Uncharacterized protein conserved in bacteria	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
arCOG07681	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG07682	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
arCOG07683 COG1637	L	Predicted nuclease of the RecB family	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
arCOG07684 COG0463	M	Glycosyltransferase	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG07685	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG07686	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07687 COG1517	V	CRISPR system related protein	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07688	S	Uncharacterized conserved membrane protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07689	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07690	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07691	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07692	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07693	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07694	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07695	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07696	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07697	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07698	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07699	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
arCOG07700 COG2730	G	Endoglucanase	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07701	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07702 COG0438	M	Glycosyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07703	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07704 COG1848	V	PIN domain containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07705	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07706	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07707	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07708	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07709	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07710	S	Cell suface protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07711	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG07712	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
arCOG07713	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07714	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07715	S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07716	S	SWIM Zn-finger	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07717	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07718	S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07719 COG0535	R	Radical SAM superfamily enzyme	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07720	S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07721	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07722	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07723	S	Uncharacterized conserved protein	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07724	S	Uncharacterized conserved protein	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07725	S	Uncharacterized conserved protein	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07726	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07727	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07728 COG1879	G	ABC-type sugar transport system, periplasmic comp	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07729	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG07730 COG0417	L	DNA polymerase elongation subunit (family B), mic	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07731	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07732 COG5558	L	Transposase	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG07733	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07734	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07735	S	Uncharacterized conserved protein	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07736	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07737	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07738	R	Transposase related protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07739	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07740	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07741 COG2427	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07742	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07743	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
arCOG07744	S	HPP family membrane protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0

arCOG07745	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07746	S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07747	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07748	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07749	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
arCOG07750	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07751	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07752	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07753	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07754	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07755	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07756	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07757	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07758	S	Uncharacterized conserved protein	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07759 COG1487	V	PIN domain containing protein	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
arCOG07760	S	Uncharacterized conserved protein	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07761	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0
arCOG07762 COG5558	L	Transposase	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
arCOG07763	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
arCOG07764 COG1318	K	Predicted transcriptional regulator	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
arCOG07765	S	Uncharacterized conserved protein	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
arCOG07766	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07767	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07768	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
arCOG07769	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07770	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07771	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07772	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07773	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07774	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07775 COG4638	P	Phenylpropionate dioxygenase or related ring-hydro	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
arCOG07776	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07777	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07778	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07779	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG07780	R	HNH/McrA nuclease domain containing protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07781	S	Cell suface protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07782	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07783 COG0846	R	SIR2 family protein	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
arCOG07784	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07785 COG3654	R	Prophage maintenance system killer protein	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07786	R	Predicted ATPase	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
arCOG07787 COG3440	V	Predicted restriction endonuclease	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
arCOG07788	S	Uncharacterized conserved protein, DUF115	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
arCOG07789 COG5659	L	FOG: Transposase	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
arCOG07790	R	D-glucuronyl C5-epimerase C-terminal domain relat	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0
arCOG07791 COG1807	M	4-amino-4-deoxy-L-arabinose transferase related pr	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07792 COG1991	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07793	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
arCOG07794 COG1401	V	GTPase subunit of restriction endonuclease	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
arCOG07795	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
arCOG07796	L	deoxyribonuclease I	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07797	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07799 COG4641	S	Uncharacterized protein conserved in bacteria	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07800	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
arCOG07801	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
arCOG07802	R	Predicted flavin-nucleotide-binding protein	0	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0
arCOG07803 COG1708	R	Predicted nucleotidyltransferase	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
arCOG07804	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07805 COG3049	M	Penicillin V acylase or related amidase	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
arCOG07806 COG1277	R	ABC-type transport system involved in multi-copper	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
arCOG07807	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
arCOG07808	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07809 COG4983	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
arCOG07810 COG2114	T	Adenylate cyclase, family 3	0	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0
arCOG07811 COG0210	L	DNA helicase, fragment?	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07813	G	Glycosyl hydrolases family 43	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	1	0
arCOG07814	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
arCOG07815	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07816	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07817	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07818 COG0454	K	Acetyltransferase (GNAT) family	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07819	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07820 COG1742	S	Uncharacterized conserved protein	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07821	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07822 COG2273	G	Beta-glucanase/Beta-glucan synthetase	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07823	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
arCOG07824	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0
arCOG07825 COG0500	Q	SAM-dependent methyltransferase	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
arCOG07826 COG1216	R	Predicted glycosyltransferase fused to methyltransfe	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0
arCOG07827 COG1479	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	1	1	0	1	0	1	0	0	0
arCOG07828	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
arCOG07829	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
arCOG07830	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
arCOG07831	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07832	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07833 COG5551	V	CRISPR system related protein, RAMP superfamily	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07834	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07835	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07836	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07837	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07838	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07839	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07840 COG3325	G	Glycosyl hydrolases family 18, contains cellulose bi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07841	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07842	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07843	S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
arCOG07844	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07845	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07846 COG1604	V	CRISPR system related protein, RAMP superfamily	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07847	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07848	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07849	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07850	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
arCOG07851	S	Uncharacterized conserved protein	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07852	R	Predicted regulatory ATPase	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07853	S	Uncharacterized conserved protein	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07854	S	Uncharacterized conserved protein	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07855 COG1409	R	Predicted phosphohydrolase	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0
arCOG07856	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07857	S	Uncharacterized conserved protein	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07858 COG2244	R	Polysaccharide biosynthesis protein, Mvin family	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07859 COG1708	R	Predicted nucleotidyltransferase	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07860	T	Signal transduction histidine kinase contains GAF d	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG07861	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
arCOG07862	S	Uncharacterized conserved protein	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
arCOG07863	S	Uncharacterized conserved protein	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07864	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07865	S	Uncharacterized conserved protein	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07866 COG1192	D	Chromosome partitioning ATPase, ParA family	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG07867	S	Uncharacterized conserved protein	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG07868 COG0346	E	Lactoylglutathione lyase or related enzyme	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
arCOG07870	R	Uncharacterized conserved domain associated with t	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0
arCOG07871	K	Helicase associated unchracterized N-terminal doma	0	0	0	2	0	0	0	1	0	0	0	0	1	0	0	0	0	0
arCOG07873	S	Uncharacterized conserved membrane protein	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
arCOG07874 COG1124	E	ABC-type dipeptide/oligopeptide/nickel transport sy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
arCOG07875 COG0679	R	Predicted permease	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
arCOG07877	H	UbiA prenyltransferase family enzyme	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0

Dostribution of arCOG in hyperthermophilic *Crenarchaeota*, *Euryarchaeota*, *Nanoarchaeota* and *C.symbiosum* in *Nitrosopulilales* was refered from Makarova et al. (2007), of *Korarchaeota* was from Elkins et al. (2008), and of *Nitrosopumilus maritimus* in *Nitrosopumilales* and *C. subterraneus* were tetntatively assigned in this study.