Table 8. *M. smithii* proteins with homologs in other sequenced Methanobacteriales

M. smithii	***Methanosphaera stadtmanae***			***Methanothermobacter thermoautotrophicus***		
ORF	**ORF**	**ANNOTATION**	**E-value**	**ORF**	**ANNOTATION**	**E-value**
MSM0001	Msp_0220	predicted glycosyltransferase	4.2E-08	NONE		
MSM0002	Msp_1355	predicted site-specific recombinase/integrase	2.0E-08	MTH_893	integrase-recombinase protein	8.1E-16
MSM0003	Msp_0548	hypothetical membrane-spanning protein	6.8E-09	NONE		
MSM0004	Msp_0803	conserved hypothetical protein	2.3E-24	NONE		
MSM0005	Msp_0783	hypothetical membrane-spanning protein	3.7E-05	MTH_1439	unknown	6.2E-04
MSM0006	Msp_0725	hypothetical protein	1.3E-05	MTH_1277	unknown	3.3E-05
MSM0007	NONE			MTH_675	unknown	1.1E-34
MSM0008	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM0009	NONE			MTH_675	unknown	8.1E-34
MSM0010	Msp_0813	conserved hypothetical protein	1.5E-36	MTH_676	unknown	1.7E-40
MSM0011	NONE			NONE		
MSM0012	Msp_0317	hypothetical protein	3.3E-04	NONE		
MSM0013	NONE			NONE		
MSM0014	NONE			MTH_1289	heat shock protein GrpE	2.6E-04
MSM0015	NONE			NONE		
MSM0016	NONE			NONE		
MSM0017	NONE			NONE		
MSM0018	NONE			NONE		
MSM0019	NONE			NONE		
MSM0020	Msp_1323	conserved hypothetical protein	1.4E-05	MTH_83	O-linked GlcNAc transferase	3.3E-07
MSM0021	Msp_0047	predicted short chain dehydrogenase	3.7E-40	NONE		
MSM0022	NONE			NONE		
MSM0023	Msp_0424	conserved hypothetical protein	1.6E-25	MTH_1084	conserved protein	4.4E-18
MSM0024	NONE			NONE		
MSM0025	Msp_0447	predicted acyl-CoA synthetase	3.7E-49	MTH_657	long-chain-fatty-acid-CoA ligase	8.7E-227
MSM0026	Msp_0265	conserved hypothetical protein	2.0E-16	MTH_659	epoxidase	4.1E-62
MSM0027	Msp_0667	putative glutamate synthase, subunit 2 with ferredoxin domain	7.9E-70	NONE	glutamate synthase (NADPH), alpha subunit	4.6E-79
MSM0028	Msp_0602	conserved hypothetical protein	1.9E-13	MTH_1876	conserved protein	1.7E-04
MSM0029	NONE			NONE		
MSM0030	Msp_0741	conserved hypothetical membrane-spanning protein	1.8E-72	MTH_1812	conserved protein	1.6E-44
MSM0031	Msp_1465	member of asn/thr-rich large protein family	2.9E-23	MTH_716	cell surface glycoprotein (s-layer protein)	3.7E-04
MSM0032	NONE			NONE		
MSM0033	Msp_0966	putative 2-dehydropantoate 2-reductase	6.8E-112	NONE		
MSM0034	Msp_0725	hypothetical protein	7.9E-06	NONE		
MSM0035	NONE			NONE		
MSM0036	NONE			NONE		
MSM0037	NONE			NONE		
MSM0038	NONE			NONE		
MSM0039	NONE			NONE		
MSM0040	Msp_1274	conserved hypothetical protein	5.5E-05	NONE		
MSM0041	NONE			NONE		
MSM0042	NONE			NONE		
MSM0043	Msp_0737	putative peptide methionine sulfoxide reductase MsrA/MsrB	1.6E-32	MTH_535	peptide methionine sulfoxide reductase	5.3E-16
MSM0044	Msp_0510	putative aspartate aminotransferase	2.0E-15	MTH_1894	aspartate aminotransferase homolog	3.9E-13

MSM0045	Msp_0283	predicted ATPase	3.9E-93	MTH_1176	nucleotide-binding protein (putative ATPase)	1.4E-70
MSM0046	Msp_1460	predicted NAD(FAD)-dependent dehydrogenase	8.4E-114	MTH_1354	NADH oxidase	2.0E-149
MSM0047	NONE			NONE		
MSM0048	Msp_0701	hypothetical protein	4.0E-20	NONE		
MSM0049	Msp_0665	F420H2:NADP oxidoreductase	3.1E-75	MTH_248	conserved protein	9.4E-56
MSM0050	Msp_1172	conserved hypothetical protein	1.7E-21	NONE		
MSM0051	Msp_1399	member of asn/thr-rich large protein family	4.0E-33	MTH_716	cell surface glycoprotein (s-layer protein)	3.9E-11
MSM0052	Msp_0145	member of asn/thr-rich large protein family	1.4E-53	MTH_716	cell surface glycoprotein (s-layer protein)	1.8E-11
MSM0053	Msp_0086	putative tRNA nucleotidyltransferase	5.0E-100	MTH_584	tRNA nucleotidyltransferase	2.5E-110
MSM0054	Msp_0089	predicted 2'-5' RNA ligase	7.2E-37	MTH_583	conserved protein	9.1E-42
MSM0055	Msp_0090	predicted 3-dehydroquinate synthase	3.5E-108	MTH_580	conserved protein	3.3E-124
MSM0056	Msp_0091	predicted fructose-bisphosphate aldolase	1.5E-100	MTH_579	conserved protein	2.9E-100
MSM0057	Msp_0762	member of asn/thr-rich large protein family	1.7E-13	MTH_716	cell surface glycoprotein (s-layer protein)	8.2E-07
MSM0058	Msp_0128	predicted helicase	8.6E-23	MTH_472	DNA helicase II	1.2E-90
MSM0059	Msp_0092	conserved hypothetical protein	9.4E-35	MTH_578	unknown	2.1E-49
MSM0060	Msp_1187	predicted archaeal kinase	8.2E-52	MTH_577	conserved protein	2.1E-49
MSM0061	Msp_0757	predicted ATPase	7.5E-97	NONE		
MSM0062	Msp_0554	hypothetical protein	2.2E-08	MTH_847	unknown	6.9E-08
MSM0063	Msp_1186	predicted hydrolase	1.3E-67	MTH_576	conserved protein	7.0E-51
MSM0064	Msp_0099	conserved hypothetical protein	4.6E-10	MTH_812	conserved protein	1.5E-09
MSM0065	Msp_1185	putative 5-amino-6-(5-phosphoribosylamino)uracil reductase	2.6E-55	MTH_235	riboflavin-specific deaminase	1.5E-66
MSM0066	Msp_0080	predicted glycosyltransferase	8.2E-107	MTH_590	N-acetylglucosamine-1-phosphate transferase	7.9E-107
MSM0067	NONE			NONE		
MSM0068	Msp_0407	conserved hypothetical protein	6.0E-04	MTH_521	unknown	8.4E-04
MSM0069	Msp_0081	conserved hypothetical protein	2.8E-26	MTH_589	conserved protein	3.1E-25
MSM0070	Msp_0082	conserved hypothetical protein	2.8E-99	MTH_588	conserved protein	4.8E-100
MSM0071	Msp_0083	MetG	5.3E-199	MTH_587	methionyl-tRNA synthetase	2.9E-235
MSM0072	Msp_0216	hypothetical membrane-spanning protein	2.2E-04	NONE		
MSM0073	Msp_0084	DNA primase, large subunit	1.4E-102	MTH_586	unknown	1.7E-118
MSM0074	NONE			NONE		
MSM0075	Msp_0085	DNA primase, small subunit	1.2E-96	NONE	DNA primase, small subunit	8.1E-105
MSM0076	Msp_0710	hypothetical protein	9.9E-04	NONE		
MSM0077	Msp_0357	putative thymidylate kinase	6.9E-16	MTH_1100	conserved protein	4.6E-47
MSM0078	NONE			MTH_1099	conserved protein	3.9E-50
MSM0079	Msp_0392	CofH	7.6E-81	MTH_820	conserved protein	1.0E-106
MSM0080	Msp_0278	ComD	1.0E-53	MTH_1206	phosphonopyruvate decarboxylase related protein	1.7E-47
MSM0081	Msp_0277	ComE	9.4E-51	MTH_1207	phosphonopyruvate decarboxylase related protein	1.7E-40
MSM0082	Msp_0127	HdrA2	1.3E-241	NONE	heterodisulfide reductase, subunit A	2.5E-133
MSM0083	Msp_0126	HdrB2	2.6E-94	NONE	heterodisulfide reductase, subunit B	8.6E-46
MSM0084	Msp_0125	HdrC2	2.6E-48	NONE	heterodisulfide reductase, subunit C	3.5E-17
MSM0085	Msp_1261	conserved hypothetical protein	6.6E-114	MTH_1684	conserved protein (contains ferredoxin domain)	2.1E-115
MSM0086	Msp_1270	ComA	5.2E-73	MTH_1674	conserved protein	3.5E-81
MSM0087	Msp_0233	conserved hypothetical protein	2.3E-22	NONE		
MSM0088	Msp_1322	conserved hypothetical protein	7.3E-44	MTH_727	conserved protein	1.6E-51
MSM0089	Msp_1314	ProC	8.2E-07	NONE		
MSM0090	NONE			MTH_224	conserved protein	8.6E-30
MSM0091	Msp_0129	putative 2,3-diphosphoglycerate synthase	8.6E-144	MTH_223	unknown	2.0E-172
MSM0092	Msp_0154	member of asn/thr-rich large protein family	5.6E-08	NONE		
MSM0093	Msp_1068	partially conserved hypothetical membrane-spanning protein	1.1E-58	MTH_1858	phage infection protein homolog	5.7E-98

MSM0094	Msp_0971	hypothetical protein	4.4E-09	MTH_1787	conserved protein	9.3E-17
MSM0095	Msp_1181	predicted phosphotransacetylase	1.3E-44	MTH_231	conserved protein	8.8E-44
MSM0096	Msp_1182	UppS	2.6E-96	MTH_232	conserved protein	2.3E-100
MSM0097	Msp_1183	predicted DNase	3.2E-57	MTH_233	conserved protein	3.4E-67
MSM0098	NONE			NONE		
MSM0099	Msp_0079	hypothetical membrane-spanning protein	2.1E-23	MTH_596	unknown	8.2E-25
MSM0100	Msp_0078	hypothetical membrane-spanning protein	7.3E-12	MTH_429	unknown	1.1E-13
MSM0101	Msp_0988	CbiF	9.8E-88	MTH_602	precorrin-3 methylase	1.5E-80
MSM0102	Msp_1236	MetE	3.4E-69	MTH_775	cobalamin-independent methionine synthase	3.8E-75
MSM0103	NONE			MTH_776	conserved protein	7.3E-33
MSM0104	NONE			MTH_777	conserved protein	2.7E-42
MSM0105	Msp_1234	conserved hypothetical membrane-spanning protein	3.8E-86	MTH_778	unknown	5.9E-118
MSM0106	Msp_1232	conserved hypothetical protein	1.8E-109	MTH_781	conserved protein	2.3E-132
MSM0107	Msp_1231	HypB	1.4E-79	MTH_782	hydrogenase expression/formation protein HypB	1.1E-84
MSM0108	Msp_1230	HypA	5.8E-35	MTH_783	hydrogenase expression/formation protein HypA	4.8E-36
MSM0109	Msp_0987	hypothetical membrane-spanning protein	8.6E-09	NONE		
MSM0110	Msp_0017	conserved hypothetical protein	1.5E-22	NONE		
MSM0111	NONE			NONE		
MSM0112	Msp_0367	predicted helicase	1.2E-208	NONE	ATP-dependent RNA helicase, eIF-4A family	1.4E-235
MSM0113	Msp_0128	predicted helicase	9.9E-137	MTH_472	DNA helicase II	6.1E-26
MSM0114	NONE			NONE		
MSM0115	Msp_1290	conserved hypothetical protein	8.0E-29	MTH_526	conserved protein	2.1E-51
MSM0116	Msp_1289	conserved hypothetical protein	3.5E-51	MTH_528	unknown	9.1E-42
MSM0117	Msp_1288	conserved hypothetical membrane-spanning protein	4.7E-56	MTH_529	unknown	1.5E-66
MSM0118	Msp_1286	conserved hypothetical protein	1.1E-86	MTH_532	UDP-N-acetylmuramyl tripeptide synthetase related protein	2.9E-86
MSM0119	Msp_0156	predicted nuclease	3.2E-18	MTH_538	unknown	2.5E-14
MSM0120	Msp_1095	DNA double-strand break repair protein Rad50	1.3E-92	MTH_540	intracellular protein transport protein	2.1E-27
MSM0121	Msp_1094	DNA double-strand break repair protein Mre11	3.7E-72	MTH_541	Rad32 related protein	1.2E-16
MSM0122	Msp_1093	predicted ATPase	1.7E-122	MTH_307	conserved protein	4.2E-124
MSM0123	Msp_1092	conserved hypothetical protein	2.4E-29	MTH_306	conserved protein	1.2E-32
MSM0124	Msp_1291	PcrB	5.1E-75	MTH_552	conserved protein	2.9E-84
MSM0125	Msp_1292	50S ribosomal protein L40e	5.5E-23	MTH_553	ribosomal protein L40	7.6E-22
MSM0126	Msp_1293	conserved hypothetical protein	9.4E-51	MTH_554	conserved protein	2.9E-54
MSM0127	NONE			NONE		
MSM0128	Msp_0853	conserved hypothetical membrane-spanning protein	2.3E-10	MTH_570	unknown	2.8E-31
MSM0129	Msp_0435	nicotinamide-nucleotide adenylyltransferase	8.1E-61	MTH_150	conserved protein	6.7E-62
MSM0130	NONE			MTH_149	molybdenum cofactor biosynthesis protein MoaE	6.6E-39
MSM0131	NONE			MTH_920	anion permease	1.5E-04
MSM0132	NONE			MTH_1797	conserved protein	7.9E-20
MSM0133	Msp_1198	predicted thioesterase	2.2E-42	MTH_658	unknown	4.8E-36
MSM0134	Msp_0565	predicted M42 glutamyl aminopeptidase	2.2E-115	NONE	endo-1,4-beta-glucanase	3.7E-116
MSM0135	Msp_0668	conserved hypothetical protein	9.1E-85	NONE	coenzyme F420-reducing hydrogenase, beta subunit homolog	4.5E-88
MSM0136	Msp_0147	ferredoxin	2.2E-06	NONE	tungsten formylmethanofuran dehydrogenase, subunit G	2.2E-06
MSM0137	Msp_0220	predicted glycosyltransferase	3.7E-12	MTH_540	intracellular protein transport protein	4.7E-05
MSM0138	NONE			MTH_491	conserved protein	2.6E-51
MSM0139	Msp_0448	predicted polysaccharide biosynthesis protein	7.6E-04	NONE		
MSM0140	Msp_0560	conserved hypothetical protein	4.0E-59	MTH_435	conserved protein	2.9E-68
MSM0141	Msp_0561	predicted dephospho-CoA kinase	5.5E-23	MTH_434	UMP/CMP kinase related protein	5.6E-42
MSM0142	Msp_0563	predicted ATPase of PP-loop superfamily	3.2E-66	MTH_432	conserved protein	2.9E-68

MSM0143	Msp_0564	partially conserved hypothetical membrane-spanning protein	1.3E-30	MTH_431	unknown	2.4E-34
MSM0144	NONE			NONE		
MSM0145	Msp_0451	hypothetical membrane-spanning protein	1.9E-13	MTH_422	unknown	1.6E-14
MSM0146	Msp_0452	conserved hypothetical membrane-spanning protein	7.0E-18	MTH_421	unknown	2.0E-21
MSM0147	Msp_0453	PyrG	2.2E-202	MTH_419	CTP synthase	2.9E-212
MSM0148	Msp_0739	predicted oxidoreductase	3.9E-93	MTH_907	conserved protein	3.1E-32
MSM0149	NONE			NONE		
MSM0150	NONE			NONE		
MSM0151	NONE			NONE		
MSM0152	Msp_1417	predicted Na+-driven multidrug efflux pump	1.1E-28	MTH_314	conserved protein	4.7E-23
MSM0153	Msp_0485	ApgM1	1.3E-110	MTH_418	phosphonopyruvate decarboxylase related protein	2.1E-106
MSM0154	Msp_0487	putative homoserine dehydrogenase	1.3E-101	MTH_417	homoserine dehydrogenase homolog	6.1E-100
MSM0155	Msp_0488	predicted allosteric regulator of homoserine dehydrogenase	1.1E-29	MTH_416	conserved protein	7.8E-36
MSM0156	Msp_0489	conserved hypothetical protein	2.6E-23	MTH_415	conserved protein	3.3E-21
MSM0157	Msp_0484	predicted type I restriction-modification system subunit	1.9E-09	NONE	type I restriction modification system, subunit S	5.3E-09
MSM0158	Msp_0483	hypothetical protein	2.3E-17	NONE	type I restriction modification system, subunit S	2.2E-13
MSM0159	Msp_0777	member of asn/thr-rich large protein family	2.1E-13	NONE		
MSM0160	Msp_0490	putative asparagine synthetase	7.9E-102	MTH_414	asparagine synthetase	2.3E-91
MSM0161	NONE			NONE		
MSM0162	NONE			NONE		
MSM0163	Msp_0425	conserved hypothetical protein	7.0E-23	MTH_1083	conserved protein	5.6E-26
MSM0164	Msp_0946	conserved hypothetical protein	1.3E-106	MTH_1084	conserved protein	4.6E-118
MSM0165	Msp_0945	predicted RecB family exonuclease	7.9E-54	MTH_1085	conserved protein	1.8E-45
MSM0166	Msp_0422	predicted helicase	2.3E-27	MTH_1086	conserved protein	9.1E-32
MSM0167	NONE			MTH_1087	unknown	8.4E-04
MSM0168	NONE			NONE		
MSM0169	Msp_0220	predicted glycosyltransferase	2.1E-04	NONE		
MSM0170	Msp_0944	conserved hypothetical protein	1.4E-63	MTH_1091	conserved protein	3.4E-35
MSM0171	Msp_0835	hypothetical membrane-spanning protein	2.7E-43	MTH_769	unknown	1.7E-34
MSM0172	NONE			NONE		
MSM0173	Msp_0145	member of asn/thr-rich large protein family	3.2E-34	MTH_1074	putative membrane protein	5.5E-31
MSM0174	Msp_0677	predicted O-acetylhomoserine sulfhydrylase	1.9E-123	NONE		
MSM0175	Msp_0676	MetX	2.3E-166	MTH_1820	homoserine O-acetyltransferase	1.5E-21
MSM0176	NONE			NONE		
MSM0177	NONE			NONE		
MSM0178	Msp_1385	conserved hypothetical protein	1.5E-27	NONE		
MSM0179	NONE			NONE		
MSM0180	NONE			MTH_698	unknown	1.6E-04
MSM0181	Msp_1174	50S ribosomal protein L37e	9.6E-26	MTH_648	ribosomal protein L37	2.8E-24
MSM0182	Msp_1175	putative snRNP Sm-like protein	1.5E-27	MTH_649	conserved protein	2.1E-33
MSM0183	Msp_1176	predicted RNA-binding protein	9.0E-46	MTH_650	conserved protein	8.6E-46
MSM0184	Msp_1177	predicted creatinine amidohydrolase	1.3E-51	MTH_651	conserved protein	1.6E-51
MSM0185	Msp_0547	hypothetical membrane-spanning protein	7.8E-08	MTH_515	unknown	4.3E-05
MSM0186	Msp_0345	conserved hypothetical protein	1.3E-14	NONE		
MSM0187	Msp_0444	rubredoxin	2.5E-09	MTH_156	rubredoxin	2.3E-13
MSM0188	Msp_0444	rubredoxin	3.4E-14	MTH_156	rubredoxin	3.5E-17
MSM0189	Msp_1301	predicted nucleoside-diphosphate-sugar pyrophosphorylase	4.6E-08	MTH_272	acetyl / acyl transferase related protein	1.3E-58
MSM0190	Msp_0617	predicted ATPase	3.1E-84	MTH_271	conserved protein	1.8E-75

MSM0191	Msp_1533	RpoM1	1.5E-04	NONE		
MSM0192	Msp_0618	ArgH	2.7E-147	MTH_269	argininosuccinate lyase	8.2E-160
MSM0193	Msp_0620	30S ribosomal protein S27Ae	1.8E-17	MTH_268	ribosomal protein S27a	8.1E-18
MSM0194	Msp_0621	30S ribosomal protein S24e	1.1E-26	MTH_267	ribosomal protein S24	1.6E-28
MSM0195	Msp_0622	conserved hypothetical protein	4.8E-31	MTH_266	conserved protein	1.3E-33
MSM0196	Msp_0623	RpoE2	9.0E-14	NONE	DNA-dependent RNA polymerase, subunit E''	1.5E-18
MSM0197	Msp_0624	RpoE1	2.2E-65	NONE	DNA-dependent RNA polymerase, subunit E'	1.3E-67
MSM0198	Msp_0625	inorganic pyrophosphatase	3.1E-68	MTH_263	inorganic pyrophosphatase	7.2E-65
MSM0199	Msp_0626	conserved hypothetical protein	2.4E-22	MTH_262	conserved protein	3.7E-29
MSM0200	Msp_0627	putative translation initiation factor 2, subunit gamma (aIF-2-gamma)(eIF2G)	3.3E-158	NONE	translation initiation factor eIF-2, gamma subunit	1.6E-163
MSM0201	Msp_0628	30S ribosomal protein S6e	9.9E-40	MTH_260	ribosomal protein S6	1.5E-41
MSM0202	Msp_0629	InfB	9.3E-202	MTH_259	translation initiation factor IF2 homolog	2.6E-218
MSM0203	Msp_0630	nucleoside diphosphate kinase	1.8E-56	MTH_258	nucleoside diphosphate kinase	1.9E-57
MSM0204	Msp_0631	50S ribosomal protein L24e	3.0E-22	MTH_257	ribosomal protein L24	8.2E-25
MSM0205	Msp_0632	30S ribosomal protein S28e	4.3E-30	MTH_256	ribosomal protein S28	2.2E-31
MSM0206	Msp_0633	50S ribosomal protein L7Ae	9.3E-44	MTH_255	ribosomal protein L7a	1.3E-44
MSM0207	NONE			MTH_1178	conserved protein	1.9E-41
MSM0208	NONE			MTH_1178	conserved protein	3.9E-08
MSM0209	Msp_0861	ferredoxin	7.3E-12	MTH_1106	ferredoxin	7.6E-22
MSM0210	Msp_0253	conserved hypothetical membrane-spanning protein	1.1E-04	NONE		
MSM0211	NONE			NONE		
MSM0212	NONE			NONE		
MSM0213	Msp_0769	archaeal histone	8.2E-20	MTH_821	histone HMtA1	3.7E-22
MSM0214	Msp_0588	ThrC	2.0E-153	MTH_253	threonine synthase	8.8E-163
MSM0215	Msp_0232	hypothetical membrane-spanning protein	2.4E-22	MTH_252	conserved protein	4.5E-24
MSM0216	Msp_0653	TrpS	5.0E-132	MTH_251	tryptophanyl-tRNA synthetase	1.8E-116
MSM0217	Msp_0652	EndA	5.0E-45	MTH_250	tRNA intron endonuclease	2.7E-49
MSM0218	Msp_0446	predicted metal-dependent transcriptional regulator	5.3E-57	MTH_214	iron repressor	6.4E-57
MSM0219	Msp_1129	partially conserved hypothetical membrane-spanning protein	1.0E-46	MTH_357	conserved protein	4.0E-67
MSM0220	Msp_0114	ThsB	1.7E-170	MTH_218	chaperonin	4.0E-183
MSM0221	Msp_0590	member of asn/thr-rich large protein family	6.9E-13	MTH_719	cell surface glycoprotein (s-layer protein)	4.2E-05
MSM0222	Msp_0787	FprA	2.5E-128	MTH_220	flavoprotein A homolog (II)	3.2E-133
MSM0223	NONE			MTH_557	unknown	1.4E-22
MSM0224	NONE			MTH_558	unknown	2.1E-28
MSM0225	Msp_1294	conserved hypothetical membrane-spanning protein	1.4E-47	MTH_559	conserved protein	1.4E-54
MSM0226	NONE			NONE		
MSM0227	Msp_0584	HmgA	2.2E-138	MTH_562	3-hydroxy-3-methylglutaryl CoA reductase	1.7E-143
MSM0228	Msp_0583	SucD	1.7E-99	NONE	succinyl-CoA synthetase, alpha subunit	1.3E-111
MSM0229	Msp_0582	conserved hypothetical protein	1.6E-69	MTH_564	conserved protein	1.5E-87
MSM0230	Msp_0233	conserved hypothetical protein	2.9E-21	NONE		
MSM0231	Msp_0577	AroD	9.9E-40	MTH_566	3-dehydroquinate dehydratase	2.9E-52
MSM0232	Msp_0145	member of asn/thr-rich large protein family	3.8E-05	MTH_567	unknown	7.5E-31
MSM0233	Msp_0664	nitrogen regulatory protein P-II	7.9E-31	MTH_664	nitrogen regulatory protein P-II	1.4E-36
MSM0234	Msp_0663	ammonium transporter	4.8E-150	MTH_663	ammonium transporter	1.2E-142
MSM0235	Msp_0119	hypothetical membrane-spanning protein	6.0E-04	MTH_181	unknown	1.4E-04
MSM0236	Msp_0434	predicted phosphohydrolase	1.2E-100	MTH_148	conserved protein	7.8E-123
MSM0237	Msp_0088	predicted 3-polyprenyl-4-hydroxybenzoate decarboxylase	3.1E-59	MTH_147	phenylacrylic acid decarboxylase	2.6E-53
MSM0238	Msp_0087	CbiT	4.2E-48	MTH_146	precorrin-8W decarboxylase	3.1E-48
MSM0239	NONE			MTH_145	conserved protein	6.9E-44

MSM0240	Msp_1289	conserved hypothetical protein	8.3E-07	MTH_143	molybdopterin-guanine dinucleotide biosynthesis MobA related protein	1.6E-30
MSM0241	Msp_1252	putative exosome complex, exonuclease 2 subunit	1.1E-61	MTH_682	conserved protein	5.6E-90
MSM0242	Msp_1251	putative exosome complex, exonuclease 1 subunit	1.4E-79	MTH_683	ribonuclease PH	1.1E-93
MSM0243	Msp_1250	putative exosome complex, RNA-binding subunit	1.6E-48	MTH_684	conserved protein	2.1E-90
MSM0244	Msp_1249	conserved hypothetical protein	1.8E-70	MTH_685	conserved protein	8.3E-80
MSM0245	Msp_1248	PsmA	6.3E-77	NONE	proteasome, alpha subunit	2.5E-94
MSM0246	Msp_1246	putative ribonuclease P, component 2	1.3E-19	MTH_687	conserved protein	2.3E-22
MSM0247	Msp_1245	putative ribonuclease P, component 3	2.1E-28	MTH_688	conserved protein	3.1E-41
MSM0248	Msp_0950	hypothetical protein	7.2E-05	NONE		
MSM0249	Msp_1548	hypothetical protein	1.8E-04	MTH_301	unknown	4.1E-23
MSM0250	Msp_0501	hypothetical membrane-spanning protein	1.0E-05	MTH_521	unknown	3.6E-10
MSM0251	Msp_0725	hypothetical protein	1.5E-04	NONE		
MSM0252	Msp_0824	predicted Na+-driven multidrug efflux pump	1.6E-96	MTH_314	conserved protein	3.7E-93
MSM0253	NONE			MTH_1725	unknown	1.4E-15
MSM0254	NONE			NONE		
MSM0255	NONE			NONE		
MSM0256	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM0257	Msp_0975	hypothetical membrane-spanning protein	4.3E-30	NONE		
MSM0258	Msp_0724	hypothetical membrane-spanning protein	1.6E-04	NONE		
MSM0259	Msp_1548	hypothetical protein	1.1E-05	MTH_521	unknown	6.8E-04
MSM0260	Msp_0507	predicted archaea-specific RecJ-like exonuclease	2.0E-199	MTH_763	conserved protein	3.4E-225
MSM0261	Msp_1384	conserved hypothetical membrane-spanning protein	1.1E-04	MTH_759	unknown	1.5E-16
MSM0262	Msp_0788	desulfoferrodoxin	1.4E-26	MTH_757	rubredoxin oxidoreductase	3.4E-26
MSM0263	Msp_1003	predicted NifU protein	1.1E-47	NONE		
MSM0264	Msp_1002	IscS	6.6E-121	MTH_1389	nifS protein	1.6E-30
MSM0265	Msp_0677	predicted O-acetylhomoserine sulfhydrylase	1.5E-148	MTH_1188	pleiotropic regulatory protein DegT	3.1E-04
MSM0266	Msp_0145	member of asn/thr-rich large protein family	2.7E-50	MTH_911	probable surface protein	6.2E-09
MSM0267	Msp_0844	predicted multimeric flavodoxin	4.4E-53	MTH_135	conserved protein	2.7E-17
MSM0268	Msp_0124	CysS	1.2E-139	MTH_587	methionyl-tRNA synthetase	9.6E-08
MSM0269	Msp_0527	conserved hypothetical protein	8.0E-38	NONE		
MSM0270	Msp_0450	predicted serine acetyltransferase	8.1E-61	MTH_1588	ferripyochelin binding protein	2.0E-06
MSM0271	Msp_0449	cysteine synthase	2.2E-97	NONE	tryptophan synthase, beta subunit	3.1E-08
MSM0272	Msp_0497	putative endonuclease III	2.2E-67	MTH_764	endonuclease III	1.1E-70
MSM0273	Msp_0498	AroA	1.1E-102	MTH_766	5-enolpyruvylshikimate 3-phosphate synthase	2.5E-62
MSM0274	NONE			NONE		
MSM0275	Msp_0499	ValS	2.4E-235	MTH_767	valyl-tRNA synthetase	0.0E+00
MSM0276	Msp_0526	hypothetical membrane-spanning protein	8.1E-29	MTH_768	unknown	2.9E-22
MSM0277	Msp_0525	PheT	3.3E-151	MTH_770	phenylalanyl-tRNA synthetase	4.2E-172
MSM0278	NONE			NONE		
MSM0279	Msp_0522	conserved hypothetical protein	4.0E-36	MTH_771	conserved protein	2.7E-35
MSM0280	Msp_0757	predicted ATPase	4.4E-13	NONE		
MSM0281	Msp_0145	member of asn/thr-rich large protein family	2.1E-09	MTH_911	probable surface protein	2.9E-10
MSM0282	Msp_0141	member of asn/thr-rich large protein family	1.3E-23	MTH_911	probable surface protein	1.1E-17
MSM0283	NONE			MTH_436	unknown	1.1E-04
MSM0284	Msp_0995	RpiA	5.8E-74	MTH_608	ribose 5-phosphate isomerase	1.3E-74
MSM0285	Msp_0996	conserved hypothetical protein	1.3E-28	MTH_609	conserved protein	1.3E-35
MSM0286	Msp_0997	EgsA	7.9E-102	MTH_610	glycerol 1-phosphate dehydrogenase	1.5E-112
MSM0287	Msp_1004	ProS	8.6E-160	MTH_611	prolyl-tRNA synthetase	1.4E-155
MSM0288	Msp_1006	conserved hypothetical protein	1.7E-53	MTH_613	conserved protein	4.2E-60
MSM0289	Msp_1007	ThiD	3.6E-58	MTH_614	transcriptional regulator	5.1E-64

MSM0290	Msp_1000	predicted ABC-type nitrate/sulfonate/bicarbonate transport system, ATB-binding protein	2.6E-71	MTH_920	anion permease	1.4E-31
MSM0291	Msp_1001	predicted ABC-type nitrate/sulfonate/bicarbonate transport system, permease protein	1.9E-84	MTH_1730	phosphate transporter permease PstC homolog	4.8E-07
MSM0292	NONE			NONE		
MSM0293	Msp_0826	predicted cation transport ATPase	1.8E-198	MTH_1535	heavy-metal transporting CPx-type ATPase	1.2E-69
MSM0294	Msp_0825	hypothetical protein	4.2E-09	NONE		
MSM0295	NONE			NONE	nitrate assimilation protein, narQ	7.1E-49
MSM0296	NONE			MTH_691	conserved protein	1.2E-30
MSM0297	Msp_1244	predicted exosome subunit	1.1E-24	MTH_689	conserved protein	2.7E-26
MSM0298	Msp_1243	50S ribosomal protein L15e	2.1E-76	MTH_690	ribosomal protein L15	1.3E-67
MSM0299	NONE			NONE		
MSM0300	Msp_0851	predicted ABC-type dipeptide/oligopeptide/nickel transport system, solute-binding protein	1.5E-139	NONE		
MSM0301	Msp_0811	ABC-type dipeptide transport system, permease protein	2.3E-120	NONE		
MSM0302	Msp_0810	ABC-type dipeptide transport system, permease protein	1.7E-99	MTH_1729	phosphate transporter permease PstC	2.3E-05
MSM0303	Msp_0848	predicted ABC-type dipeptide/oligopeptide/nickel transport system, ATP-binding protein	3.4E-101	MTH_696	ABC transporter (glutamine transport ATP-binding protein)	1.4E-20
MSM0304	Msp_0847	predicted ABC-type dipeptide/oligopeptide/nickel transport system, ATP-binding protein	4.8E-63	NONE	methyl coenzyme M reductase system, component A2	7.3E-21
MSM0305	Msp_0431	GuaB	6.1E-10	MTH_406	conserved protein	7.6E-70
MSM0306	Msp_1447	EhbK	3.0E-18	MTH_405	polyferredoxin	1.6E-37
MSM0307	Msp_0071	predicted ribokinase	3.4E-62	MTH_404	ribokinase	3.5E-65
MSM0308	Msp_0070	formylmethanofuran-tetrahydromethanopterin formyltransferase	6.7E-89	MTH_403	formylmethanofuran:tetrahydromethanopterin formyltransferase II	1.7E-95
MSM0309	Msp_0069	conserved hypothetical membrane-spanning protein	2.4E-68	MTH_402	unknown	3.9E-57
MSM0310	Msp_1447	EhbK	1.7E-23	MTH_401	polyferredoxin	7.7E-77
MSM0311	Msp_1447	EhbK	2.1E-13	MTH_399	polyferredoxin	7.4E-111
MSM0312	Msp_1444	EhbN	2.2E-51	NONE	formate hydrogenlyase, subunit 5	7.8E-139
MSM0313	Msp_1445	EhbM	5.4E-32	NONE	formate hydrogenlyase, subunit 7	6.3E-66
MSM0314	NONE			MTH_396	conserved protein	2.9E-29
MSM0315	NONE			MTH_395	conserved protein	1.9E-18
MSM0316	Msp_0616	partially conserved hypothetical membrane-spanning protein	9.5E-04	MTH_394	unknown	5.8E-08
MSM0317	Msp_1443	EhbO	1.1E-16	NONE	NADH dehydrogenase (ubiquinone), subunit 1 related protein	1.9E-105
MSM0318	NONE			MTH_392	unknown	1.4E-15
MSM0319	Msp_1452	EhbF	4.0E-06	NONE	NADH dehydrogenase I, subunit N related protein	5.5E-83
MSM0320	NONE			MTH_390	conserved protein	7.0E-67
MSM0321	NONE			MTH_389	conserved protein	6.6E-55
MSM0322	NONE			MTH_388	unknown	1.5E-25
MSM0323	NONE			MTH_387	conserved protein	3.9E-18
MSM0324	NONE			MTH_386	unknown	6.4E-18
MSM0325	NONE			MTH_385	conserved protein	4.1E-55
MSM0326	NONE			MTH_384	unknown	3.5E-17
MSM0327	Msp_0067	putative UDP-glucose 4-epimerase	1.2E-73	MTH_380	UDP-glucose 4-epimerase homolog	1.7E-86
MSM0328	NONE			MTH_698	unknown	2.7E-10
MSM0329	Msp_0265	conserved hypothetical protein	7.4E-51	MTH_700	conserved protein	5.1E-64
MSM0330	Msp_0266	predicted acyl-CoA synthetase	1.1E-184	MTH_701	acetyl-CoA synthetase related protein	1.0E-138
MSM0331	Msp_1390	KorD	7.0E-07	NONE	2-oxoisovalerate oxidoreductase, gamma subunit	7.9E-20
MSM0332	Msp_1389	KorA	1.6E-56	NONE	2-oxoisovalerate oxidoreductase, beta subunit	6.4E-144

MSM0333	Msp_1388	KorB	2.0E-28	NONE	2-oxoisovalerate oxidoreductase, alpha subunit	8.0E-169
MSM0334	Msp_1411	GatD	9.1E-140	MTH_706	L-asparaginase I	6.4E-144
MSM0335	Msp_1412	GatE	8.1E-187	MTH_707	PET112-like protein	7.1E-209
MSM0336	NONE			NONE		
MSM0337	Msp_0145	member of asn/thr-rich large protein family	1.1E-08	NONE		
MSM0338	NONE			NONE		
MSM0339	NONE			NONE		
MSM0340	Msp_1413	predicted thioredoxin reductase	1.4E-70	MTH_708	thioredoxin reductase	6.9E-92
MSM0341	NONE			NONE		
MSM0342	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM0343	Msp_1311	GMP synthase [glutamine hydrolyzing], subunit A	4.2E-64	NONE	GMP synthetase, subunit A	1.1E-68
MSM0344	NONE			NONE		
MSM0345	Msp_1312	GMP synthase [glutamine hydrolyzing], subunit B	3.4E-117	NONE	GMP synthetase, subunit B	7.1E-122
MSM0346	Msp_1315	conserved hypothetical protein	8.0E-125	MTH_720	unknown	3.1E-128
MSM0347	Msp_1316	conserved hypothetical protein	6.5E-43	MTH_721	conserved protein	8.6E-62
MSM0348	Msp_1317	conserved hypothetical protein	7.1E-14	MTH_722	conserved protein	2.3E-22
MSM0349	Msp_1317	conserved hypothetical protein	1.5E-05	MTH_722	conserved protein	1.2E-04
MSM0350	Msp_1318	predicted isopropylmalate/homocitrate/citramalate synthase	3.9E-155	MTH_723	2-isopropylmalate synthase	6.2E-162
MSM0351	NONE			NONE		
MSM0352	Msp_1319	predicted DNA modification methylase	1.4E-72	MTH_724	methyltransferase related protein	4.3E-83
MSM0353	Msp_1321	hypothetical membrane-spanning protein	4.8E-11	NONE		
MSM0354	Msp_1206	proteasome-activating nucleotidase	4.1E-144	MTH_728	ATP-dependent 26S protease regulatory subunit 4	1.2E-172
MSM0355	Msp_1207	predicted transcriptional regulator	7.4E-35	MTH_729	conserved protein	2.7E-33
MSM0356	Msp_1208	conserved hypothetical protein	2.3E-24	MTH_730	conserved protein	6.2E-27
MSM0357	Msp_1209	conserved hypothetical membrane-spanning protein	1.6E-128	MTH_731	unknown	1.5E-110
MSM0358	Msp_1210	conserved hypothetical membrane-spanning protein	7.3E-44	MTH_733	unknown	3.7E-45
MSM0359	Msp_1213	predicted UDP-N-acetylmuramyl tripeptide synthase	1.7E-108	MTH_530	UDP-N-acetylmuramyl tripeptide synthetase related protein	5.2E-14
MSM0360	Msp_1214	predicted UDP-N-acetylmuramyl pentapeptide phosphotransferase	1.9E-91	MTH_735	phospho-N-acetylmuramoyl-pentapeptide- transferase	2.8E-102
MSM0361	Msp_1215	partially conserved hypothetical protein, predicted carbamoyl-phosphate synthase, large chain	6.8E-96	MTH_736	conserved protein	2.0E-76
MSM0362	Msp_1216	partially conserved hypothetical protein	5.4E-16	NONE	coenzyme F420-reducing hydrogenase, delta subunit homolog	5.3E-30
MSM0363	Msp_1217	predicted RNA methylase	3.2E-50	MTH_738	conserved protein	1.0E-56
MSM0364	Msp_1218	putative nickel responsive regulator	3.0E-54	MTH_739	conserved protein	9.1E-58
MSM0365	Msp_1090	hypothetical protein	2.1E-23	MTH_741	unknown	1.8E-22
MSM0366	NONE			NONE		
MSM0367	Msp_0099	conserved hypothetical protein	6.0E-17	MTH_812	conserved protein	5.6E-26
MSM0368	Msp_0667	putative glutamate synthase, subunit 2 with ferredoxin domain	1.3E-193	NONE	glutamate synthase (NADPH), alpha subunit	1.3E-216
MSM0369	Msp_0669	putative glutamate synthase, subunit 3	1.2E-68	NONE	tungsten formylmethanofuran dehydrogenase, subunit C homolog	1.1E-82
MSM0370	Msp_0670	putative glutamate synthase, subunit 1	5.7E-115	MTH_191	glutamine PRPP amidotransferase	2.2E-127
MSM0371	Msp_0671	predicted glutamine amidotransferase	6.2E-54	MTH_190	conserved protein	3.3E-60
MSM0372	Msp_0673	partially conserved hypothetical protein	1.3E-23	MTH_187	conserved protein	2.8E-24
MSM0373	Msp_1484	LeuB	3.3E-96	MTH_184	isocitrate dehydrogenase	4.5E-104
MSM0374	Msp_0447	predicted acyl-CoA synthetase	8.3E-178	MTH_657	long-chain-fatty-acid-CoA ligase	5.0E-58
MSM0375	Msp_0550	ArgB	2.3E-111	MTH_183	acetylglutamate kinase	2.5E-110
MSM0376	Msp_0967	putative NADP-dependent alcohol dehydrogenase	6.2E-06	NONE		

MSM0377	Msp_0310	predicted GTP:adenosylcobinamide-phosphate guanylyltransferase	4.9E-07	MTH_1152	conserved protein	6.5E-05
MSM0378	NONE			MTH_1876	conserved protein	1.3E-24
MSM0379	Msp_0549	ArgJ	6.5E-107	MTH_182	glutamate N-acetyltransferase	1.9E-103
MSM0380	Msp_0506	hypothetical membrane-spanning protein	2.1E-05	MTH_181	unknown	1.8E-04
MSM0381	Msp_0546	conserved hypothetical membrane-spanning protein	2.8E-99	MTH_180	unknown	1.4E-114
MSM0382	Msp_0545	conserved hypothetical protein	3.7E-95	MTH_179	unknown	1.9E-103
MSM0383	Msp_0544	predicted phosphohydrolase	1.0E-62	MTH_178	Icc related protein	2.6E-53
MSM0384	Msp_0543	conserved hypothetical protein	4.1E-34	MTH_177	conserved protein	1.9E-34
MSM0385	Msp_0511	predicted Fe-S oxidoreductase	3.2E-07	MTH_1784	Mg-protoporphyrin IX monomethyl ester oxidative cyclase	9.9E-84
MSM0386	Msp_0148	predicted sodium:solute symporter	1.9E-178	MTH_1856	sodium/proline symporter (proline permease)	1.5E-181
MSM0387	Msp_1040	coenzyme F390 synthetase II	2.2E-145	MTH_1855	coenzyme F390 synthetase II	1.4E-162
MSM0388	Msp_1041	predicted regulatory protein	4.1E-34	MTH_1854	unknown	2.6E-37
MSM0389	Msp_0136	hypothetical protein	1.5E-06	NONE		
MSM0390	NONE			NONE		
MSM0391	Msp_1042	IorB	5.6E-53	NONE	indolepyruvate oxidoreductase, beta subunit	2.4E-50
MSM0392	Msp_1043	IorA	6.7E-185	NONE	indolepyruvate oxidoreductase, alpha subunit	4.1E-192
MSM0393	Msp_1044	TfrB	3.3E-135	MTH_1850	fumarate reductase	1.4E-155
MSM0394	Msp_1047	predicted rRNA methylase	2.2E-65	MTH_1849	conserved protein	1.2E-69
MSM0395	Msp_1581	partially conserved hypothetical protein	2.7E-46	MTH_745	unknown (contains ferredoxin domain)	3.9E-57
MSM0396	Msp_0233	conserved hypothetical protein	2.3E-22	NONE		
MSM0397	NONE			NONE		
MSM0398	Msp_1229	ribose-phosphate pyrophosphokinase	6.6E-04	MTH_1114	uracil phosphoribosyltransferase	6.6E-23
MSM0399	NONE			NONE		
MSM0400	NONE			NONE		
MSM0401	NONE			MTH_75	surface protease related protein	2.7E-27
MSM0402	Msp_1048	deoxycytidine triphosphate deaminase	3.5E-76	MTH_1847	deoxycytidine triphosphate deaminase	1.1E-75
MSM0403	Msp_1049	GlyS	2.1E-188	MTH_1846	glycyl-tRNA synthetase	7.6E-196
MSM0404	Msp_0799	predicted transcriptional regulator	1.6E-25	MTH_1843	unknown	9.1E-26
MSM0405	Msp_1050	predicted metal-dependent hydrolase	1.7E-58	MTH_1842	conserved protein	2.5E-46
MSM0406	Msp_1052	hypothetical protein	1.7E-10	MTH_1838	unknown	6.6E-23
MSM0407	Msp_1053	conserved hypothetical membrane-spanning protein	1.7E-115	MTH_1837	unknown	1.2E-124
MSM0408	Msp_0406	2-phosphoglycerate kinase-like/predicted small molecule-binding domain fusion	4.2E-80	MTH_1835	2-phosphoglycerate kinase homolog	2.3E-91
MSM0409	Msp_0407	conserved hypothetical protein	2.2E-42	MTH_1834	conserved protein	9.5E-47
MSM0410	Msp_0409	conserved hypothetical protein	3.9E-52	MTH_1833	unknown	4.6E-47
MSM0411	Msp_0145	member of asn/thr-rich large protein family	1.3E-25	MTH_1074	putative membrane protein	1.3E-115
MSM0412	Msp_0046	member of asn/thr-rich large protein family	1.3E-06	MTH_117	unknown	2.4E-41
MSM0413	Msp_0512	predicted transcriptional regulator	2.7E-21	MTH_313	transcriptional regulator	1.9E-16
MSM0414	Msp_0824	predicted Na+-driven multidrug efflux pump	2.8E-138	MTH_314	conserved protein	6.7E-110
MSM0415	Msp_1362	PyrH	3.5E-76	MTH_879	uridine monophosphate kinase	2.8E-79
MSM0416	Msp_0974	predicted Mg-dependent DNase	1.5E-93	MTH_233	conserved protein	8.0E-27
MSM0417	Msp_1361	hypothetical membrane-spanning protein	3.8E-15	MTH_880	unknown	3.2E-14
MSM0418	Msp_1045	conserved hypothetical protein	2.5E-34	MTH_507	conserved protein	2.5E-32
MSM0419	Msp_0253	conserved hypothetical membrane-spanning protein	1.4E-24	MTH_506	unknown	4.2E-21
MSM0420	Msp_0355	conserved hypothetical membrane-spanning protein	3.0E-22	MTH_882	conserved protein	1.1E-27
MSM0421	NONE			NONE		
MSM0422	Msp_0644	conserved hypothetical membrane-spanning protein	1.1E-36	MTH_883	unknown	6.3E-48
MSM0423	Msp_0645	predicted glycosyltransferase	6.9E-157	MTH_884	teichoic acid biosynthesis related protein	4.5E-184
MSM0424	Msp_1360	transcription initiation factor IIB (TFIIB)	8.1E-148	MTH_885	transcription initiation factor TFIIB	9.2E-152
MSM0425	Msp_1359	hypothetical protein	2.3E-15	MTH_886	conserved protein	3.4E-19

MSM0426	Msp_1358	predicted demethylmenaquinone methyltransferase	3.7E-33	MTH_888	conserved protein	3.2E-46
MSM0427	Msp_1356	predicted DNA primase	7.2E-108	MTH_891	conserved protein	2.9E-141
MSM0428	Msp_1355	predicted site-specific recombinase/integrase	2.5E-66	MTH_893	integrase-recombinase protein	7.7E-77
MSM0429	Msp_1354	conserved hypothetical protein	4.3E-46	MTH_905	conserved protein	1.8E-38
MSM0430	NONE			MTH_906	unknown	2.7E-17
MSM0431	Msp_1132	predicted ATP-dependent carboligase	1.7E-44	MTH_947	conserved protein	2.8E-40
MSM0432	Msp_1131	hypothetical membrane-spanning protein	5.5E-07	NONE		
MSM0433	Msp_1133	AhaD	1.6E-69	NONE	ATP synthase, subunit D	1.5E-73
MSM0434	Msp_1134	AhaB	1.4E-212	NONE	ATP synthase, subunit B	4.5E-214
MSM0435	Msp_1135	AhaA	1.4E-246	NONE	ATP synthase, subunit A	2.8E-260
MSM0436	Msp_1136	AhaF	8.6E-25	NONE	ATP synthase, subunit F	3.1E-25
MSM0437	Msp_1137	AhaC	1.5E-105	NONE	ATP synthase, subunit C	7.7E-116
MSM0438	Msp_1138	AhaE	3.2E-50	NONE	ATP synthase, subunit E	5.9E-54
MSM0439	Msp_1139	AhaK	7.0E-62	NONE	ATP synthase, subunit K	9.7E-70
MSM0440	Msp_1140	AhaI	1.9E-148	NONE	ATP synthase, subunit I	3.5E-191
MSM0441	Msp_1141	AhaH	7.6E-17	MTH_961	unknown	3.1E-18
MSM0442	NONE			NONE		
MSM0443	NONE			NONE		
MSM0444	NONE			NONE		
MSM0445	Msp_0408	putative nitroreductase protein	2.0E-55	MTH_120	NADPH-oxidoreductase	1.4E-13
MSM0446	NONE			MTH_962	citrate synthase I	6.2E-75
MSM0447	Msp_0338	fumarate hydratase	2.6E-15	NONE	fumarate hydratase, class I related protein	3.8E-75
MSM0448	NONE			MTH_964	unknown	4.6E-102
MSM0449	NONE			MTH_965	conserved protein	1.1E-86
MSM0450	Msp_0680	conserved hypothetical membrane-spanning protein	2.4E-38	NONE		
MSM0451	Msp_0679	conserved hypothetical membrane-spanning protein	7.8E-79	NONE		
MSM0452	Msp_1142	predicted DNA-binding protein	3.9E-132	MTH_966	conserved protein	1.8E-130
MSM0453	Msp_1143	putative transcriptional regulator	7.5E-58	MTH_967	conserved protein	1.3E-88
MSM0454	NONE			NONE		
MSM0455	Msp_1144	conserved hypothetical protein	2.2E-35	MTH_969	unknown	1.0E-43
MSM0456	Msp_1005	conserved hypothetical protein	2.3E-17	MTH_544	conserved protein	2.7E-35
MSM0457	Msp_1145	SerA	8.8E-158	MTH_970	phosphoglycerate dehydrogenase	1.3E-177
MSM0458	NONE			NONE		
MSM0459	NONE			NONE		
MSM0460	NONE			NONE		
MSM0461	Msp_0983	member of asn/thr-rich large protein family	3.0E-39	MTH_911	probable surface protein	2.9E-18
MSM0462	Msp_1146	partially conserved hypothetical protein	1.8E-38	MTH_971	unknown	1.0E-33
MSM0463	Msp_1147	conserved hypothetical protein	2.0E-57	MTH_972	conserved protein	3.7E-61
MSM0464	Msp_1148	predicted dinucleotide-utilizing protein	4.0E-59	MTH_973	conserved protein	1.1E-77
MSM0465	Msp_1149	conserved hypothetical protein	1.1E-17	MTH_974	unknown	4.1E-23
MSM0466	Msp_1150	predicted tRNA-binding protein	2.4E-68	MTH_975	conserved protein	1.4E-70
MSM0467	NONE			MTH_978	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	8.1E-137
MSM0468	NONE			MTH_1490	unknown	2.2E-10
MSM0469	NONE			MTH_1490	unknown	1.8E-11
MSM0470	Msp_1151	hypothetical membrane-spanning protein	1.4E-10	MTH_979	unknown	7.2E-10
MSM0471	Msp_1152	conserved hypothetical membrane-spanning protein	7.1E-53	MTH_980	conserved protein	5.9E-70
MSM0472	Msp_1153	PepQ	2.7E-69	MTH_981	aminopeptidase P	1.0E-65
MSM0473	Msp_0417	hypothetical membrane-spanning protein	2.5E-04	NONE		
MSM0474	NONE			NONE		
MSM0475	Msp_0417	hypothetical membrane-spanning protein	1.8E-04	NONE		

MSM0476	NONE			MTH_93	unknown	8.5E-04
MSM0477	NONE			NONE		
MSM0478	NONE			NONE		
MSM0479	Msp_1154	conserved hypothetical membrane-spanning protein	2.4E-45	MTH_986	conserved protein	2.1E-42
MSM0480	Msp_1155	conserved hypothetical protein	2.3E-95	MTH_987	conserved protein	6.0E-109
MSM0481	Msp_1274	conserved hypothetical protein	4.4E-53	MTH_989	conserved protein	2.2E-24
MSM0482	Msp_1275	predicted ATP-utilizing enzyme	4.6E-58	MTH_990	conserved protein	2.6E-51
MSM0483	NONE			MTH_991	unknown	8.6E-14
MSM0484	Msp_1276	conserved hypothetical protein	9.2E-76	MTH_992	inosine-5'-monophosphate dehydrogenase related protein IX	2.8E-86
MSM0485	Msp_1410	predicted universal stress protein	9.6E-26	MTH_993	conserved protein	1.0E-33
MSM0486	Msp_1199	predicted metal-dependent hydrolase	3.1E-84	MTH_994	N-ethylammeline chlorohydrolase related protein	4.2E-85
MSM0487	NONE			NONE		
MSM0488	Msp_1200	CarB	0.0E+00	NONE	carbamoyl-phosphate synthase, large subunit	0.0E+00
MSM0489	Msp_1201	CarA	1.5E-121	NONE	carbamoyl-phosphate synthase, small subunit	6.0E-125
MSM0490	Msp_0602	conserved hypothetical protein	1.0E-28	MTH_738	conserved protein	3.0E-06
MSM0491	Msp_0410	NadC	2.0E-64	MTH_1832	quinolinate phosphoribosyltransferase	7.7E-61
MSM0492	Msp_0411	putative ribonuclease Z	1.7E-76	MTH_1831	conserved protein	2.6E-92
MSM0493	Msp_0982	predicted mechanosensitive ion channel	6.7E-25	MTH_1830	conserved protein	1.7E-40
MSM0494	Msp_0643	NadA	3.6E-90	MTH_1827	quinolinate synthetase	6.8E-101
MSM0495	NONE			MTH_1821	unknown	2.7E-19
MSM0496	Msp_1526	putative homoserine O-acetyltransferase	1.2E-84	MTH_1820	homoserine O-acetyltransferase	1.3E-67
MSM0497	Msp_0157	hypothetical protein	6.9E-55	MTH_1816	conserved protein	2.6E-76
MSM0498	NONE			NONE		
MSM0499	Msp_1548	hypothetical protein	1.0E-05	MTH_1277	unknown	1.8E-06
MSM0500	Msp_0155	predicted amidohydrolase	3.1E-75	MTH_1811	N-carbamoyl-D-amino acid amidohydrolase	3.7E-77
MSM0501	Msp_0153	conserved hypothetical protein	1.8E-31	MTH_1806	phycocyanin alpha phycocyanobilin lyase CpcE	8.1E-34
MSM0502	Msp_0150	predicted helicase	2.9e-310	MTH_1802	ATP-dependent helicase	0.0E+00
MSM0503	Msp_0553	hypothetical protein	9.4E-19	MTH_1799	unknown	3.9E-18
MSM0504	Msp_0927	hypothetical protein	2.1E-05	MTH_1641	unknown	1.4E-06
MSM0505	NONE			NONE		
MSM0506	Msp_0240	predicted ATP-utilizing enzyme	3.0E-148	MTH_1201	conserved protein	3.4E-145
MSM0507	Msp_0365	predicted phosphoesterase	6.0E-49	MTH_1774	conserved protein	2.9E-52
MSM0508	Msp_0364	putative 23S rRNA methylase	1.9E-61	MTH_1773	cell division protein J	5.9E-70
MSM0509	Msp_0363	hypothetical membrane-spanning protein	1.4E-24	MTH_1772	unknown	9.1E-26
MSM0510	Msp_0362	predicted minichromosome maintenance protein	1.4E-255	MTH_1770	DNA replication initiator (Cdc21/Cdc54)	1.4E-260
MSM0511	Msp_0361	translation initiation factor aIF-2, beta subunit (eIF2B)	2.3E-54	NONE	translation initiation factor eIF-2, beta subunit	6.9E-60
MSM0512	Msp_0360	predicted NMD3-related protein	5.2E-73	MTH_1768	conserved protein	2.1E-90
MSM0513	Msp_0359	TyrS	2.4E-100	MTH_1767	tyrosyl-tRNA synthetase	1.1E-109
MSM0514	Msp_0358	hypothetical protein	3.5E-05	MTH_1766	unknown	1.1E-08
MSM0515	Msp_0186	MtaB2	1.3E-156	NONE		
MSM0516	Msp_0185	MtaC3	5.2E-89	NONE		
MSM0517	Msp_0190	MapA	8.7E-167	MTH_278	ferredoxin	7.0E-04
MSM0518	Msp_0112	MtaA2	2.1E-94	MTH_775	cobalamin-independent methionine synthase	3.4E-05
MSM0519	Msp_0183	hypothetical protein	1.2E-32	NONE		
MSM0520	Msp_0357	putative thymidylate kinase	2.1E-46	MTH_1765	thymidylate kinase	7.5E-47
MSM0521	NONE			NONE		
MSM0522	Msp_0984	predicted peptidase	2.7E-234	MTH_1763	collagenase	3.4E-99
MSM0523	Msp_0984	predicted peptidase	1.6E-96	MTH_1763	collagenase	6.8E-108
MSM0524	Msp_0354	MutS	4.3E-133	MTH_1762	DNA mismatch recognition protein MutS	1.9E-176
MSM0525	Msp_1282	predicted protein kinase	1.8E-104	MTH_1645	ABC transporter	3.1E-112

MSM0526	NONE			NONE		
MSM0527	Msp_0017	conserved hypothetical protein	3.5E-28	NONE		
MSM0528	Msp_0233	conserved hypothetical protein	1.4E-10	NONE		
MSM0529	Msp_0725	hypothetical protein	1.0E-04	NONE		
MSM0530	Msp_1323	conserved hypothetical protein	3.3E-04	MTH_72	O-linked GlcNAc transferase	5.5E-06
MSM0531	NONE			NONE		
MSM0532	Msp_0233	conserved hypothetical protein	3.4E-08	NONE		
MSM0533	Msp_0017	conserved hypothetical protein	3.1E-16	NONE		
MSM0534	NONE			NONE		
MSM0535	Msp_0466	hypothetical protein	7.1E-05	NONE		
MSM0536	NONE			NONE		
MSM0537	NONE			NONE		
MSM0538	Msp_1324	predicted glycyl radical activating enzyme	5.1E-07	MTH_1586	pyruvate formate-lyase activating enzyme	1.3E-05
MSM0539	Msp_0219	conserved hypothetical protein	3.1E-04	NONE		
MSM0540	NONE			NONE		
MSM0541	NONE			NONE		
MSM0542	Msp_1128	F420-dependent N5,N10-methylenetetrahydromethanopterin reductase	3.4E-94	NONE	coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase	1.4E-132
MSM0543	Msp_0646	predicted DNA repair photolyase	9.3E-28	NONE		
MSM0544	Msp_1127	predicted Fe-S oxidoreductase	4.4E-92	MTH_1751	conserved protein	1.3E-90
MSM0545	NONE			NONE		
MSM0546	Msp_1046	hypothetical membrane-spanning protein	2.6E-23	MTH_813	unknown	2.4E-27
MSM0547	Msp_0324	predicted nucleotidyltransferase	1.6E-08	MTH_1749	unknown	7.2E-81
MSM0548	Msp_1148	predicted dinucleotide-utilizing protein	4.4E-04	MTH_1747	conserved protein	5.4E-37
MSM0549	Msp_0830	Trk-type potassium transport system, membrane protein	3.9E-04	MTH_1746	cytochrome C-type biogenesis protein	2.1E-28
MSM0550	Msp_0656	hypothetical membrane-spanning protein	2.0E-04	MTH_1745	protein disulphide isomerase	7.9E-20
MSM0551	Msp_1124	conserved hypothetical protein	1.9E-68	MTH_1744	conserved protein	2.4E-73
MSM0552	Msp_0330	hypothetical protein	4.6E-10	MTH_1743	unknown	8.9E-12
MSM0553	Msp_0331	predicted ATPase	3.5E-92	MTH_1742	conserved protein	1.2E-80
MSM0554	Msp_0161	conserved hypothetical protein	2.8E-74	MTH_1815	conserved protein	2.6E-83
MSM0555	Msp_0192	predicted MoxR-like ATPase	3.9E-93	MTH_1814	conserved protein	1.9E-87
MSM0556	Msp_0333	predicted pterin-binding enzyme	4.1E-121	MTH_1741	conserved protein	1.1E-153
MSM0557	Msp_0334	PorC	2.1E-53	NONE	pyruvate oxidoreductase, gamma subunit	2.1E-65
MSM0558	Msp_0335	PorD	4.3E-30	NONE	pyruvate oxidoreductase, gamma subunit	1.2E-32
MSM0559	Msp_0336	PorA	2.1E-140	NONE	pyruvate oxidoreductase, alpha subunit	2.3E-148
MSM0560	Msp_0337	PorB	1.8E-118	NONE	pyruvate oxidoreductase, beta subunit	2.2E-127
MSM0561	Msp_1447	EhbK	8.6E-08	NONE	formate hydrogenlyase, iron-sulfur subunit I	4.5E-40
MSM0562	Msp_1447	EhbK	4.0E-09	NONE	formate hydrogenlyase, iron-sulfur subunit 2	5.3E-14
MSM0563	Msp_0338	fumarate hydratase	3.3E-96	NONE	fumarate hydratase, class I	8.3E-96
MSM0564	Msp_0339	predicted phosphate uptake regulator	4.8E-31	MTH_1734	phosphate transport system regulator	2.8E-47
MSM0565	Msp_0340	PstB	4.0E-107	MTH_1731	phosphate transport system ATP-binding	1.5E-105
MSM0566	Msp_0341	PstA	1.3E-94	MTH_1730	phosphate transporter permease PstC homolog	4.5E-111
MSM0567	Msp_0342	PstC	7.0E-94	MTH_1729	phosphate transporter permease PstC	4.8E-100
MSM0568	Msp_0343	PstS	1.6E-64	MTH_1727	phosphate-binding protein PstS	2.7E-81
MSM0569	Msp_0344	predicted phosphate uptake regulator	5.5E-62	MTH_1724	phosphate transport system regulator related protein	2.4E-82
MSM0570	Msp_0346	conserved hypothetical membrane-spanning protein	5.2E-17	MTH_1723	unknown	9.1E-26
MSM0571	NONE			MTH_1137	conserved protein (FlpA)	5.2E-165
MSM0572	NONE			NONE	H(2)-dependent N5,N10-methylenetetrahydromethanopterin dehydrogenase	2.4E-128
MSM0573	Msp_0296	CofG	1.4E-15	MTH_1143	biotin synthetase (BioB)	5.1E-112
MSM0574	NONE			MTH_1144	conserved protein	2.9E-38

MSM0575	Msp_1393	conserved hypothetical membrane-spanning protein	8.5E-05	MTH_1145	conserved protein	2.9E-38
MSM0576	NONE			MTH_1146	conserved protein	2.9E-38
MSM0577	NONE			MTH_1147	conserved protein	6.1E-52
MSM0578	NONE			MTH_1148	conserved protein	8.1E-34
MSM0579	Msp_1581	partially conserved hypothetical protein	7.5E-10	MTH_1106	ferredoxin	1.3E-10
MSM0580	Msp_0911	member of asn/thr-rich large protein family	2.5E-05	MTH_654	unknown	5.2E-39
MSM0581	Msp_0166	conserved hypothetical membrane-spanning protein	3.9E-29	MTH_655	conserved protein	6.7E-94
MSM0582	Msp_0737	putative peptide methionine sulfoxide reductase MsrA/MsrB	4.5E-122	MTH_535	peptide methionine sulfoxide reductase	2.4E-34
MSM0583	Msp_0655	CbiM2	2.7E-69	MTH_1707	cobalamin biosynthesis protein M	1.5E-64
MSM0584	Msp_0656	hypothetical membrane-spanning protein	2.2E-12	MTH_1706	unknown	3.4E-12
MSM0585	Msp_0657	CbiQ2	5.4E-55	MTH_1705	cobalt transport membrane protein	4.2E-60
MSM0586	Msp_0401	CbiO1	7.6E-81	MTH_1704	cobalt transport ATP-binding protein O	1.2E-85
MSM0587	Msp_1438	hypothetical protein	5.9E-10	NONE		
MSM0588	Msp_1441	FeoA	1.7E-12	MTH_1362	unknown	2.4E-11
MSM0589	Msp_1440	FeoB	3.6E-200	MTH_1361	ferrous iron transport protein B	5.7E-152
MSM0590	NONE			NONE		
MSM0591	NONE			NONE		
MSM0592	Msp_0202	conserved hypothetical membrane-spanning protein	2.3E-40	MTH_230	unknown	1.2E-48
MSM0593	Msp_0610	predicted ABC-type multidrug transport system, ATP-binding protein	3.9E-77	MTH_1487	ABC transporter (ATP-binding	2.0E-37
MSM0594	Msp_0609	conserved hypothetical membrane-spanning protein	2.7E-44	NONE		
MSM0595	Msp_0609	conserved hypothetical membrane-spanning protein	1.8E-40	NONE		
MSM0596	Msp_1163	predicted type II secretion protein F	3.0E-47	MTH_1703	unknown	4.9E-59
MSM0597	Msp_1162	predicted type II/IV secretion protein	4.1E-121	MTH_1702	secretory protein kinase	2.9E-157
MSM0598	Msp_1161	conserved hypothetical protein	3.5E-44	MTH_1701	unknown	5.6E-42
MSM0599	Msp_1160	conserved hypothetical membrane-spanning protein	1.3E-94	MTH_1700	conserved protein	8.9E-99
MSM0600	Msp_0512	predicted transcriptional regulator	7.9E-15	MTH_313	transcriptional regulator	5.5E-12
MSM0601	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM0602	Msp_1159	elongation factor 1-beta (aEF-1beta) (ef1B)	2.2E-26	MTH_1699	translation elongation factor EF-1b	1.3E-28
MSM0603	Msp_1158	predicted Zn-ribbon RNA-binding protein	4.7E-17	MTH_1178	conserved protein	8.3E-04
MSM0604	Msp_1157	predicted amino acid kinase	1.7E-42	MTH_1698	delta 1-pyrroline-5-carboxylate synthetase	6.2E-43
MSM0605	Msp_1156	putative peptidyl-tRNA hydrolase	1.5E-29	MTH_1697	conserved protein	1.1E-36
MSM0606	NONE			NONE		
MSM0607	Msp_0613	predicted ATPase	4.1E-224	MTH_1695	RNase L inhibitor	6.8E-227
MSM0608	NONE			NONE		
MSM0609	Msp_0147	ferredoxin	2.6E-04	MTH_221	unknown	6.4E-25
MSM0610	Msp_0370	putative aspartate aminotransferase	8.5E-121	MTH_1694	aspartate aminotransferase related protein	9.6E-134
MSM0611	Msp_0369	RadB	3.9E-61	MTH_1693	DNA repair protein Rad51 homolog	3.6E-63
MSM0612	Msp_0096	conserved hypothetical protein	1.9E-36	MTH_1692	conserved protein	3.8E-43
MSM0613	Msp_0095	predicted phosphatidylglycerophosphate synthase	1.0E-46	MTH_1691	conserved protein	4.3E-44
MSM0614	Msp_0094	conserved hypothetical protein	2.1E-14	MTH_1690	unknown	1.7E-17
MSM0615	Msp_0675	conserved hypothetical protein	4.7E-159	MTH_1686	conserved protein	7.7E-164
MSM0616	Msp_0440	member of asn/thr-rich large protein family	1.1E-93	MTH_716	cell surface glycoprotein (s-layer protein)	1.4E-14
MSM0617	Msp_0160	ThiI	1.4E-102	MTH_1685	conserved protein	1.1E-118
MSM0618	Msp_1489	predicted potassium transport system, membrane component	3.0E-09	MTH_760	Na+/H+-exchanging protein:Na+/H+ antiporter	2.3E-16
MSM0619	Msp_1262	AlaS	7.0E-300	MTH_1683	alanyl-tRNA synthetase	1.5e-316
MSM0620	Msp_1263	50S ribosomal protein L12P	1.9E-36	MTH_1682	ribosomal protein Lp1	9.4E-40
MSM0621	Msp_1264	50S ribosomal protein L10P	5.3E-96	MTH_1681	ribosomal protein Lp0 (E.coli)	2.7E-106
MSM0622	Msp_1265	50S ribosomal protein L1P	9.5E-74	MTH_1680	ribosomal protein L10a (E.coli)	1.3E-81

MSM0623	Msp_1266	50S ribosomal protein L11P	1.3E-62	MTH_1679	ribosomal protein L12 (E.coli)	2.2E-63
MSM0624	Msp_1267	putative transcription antiterminator	1.3E-46	MTH_1678	transcription termination factor NusG	1.1E-61
MSM0625	Msp_1268	partially conserved hypothetical membrane-spanning protein	1.3E-12	MTH_1677	protein translocation complex sec61 gamma subunit related protein	1.1E-13
MSM0626	Msp_1269	FtsZ	8.7E-135	MTH_1676	cell division protein FtsZ	1.7E-143
MSM0627	Msp_0307	MtrH	8.5E-105	MTH_1156	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit H	3.7E-116
MSM0628	NONE			MTH_1675	conserved protein	7.2E-49
MSM0629	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM0630	Msp_1271	conserved hypothetical protein	7.1E-69	MTH_1670	conserved protein	4.2E-76
MSM0631	Msp_1272	predicted transcription initiation factor IIE, alpha subunit	3.4E-37	MTH_1669	conserved protein	4.6E-47
MSM0632	Msp_1273	conserved hypothetical protein	6.2E-38	MTH_1668	conserved protein	1.7E-40
MSM0633	Msp_1063	predicted RNA-binding protein	9.2E-92	MTH_1665	conserved protein	6.9E-92
MSM0634	Msp_1064	conserved hypothetical protein	1.8E-24	MTH_1664	conserved protein	6.2E-27
MSM0635	Msp_1069	predicted regulator of aminoacid metabolism	1.6E-41	MTH_1654	unknown	1.8E-45
MSM0636	Msp_1067	hypothetical protein	1.6E-23	MTH_1649	hydrogenase expression/formation protein HypC	1.2E-25
MSM0637	Msp_1077	predicted dihydrolipoamide dehydrogenase-related protein	2.4E-93	MTH_1648	dihydrolipoamide dehydrogenase	1.2E-92
MSM0638	Msp_1343	hypothetical membrane-spanning multicopy protein A 3	2.6E-78	MTH_1646	unknown	5.9E-54
MSM0639	Msp_1080	conserved hypothetical membrane-spanning protein	4.5E-67	MTH_1644	unknown	1.8E-52
MSM0640	Msp_1081	predicted release factor aRF1	2.2E-106	MTH_1642	cell division protein	9.6E-118
MSM0641	Msp_1083	putative prephenate dehydrogenase	4.4E-92	MTH_1640	chorismate mutase	1.8E-100
MSM0642	Msp_1084	CdcH	9.3E-273	MTH_1639	cell division control protein Cdc48	4.7E-299
MSM0643	Msp_0227	conserved hypothetical protein	3.3E-71	MTH_1574	conserved protein	5.2E-78
MSM0644	Msp_0228	ThiC1	1.2E-144	MTH_1576	thiamine biosynthesis protein	3.2E-158
MSM0645	Msp_0258	ATP-dependent DNA ligase	1.1E-148	MTH_1580	DNA ligase	3.9E-176
MSM0646	Msp_0504	conserved hypothetical membrane-spanning protein	5.5E-30	NONE		
MSM0647	Msp_0259	hypothetical protein	3.8E-15	MTH_1581	conserved protein	4.8E-20
MSM0648	Msp_0263	predicted phosphomannomutase	1.2E-169	MTH_1584	phosphomannomutase	9.9E-171
MSM0649	Msp_0970	hypothetical membrane-spanning protein	3.5E-44	MTH_559	conserved protein	1.0E-06
MSM0650	Msp_0971	hypothetical protein	1.2E-36	MTH_1787	conserved protein	1.3E-07
MSM0651	Msp_1323	conserved hypothetical protein	1.5E-98	MTH_1585	O-linked GlcNAc transferase	1.9E-105
MSM0652	Msp_1324	predicted glycyl radical activating enzyme	6.3E-45	MTH_1586	pyruvate formate-lyase activating enzyme	1.5E-50
MSM0653	Msp_1326	HisC	2.5E-112	MTH_1587	histidinol-phosphate aminotransferase	1.2E-119
MSM0654	Msp_1325	predicted carbonic anhydrase/acetyltransferase	1.8E-47	MTH_1588	ferripyochelin binding protein	4.6E-47
MSM0655	Msp_1301	predicted nucleoside-diphosphate-sugar pyrophosphorylase	3.0E-134	MTH_1589	glucose-1-phosphate thymidylyltransferase homolog	8.1E-137
MSM0656	Msp_1300	predicted phosphomannomutase	9.7E-136	MTH_1590	phosphomannomutase	7.6E-141
MSM0657	Msp_1299	ApgM2	6.1E-150	MTH_1591	phosphonopyruvate decarboxylase	6.0E-148
MSM0658	NONE			NONE		
MSM0659	Msp_1298	conserved hypothetical membrane-spanning protein	4.8E-63	MTH_1592	conserved protein	1.1E-77
MSM0660	Msp_1568	conserved hypothetical membrane-spanning protein	3.9E-52	NONE		
MSM0661	Msp_1297	30S ribosomal protein S3Ae	3.2E-66	MTH_1593	ribosomal protein S3a	8.4E-71
MSM0662	Msp_0712	hypothetical membrane-spanning protein	8.9E-07	NONE		
MSM0663	Msp_1295	predicted iron-molybdenum cluster-binding protein	1.4E-08	MTH_1594	conserved protein	1.2E-16
MSM0664	Msp_0540	predicted multimeric flavodoxin	2.4E-22	MTH_1595	conserved protein	5.0E-57
MSM0665	Msp_0642	predicted purine nucleoside phosphorylase	7.4E-74	MTH_1596	methylthioadenosine phosphorylase	3.7E-77
MSM0666	Msp_0641	conserved hypothetical membrane-spanning protein	6.7E-176	MTH_1597	conserved protein	3.5E-184
MSM0667	Msp_0587	hypothetical membrane-spanning protein	1.8E-05	MTH_520	unknown	3.7E-13
MSM0668	Msp_0637	conserved hypothetical protein	4.9E-22	MTH_1598	conserved protein	5.8E-40
MSM0669	NONE			NONE		
MSM0670	NONE			NONE		

MSM0671	Msp_0635	cell division control protein 6-like 2	2.7E-108	MTH_1599	Cdc6 related protein	5.4E-131
MSM0672	Msp_0661	conserved hypothetical protein	1.4E-56	MTH_1600	conserved protein	7.0E-67
MSM0673	Msp_1557	conserved hypothetical membrane-spanning protein	5.1E-27	NONE		
MSM0674	NONE			NONE		
MSM0675	NONE			NONE		
MSM0676	Msp_1557	conserved hypothetical membrane-spanning protein	9.7E-33	NONE		
MSM0677	Msp_0662	putative aspartate aminotransferase	1.3E-131	MTH_1601	aspartate aminotransferase	7.3E-136
MSM0678	Msp_0505	conserved hypothetical membrane-spanning protein	8.1E-29	MTH_519	unknown	1.1E-20
MSM0679	Msp_0587	hypothetical membrane-spanning protein	8.1E-12	MTH_520	unknown	8.1E-34
MSM0680	Msp_0757	predicted ATPase	2.4E-109	NONE		
MSM0681	NONE			NONE		
MSM0682	NONE			NONE		
MSM0683	Msp_0380	hypothetical protein	3.1E-13	MTH_626	unknown	9.7E-22
MSM0684	Msp_0381	hypothetical membrane-spanning protein	1.2E-09	MTH_625	unknown	1.5E-04
MSM0685	NONE			NONE		
MSM0686	Msp_0605	predicted thiamine pyrophosphate-requiring enzyme	2.1E-94	NONE	acetolactate synthase, large subunit homolog	8.5E-94
MSM0687	Msp_0604	predicted deoxycytidine triphosphate deaminase	1.6E-57	MTH_1605	deoxycytidine-triphosphate deaminase related protein	8.2E-57
MSM0688	Msp_1409	predicted tautomerase	3.2E-11	MTH_1606	unknown	1.7E-08
MSM0689	NONE			NONE		
MSM0690	Msp_0767	predicted helicase	2.1E-243	NONE	ATP-dependent RNA helicase, eIF-4A family	9.5E-09
MSM0691	Msp_0006	predicted NUDIX-related protein	1.4E-40	MTH_1336	mutator MutT protein homolog	4.1E-14
MSM0692	NONE			NONE		
MSM0693	Msp_0113	conserved hypothetical protein	1.4E-13	MTH_540	intracellular protein transport protein	7.2E-10
MSM0694	NONE			NONE		
MSM0695	Msp_0767	predicted helicase	1.0E-13	NONE	ATP-dependent RNA helicase, eIF-4A family	3.7E-10
MSM0696	Msp_1095	DNA double-strand break repair protein Rad50	4.0E-04	NONE		
MSM0697	NONE			NONE		
MSM0698	NONE			NONE		
MSM0699	Msp_0738	predicted Na+-dependent transporter	4.1E-137	MTH_1909	unknown	5.8E-04
MSM0700	Msp_0921	putative poly-gamma-glutamate biosynthesis protein	1.0E-108	NONE		
MSM0701	Msp_0601	partially conserved hypothetical protein, predicted GTPase	2.4E-116	MTH_1608	signal recognition particle protein (docking protein)	3.6E-111
MSM0702	Msp_0600	conserved hypothetical protein	1.5E-20	MTH_1609	conserved protein	1.1E-36
MSM0703	Msp_0599	RplX	4.1E-18	MTH_1610	ribosomal protein L18a	1.0E-17
MSM0704	Msp_0598	translation initiation factor 6 (aIF-6)	3.7E-56	MTH_1611	conserved protein	3.8E-59
MSM0705	Msp_0597	50S ribosomal protein L31e	1.4E-22	MTH_1612	ribosomal protein L31	4.7E-29
MSM0706	NONE			MTH_1613	ribosomal protein L39	1.2E-16
MSM0707	Msp_0596	predicted subunit of tRNA methyltransferase	2.8E-58	MTH_1614	conserved protein	3.8E-59
MSM0708	Msp_0595	partially conserved hypothetical protein	1.4E-31	MTH_1615	conserved protein	3.1E-32
MSM0709	Msp_0594	30S ribosomal protein S19e	1.5E-52	MTH_1616	ribosomal protein S19	5.9E-54
MSM0710	Msp_0593	hypothetical protein	1.3E-28	MTH_1617	conserved protein	1.3E-19
MSM0711	Msp_0592	putative ribonuclease P, subunit 4	8.7E-32	MTH_1618	conserved protein	3.0E-34
MSM0712	NONE			NONE		
MSM0713	Msp_0589	predicted nucleotide kinase	3.1E-36	MTH_1619	conserved protein (adenylate kinase related)	2.4E-34
MSM0714	Msp_0660	predicted GTPase	2.1E-46	NONE	GTP-binding protein, GTP1/OBG family	3.9E-50
MSM0715	Msp_0660	predicted GTPase	2.4E-77	NONE	GTP-binding protein, GTP1/OBG family	1.2E-87
MSM0716	Msp_0368	conserved hypothetical membrane-spanning protein	1.1E-141	MTH_1623	oligosaccharyl transferase STT3 subunit related protein	7.3E-88
MSM0717	Msp_0366	TopA	8.0E-228	MTH_1624	DNA topoisomerase I	3.1E-247
MSM0718	NONE			MTH_1625	unknown	4.6E-15
MSM0719	Msp_1096	putative phosphoserine phosphatase	2.7E-124	MTH_1626	phosphoserine phosphatase	1.3E-83
MSM0720	Msp_1097	TATA-box binding protein	5.0E-68	MTH_1627	TATA-binding transcription initiation factor	1.2E-73

MSM0721	Msp_1098	predicted adenylate cyclase	2.6E-39	MTH_1629	conserved protein	1.3E-42
MSM0722	Msp_1099	LeuA2	1.9E-91	MTH_1630	2-isopropylmalate synthase	1.5E-151
MSM0723	Msp_1100	LeuC2	2.7E-140	NONE	3-isopropylmalate dehydratase, LeuC subunit	5.8E-150
MSM0724	Msp_0326	hypothetical protein	9.1E-04	MTH_1632	conserved protein	1.0E-40
MSM0725	Msp_1086	flap structure-specific endonuclease	9.2E-92	MTH_1633	DNA repair protein Rad2	7.8E-100
MSM0726	NONE			MTH_1635	conserved protein	7.1E-42
MSM0727	Msp_1085	AhcY	1.3E-163	MTH_1636	S-adenosylhomocysteine hydrolase	3.7E-164
MSM0728	Msp_0524	predicted oxidoreductase	4.4E-92	MTH_907	conserved protein	2.5E-62
MSM0729	Msp_0231	predicted E1-like enzyme	2.1E-46	MTH_1571	molybdopterin biosynthesis protein MoeB homolog	1.7E-65
MSM0730	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM0731	Msp_0113	conserved hypothetical protein	1.6E-13	MTH_511	DNA helicase II	4.6E-07
MSM0732	Msp_0873	TruB	3.2E-105	MTH_32	centromere/microtubule-binding protein	3.2E-110
MSM0733	Msp_0880	50S ribosomal protein L14e	2.3E-24	MTH_31	ribosomal protein L14	4.1E-23
MSM0734	Msp_0881	putative cytidylate kinase	1.8E-56	MTH_30	cytidylate kinase	3.8E-52
MSM0735	Msp_0882	50S ribosomal protein L34e	2.4E-29	MTH_29	ribosomal protein L34 (E.coli)	3.3E-37
MSM0736	Msp_0883	hypothetical membrane-spanning protein	1.2E-34	MTH_28	conserved protein	1.1E-50
MSM0737	Msp_0884	AdkA	1.1E-61	MTH_27	adenylate kinase	1.1E-63
MSM0738	Msp_0885	SecY	6.6E-153	MTH_26	preprotein translocase SecY	1.0E-145
MSM0739	Msp_0886	50S ribosomal protein L15P	1.9E-43	MTH_25	ribosomal protein L27a (E.coli)	4.1E-46
MSM0740	Msp_0887	50S ribosomal protein L30P	9.7E-49	MTH_24	ribosomal protein L7 (E.coli)	1.2E-53
MSM0741	Msp_0888	30S ribosomal protein S5P	3.5E-92	MTH_23	ribosomal protein S2 (E.coli)	3.7E-93
MSM0742	Msp_0889	50S ribosomal protein L18P	6.7E-57	MTH_22	ribosomal protein L5	8.9E-67
MSM0743	Msp_0890	50S ribosomal protein L19e	4.6E-58	MTH_21	ribosomal protein L19	1.5E-64
MSM0744	Msp_0891	50S ribosomal protein L32e	6.6E-34	MTH_20	ribosomal protein L32	3.1E-41
MSM0745	Msp_0892	50S ribosomal protein L6P	5.7E-60	MTH_19	ribosomal protein L9 (E.coli)	4.3E-67
MSM0746	Msp_0893	30S ribosomal protein S8P	9.5E-58	MTH_18	ribosomal protein S15a (E.coli)	1.2E-55
MSM0747	Msp_0894	30S ribosomal protein S14P	2.1E-21	MTH_17	ribosomal protein S29 (E.coli)	7.6E-22
MSM0748	Msp_0895	50S ribosomal protein L5P	2.4E-61	MTH_16	ribosomal protein L11 (E.coli)	2.9E-61
MSM0749	Msp_0896	30S ribosomal protein S4e	3.0E-70	MTH_15	ribosomal protein S4	1.8E-77
MSM0750	Msp_0897	50S ribosomal protein L24P	2.4E-29	MTH_14	ribosomal protein L26 (E.coli)	1.3E-35
MSM0751	Msp_0898	50S ribosomal protein L14P	1.4E-56	MTH_13	ribosomal protein L23 (E.coli)	1.0E-56
MSM0752	Msp_0899	30S ribosomal protein S17P	1.4E-42	MTH_12	ribosomal protein S11 (E.coli)	1.4E-45
MSM0753	Msp_0900	putative ribonuclease P, component 1	4.8E-24	MTH_11	conserved protein	8.7E-21
MSM0754	Msp_0901	protein translation factor SUI1-like protein	2.4E-45	MTH_10	ribosomal protein SUI1	3.6E-47
MSM0755	Msp_0902	50S ribosomal protein L29P	3.3E-16	MTH_9	ribosomal protein L35 (E.coli)	7.9E-20
MSM0756	Msp_0903	30S ribosomal protein S3P	6.8E-96	MTH_8	ribosomal protein S3 (E.coli)	1.2E-96
MSM0757	Msp_0904	50S ribosomal protein L22P	1.3E-46	MTH_7	ribosomal protein L17 (E.coli)	3.5E-56
MSM0758	Msp_0905	30S ribosomal protein S19P	1.4E-58	MTH_6	ribosomal protein S15 (E.coli)	1.3E-58
MSM0759	Msp_0906	50S ribosomal protein L2P	3.1E-107	MTH_5	ribosomal protein L8 (E.coli)	1.9E-105
MSM0760	Msp_0907	50S ribosomal protein L23P	2.8E-26	MTH_4	ribosomal protein L23a (E.coli)	5.4E-28
MSM0761	Msp_0908	50S ribosomal protein L1e	4.5E-99	MTH_3	ribosomal protein L4 (E.coli)	2.6E-99
MSM0762	Msp_0909	50S ribosomal protein L3P	1.5E-121	MTH_2	ribosomal protein L3 (E.coli)	1.1E-132
MSM0763	Msp_0910	conserved hypothetical protein	1.1E-79	MTH_1	conserved protein	1.2E-73
MSM0764	Msp_1319	predicted DNA modification methylase	1.7E-04	MTH_1918	possible protein methyltransferase	3.7E-45
MSM0765	Msp_0914	PycA	1.7E-186	MTH_1917	biotin carboxylase	5.5E-202
MSM0766	Msp_0915	partially conserved hypothetical protein	4.0E-36	MTH_1916	biotin acetyl-CoA carboxylase ligase/biotin operon repressor	5.3E-62
MSM0767	Msp_0916	predicted selenocysteine synthase	2.8E-99	MTH_1914	conserved protein	2.3E-100
MSM0768	Msp_0917	hypothetical protein	7.5E-04	MTH_1912	unknown	1.1E-11
MSM0769	Msp_0791	fumarate hydratase	3.1E-59	NONE	fumarate hydratase, class I related protein	1.5E-50

MSM0770	Msp_1112	CbiO2	1.2E-43	NONE	methyl coenzyme M reductase system, component A2 homolog	8.3E-64
MSM0771	Msp_0657	CbiQ2	1.4E-05	MTH_453	conserved protein	2.6E-12
MSM0772	NONE			MTH_452	unknown	9.2E-07
MSM0773	Msp_0958	predicted ABC-type polar amino acid transport system, ATP-binding protein	1.4E-26	MTH_1704	cobalt transport ATP-binding protein O	5.9E-25
MSM0774	Msp_0340	PstB	1.6E-26	MTH_1731	phosphate transport system ATP-binding	5.2E-26
MSM0775	Msp_0149	predicted transcriptional regulator	2.0E-34	NONE		
MSM0776	Msp_0790	conserved hypothetical membrane-spanning protein	2.2E-138	MTH_1909	unknown	2.8E-159
MSM0777	Msp_0491	hypothetical membrane-spanning protein	3.6E-10	MTH_1908	unknown	3.2E-16
MSM0778	Msp_0517	predicted RNA-binding protein	3.6E-184	MTH_1907	conserved protein	2.0E-188
MSM0779	Msp_0516	predicted Zn-dependent hydrolase of the beta-lactamase superfamily	2.3E-70	MTH_1902	conserved protein	3.5E-72
MSM0780	NONE			MTH_1901	unknown	2.9E-16
MSM0781	Msp_1151	hypothetical membrane-spanning protein	1.2E-09	MTH_1533	unknown	1.3E-10
MSM0782	Msp_1151	hypothetical membrane-spanning protein	2.4E-04	MTH_979	unknown	1.2E-05
MSM0783	Msp_1447	EhbK	3.3E-20	NONE	tungsten formylmethanofuran dehydrogenase, subunit F homolog	3.5E-88
MSM0784	Msp_0236	ferredoxin	5.5E-14	MTH_927	ferredoxin	5.1E-16
MSM0785	Msp_0514	putative phosphopantetheine adenylyltransferase	1.0E-37	MTH_1896	conserved protein	1.3E-42
MSM0786	Msp_1129	partially conserved hypothetical membrane-spanning protein	1.1E-49	MTH_412	conserved protein	1.3E-69
MSM0787	Msp_0511	predicted Fe-S oxidoreductase	7.6E-120	MTH_1895	conserved protein	8.7E-124
MSM0788	Msp_0510	putative aspartate aminotransferase	5.5E-117	MTH_1894	aspartate aminotransferase homolog	3.3E-108
MSM0789	Msp_0519	predicted Co/Zn/Cd cation transporter	7.6E-33	MTH_1893	cation efflux system protein (zinc/cadmium)	1.8E-77
MSM0790	Msp_1428	conserved hypothetical protein	1.3E-15	MTH_1884	conserved protein	3.0E-36
MSM0791	Msp_0443	2-phosphoglycerate kinase	3.6E-81	MTH_1883	2-phosphoglycerate kinase	3.7E-84
MSM0792	Msp_1010	predicted phosphoesterase	1.8E-47	MTH_1882	conserved protein	2.3E-52
MSM0793	Msp_1011	conserved hypothetical protein	1.9E-29	MTH_1881	conserved protein	4.4E-42
MSM0794	Msp_1012	conserved hypothetical protein	1.9E-20	MTH_1880	conserved protein	2.1E-28
MSM0795	Msp_1013	HdrB1	1.9E-116	NONE	heterodisulfide reductase, subunit B	4.3E-115
MSM0796	Msp_1014	HdrC1	1.6E-69	NONE	heterodisulfide reductase, subunit C	4.7E-77
MSM0797	Msp_1015	conserved hypothetical protein	2.5E-50	MTH_1877	conserved protein	1.6E-53
MSM0798	NONE			NONE		
MSM0799	Msp_0113	conserved hypothetical protein	1.6E-12	MTH_1626	phosphoserine phosphatase	2.2E-06
MSM0800	NONE			NONE		
MSM0801	Msp_1017	DphB	1.7E-74	MTH_1874	diphthine synthase	2.9E-77
MSM0802	Msp_1022	predicted methyltransferase	3.6E-81	MTH_1873	met-10+ protein	1.3E-74
MSM0803	NONE			MTH_633	conserved protein	4.3E-04
MSM0804	Msp_1023	putative translation initiation factor aIF-2B, subunit 1	5.0E-100	NONE	translation initiation factor eIF-2B, alpha subunit	2.2E-125
MSM0805	Msp_0958	predicted ABC-type polar amino acid transport system, ATP-binding protein	5.0E-100	MTH_696	ABC transporter (glutamine transport ATP-binding protein)	2.7E-35
MSM0806	Msp_0959	predicted ABC-type polar amino acid transport system, permease protein	2.1E-92	NONE		
MSM0807	Msp_0960	predicted ABC-type polar amino acid transport system, periplasmic substrate-binding protein	3.5E-108	NONE		
MSM0808	Msp_1024	conserved hypothetical protein	2.9E-104	MTH_1871	nitrogenase iron-molybdenum cofactor biosynthesis protein NifB	1.6E-115
MSM0809	Msp_1025	conserved hypothetical protein	2.3E-40	MTH_1870	conserved protein	3.1E-41
MSM0810	Msp_1026	predicted activator of 2-hydroxyglutaryl-CoA dehydratase	5.5E-165	MTH_1869	activator of (R)-2-hydroxyglutaryl-CoA	1.7E-175
MSM0811	Msp_1027	conserved hypothetical protein	1.7E-53	MTH_1868	conserved protein	1.2E-57

MSM0812	Msp_1029	conserved hypothetical protein	1.3E-39	MTH_1866	conserved protein	1.0E-40
MSM0813	Msp_1030	predicted peptidyl-prolyl cis-trans isomerase	2.6E-135	MTH_1865	conserved protein	2.3E-146
MSM0814	Msp_1032	predicted selenophosphate synthetase-related protein	3.3E-87	MTH_1864	phosphoribosylformylglycinamidine synthase II related protein	6.2E-91
MSM0815	Msp_1033	conserved hypothetical protein	4.5E-99	MTH_1863	conserved protein	4.4E-97
MSM0816	Msp_1034	predicted nucleic acid-binding protein	3.7E-33	MTH_1862	conserved protein	3.5E-40
MSM0817	Msp_0799	predicted transcriptional regulator	6.6E-34	MTH_1843	unknown	1.0E-33
MSM0818	Msp_0798	predicted transcriptional regulator	5.0E-36	MTH_1843	unknown	2.1E-26
MSM0819	NONE			MTH_1438	unknown	4.6E-15
MSM0820	NONE			MTH_1861	molybdenum cofactor biosynthesis MoaB	2.5E-46
MSM0821	Msp_1036	PyrE	3.1E-59	MTH_1860	uridine 5'-monophosphate synthase	5.2E-55
MSM0822	Msp_1035	hypothetical protein	3.1E-13	MTH_1859	unknown	1.4E-15
MSM0823	NONE			NONE		
MSM0824	NONE			NONE	N-terminal acetyltransferase complex, subunit ARD1	3.1E-06
MSM0825	Msp_0437	conserved hypothetical protein	4.7E-56	NONE		
MSM0826	Msp_0114	ThsB	8.2E-226	MTH_794	chaperonin	2.4E-231
MSM0827	Msp_0747	member of asn/thr-rich large protein family	5.9E-04	MTH_796	conserved protein	4.5E-33
MSM0828	Msp_0220	predicted glycosyltransferase	2.0E-14	MTH_540	intracellular protein transport protein	8.1E-06
MSM0829	Msp_0110	aspartate-semialdehyde dehydrogenase	6.6E-121	MTH_799	aspartate-semialdehyde dehydrogenase	2.3E-132
MSM0830	Msp_0109	DapB	1.0E-85	MTH_800	dihydrodipicolinate reductase	3.2E-87
MSM0831	Msp_0108	DapA	4.9E-86	MTH_801	dihydrodipicolinate synthase	2.0E-85
MSM0832	Msp_0107	putative aspartokinase	2.2E-129	MTH_802	aspartokinase II alpha subunit	6.7E-149
MSM0833	Msp_0106	30S ribosomal protein S17e	1.3E-19	MTH_803	ribosomal protein S17	1.5E-23
MSM0834	Msp_0105	putative chorismate mutase	3.8E-15	NONE	chorismate mutase, subunit A	9.3E-17
MSM0835	Msp_0104	AroK	4.7E-56	MTH_805	conserved protein (homoserine kinase related)	2.6E-76
MSM0836	Msp_0101	predicted glycosyltransferase	2.6E-64	MTH_450	LPS biosynthesis RfbU related protein	9.6E-31
MSM0837	Msp_0102	CbiD	6.5E-91	MTH_808	cobalamin biosynthesis protein D	4.0E-87
MSM0838	Msp_0103	putative thioredoxin	2.5E-18	MTH_807	thioredoxin	7.1E-19
MSM0839	Msp_0100	predicted helicase	2.1E-227	MTH_810	DNA helicase related protein	9.1E-248
MSM0840	Msp_0097	conserved hypothetical protein	3.0E-15	MTH_814	conserved protein	1.6E-14
MSM0841	Msp_0371	hypothetical protein	6.6E-11	MTH_815	unknown	2.2E-15
MSM0842	Msp_0372	predicted histone acetyltransferase	1.5E-187	MTH_817	conserved protein	6.2E-189
MSM0843	NONE			MTH_818	deoxyribose-phosphate aldolase	2.1E-26
MSM0844	Msp_0122	archaeal histone	3.5E-21	MTH_821	histone HMtA1	2.5E-23
MSM0845	Msp_0376	predicted 2-methylthioadenine synthetase	8.9E-126	MTH_826	conserved protein	3.8E-130
MSM0846	Msp_0375	conserved hypothetical protein	1.6E-39	MTH_828	conserved protein	1.6E-46
MSM0847	Msp_0374	LeuD2	4.1E-57	NONE	3-isopropylmalate dehydratase, LeuD subunit	7.4E-56
MSM0848	Msp_0373	predicted archaeal sugar kinase	1.5E-73	MTH_830	conserved protein	3.0E-82
MSM0849	Msp_0384	predicted Fe-S oxidoreductase	6.6E-169	MTH_831	molybdenum cofactor biosynthesis MoaA homolog	2.7E-177
MSM0850	Msp_0385	conserved hypothetical membrane-spanning protein	2.4E-45	MTH_832	conserved protein	1.4E-43
MSM0851	Msp_0386	predicted transcriptional regulator	1.1E-70	MTH_834	conserved protein	3.0E-98
MSM0852	Msp_0387	predicted ATP-utilizing enzyme	2.3E-40	MTH_835	conserved protein	1.0E-53
MSM0853	Msp_0217	predicted UDP-N-acetylglucosamine 2-epimerase	1.4E-120	MTH_837	UDP-N-acetylglucosamine 2-epimerase	1.3E-136
MSM0854	NONE			NONE		
MSM0855	Msp_0388	TruA	5.2E-50	MTH_840	pseudouridylate synthase I	1.6E-51
MSM0856	NONE			MTH_695	conserved protein	1.7E-08
MSM0857	Msp_1000	predicted ABC-type nitrate/sulfonate/bicarbonate transport system, ATB-binding protein	1.5E-29	MTH_696	ABC transporter (glutamine transport ATP-binding protein)	3.3E-44
MSM0858	Msp_0389	HisA	6.3E-77	MTH_843	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	7.4E-79
MSM0859	Msp_0390	putative cytidylyltransferase	5.1E-43	MTH_844	autotrophic growth protein	1.5E-48

MSM0860	Msp_0552	ArgC	4.9E-109	MTH_846	N-acetyl-gamma-glutamyl-phosphate reductase	2.0E-108
MSM0861	Msp_0554	hypothetical protein	4.8E-31	MTH_847	unknown	3.3E-44
MSM0862	Msp_0521	PyrI	2.1E-44	MTH_850	aspartate carbamoyltransferase regulatory subunit	7.5E-47
MSM0863	Msp_1419	hypothetical protein	3.1E-20	NONE		
MSM0864	NONE			MTH_1285	conserved protein	2.7E-10
MSM0865	Msp_0159	conserved hypothetical protein	1.1E-79	MTH_853	conserved protein	2.4E-96
MSM0866	Msp_0402	predicted zinc metalloprotease	4.7E-143	MTH_856	zinc metalloproteinase	8.2E-144
MSM0867	Msp_0403	conserved hypothetical protein	1.1E-47	MTH_857	conserved protein	4.0E-48
MSM0868	NONE			NONE		
MSM0869	Msp_0404	predicted GTPase	3.0E-93	NONE	GTP-binding protein, GTP1/OBG family	8.2E-112
MSM0870	Msp_0405	putative small heat shock protein	1.2E-16	NONE	heat shock protein, class I	3.8E-20
MSM0871	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM0872	Msp_1054	predicted phosphosugar isomerase	1.2E-103	MTH_860	glucosamine--fructose-6-phosphate aminotransferase	5.6E-113
MSM0873	Msp_1309	conserved hypothetical protein	7.6E-17	MTH_863	conserved protein	5.4E-28
MSM0874	Msp_1308	adenine deaminase	1.5E-139	MTH_866	adenine deaminase	1.3E-132
MSM0875	Msp_1347	conserved hypothetical protein	6.0E-136	MTH_867	conserved protein	6.4E-144
MSM0876	Msp_0415	predicted arginase/agmatinase/formimionoglutamate hydrolase	1.3E-71	MTH_868	agmatine ureohydrolase	1.2E-73
MSM0877	Msp_1352	translation initiation factor 5A (aIF-5A)	4.4E-53	NONE	translation initiation factor, eIF-5A	1.7E-49
MSM0878	Msp_1327	PdaD	2.1E-37	MTH_870	conserved protein	3.4E-42
MSM0879	Msp_1330	PpnK	7.2E-60	MTH_872	conserved protein	9.0E-77
MSM0880	Msp_1331	predicted UDP-N-acetylmuramyl pentapeptide synthase	1.1E-47	MTH_873	UDP-N-acetylmuramyl tripeptide synthetase related protein	5.4E-81
MSM0881	Msp_1332	HemC	7.3E-83	MTH_874	porphobilinogen deaminase	2.0E-85
MSM0882	Msp_1333	predicted dehydrogenase	2.7E-101	NONE	3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein	3.0E-130
MSM0883	Msp_1334	predicted orotate phosphoribosyltransferase	5.6E-53	MTH_876	orotate phosphoribosyltransferase	9.7E-70
MSM0884	Msp_0747	member of asn/thr-rich large protein family	1.5E-18	MTH_716	cell surface glycoprotein (s-layer protein)	4.1E-07
MSM0885	Msp_1465	member of asn/thr-rich large protein family	2.4E-39	MTH_716	cell surface glycoprotein (s-layer protein)	1.7E-08
MSM0886	NONE			NONE		
MSM0887	Msp_1410	predicted universal stress protein	2.5E-18	MTH_898	conserved protein	1.5E-18
MSM0888	Msp_1416	GdhA	2.6E-181	NONE		
MSM0889	NONE			NONE		
MSM0890	NONE			NONE		
MSM0891	Msp_1363	peptide chain release factor, subunit 1 (aRF-1)	3.4E-149	NONE	peptide chain release factor eRF, subunit 1	8.7E-156
MSM0892	Msp_1056	hypothetical membrane-spanning protein	5.4E-06	MTH_1905	unknown	3.2E-06
MSM0893	Msp_1202	predicted acetyltransferase	2.4E-29	NONE	N-terminal acetyltransferase complex, subunit ARD1	3.7E-38
MSM0894	Msp_1203	conserved hypothetical protein	5.7E-28	MTH_1000	conserved protein	1.2E-25
MSM0895	Msp_1204	predicted cation transport ATPase	3.9E-235	MTH_1001	cation-transporting P-ATPase PacL	9.8E-251
MSM0896	Msp_1205	CbiJ	6.5E-43	MTH_1002	cobalamin biosynthesis protein J	8.5E-39
MSM0897	Msp_1365	30S ribosomal protein S10P	1.6E-48	MTH_1059	ribosomal protein S20 (E.coli)	1.3E-49
MSM0898	Msp_1366	translation elongation factor 1-alpha (EF-Tu)	1.9E-185	NONE	translation elongation factor, EF-1 alpha	3.9E-192
MSM0899	Msp_1367	FusA	1.7e-319	NONE	translation elongation factor, EF-2	1.9e-318
MSM0900	Msp_1368	30S ribosomal protein S7P	3.3E-80	MTH_1056	ribosomal protein S5 (E.coli)	9.2E-81
MSM0901	Msp_1369	30S ribosomal protein S12P	4.4E-69	MTH_1055	ribosomal protein S23 (E.coli)	7.8E-68
MSM0902	Msp_0321	MrtA	5.7E-250	NONE	methyl coenzyme M reductase II, alpha subunit	2.0E-250
MSM0903	Msp_0320	MrtG	1.6E-103	NONE	methyl coenzyme M reductase II, gamma subunit	1.8E-116
MSM0904	Msp_0319	MrtD	1.9E-45	NONE	methyl coenzyme M reductase II, D protein	2.2E-40
MSM0905	Msp_0318	MrtB	9.8E-159	NONE	methyl coenzyme M reductase II, beta subunit	4.1E-181
MSM0906	Msp_1370	NusA	1.7E-44	MTH_1054	transcription termination factor NusA	2.5E-55
MSM0907	Msp_1371	50S ribosomal protein L30e	6.0E-33	MTH_1053	ribosomal protein L30	3.0E-36
MSM0908	Msp_1372	RpoA2	2.1E-126	NONE	DNA-dependent RNA polymerase, subunit A"	4.7E-141

MSM0909	Msp_1373	RpoA1	0.0E+00	NONE	DNA-dependent RNA polymerase, subunit A'	0.0E+00
MSM0910	Msp_1374	RpoB1	6.1E-253	NONE	DNA-dependent RNA polymerase, subunit B'	4.6E-276
MSM0911	Msp_1375	RpoB2	3.3E-103	NONE	DNA-dependent RNA polymerase, subunit B''	8.6E-220
MSM0912	Msp_1376	RpoH	7.6E-17	NONE	DNA-dependent RNA polymerase, subunit H	4.6E-15
MSM0913	NONE			NONE		
MSM0914	NONE			MTH_72	O-linked GlcNAc transferase	3.0E-04
MSM0915	NONE			NONE		
MSM0916	Msp_0682	ThiM1	1.2E-73	NONE		
MSM0917	Msp_0683	hypothetical protein	7.7E-56	NONE		
MSM0918	Msp_1381	phosphoglycerate kinase	1.1E-120	MTH_1042	3-phosphoglycerate kinase	4.3E-131
MSM0919	Msp_1382	TpiA	4.9E-77	MTH_1041	triosephosphate isomerase	3.2E-71
MSM0920	Msp_1103	member of asn/thr-rich large protein family	4.2E-04	NONE		
MSM0921	Msp_0548	hypothetical membrane-spanning protein	1.1E-05	NONE		
MSM0922	Msp_1383	predicted Fe-S oxidoreductase	1.7E-97	MTH_1039	conserved protein	4.9E-98
MSM0923	Msp_0540	predicted multimeric flavodoxin	1.2E-16	MTH_135	conserved protein	1.3E-17
MSM0924	Msp_1386	SucC	3.4E-101	NONE	succinyl-CoA synthetase, beta subunit	3.7E-116
MSM0925	Msp_1387	KorC	9.5E-58	NONE	2-oxoglutarate oxidoreductase, gamma subunit	8.8E-60
MSM0926	Msp_1388	KorB	1.3E-99	NONE	2-oxoglutarate oxidoreductase, beta subunit	2.2E-102
MSM0927	Msp_1389	KorA	4.5E-138	NONE	2-oxoglutarate oxidoreductase, alpha subunit	6.2E-130
MSM0928	Msp_1390	KorD	3.0E-15	NONE	ferredoxin (putative 2-oxoglutarate oxidoreductase, delat subunit)	8.6E-14
MSM0929	Msp_0791	fumarate hydratase	3.7E-17	NONE	fumarate hydratase, class I	3.5E-40
MSM0930	Msp_0325	predicted peptidyl-prolyl cis-trans isomerase 2	3.5E-67	MTH_1125	fkbp-type peptidyl-prolyl cis-trans isomerase	1.8E-77
MSM0931	Msp_0801	conserved hypothetical protein	7.0E-94	MTH_448	unknown	4.8E-68
MSM0932	Msp_1167	conserved hypothetical protein	4.7E-49	MTH_1113	conserved protein	1.6E-58
MSM0933	Msp_1168	CobS	1.2E-50	MTH_1112	cobalamin (5'-phosphate) synthase	1.9E-41
MSM0934	Msp_1169	hypothetical protein	1.1E-06	MTH_1111	conserved protein	1.5E-41
MSM0935	Msp_1170	conserved hypothetical protein	4.5E-106	MTH_1109	conserved protein	4.2E-92
MSM0936	Msp_1171	predicted ATPase	6.3E-77	MTH_1108	conserved protein	1.0E-65
MSM0937	NONE			NONE		
MSM0938	NONE			NONE		
MSM0939	Msp_1173	PycB	1.4E-212	NONE	oxaloacetate decarboxylase, alpha subunit	2.8E-221
MSM0940	Msp_1166	predicted myo-inositol-1-phosphate synthase	5.3E-151	MTH_1105	conserved protein	9.4E-159
MSM0941	Msp_0634	predicted prenyltransferase	2.3E-70	MTH_1098	bacteriochlorophyll synthase related protein	4.2E-69
MSM0942	Msp_0616	partially conserved hypothetical membrane-spanning protein	5.0E-52	MTH_371	unknown	5.1E-35
MSM0943	NONE			MTH_466	unknown	5.6E-09
MSM0944	NONE			NONE		
MSM0945	Msp_1285	hydrogenase expression/formation protein	9.3E-147	MTH_1072	hydrogenase expression/formation protein HypD	2.2E-141
MSM0946	Msp_0215	predicted glycosyltransferase	6.1E-04	MTH_1071	conserved protein	3.9E-50
MSM0947	Msp_1284	predicted modulator of DNA gyrase	3.7E-95	MTH_1070	conserved protein	1.5E-96
MSM0948	Msp_0220	predicted glycosyltransferase	4.0E-04	NONE		
MSM0949	Msp_1351	predicted transcriptional activator	6.7E-18	MTH_628	unknown	1.6E-19
MSM0950	NONE			MTH_1003	molybdenum cofactor biosynthesis protein MoeA	6.8E-101
MSM0951	Msp_1335	translation initiation factor 1A (aIF-1A) (eIF1A)	1.6E-41	NONE	translation initiation factor, eIF-1A	1.3E-44
MSM0952	Msp_1337	predicted serine/threonine protein kinase	5.1E-59	MTH_1005	conserved protein	1.1E-75
MSM0953	NONE			MTH_630	unknown	1.5E-04
MSM0954	Msp_1338	predicted RNA-binding protein	1.4E-56	MTH_1006	conserved protein	2.0E-60
MSM0955	Msp_1339	type II DNA topoisomerase VI, subunit B	2.4E-203	MTH_1007	conserved protein	1.5E-213
MSM0956	Msp_1340	type II DNA topoisomerase VI, subunit A	4.3E-149	MTH_1008	conserved protein	1.8E-155
MSM0957	Msp_0119	hypothetical membrane-spanning protein	6.8E-20	MTH_524	unknown	4.9E-35

MSM0958	Msp_1110	CobN	5.3E-11	MTH_515	unknown	1.1E-08
MSM0959	Msp_0994	conserved hypothetical protein	3.0E-31	NONE		
MSM0960	Msp_0678	predicted cation transport ATPase	4.8E-134	MTH_411	cadmium efflux ATPase	1.9E-80
MSM0961	Msp_0224	predicted cation transport ATPase	9.6E-07	MTH_1535	heavy-metal transporting CPx-type ATPase	1.4E-08
MSM0962	Msp_1346	glyceraldehyde 3-phosphate dehydrogenase	4.7E-127	MTH_1009	glyceraldehyde 3-phosphate dehydrogenase	5.9E-134
MSM0963	Msp_0992	putative endonuclease IV	9.5E-06	MTH_1010	endonuclease IV	6.6E-71
MSM0964	Msp_1349	predicted phosphohydrolase	8.0E-19	MTH_1179	conserved protein	1.1E-38
MSM0965	Msp_0718	preducted 3-hydroxyacyl-CoA dehydrogenase	2.6E-126	NONE		
MSM0966	Msp_1415	putative 26S protease, regulatory subunit	6.5E-107	MTH_1011	ATP-dependent 26S protease regulatory subunit 8	7.4E-111
MSM0967	Msp_1408	HemA	4.6E-90	MTH_1012	glutamyl-tRNA reductase	3.2E-94
MSM0968	Msp_1407	predicted siroheme synthase	2.4E-45	MTH_1013	conserved protein	1.9E-41
MSM0969	Msp_1406	predicted metal-binding transcription factor	4.9E-54	MTH_1014	conserved protein	5.6E-58
MSM0970	Msp_0784	hypothetical protein	1.3E-21	NONE		
MSM0971	Msp_0393	methyl-coenzyme M reductase, component A2	7.6E-191	NONE	methyl coenzyme M reductase system, component A2	4.3E-209
MSM0972	Msp_1405	conserved hypothetical protein	1.3E-46	MTH_1016	conserved protein	5.5E-51
MSM0973	Msp_1404	putative GTP cyclohydrolase III	9.2E-76	MTH_1017	conserved protein	1.3E-88
MSM0974	Msp_1403	CofD	3.6E-90	MTH_1018	conserved protein	8.0E-98
MSM0975	Msp_1402	CofE	3.8E-63	MTH_1019	conserved protein	1.6E-76
MSM0976	Msp_1398	PurO	2.8E-51	MTH_1020	conserved protein	1.0E-51
MSM0977	Msp_1397	conserved hypothetical membrane-spanning protein	3.7E-24	MTH_1021	unknown	3.2E-30
MSM0978	Msp_1396	predicted biopolymer transport protein	1.5E-77	MTH_1022	biopolymer transport protein	4.1E-94
MSM0979	Msp_1395	RnhB	1.6E-48	MTH_1023	ribonuclease HII	9.8E-61
MSM0980	Msp_1517	DnaK	5.3E-16	MTH_1024	rod shape-determining protein	7.3E-136
MSM0981	NONE			MTH_1025	unknown	2.6E-51
MSM0982	Msp_1394	partially conserved hypothetical membrane-spanning protein	2.4E-38	MTH_1027	CDP-diacylglycerol-serine O-phosphatidyltransferase	8.2E-41
MSM0983	Msp_1393	conserved hypothetical membrane-spanning protein	8.7E-48	MTH_1028	unknown	1.7E-70
MSM0984	NONE			MTH_1030	unknown	1.4E-45
MSM0985	Msp_1392	conserved hypothetical protein	1.1E-29	MTH_1031	conserved protein	6.3E-34
MSM0986	Msp_0760	putative bile salt acid hydrolase	4.3E-110	NONE		
MSM0987	Msp_0329	MfnA	3.9E-100	MTH_1116	glutamate decarboxylase	6.1E-123
MSM0988	Msp_0328	PpsA	1.7E-273	MTH_1118	phosphoenolpyruvate synthase	2.0E-250
MSM0989	Msp_0327	50S ribosomal protein L10e	2.8E-58	MTH_1119	ribosomal protein L10	2.1E-65
MSM0990	Msp_1000	predicted ABC-type nitrate/sulfonate/bicarbonate transport system, ATB-binding protein	4.7E-40	MTH_920	anion permease	4.2E-37
MSM0991	Msp_1001	predicted ABC-type nitrate/sulfonate/bicarbonate transport system, permease protein	2.4E-11	MTH_478	sulfate transport system permease protein	4.1E-09
MSM0992	Msp_0326	hypothetical protein	1.0E-12	MTH_1121	unknown	8.9E-12
MSM0993	Msp_0601	partially conserved hypothetical protein, predicted GTPase	3.9E-04	MTH_1123	unknown	1.9E-15
MSM0994	Msp_0324	predicted nucleotidyltransferase	3.4E-101	MTH_1126	conserved protein	2.7E-90
MSM0995	Msp_0590	member of asn/thr-rich large protein family	8.7E-33	MTH_716	cell surface glycoprotein (s-layer protein)	1.3E-09
MSM0996	Msp_0983	member of asn/thr-rich large protein family	2.6E-26	MTH_716	cell surface glycoprotein (s-layer protein)	1.1E-09
MSM0997	Msp_0323	PyrC	1.1E-97	MTH_1127	dihydroorotase	7.8E-100
MSM0998	Msp_1447	EhbK	1.0E-30	MTH_1133	polyferredoxin (MvhB)	4.4E-145
MSM0999	Msp_0316	MvhA	3.4E-181	NONE	methyl viologen-reducing hydrogenase, alpha subunit	2.1E-207
MSM1000	Msp_0315	MvhG	3.2E-128	NONE	methyl viologen-reducing hydrogenase, gamma subunit	5.5E-138
MSM1001	Msp_0314	MvhD1	3.9E-61	NONE	methyl viologen-reducing hydrogenase, delta subunit	1.6E-67
MSM1002	Msp_0312	conserved hypothetical protein	1.2E-130	MTH_1150	ABC transporter subunit Ycf24	3.5E-152
MSM1003	Msp_0313	predicted ABC-type transport system	3.2E-82	MTH_1149	ABC transporter subunit Ycf16	8.0E-98
MSM1004	Msp_0311	conserved hypothetical protein	1.2E-27	MTH_1151	unknown	9.3E-33

MSM1005	Msp_0310	predicted GTP:adenosylcobinamide-phosphate guanylyltransferase	4.0E-36	MTH_1152	conserved protein	7.0E-35
MSM1006	Msp_0308	conserved hypothetical protein	2.2E-90	MTH_1153	conserved protein	5.2E-165
MSM1007	Msp_0307	MtrH	2.1E-108	MTH_1156	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit H	2.9E-125
MSM1008	Msp_0306	MtrG	5.7E-12	MTH_1157	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit G	4.2E-21
MSM1009	Msp_0305	MtrF	5.5E-07	MTH_1158	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit F	9.3E-17
MSM1010	Msp_0304	MtrA	9.0E-62	MTH_1159	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit A	9.8E-93
MSM1011	Msp_0303	MtrB	1.0E-12	MTH_1160	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit B	1.7E-31
MSM1012	Msp_0302	MtrC	7.6E-49	MTH_1161	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit C	7.2E-81
MSM1013	Msp_0301	MtrD	2.0E-57	MTH_1162	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit D	1.0E-81
MSM1014	Msp_0300	MtrE	9.5E-74	MTH_1163	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit E	1.5E-121
MSM1015	Msp_0321	MrtA	7.6E-207	NONE	methyl coenzyme M reductase I, alpha subunit	1.7E-253
MSM1016	Msp_0320	MrtG	6.2E-86	NONE	methyl coenzyme M reductase I, gamma subunit	2.9E-109
MSM1017	Msp_0299	McrC	2.8E-67	NONE	methyl coenzyme M reductase I, C protein	2.6E-83
MSM1018	Msp_0319	MrtD	7.4E-19	NONE	methyl coenzyme M reductase I, D protein	1.1E-34
MSM1019	Msp_0318	MrtB	1.6E-133	NONE	methyl coenzyme M reductase I, beta subunit	3.4E-177
MSM1020	Msp_0298	predicted Fe-S oxidoreductase	2.0E-119	MTH_1170	conserved protein	1.7E-136
MSM1021	Msp_0284	conserved hypothetical protein	1.7E-99	MTH_1180	conserved protein	6.7E-117
MSM1022	Msp_0285	conserved hypothetical protein	8.5E-34	MTH_1181	unknown	2.0E-23
MSM1023	Msp_0973	ComB2	1.3E-44	MTH_1182	conserved protein	2.7E-42
MSM1024	Msp_0287	conserved hypothetical membrane-spanning protein	1.9E-98	MTH_1183	pheromone shutdown protein TraB	4.4E-58
MSM1025	Msp_0288	hypothetical protein	1.5E-20	MTH_1184	unknown	3.0E-20
MSM1026	NONE			MTH_1224	inosine-5'-monophosphate dehydrogenase related protein III	5.6E-04
MSM1027	NONE			MTH_1155	Na+/Ca+ exchanging protein related	2.1E-42
MSM1028	Msp_0289	predicted ATPase	9.5E-74	MTH_1186	conserved protein	2.0E-85
MSM1029	Msp_0693	conserved hypothetical protein	1.3E-39	MTH_1187	conserved protein	3.2E-23
MSM1030	Msp_0290	predicted pyridoxal phosphate-dependent enzyme	1.3E-124	MTH_1188	pleiotropic regulatory protein DegT	6.1E-123
MSM1031	Msp_0291	N2,N2-dimethylguanosine tRNA methyltransferase	1.1E-109	NONE	N2,N2-dimethylguanosine tRNA methyltransferase	4.1E-110
MSM1032	Msp_0293	predicted transcriptional regulator	9.3E-44	MTH_1193	transcriptional regulator	2.9E-52
MSM1033	Msp_0294	conserved hypothetical protein	1.8E-109	MTH_1196	conserved protein	7.7E-116
MSM1034	Msp_0295	conserved hypothetical protein	6.0E-17	MTH_1197	conserved protein	1.1E-22
MSM1035	Msp_0296	CofG	4.2E-96	MTH_1198	biotin synthetase related protein	6.4E-105
MSM1036	Msp_0297	predicted methyltransferase	2.3E-70	MTH_1200	met-10+ related protein	5.7E-72
MSM1037	Msp_0282	PsmB	7.5E-58	NONE	proteasome, beta subunit	7.8E-68
MSM1038	Msp_0281	predicted exonuclease	5.4E-245	MTH_1203	cleavage and polyadenylation specificity factor	3.5E-278
MSM1039	Msp_0280	PurM	1.6E-103	MTH_1204	phosphoribosylformylglycinamidine cyclo-ligase	4.0E-112
MSM1040	Msp_0279	ComC	7.6E-104	MTH_1205	malate dehydrogenase	5.7E-104
MSM1041	Msp_1507	putative DNA polymerase	6.8E-167	MTH_1208	DNA-dependent DNA polymerase family B (PolB1)	5.1E-183
MSM1042	NONE			MTH_1211	conserved protein	4.0E-71
MSM1043	Msp_1420	PyrK	4.4E-69	NONE	cytochrome-c3 hydrogenase, gamma subunit	1.6E-74
MSM1044	Msp_1421	PyrD	7.4E-90	MTH_1213	dihydroorotate oxidase	1.3E-106
MSM1045	Msp_0220	predicted glycosyltransferase	1.9E-12	MTH_1626	phosphoserine phosphatase	2.4E-05

MSM1046	Msp_1422	predicted ribosomal biogenesis protein	1.2E-89	MTH_1214	pre-mRNA splicing protein PRP31	1.4E-88
MSM1047	Msp_1423	FlpA	5.3E-64	MTH_1215	fibrillarin-like pre-rRNA processing protein	2.5E-62
MSM1048	Msp_1424	predicted phosphopantothenoylcysteine synthetase/decarboxylase	1.9E-43	MTH_1216	pantothenate metabolism flavoprotein	2.3E-52
MSM1049	Msp_1424	predicted phosphopantothenoylcysteine synthetase/decarboxylase	2.0E-55	MTH_1216	pantothenate metabolism flavoprotein	2.2E-54
MSM1050	Msp_1425	conserved hypothetical membrane-spanning protein	4.7E-11	MTH_1218	unknown	3.3E-21
MSM1051	Msp_1426	hypothetical membrane-spanning protein	3.5E-05	MTH_1219	unknown	9.0E-19
MSM1052	Msp_1427	PheA	2.5E-59	MTH_1220	chorismate mutase	1.1E-70
MSM1053	Msp_1428	conserved hypothetical protein	4.4E-60	MTH_1222	inosine-5'-monophosphate dehydrogenase related protein I	4.5E-72
MSM1054	Msp_1429	conserved hypothetical protein	2.2E-74	MTH_1224	inosine-5'-monophosphate dehydrogenase related protein III	1.3E-83
MSM1055	Msp_1431	partially conserved hypothetical protein	1.9E-36	MTH_1227	coenzyme PQQ synthesis protein III	1.9E-57
MSM1056	Msp_1432	putative 6-pyruvoyl tetrahydrobiopterin synthase	1.4E-38	MTH_1228	conserved protein	4.6E-47
MSM1057	Msp_1433	conserved hypothetical protein	2.1E-53	MTH_1229	conserved protein	2.1E-49
MSM1058	Msp_1434	conserved hypothetical protein	5.6E-85	MTH_1231	conserved protein	1.1E-95
MSM1059	Msp_0945	predicted RecB family exonuclease	1.2E-06	MTH_1233	unknown	1.4E-36
MSM1060	Msp_1436	EhbQ	4.9E-61	MTH_1235	conserved protein	1.2E-69
MSM1061	Msp_1442	EhbP	6.3E-22	MTH_1236	conserved protein	1.6E-28
MSM1062	Msp_1443	EhbO	6.1E-79	NONE	NADH dehydrogenase (ubiquinone), subunit 1 related protein	5.8E-111
MSM1063	Msp_1444	EhbN	8.0E-141	NONE	formate hydrogenlyase, subunit 5	2.8E-143
MSM1064	Msp_1445	EhbM	1.0E-62	NONE	formate hydrogenlyase, subunit 7	1.6E-67
MSM1065	Msp_1446	EhbL	8.6E-41	MTH_1240	ferredoxin-like protein	3.4E-51
MSM1066	Msp_1447	EhbK	7.7E-72	MTH_1241	polyferredoxin	1.7E-97
MSM1067	Msp_1448	EhbJ	4.5E-12	MTH_1242	unknown	5.5E-19
MSM1068	Msp_1449	EhbI	4.2E-48	MTH_1243	conserved protein	1.0E-49
MSM1069	Msp_1450	EhbH	3.5E-21	MTH_1244	conserved protein	5.0E-25
MSM1070	Msp_1451	EhbG	4.8E-15	MTH_1245	unknown	6.6E-16
MSM1071	Msp_1452	EhbF	1.1E-134	NONE	NADH dehydrogenase I, subunit N	8.4E-142
MSM1072	Msp_1453	EhbE	2.0E-32	MTH_1247	conserved protein	4.5E-40
MSM1073	Msp_1454	EhbD	4.1E-18	MTH_1248	conserved protein	9.4E-24
MSM1074	Msp_1455	EhbC	1.4E-10	MTH_1249	conserved protein	1.5E-18
MSM1075	Msp_1456	EhbB	2.2E-10	MTH_1250	unknown	1.1E-13
MSM1076	Msp_1457	EhbA	1.2E-27	MTH_1251	conserved protein	6.8E-37
MSM1077	Msp_1336	predicted permease	2.3E-05	NONE		
MSM1078	Msp_1336	predicted permease	9.6E-97	MTH_900	conserved protein	3.1E-32
MSM1079	Msp_1458	conserved hypothetical membrane-spanning protein	2.1E-28	MTH_1252	conserved protein	1.6E-35
MSM1080	NONE			MTH_1253	unknown	2.5E-48
MSM1081	Msp_0795	partially conserved hypothetical protein	1.4E-56	MTH_1634	transcriptional control factor (enhancer-binding protein)	5.0E-176
MSM1082	NONE			NONE		
MSM1083	Msp_0202	conserved hypothetical membrane-spanning protein	4.5E-35	MTH_230	unknown	1.0E-33
MSM1084	Msp_1459	ArgG	7.4E-138	MTH_1254	argininosuccinate synthase	2.1E-136
MSM1085	Msp_1240	AqpM2	1.8E-54	MTH_103	water channel protein	1.5E-71
MSM1086	NONE			MTH_101	unknown	3.8E-194
MSM1087	NONE			NONE		
MSM1088	NONE			NONE		
MSM1089	Msp_0506	hypothetical membrane-spanning protein	3.3E-04	NONE		
MSM1090	Msp_1057	SfsA	6.0E-33	MTH_1521	sugar fermentation stimulation protein	3.6E-31
MSM1091	Msp_1501	predicted sugar kinase	3.6E-97	MTH_1256	conserved protein	1.4E-114

MSM1092	Msp_1502	formylmethanofuran-tetrahydromethanopterin formyltransferase	1.2E-91	MTH_1259	formylmethanofuran:tetrahydromethanopterin formyltransferase	1.3E-127
MSM1093	Msp_0233	conserved hypothetical protein	2.3E-22	NONE		
MSM1094	Msp_1503	conserved hypothetical membrane-spanning protein	2.8E-81	MTH_1261	conserved protein	7.2E-97
MSM1095	Msp_0830	Trk-type potassium transport system, membrane protein	2.6E-62	MTH_1264	TRK system potassium uptake protein TrkH	2.1E-122
MSM1096	Msp_0250	TrkA1	3.1E-52	MTH_1265	TRK system potassium uptake protein TrkA	3.6E-79
MSM1097	Msp_1505	putative Zn-dependent hydrolase	2.3E-40	MTH_1267	conserved protein	1.2E-53
MSM1098	Msp_1418	putative archaeal holliday junction resolvase	1.4E-38	MTH_1270	conserved protein	1.4E-43
MSM1099	Msp_0270	predicted biotin synthase related protein	7.4E-106	MTH_1279	conserved protein	2.3E-75
MSM1100	NONE			MTH_627	unknown	7.2E-10
MSM1101	Msp_0269	GatB	1.4E-175	MTH_1280	PET112-like protein	3.6E-182
MSM1102	Msp_0268	conserved hypothetical protein	3.4E-78	MTH_1282	inosine-5'-monophosphate dehydrogenase related protein VI	2.3E-93
MSM1103	Msp_0267	HisE	4.8E-31	MTH_1283	phosphoribosyl-AMP cyclohydrolase homolog	3.0E-34
MSM1104	Msp_1506	predicted acetyltransferase	2.6E-11	MTH_1284	conserved protein	3.2E-16
MSM1105	Msp_1492	conserved hypothetical protein	7.0E-62	MTH_1286	phosphoribosylaminoimidazole carboxylase related protein	1.7E-65
MSM1106	Msp_1497	HypF	8.5E-208	MTH_1287	transcriptional regulator HypF homolog	2.3E-219
MSM1107	Msp_1519	predicted transcriptional regulator	6.6E-34	MTH_1288	unknown	1.8E-52
MSM1108	Msp_1518	GrpE	2.1E-44	MTH_1289	heat shock protein GrpE	1.6E-44
MSM1109	Msp_1517	DnaK	8.6E-247	MTH_1290	DnaK protein (Hsp70)	7.7E-251
MSM1110	Msp_1516	DnaJ	3.0E-118	MTH_1291	DnaJ protein	1.0E-122
MSM1111	Msp_0145	member of asn/thr-rich large protein family	5.9E-49	MTH_716	cell surface glycoprotein (s-layer protein)	7.7E-12
MSM1112	Msp_0762	member of asn/thr-rich large protein family	1.6E-40	MTH_716	cell surface glycoprotein (s-layer protein)	3.3E-11
MSM1113	Msp_0762	member of asn/thr-rich large protein family	2.9E-70	MTH_716	cell surface glycoprotein (s-layer protein)	1.2E-05
MSM1114	Msp_0145	member of asn/thr-rich large protein family	1.3E-24	MTH_716	cell surface glycoprotein (s-layer protein)	3.3E-15
MSM1115	Msp_0017	conserved hypothetical protein	2.2E-21	NONE		
MSM1116	Msp_1108	member of asn/thr-rich large protein family	4.2E-137	MTH_911	probable surface protein	1.5E-12
MSM1117	Msp_1110	CobN	8.5E-304	MTH_514	cobalamin biosynthesis protein N	1.4E-239
MSM1118	Msp_1494	hypothetical membrane-spanning protein	1.5E-18	MTH_1294	unknown	2.5E-23
MSM1119	Msp_1495	hypothetical membrane-spanning protein	4.1E-25	MTH_1295	unknown	4.8E-36
MSM1120	Msp_1496	methionine aminopeptidase	3.4E-53	MTH_1296	methionine aminopeptidase	2.8E-86
MSM1121	Msp_1305	FrhB	3.9E-77	NONE	coenzyme F420-reducing hydrogenase, beta subunit	2.1E-97
MSM1122	Msp_1304	FrhG	4.6E-81	NONE	coenzyme F420-reducing hydrogenase, gamma subunit	2.2E-102
MSM1123	Msp_1514	putative coenzyme F420 hydrogenase, delta subunit-like protein	9.3E-44	NONE	coenzyme F420-reducing hydrogenase, delta subunit	4.7E-61
MSM1124	Msp_1302	FrhA	9.4E-138	NONE	coenzyme F420-reducing hydrogenase, alpha subunit	8.8E-163
MSM1125	Msp_1110	CobN	2.3E-10	MTH_1301	unknown	3.8E-11
MSM1126	Msp_0120	predicted transcriptional regulator	3.1E-20	MTH_1795	transcriptional regulator	1.1E-20
MSM1127	Msp_0121	predicted cation transport ATPase	1.2E-162	MTH_411	cadmium efflux ATPase	1.2E-119
MSM1128	NONE			NONE		
MSM1129	Msp_1523	conserved hypothetical protein	2.3E-118	MTH_1305	conserved protein	3.6E-134
MSM1130	Msp_1028	conserved hypothetical protein	4.5E-44	MTH_1868	conserved protein	1.4E-15
MSM1131	Msp_1524	conserved hypothetical protein	1.1E-56	MTH_1306	conserved protein	1.1E-59
MSM1132	Msp_1525	ribosome biogenesis protein Nop10	2.3E-15	MTH_1307	unknown	4.0E-16
MSM1133	Msp_1527	putative translation initiation factor 2, alpha subunit (aIF-2-alpha) (eIF2A)	3.4E-94	NONE	translation initiation factor eIF-2, alpha subunit	3.5E-104
MSM1134	Msp_1528	30S ribosomal protein S27e	2.3E-17	MTH_1309	ribosomal protein S27	8.1E-18
MSM1135	Msp_1529	50S ribosomal protein L44e	1.6E-41	MTH_1310	ribosomal protein L36a	2.7E-42
MSM1136	Msp_1530	partially conserved hypothetical protein	1.6E-30	MTH_1311	unknown	2.1E-49
MSM1137	Msp_1531	DNA polymerase sliding clamp (PCNA)	1.5E-73	MTH_1312	proliferating-cell nuclear antigen	6.0E-93
MSM1138	Msp_0580	predicted glutamine amidotransferase	5.2E-73	MTH_787	cobyric acid synthase	9.2E-10

MSM1139	Msp_0581	predicted UDP-N-acetylmuramyl tripeptide synthase	3.6E-90	MTH_530	UDP-N-acetylmuramyl tripeptide synthetase related protein	6.8E-16
MSM1140	Msp_0417	hypothetical membrane-spanning protein	2.7E-04	NONE		
MSM1141	Msp_1075	TrpA	7.3E-44	NONE	tryptophan synthase, subunit alpha	6.5E-48
MSM1142	Msp_1074	TrpB	6.4E-123	NONE	tryptophan synthase, beta subunit	1.3E-120
MSM1143	Msp_1072	TrpC	1.7E-42	MTH_1657	indole-3-glycerol phosphate synthase	1.4E-38
MSM1144	Msp_1076	TrpD	2.0E-71	MTH_1661	anthranilate phosphoribosyltransferase	2.3E-68
MSM1145	Msp_1071	TrpG	7.4E-51	MTH_1656	anthranilate synthase component II	1.1E-43
MSM1146	Msp_1070	TrpE	6.5E-78	MTH_1655	anthranilate synthase component I	9.9E-84
MSM1147	NONE			NONE		
MSM1148	NONE			MTH_1189	conserved protein	8.2E-08
MSM1149	Msp_0607	hypothetical membrane-spanning protein	6.0E-33	MTH_1192	conserved protein	2.8E-31
MSM1150	Msp_0608	predicted transcriptional regulator	9.4E-19	MTH_1328	conserved protein	1.3E-17
MSM1151	Msp_1247	PurB	6.0E-159	MTH_1537	adenylosuccinate lyase	8.4E-174
MSM1152	Msp_0879	hypothetical membrane-spanning protein	2.8E-04	MTH_1538	unknown	6.4E-25
MSM1153	Msp_0224	predicted cation transport ATPase	1.1E-205	MTH_1535	heavy-metal transporting CPx-type ATPase	5.1E-199
MSM1154	Msp_0200	predicted metal-dependent hydrolase	1.2E-07	MTH_1534	aryldialkylphosphatase related protein	5.0E-89
MSM1155	Msp_0225	conserved hypothetical protein	1.4E-40	MTH_1530	conserved protein	1.7E-42
MSM1156	Msp_0221	TruD	6.2E-125	MTH_1529	conserved protein	4.6E-134
MSM1157	Msp_1512	hypothetical membrane-spanning protein	3.5E-05	MTH_1526	conserved protein	8.9E-04
MSM1158	Msp_1511	HypE2	8.9E-126	MTH_1525	hydrogenase expression/formation protein HypE related protein	4.2E-156
MSM1159	Msp_1510	HisH	3.0E-38	MTH_1524	imidazoleglycerol-phosphate synthase	9.1E-58
MSM1160	Msp_1461	predicted nitrogenase molybdenum-iron protein	3.8E-118	MTH_1522	nitrogenase alpha chain (NifD) related protein	8.9E-131
MSM1161	Msp_0719	partially conserved hypothetical membrane-spanning protein	2.8E-05	NONE		
MSM1162	NONE			NONE		
MSM1163	NONE			NONE		
MSM1164	Msp_1463	predicted GTPase	1.4E-143	MTH_1515	GTP-binding protein	2.4E-153
MSM1165	Msp_1472	predicted phosphohydrolase	2.2E-67	MTH_1179	conserved protein	9.0E-10
MSM1166	Msp_1474	conserved hypothetical membrane-spanning protein	1.5E-146	NONE		
MSM1167	Msp_1464	CbiE	6.8E-48	MTH_1514	precorrin-6Y methylase	3.9E-50
MSM1168	Msp_0590	member of asn/thr-rich large protein family	1.7E-16	MTH_75	surface protease related protein	2.1E-11
MSM1169	NONE			NONE		
MSM1170	Msp_0169	putative arsenical prump-driving ATPase	5.3E-96	MTH_1511	arsenical pump-driving ATPase	6.9E-108
MSM1171	Msp_0170	NadE	1.1E-63	MTH_1510	NH(3)-dependent NAD+ synthetase	1.3E-60
MSM1172	Msp_0171	LeuS	0.0E+00	MTH_1508	leucyl-tRNA synthetase	0.0E+00
MSM1173	Msp_0004	predicted tRNA(1-methyladenosine) methyltransferase	1.0E-62	MTH_1414	protein-L-isoaspartate methyltransferase homolog	1.4E-77
MSM1174	Msp_0309	HtpX	1.8E-38	MTH_569	heat shock protein X	2.1E-67
MSM1175	Msp_0548	hypothetical membrane-spanning protein	6.6E-11	NONE		
MSM1176	Msp_0413	RfcS	2.2E-115	NONE	replication factor C, small subunit	3.7E-125
MSM1177	Msp_0414	RfcL	1.1E-113	NONE	replication factor C, large subunit	3.8E-123
MSM1178	Msp_0578	conserved hypothetical protein	4.1E-34	MTH_239	unknown	9.7E-38
MSM1179	Msp_0647	AroE	1.8E-72	MTH_242	shikimate 5-dehydrogenase	1.2E-71
MSM1180	NONE			MTH_1189	conserved protein	1.6E-08
MSM1181	Msp_0648	HisS	5.1E-114	MTH_244	histidyl-tRNA synthetase	3.8E-130
MSM1182	Msp_0649	HisI	1.6E-39	MTH_245	phosphoribosyl-AMP cyclohydrolase	1.0E-40
MSM1183	Msp_0650	predicted ATPase	1.5E-155	MTH_246	twitching mobility (PilT) related protein	8.0E-185
MSM1184	Msp_0651	predicted sugar phosphate isomerase/epimerase or endonuclease	8.7E-48	MTH_247	conserved protein	4.5E-49
MSM1185	Msp_1499	putative methylated-DNA--protein-cysteine methyltransferase	1.3E-12	MTH_618	O6-methylguanidine-DNA methyltransferase	2.8E-15

MSM1186	Msp_1489	predicted potassium transport system, membrane component	9.9E-111	NONE		
MSM1187	Msp_0007	predicted ERCC4-like helicase	5.4E-213	NONE	ATP-dependent RNA helicase, eIF-4A family	3.5E-241
MSM1188	Msp_0590	member of asn/thr-rich large protein family	1.4E-49	MTH_716	cell surface glycoprotein (s-layer protein)	6.9E-13
MSM1189	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM1190	Msp_1211	partially conserved hypothetical membrane-spanning protein	6.7E-128	MTH_530	UDP-N-acetylmuramyl tripeptide synthetase related protein	3.1E-57
MSM1191	Msp_1212	predicted UDP-N-acetylmuramoylalanine--D-glutamate ligase	7.9E-102	MTH_531	UDP-N-acetylmuramyl tripeptide synthetase related protein	1.3E-40
MSM1192	Msp_0008	conserved hypothetical protein	9.1E-124	MTH_1421	conserved protein	5.0E-137
MSM1193	Msp_0009	putative single-stranded-DNA-specific exonuclease	9.9E-111	MTH_1422	conserved protein	9.3E-136
MSM1194	Msp_0010	30S ribosomal protein S15P	5.3E-48	MTH_1423	ribosomal protein S13 (E.coli)	2.1E-49
MSM1195	Msp_0011	putative xanthosine triphosphate pyrophosphatase	1.9E-61	MTH_1424	conserved protein	1.2E-62
MSM1196	Msp_0635	cell division control protein 6-like 2	9.7E-06	NONE		
MSM1197	NONE			NONE		
MSM1198	Msp_0013	putative O-sialoglycoprotein endopeptidase	7.7E-159	MTH_1425	O-sialoglycoprotein endopeptidase	1.9E-174
MSM1199	Msp_0999	hypothetical protein	7.0E-06	NONE		
MSM1200	Msp_0012	predicted phosphoribosyltransferase	1.4E-88	MTH_1426	conserved protein	3.4E-99
MSM1201	Msp_0014	UppP	6.0E-72	MTH_1428	bacitracin resistance protein	1.1E-43
MSM1202	Msp_0015	IlvE	4.0E-114	MTH_1430	branched-chain amino-acid aminotransferase	5.2E-110
MSM1203	Msp_0724	hypothetical membrane-spanning protein	6.7E-09	MTH_470	conserved protein	7.9E-05
MSM1204	Msp_0163	F420-dependent methylenetetrahydromethanopterin dehydrogenase	4.0E-82	NONE	coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin dehydrogenase	2.2E-102
MSM1205	Msp_0417	hypothetical membrane-spanning protein	5.3E-04	MTH_1490	unknown	3.5E-17
MSM1206	Msp_0164	HisB	2.5E-57	MTH_1467	imidazoleglycerol-phosphate dehydratase	9.7E-54
MSM1207	NONE			MTH_1470	molybdenum transport protein ModA related protein	2.2E-17
MSM1208	Msp_0165	predicted polysaccharide biosynthesis protein	5.0E-116	MTH_1471	O-antigen transporter homolog	3.2E-87
MSM1209	Msp_0540	predicted multimeric flavodoxin	6.7E-25	MTH_1473	conserved protein	4.7E-54
MSM1210	Msp_0925	predicted arabinose efflux permease	7.5E-22	MTH_195	efflux pump antibiotic resistance protein	2.5E-24
MSM1211	Msp_0260	hypothetical protein	4.6E-16	MTH_1626	phosphoserine phosphatase	4.3E-06
MSM1212	NONE			NONE		
MSM1213	Msp_1498	formaldehyde activating enzyme fused to 3-hexulose-6-phosphate synthase	8.3E-162	MTH_1474	D-arabino 3-hexulose 6-phosphate formaldehyde lyase related protein	6.3E-169
MSM1214	Msp_1573	ThrS	7.3E-202	MTH_1455	threonyl-tRNA synthetase	1.3E-225
MSM1215	Msp_0162	CbiA	1.7E-147	NONE	cobyrinic acid a,c-diamide synthase	9.4E-143
MSM1216	Msp_0166	conserved hypothetical membrane-spanning protein	1.3E-74	MTH_1461	conserved protein	2.1E-67
MSM1217	Msp_0019	partially conserved hypothetical protein	5.0E-45	MTH_1434	unknown	1.3E-55
MSM1218	Msp_0020	SurE	1.2E-68	MTH_1435	survival protein SurE	1.5E-73
MSM1219	NONE			NONE		
MSM1220	NONE			MTH_1440	unknown	8.6E-14
MSM1221	Msp_0021	conserved hypothetical protein	5.2E-89	MTH_1441	conserved protein	3.4E-106
MSM1222	Msp_0022	IlvC	6.9E-126	MTH_1442	ketol-acid reductoisomerase	2.7E-122
MSM1223	Msp_0591	predicted carbonic anhydrase	8.1E-13	MTH_1582	carbonic anhydrase	3.7E-38
MSM1224	Msp_0025	IlvH1	1.1E-45	NONE	acetolactate synthase, small subunit	4.1E-55
MSM1225	Msp_0026	IlvB1	6.3E-180	NONE	acetolactate synthase, large subunit	3.5E-207
MSM1226	Msp_0031	ArgF	2.3E-102	MTH_1446	ornithine carbamoyltransferase	4.6E-102
MSM1227	Msp_0030	PurD	1.1E-150	MTH_1445	glycinamide ribonucleotide synthetase	4.2E-147
MSM1228	Msp_0513	predicted Na+-driven multidrug efflux pump	5.6E-108	MTH_314	conserved protein	2.8E-95
MSM1229	Msp_0513	predicted Na+-driven multidrug efflux pump	1.1E-125	MTH_314	conserved protein	3.1E-105
MSM1230	Msp_0512	predicted transcriptional regulator	5.3E-25	MTH_313	transcriptional regulator	2.2E-17
MSM1231	Msp_1574	ArgS	1.4E-157	MTH_1447	arginyl-tRNA synthetase	9.3E-175

MSM1232	Msp_1575	putative signal peptidase	3.6E-42	MTH_1448	signal peptidase	2.7E-42
MSM1233	Msp_1180	HemL	5.8E-138	MTH_228	glutamate-1-semialdehyde aminotransferase	2.1E-136
MSM1234	Msp_1179	CbiC	8.2E-68	MTH_227	precorrin isomerase	7.1E-58
MSM1235	Msp_0093	predicted flavoprotein	2.5E-59	NONE		
MSM1236	Msp_0135	AspS	1.9E-164	MTH_226	aspartyl-tRNA synthetase	1.2E-165
MSM1237	Msp_1576	IlvD	7.2E-195	MTH_1449	dihydroxy-acid dehydratase	3.4E-177
MSM1238	Msp_0134	HisD	2.7E-131	MTH_225	histidinol dehydrogenase	2.7E-138
MSM1239	Msp_1569	predicted DNA-binding protein	2.7E-92	MTH_1458	unknown	5.1E-96
MSM1240	Msp_1570	conserved hypothetical protein	8.9E-23	MTH_1457	unknown	3.0E-24
MSM1241	Msp_1571	predicted ATPase	5.2E-82	MTH_1456	chromosome partitioning protein Soj	1.9E-73
MSM1242	Msp_1074	TrpB	7.2E-37	NONE	tryptophan synthase, beta subunit homolog	1.0E-168
MSM1243	NONE			MTH_1477	unknown	3.1E-73
MSM1244	Msp_1491	predicted metal-dependent phosphoesterase	1.9E-45	MTH_1478	conserved protein	8.9E-28
MSM1245	Msp_0198	AlbA	2.2E-26	MTH_1483	conserved protein	3.8E-27
MSM1246	Msp_0199	LeuA1	8.3E-162	MTH_1481	isopropylmalate synthase	2.8E-175
MSM1247	Msp_0197	conserved hypothetical membrane-spanning protein	2.6E-78	MTH_1485	serine/threonine protein kinase related protein	1.2E-92
MSM1248	Msp_0196	ABC-type multidrug transport system, permease protein	4.6E-74	MTH_1486	conserved protein	1.5E-82
MSM1249	Msp_0195	ABC-type multidrug transport system, ATP-binding protein	1.6E-94	MTH_1487	ABC transporter (ATP-binding	5.1E-103
MSM1250	Msp_0194	predicted transcriptional regulator	3.6E-19	MTH_1488	unknown	1.6E-19
MSM1251	Msp_0651	predicted sugar phosphate isomerase/epimerase or endonuclease	7.5E-26	MTH_1489	conserved protein	8.8E-60
MSM1252	Msp_0191	MapB	8.0E-38	MTH_1493	cation transporting P-type ATPase related protein	1.8E-54
MSM1253	Msp_0181	GatA	2.1E-165	MTH_1496	amidase	1.1E-164
MSM1254	Msp_0174	predicted cobyric acid synthase	7.3E-115	NONE	cobyrinic acid a,c-diamide synthase related protein	8.9E-115
MSM1255	NONE			NONE		
MSM1256	Msp_0175	RibB	2.5E-59	MTH_1499	GTP cyclohydrolase II	2.8E-63
MSM1257	Msp_0177	predicted transcriptional regulator	1.7E-19	MTH_1500	conserved protein	9.4E-24
MSM1258	Msp_0180	TfrA	2.0E-174	NONE	succinate dehydrogenase, flavoprotein subunit	3.9E-185
MSM1259	Msp_0200	predicted metal-dependent hydrolase	1.0E-115	MTH_1505	N-ethylammeline chlorohydrolase homolog	9.3E-120
MSM1260	Msp_0383	archaeal histone	8.8E-16	MTH_1696	histone HMtA2	8.4E-16
MSM1261	Msp_0178	HisG	1.4E-88	MTH_1506	ATP phosphoribosyltransferase	1.3E-90
MSM1262	NONE			NONE		
MSM1263	Msp_0003	PyrB	8.4E-98	MTH_1413	aspartate carbamoyltransferase	5.1E-96
MSM1264	Msp_0001	cell division control protein 6-like 1	4.9E-141	MTH_1412	Cdc6 related protein	8.2E-160
MSM1265	NONE			MTH_1410	unknown	1.4E-31
MSM1266	Msp_1588	CobD	4.4E-76	MTH_1409	cobalamin biosynthesis protein B	7.6E-54
MSM1267	Msp_1587	CbiG	2.3E-70	MTH_1408	cobalamin biosynthesis protein G	3.0E-50
MSM1268	Msp_1586	conserved hypothetical protein	2.7E-21	MTH_1407	conserved protein	2.6E-28
MSM1269	NONE			NONE		
MSM1270	Msp_1585	predicted class II aldolase	4.7E-40	MTH_1406	fuculose-1-phosphate aldolase	4.9E-43
MSM1271	Msp_1584	PolB	4.5E-131	MTH_1405	DNA polymerase delta small subunit	3.6E-156
MSM1272	Msp_1583	hypothetical membrane-spanning protein	5.8E-19	MTH_1404	unknown	4.3E-28
MSM1273	Msp_1582	CbiH	2.5E-98	MTH_1403	precorrin-3 methylase	1.2E-101
MSM1274	NONE			MTH_1402	conserved protein	6.4E-73
MSM1275	Msp_0962	hypothetical membrane-spanning protein	2.4E-04	MTH_1401	unknown	5.4E-108
MSM1276	Msp_1558	hypothetical protein	1.7E-10	MTH_1400	unknown	1.3E-16
MSM1277	Msp_1559	conserved hypothetical membrane-spanning protein	8.0E-38	MTH_1399	unknown	2.0E-46
MSM1278	Msp_0757	predicted ATPase	4.3E-101	NONE		
MSM1279	Msp_1562	conserved hypothetical protein	1.5E-50	MTH_1398	conserved protein	2.3E-52
MSM1280	Msp_1561	conserved hypothetical protein	5.0E-52	MTH_1397	conserved protein	1.2E-25
MSM1281	Msp_1563	CbiX	7.5E-42	MTH_1397	conserved protein	8.6E-30

MSM1282	Msp_0590	member of asn/thr-rich large protein family	3.1E-13	MTH_716	cell surface glycoprotein (s-layer protein)	2.7E-05
MSM1283	Msp_1564	ThiL	6.8E-48	MTH_1396	thiamine monphosphate kinase	3.1E-57
MSM1284	Msp_1565	predicted pyruvate-formate lyase-activating enzyme	1.5E-66	MTH_1395	pyruvate formate-lyase activating enzyme related protein	3.5E-81
MSM1285	Msp_0615	partially conserved hypothetical membrane-spanning protein	6.8E-05	NONE		
MSM1286	Msp_1479	predicted 3-octaprenyl-4-hydroxybenzoate carboxy-lyase	5.7E-147	MTH_1394	conserved protein	3.5E-152
MSM1287	Msp_1480	PurE	6.4E-68	MTH_1393	phosphoribosylaminoimidazole carboxylase	1.9E-80
MSM1288	NONE			NONE		
MSM1289	Msp_1168	CobS	6.5E-04	NONE		
MSM1290	Msp_0054	predicted glycosyltransferase	1.4E-33	MTH_374	dolichyl-phosphate mannose synthase related protein	7.5E-31
MSM1291	NONE			NONE		
MSM1292	Msp_0920	predicted transcriptional accessory protein	9.5E-232	NONE	translation initiation factor eIF-2, alpha subunit	2.1E-04
MSM1293	Msp_0965	predicted nitroreductase	3.3E-16	MTH_120	NADPH-oxidoreductase	2.1E-33
MSM1294	Msp_1481	conserved hypothetical membrane-spanning protein	3.4E-124	MTH_1392	dolichyl-phosphate mannoosyltransferase related protein	5.8E-150
MSM1295	Msp_1482	conserved hypothetical membrane-spanning protein	7.0E-94	MTH_1391	conserved protein	3.8E-114
MSM1296	Msp_1483	RibH	2.0E-50	MTH_1390	riboflavin synthase beta subunit	1.4E-54
MSM1297	Msp_0219	conserved hypothetical protein	3.0E-70	NONE		
MSM1298	Msp_1484	LeuB	3.8E-109	MTH_1388	3-isopropylmalate dehydrogenase	3.2E-103
MSM1299	Msp_1485	LeuD1	3.1E-43	NONE	3-isopropylmalate dehydratase, LeuC subunit	3.3E-60
MSM1300	Msp_1486	LeuC1	1.3E-165	NONE	3-isopropylmalate dehydratase, LeuD subunit	1.7E-175
MSM1301	NONE			NONE		
MSM1302	NONE			NONE		
MSM1303	Msp_0214	predicted UDP-N-acetyl-D-mannosaminuronate dehydrogenase	2.3E-143	MTH_836	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	2.8E-79
MSM1304	Msp_1116	predicted dTDP-4-dehydrorhamnose reductase	9.6E-42	MTH_1792	dTDP-4-dehydrorhamnose reductase	1.9E-73
MSM1305	Msp_0762	member of asn/thr-rich large protein family	5.3E-36	MTH_716	cell surface glycoprotein (s-layer protein)	2.2E-12
MSM1306	Msp_0590	member of asn/thr-rich large protein family	3.5E-45	MTH_716	cell surface glycoprotein (s-layer protein)	1.8E-07
MSM1307	Msp_1102	predicted dTDP-glucose pyrophosphorylase	4.1E-41	MTH_1791	glucose-1-phosphate thymidylyltransferase	1.4E-123
MSM1308	Msp_0539	predicted dTDP-4-dehydrorhamnose 3,5-epimerase	1.9E-68	NONE	dTDP-4-dehydrorhamnose 3,5-epimerase	5.4E-60
MSM1309	Msp_1114	predicted dTDP-D-glucose 4,6-dehydratase	4.5E-106	NONE	dTDP-glucose 4,6-dehydratase	3.0E-137
MSM1310	Msp_0212	predicted glycosyltransferase	1.8E-54	MTH_884	teichoic acid biosynthesis related protein	7.1E-10
MSM1311	Msp_0496	predicted glycosyltransferase	2.8E-34	MTH_136	dolichyl-phosphate mannose synthase	2.2E-05
MSM1312	Msp_0500	predicted glycosyltransferase	4.8E-79	MTH_172	conserved protein	6.5E-19
MSM1313	Msp_0492	predicted glycosyltransferase	6.1E-57	MTH_338	LPS biosynthesis RfbU related protein	2.9E-07
MSM1314	NONE			NONE		
MSM1315	NONE			NONE		
MSM1316	Msp_0495	predicted glycosyltransferase	2.3E-33	MTH_884	teichoic acid biosynthesis related protein	8.9E-09
MSM1317	Msp_0500	predicted glycosyltransferase	2.9E-07	NONE		
MSM1318	Msp_0927	hypothetical protein	2.1E-30	NONE		
MSM1319	Msp_0928	hypothetical protein	3.0E-31	NONE		
MSM1320	Msp_0492	predicted glycosyltransferase	4.1E-58	NONE		
MSM1321	Msp_0500	predicted glycosyltransferase	4.4E-76	MTH_172	conserved protein	9.5E-17
MSM1322	Msp_0492	predicted glycosyltransferase	6.5E-62	MTH_338	LPS biosynthesis RfbU related protein	9.6E-12
MSM1323	Msp_0495	predicted glycosyltransferase	5.3E-34	MTH_884	teichoic acid biosynthesis related protein	2.0E-08
MSM1324	Msp_0215	predicted glycosyltransferase	1.0E-32	MTH_884	teichoic acid biosynthesis related protein	1.5E-08
MSM1325	Msp_0204	predicted ABC-type polysaccharide/polyol phosphate export system, permease protein	1.2E-64	MTH_1092	putative membrane protein	6.6E-06
MSM1326	Msp_0205	predicted ABC-type polysaccharide/polyol phosphate export system, ATP-binding protein	3.7E-79	MTH_1370	ABC transporter (ATP-binding protein)	2.0E-16
MSM1327	NONE			MTH_361	teichoic acid biosynthesis protein RodC related protein	2.4E-17
MSM1328	Msp_0212	predicted glycosyltransferase	2.9E-26	MTH_884	teichoic acid biosynthesis related protein	2.0E-12

MSM1329	Msp_0206	predicted glycosyltransferase	5.2E-82	MTH_172	conserved protein	2.5E-46
MSM1330	Msp_0207	predicted glycosyltransferase	9.1E-69	MTH_172	conserved protein	1.1E-20
MSM1331	Msp_0208	predicted bacterial sugar transferase	9.0E-117	NONE		
MSM1332	Msp_1487	predicted ssDNA-binding protein	6.2E-157	MTH_1385	replication factor A related protein	7.8E-152
MSM1333	Msp_1488	RadA	6.9E-142	MTH_1383	DNA repair protein RadA	6.4E-144
MSM1334	Msp_1477	predicted permease	1.4E-56	MTH_1382	conserved protein	1.2E-57
MSM1335	NONE			NONE		
MSM1336	Msp_1476	HdrA1	6.9E-277	NONE	heterodisulfide reductase, subunit A	2.0E-298
MSM1337	Msp_1475	GlyA	5.9E-145	MTH_1380	serine hydroxymethyltransferase	6.5E-151
MSM1338	Msp_1473	predicted flavoprotein	3.4E-53	MTH_1379	conserved protein (contains ferredoxin domain)	5.0E-73
MSM1339	Msp_1471	conserved hypothetical protein	2.5E-11	MTH_1377	conserved protein	9.7E-22
MSM1340	Msp_1470	S-adenosylmethionine synthetase	2.2E-138	MTH_1376	conserved protein	3.7E-148
MSM1341	Msp_1468	IleS	0.0E+00	MTH_1375	isoleucyl-tRNA synthetase	0.0E+00
MSM1342	Msp_1467	PurL	5.9E-239	MTH_1374	phosphoribosylformylglycinamidine synthase II	4.4E-255
MSM1343	NONE			MTH_1369	molybdenum cofactor biosynthesis MoeA	2.5E-110
MSM1344	Msp_1466	predicted membrane-associated Zn-dependent protease	1.4E-81	MTH_1368	conserved protein	3.4E-99
MSM1345	NONE			NONE		
MSM1346	Msp_0822	hypothetical protein	1.6E-06	NONE		
MSM1347	NONE			NONE		
MSM1348	Msp_0789	rubrerythrin	2.7E-04	MTH_1351	conserved protein	4.2E-37
MSM1349	Msp_0787	FprA	2.9E-136	MTH_1350	flavoprotein AI	2.7E-152
MSM1350	Msp_0061	conserved hypothetical protein	5.4E-32	MTH_1349	conserved protein	3.1E-48
MSM1351	Msp_0038	CbiL	1.1E-58	MTH_1348	precorrin-2 methyltransferase	9.8E-61
MSM1352	Msp_0036	putative ATP-dependent helicase	1.1E-175	MTH_1347	probable ATP-dependent helicase	3.4E-212
MSM1353	Msp_1532	hypothetical membrane-spanning protein	1.6E-08	MTH_1313	unknown	9.0E-13
MSM1354	Msp_1533	RpoM1	4.7E-33	MTH_1314	transcription elongation factor TFIIS	4.8E-36
MSM1355	Msp_1534	putative ADP-ribose pyrophosphatase	4.9E-38	MTH_1315	mutator MutT protein	1.1E-34
MSM1356	Msp_1535	RpoL	2.1E-14	NONE	DNA-dependent RNA polymerase, subunit L	5.5E-19
MSM1357	Msp_1536	predicted RNA-binding protein	2.6E-32	MTH_1318	conserved protein	1.6E-46
MSM1358	Msp_1537	predicted diphthamide synthase, subunit DPH2	6.1E-95	MTH_1319	conserved protein	1.1E-109
MSM1359	Msp_1538	putative adenine phosphoribosyltransferase	5.0E-52	MTH_1320	adenine phosphoribosyltransferase	2.2E-54
MSM1360	Msp_1539	signal recognition particle, 54 kDa protein	2.0E-151	MTH_1321	signal recognition particle protein SRP54	5.8E-159
MSM1361	Msp_1541	predicted pseudouridylate synthase	4.0E-82	MTH_1322	conserved protein	1.0E-104
MSM1362	NONE			MTH_809	molybdenum cofactor biosynthesis protein MoaC	2.2E-47
MSM1363	Msp_0229	SecG	2.2E-12	NONE		
MSM1364	Msp_0032	HisF	1.6E-112	MTH_1343	imidazoleglycerol-phosphate synthase (cyclase)	3.7E-109
MSM1365	Msp_0034	putative 3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase	2.1E-37	MTH_1342	8-oxoguanine DNA glycosylase	1.1E-68
MSM1366	NONE			MTH_758	S-D-lactoylglutathione methylglyoxal lyase	7.2E-26
MSM1367	Msp_0035	predicted peptidyl-prolyl cis-trans isomerase 1	2.3E-63	MTH_1338	peptidyl-prolyl cis-trans isomerase B	1.9E-57
MSM1368	Msp_0037	ArgD	6.6E-121	MTH_1337	N-acetylornithine aminotransferase	8.1E-121
MSM1369	Msp_0006	predicted NUDIX-related protein	4.5E-12	MTH_1336	mutator MutT protein homolog	1.0E-17
MSM1370	Msp_0715	conserved hypothetical membrane-spanning protein	9.6E-97	NONE		
MSM1371	Msp_1578	LysA	2.9E-152	MTH_1335	diaminopimelate decarboxylase	2.3E-155
MSM1372	Msp_1579	DapF	1.3E-74	MTH_1334	diaminopimelate epimerase	2.8E-86
MSM1373	Msp_1545	conserved hypothetical protein	3.2E-50	MTH_1329	methyltransferase related protein	4.1E-46
MSM1374	Msp_1544	KsgA	1.6E-62	MTH_1326	dimethyladenosine transferase	1.3E-56
MSM1375	NONE			MTH_1325	conserved protein	2.9E-61
MSM1376	Msp_1543	conserved hypothetical protein	5.1E-20	MTH_1324	conserved protein	2.1E-28
MSM1377	Msp_1542	50S ribosomal protein L21e	3.3E-32	MTH_1323	ribosomal protein L21	2.7E-35
MSM1378	Msp_0981	conserved hypothetical protein	7.4E-19	NONE		

MSM1379	Msp_0967	putative NADP-dependent alcohol dehydrogenase	1.4E-24	NONE		
MSM1380	Msp_0967	putative NADP-dependent alcohol dehydrogenase	4.6E-74	NONE		
MSM1381	Msp_0967	putative NADP-dependent alcohol dehydrogenase	2.2E-11	NONE		
MSM1382	Msp_0504	conserved hypothetical membrane-spanning protein	2.7E-53	NONE		
MSM1383	Msp_0254	anaerobic ribonucleotide-triphosphate reductase	1.6E-307	MTH_1539	anaerobic ribonucleoside-triphosphate reductase	9.9E-306
MSM1384	Msp_0255	PolC	3.9E-290	MTH_1536	conserved protein	0.0E+00
MSM1385	Msp_0113	conserved hypothetical protein	7.7E-16	MTH_1626	phosphoserine phosphatase	2.3E-09
MSM1386	NONE			NONE		
MSM1387	Msp_0249	LysS	4.8E-205	MTH_1542	conserved protein	2.6E-202
MSM1388	Msp_0251	ThiC2	1.0E-156	MTH_1543	thiamine biosynthesis protein	5.3E-172
MSM1389	Msp_0252	predicted ribokinase	1.3E-78	MTH_1544	ribokinase	3.8E-91
MSM1390	Msp_0248	conserved hypothetical protein	2.5E-50	MTH_1545	conserved protein	1.5E-55
MSM1391	Msp_0247	predicted sugar phosphate isomerase	1.2E-52	MTH_1546	conserved protein	1.3E-51
MSM1392	NONE			NONE	nitrate assimilation protein, narQ	4.4E-58
MSM1393	NONE			NONE		
MSM1394	Msp_0355	conserved hypothetical membrane-spanning protein	1.5E-04	NONE		
MSM1395	Msp_0340	PstB	3.1E-27	MTH_605	ABC transporter	3.2E-30
MSM1396	NONE			MTH_1345	conserved protein	4.7E-22
MSM1397	Msp_0432	member of asn/thr-rich large protein family	7.3E-30	MTH_911	probable surface protein	3.0E-12
MSM1398	Msp_0762	member of asn/thr-rich large protein family	4.2E-21	MTH_716	cell surface glycoprotein (s-layer protein)	2.4E-10
MSM1399	Msp_0911	member of asn/thr-rich large protein family	5.8E-13	MTH_716	cell surface glycoprotein (s-layer protein)	4.7E-13
MSM1400	Msp_0615	partially conserved hypothetical membrane-spanning protein	5.3E-05	MTH_672	unknown	1.6E-04
MSM1401	Msp_1106	conserved hypothetical membrane-spanning protein	5.9E-42	MTH_671	unknown	1.9E-48
MSM1402	Msp_1107	conserved hypothetical membrane-spanning protein	4.2E-16	MTH_670	unknown	2.4E-11
MSM1403	NONE			NONE		
MSM1404	Msp_0243	FwdB	5.2E-23	NONE	formate dehydrogenase, alpha subunit homolog	1.9E-153
MSM1405	Msp_0639	FdhB	5.0E-84	NONE	formate dehydrogenase, beta subunit related protein FlpB	7.8E-84
MSM1406	Msp_0384	predicted Fe-S oxidoreductase	2.7E-19	MTH_1550	molybdenum cofactor biosynthesis MoaA	2.6E-99
MSM1407	Msp_0488	predicted allosteric regulator of homoserine dehydrogenase	9.7E-04	MTH_1551	molybdopterin-guanine dinucleotide biosynthesis protein B related	2.3E-36
MSM1408	Msp_0147	ferredoxin	7.5E-10	NONE	tungsten formylmethanofuran dehydrogenase, subunit H	8.3E-48
MSM1409	Msp_1447	EhbK	6.0E-18	NONE	tungsten formylmethanofuran dehydrogenase, subunit F	3.1E-97
MSM1410	Msp_0241	FwdG	1.8E-22	NONE	tungsten formylmethanofuran dehydrogenase, subunit G	2.7E-19
MSM1411	Msp_0242	FwdD	5.4E-39	NONE	tungsten formylmethanofuran dehydrogenase, subunit D	6.9E-21
MSM1412	Msp_0243	FwdB	1.6E-156	NONE	tungsten formylmethanofuran dehydrogenase, subunit B	5.3E-117
MSM1413	Msp_0244	FwdA	6.4E-203	NONE	tungsten formylmethanofuran dehydrogenase, subunit A	1.7E-182
MSM1414	Msp_0245	FwdC	1.9E-66	NONE	tungsten formylmethanofuran dehydrogenase, subunit C	2.9E-52
MSM1415	Msp_0246	hypothetical protein	3.9E-13	MTH_1568	unknown	1.1E-08
MSM1416	Msp_0246	hypothetical protein	6.8E-09	MTH_1568	unknown	1.6E-05
MSM1417	Msp_0235	conserved hypothetical membrane-spanning protein	2.9E-150	MTH_1569	conserved protein	6.5E-151
MSM1418	Msp_0234	GlnA	3.8E-157	MTH_1570	glutamine synthetase	4.7E-164
MSM1419	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM1420	Msp_0128	predicted helicase	5.7E-11	MTH_511	DNA helicase II	1.5E-13
MSM1421	Msp_1566	conserved hypothetical membrane-spanning protein	4.4E-92	NONE		
MSM1422	Msp_1568	conserved hypothetical membrane-spanning protein	3.5E-67	NONE		
MSM1423	Msp_0721	partially conserved hypothetical protein	5.9E-42	NONE		
MSM1424	Msp_0720	polyphosphate kinase	2.4E-258	NONE		
MSM1425	Msp_0871	30S ribosomal protein S13P	7.7E-56	MTH_34	ribosomal protein S18 (E.coli)	2.9E-54
MSM1426	Msp_0870	30S ribosomal protein S4P	6.5E-59	MTH_35	ribosomal protein S9 (E.coli)	4.4E-65
MSM1427	Msp_0869	30S ribosomal protein S11P	2.5E-59	MTH_36	ribosomal protein S14 (E.coli)	2.9E-61

MSM1428	Msp_0868	RpoD	6.3E-61	NONE	DNA-dependent RNA polymerase, subunit D	9.1E-74
MSM1429	Msp_0867	50S ribosomal protein L18e	1.1E-33	MTH_38	ribosomal protein L18 (E.coli)	5.5E-35
MSM1430	Msp_0866	50S ribosomal protein L13P	1.3E-51	MTH_39	ribosomal protein S16 (E.coli)	7.1E-58
MSM1431	Msp_0865	30S ribosomal protein S9P	2.9E-56	MTH_39	ribosomal protein S16 (E.coli)	1.3E-56
MSM1432	Msp_0864	RpoN	9.4E-19	NONE	DNA-dependent RNA polymerase, subunit N	1.3E-24
MSM1433	Msp_0863	RpoK	6.9E-16	NONE	DNA-dependent RNA polymerase, subunit K	2.4E-18
MSM1434	NONE			NONE		
MSM1435	Msp_0862	enolase	2.2E-113	MTH_43	enolase	3.0E-121
MSM1436	Msp_0861	ferredoxin	3.0E-15	MTH_1106	ferredoxin	6.2E-20
MSM1437	Msp_0860	ribosomal protein S2P	3.9E-84	MTH_44	ribosomal protein Sa (E.coli)	5.5E-83
MSM1438	Msp_0859	conserved hypothetical protein	1.9E-59	MTH_45	conserved protein	5.1E-64
MSM1439	Msp_0858	putative mevalonate kinase	2.1E-60	MTH_46	mevalonate kinase	4.6E-63
MSM1440	Msp_0857	predicted archaeal kinase	9.2E-60	MTH_47	conserved protein	3.6E-70
MSM1441	Msp_0856	isopentenyl-diphosphate delta-isomerase	6.2E-118	MTH_48	conserved protein	4.1E-117
MSM1442	Msp_0855	predicted hydrolase	8.3E-178	MTH_49	conserved protein	8.6E-188
MSM1443	Msp_0854	IdsA	1.3E-90	MTH_50	bifunctional short chain isoprenyl diphosphate synthase	4.1E-94
MSM1444	NONE			NONE		
MSM1445	Msp_1125	predicted transcriptional regulator	1.4E-38	MTH_1454	conserved protein	2.9E-45
MSM1446	Msp_1126	putative hydroxylamine reductase	1.8E-152	MTH_1453	6Fe-6S prismane-containing protein	3.6E-173
MSM1447	Msp_0002	conserved hypothetical protein	1.1E-31	MTH_1452	unknown	2.3E-36
MSM1448	Msp_1545	conserved hypothetical protein	1.9E-08	MTH_146	precorrin-8W decarboxylase	1.7E-05
MSM1449	Msp_0219	conserved hypothetical protein	7.9E-04	MTH_83	O-linked GlcNAc transferase	9.2E-05
MSM1450	Msp_0524	predicted oxidoreductase	8.4E-25	MTH_907	conserved protein	6.8E-08
MSM1451	Msp_0039	predicted glycosyltransferase	2.2E-06	MTH_83	O-linked GlcNAc transferase	3.2E-10
MSM1452	Msp_0923	GltX	1.1E-184	MTH_51	glutamyl-tRNA synthetase	8.5E-181
MSM1453	NONE			NONE		
MSM1454	Msp_0226	hypothetical protein	9.5E-14	NONE	heterodisulfide reductase, subunit C	6.6E-06
MSM1455	Msp_0924	predicted aspartate/tyrosine/aromatic aminotransferase	3.8E-166	MTH_52	aspartate aminotransferase related protein	6.6E-158
MSM1456	NONE			NONE		
MSM1457	NONE			NONE		
MSM1458	NONE			NONE		
MSM1459	Msp_0925	predicted arabinose efflux permease	7.3E-115	MTH_195	efflux pump antibiotic resistance protein	7.7E-93
MSM1460	Msp_1447	EhbK	1.8E-33	MTH_1133	polyferredoxin (MvhB)	5.8E-143
MSM1461	Msp_0638	MvhD2	1.3E-53	NONE	methyl viologen-reducing hydrogenase, delta subunit homolog FlpD	2.7E-58
MSM1462	Msp_0639	FdhB	1.2E-119	NONE	formate dehydrogenase, beta subunit related protein FlpB	1.9E-135
MSM1463	Msp_0640	FdhA	4.1E-50	NONE	formate dehydrogenase, alpha subunit related protein FlpC	2.0E-39
MSM1464	NONE			MTH_1141	conserved protein (FlpE)	1.2E-18
MSM1465	Msp_0925	predicted arabinose efflux permease	1.3E-115	MTH_195	efflux pump antibiotic resistance protein	9.5E-95
MSM1466	NONE			NONE		
MSM1467	NONE			NONE		
MSM1468	Msp_0986	PurA	7.6E-136	MTH_615	adenylosuccinate synthetase	9.4E-143
MSM1469	Msp_1164	predicted ABC-type nitrate/sulfonate/bicarbonate transport system, periplasmic solute-binding protein	2.4E-91	MTH_924	molybdate-binding periplasmic protein	5.9E-06
MSM1470	NONE			NONE		
MSM1471	Msp_0919	predicted acyl-CoA synthetase	2.3E-237	NONE	succinyl-CoA synthetase, alpha subunit	2.5E-07
MSM1472	NONE			MTH_752	conserved protein	3.7E-77
MSM1473	Msp_0575	predicted metal-dependent hydrolase	2.9E-79	MTH_751	conserved protein	9.4E-72
MSM1474	Msp_0579	AroC	7.2E-124	MTH_748	chorismate synthase	4.7E-125
MSM1475	Msp_0497	putative endonuclease III	1.0E-14	MTH_746	endonuclease III related protein	2.1E-51
MSM1476	Msp_0416	HemB	6.2E-102	MTH_744	porphobilinogen synthase	3.6E-102

MSM1477	Msp_0428	predicted ATP:dephospho-CoA triphosphoribosyl transferase	1.7E-58	MTH_743	conserved protein	5.9E-70
MSM1478	Msp_0429	PheS	2.6E-165	MTH_742	phenylalanyl-tRNA synthetase	5.5E-170
MSM1479	NONE			MTH_212	exodeoxyribonuclease	2.4E-73
MSM1480	Msp_1260	predicted hydrolase	1.5E-59	MTH_209	conserved protein	1.1E-77
MSM1481	Msp_1281	conserved hypothetical protein	6.5E-59	MTH_208	DNA-dependent DNA polymerase family B (PolB2)	2.0E-69
MSM1482	NONE			NONE		
MSM1483	Msp_0195	ABC-type multidrug transport system, ATP-binding protein	2.0E-41	MTH_1093	ABC transporter (ATP-binding	1.4E-54
MSM1484	Msp_0196	ABC-type multidrug transport system, permease protein	8.1E-29	MTH_1486	conserved protein	1.0E-19
MSM1485	Msp_0440	member of asn/thr-rich large protein family	3.3E-06	NONE		
MSM1486	Msp_1280	30S ribosomal protein S8e	6.6E-34	MTH_207	ribosomal protein S8	1.5E-41
MSM1487	NONE			MTH_199	unknown	9.6E-31
MSM1488	Msp_0977	conserved hypothetical protein	3.1E-27	MTH_200	cobalamin biosynthesis protein M related protein	3.0E-50
MSM1489	Msp_0474	hypothetical protein	1.2E-09	MTH_1346	unknown	1.3E-177
MSM1490	Msp_0474	hypothetical protein	7.1E-06	MTH_201	unknown	4.9E-11
MSM1491	Msp_0474	hypothetical protein	9.8E-08	MTH_1346	unknown	1.3E-159
MSM1492	Msp_1279	HypE1	1.0E-122	MTH_205	hydrogenase expression/formation protein HypE	3.2E-126
MSM1493	Msp_1278	conserved hypothetical membrane-spanning protein	1.3E-21	MTH_204	conserved protein	4.3E-19
MSM1494	NONE			NONE		
MSM1495	Msp_1089	predicted nuclease	1.8E-40	MTH_494	thermonuclease precursor	8.5E-39
MSM1496	Msp_0024	hypothetical protein	4.5E-67	NONE		
MSM1497	NONE			MTH_1785	coenzyme PQQ synthesis protein	6.4E-57
MSM1498	Msp_1228	predicted helicase	2.1E-131	NONE	ATP-dependent RNA helicase, eIF-4A family	3.8E-114
MSM1499	Msp_1188	predicted transcriptional regulator	8.1E-61	MTH_163	conserved protein	2.5E-62
MSM1500	Msp_1189	RecJ	1.5E-114	MTH_164	single-stranded DNA exonuclease RecJ related protein	1.1E-116
MSM1501	Msp_1190	signal recognition particle, 19 kDa protein	4.0E-20	MTH_165	signal recognition particle 19 kDa protein	9.3E-17
MSM1502	Msp_0223	predicted UDP-galactopyranose mutase	3.6E-65	MTH_344	UDP-galactopyranose mutase	2.4E-80
MSM1503	Msp_0215	predicted glycosyltransferase	4.0E-39	MTH_884	teichoic acid biosynthesis related protein	2.4E-06
MSM1504	Msp_1191	HemD	2.2E-49	MTH_166	uroporphyrinogen III synthase	1.1E-52
MSM1505	NONE			NONE		
MSM1506	NONE			NONE		
MSM1507	Msp_0215	predicted glycosyltransferase	5.6E-34	MTH_884	teichoic acid biosynthesis related protein	7.4E-10
MSM1508	NONE			NONE		
MSM1509	NONE			NONE		
MSM1510	NONE			NONE		
MSM1511	NONE			NONE		
MSM1512	Msp_0060	putative lipooligosaccharide cholinephosphotransferase	7.0E-62	NONE		
MSM1513	Msp_0662	putative aspartate aminotransferase	2.7E-37	MTH_1601	aspartate aminotransferase	1.9E-41
MSM1514	Msp_1333	predicted dehydrogenase	1.3E-06	NONE	3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein	8.7E-09
MSM1515	Msp_0060	putative lipooligosaccharide cholinephosphotransferase	1.1E-24	NONE		
MSM1516	Msp_1326	HisC	1.7E-26	MTH_1587	histidinol-phosphate aminotransferase	5.5E-22
MSM1517	NONE			MTH_1495	ornithine cyclodeaminase	1.2E-15
MSM1518	Msp_0017	conserved hypothetical protein	1.2E-11	NONE		
MSM1519	NONE			NONE		
MSM1520	NONE			NONE		
MSM1521	NONE			NONE		
MSM1522	NONE			NONE		
MSM1523	NONE			NONE		
MSM1524	NONE			NONE		
MSM1525	NONE			NONE		

MSM1526	Msp_0772	hypothetical membrane-spanning protein	2.3E-15	MTH_252	conserved protein	7.1E-19
MSM1527	NONE			NONE		
MSM1528	Msp_0608	predicted transcriptional regulator	1.9E-04	MTH_700	conserved protein	1.1E-04
MSM1529	NONE			NONE		
MSM1530	NONE			NONE		
MSM1531	Msp_0691	predicted Na+-dependent transporter	1.3E-131	NONE		
MSM1532	Msp_0691	predicted Na+-dependent transporter	2.0E-137	NONE		
MSM1533	Msp_1465	member of asn/thr-rich large protein family	7.2E-12	MTH_1074	putative membrane protein	3.7E-06
MSM1534	Msp_0590	member of asn/thr-rich large protein family	2.0E-24	MTH_1074	putative membrane protein	3.0E-123
MSM1535	Msp_1114	predicted dTDP-D-glucose 4,6-dehydratase	1.3E-10	NONE	dTDP-glucose 4,6-dehydratase	1.2E-06
MSM1536	Msp_0290	predicted pyridoxal phosphate-dependent enzyme	6.9E-71	MTH_1188	pleiotropic regulatory protein DegT	6.6E-71
MSM1537	Msp_0310	predicted GTP:adenosylcobinamide-phosphate guanylyltransferase	4.2E-04	NONE		
MSM1538	Msp_1202	predicted acetyltransferase	1.9E-08	NONE	N-terminal acetyltransferase complex, subunit ARD1	3.5E-06
MSM1539	NONE			NONE		
MSM1540	NONE			MTH_368	glycerol-3-phosphate dehydrogenase (NAD)	6.5E-48
MSM1541	NONE			NONE		
MSM1542	Msp_0310	predicted GTP:adenosylcobinamide-phosphate guanylyltransferase	4.6E-06	MTH_1152	conserved protein	1.4E-04
MSM1543	NONE			NONE		
MSM1544	Msp_0060	putative lipooligosaccharide cholinephosphotransferase	3.9E-22	NONE		
MSM1545	Msp_0495	predicted glycosyltransferase	1.3E-31	MTH_136	dolichyl-phosphate mannose synthase	1.4E-08
MSM1546	NONE			NONE		
MSM1547	Msp_1195	PurC	3.9E-77	MTH_170	phosphoribosylaminoimidazolesuccinocarboxamide synthase	6.8E-69
MSM1548	Msp_1194	predicted phosphoribosylformylglycinamidine synthase	1.2E-25	MTH_169	conserved protein	4.5E-24
MSM1549	Msp_1193	PurQ	2.4E-75	MTH_168	phosphoribosylformylglycinamidine synthase I	6.8E-85
MSM1550	Msp_1192	CobA	6.2E-86	MTH_167	S-adenosyl-L-methionine uroporphyrinogen methyltransferase	7.1E-90
MSM1551	Msp_1196	GlmS	1.5E-201	MTH_171	glutamine-fructose-6-phosphate transaminase	1.5E-208
MSM1552	NONE			NONE		
MSM1553	NONE			NONE		
MSM1554	Msp_0141	member of asn/thr-rich large protein family	1.1E-09	NONE		
MSM1555	Msp_0076	conserved hypothetical protein	3.5E-60	MTH_175	conserved protein	4.7E-77
MSM1556	Msp_1344	conserved hypothetical membrane-spanning protein	6.5E-75	NONE		
MSM1557	Msp_0520	predicted queuine/archaeosine tRNA-ribosyltransferase	5.0E-219	MTH_176	tRNA-guanine transglycosylase	1.2E-206
MSM1558	NONE			MTH_1329	methyltransferase related protein	3.1E-04
MSM1559	Msp_0063	predicted polysaccharide biosynthesis protein	9.5E-74	MTH_379	O-antigen transporter related protein	1.7E-72
MSM1560	Msp_0448	predicted polysaccharide biosynthesis protein	1.3E-78	MTH_379	O-antigen transporter related protein	4.9E-75
MSM1561	Msp_0117	predicted 3-hydroxy-3-methylglutaryl CoA synthase	3.6E-145	MTH_792	3-hydroxy-3-methylglutaryl-CoA-synthase	3.4E-145
MSM1562	Msp_0116	predicted thiolase	2.1E-156	MTH_793	lipid-transfer protein (sterol or nonspecific)	3.5E-168
MSM1563	NONE			NONE		
MSM1564	Msp_0087	CbiT	4.6E-05	NONE		
MSM1565	Msp_1226	CobQ	9.4E-154	MTH_787	cobyric acid synthase	1.1E-162
MSM1566	Msp_0233	conserved hypothetical protein	2.3E-22	NONE		
MSM1567	Msp_0762	member of asn/thr-rich large protein family	7.2E-35	MTH_1485	serine/threonine protein kinase related protein	5.1E-13
MSM1568	NONE			NONE		
MSM1569	Msp_1227	predicted ATP-dependent protease	2.4E-226	MTH_785	ATP-dependent protease LA	9.0E-241
MSM1570	Msp_0557	hypothetical protein	1.1E-127	MTH_530	UDP-N-acetylmuramyl tripeptide synthetase related protein	2.6E-25
MSM1571	NONE			NONE		
MSM1572	Msp_0683	hypothetical protein	4.9E-61	NONE		

MSM1573	NONE			NONE		
MSM1574	Msp_0797	predicted nitroreductase	6.3E-10	MTH_120	NADPH-oxidoreductase	4.2E-11
MSM1575	Msp_1055	hypothetical membrane-spanning protein	7.8E-04	MTH_521	unknown	8.2E-05
MSM1576	NONE			NONE		
MSM1577	Msp_1229	ribose-phosphate pyrophosphokinase	1.2E-84	MTH_784	ribose-phosphate pyrophosphokinase	1.0E-88
MSM1578	NONE			NONE		
MSM1579	Msp_0573	UvrB	1.2E-247	MTH_442	excinuclease ABC subunit B	1.2E-261
MSM1580	NONE			NONE		
MSM1581	Msp_0574	UvrA	0.0E+00	MTH_443	excinuclease ABC subunit A	0.0E+00
MSM1582	Msp_0603	conserved hypothetical membrane-spanning protein	5.6E-85	MTH_465	unknown	4.8E-84
MSM1583	Msp_1178	predicted helicase	7.4E-193	MTH_656	ATP-dependent RNA helicase related protein	2.1E-232
MSM1584	Msp_1119	conserved hypothetical protein	1.0E-37	MTH_641	conserved protein	2.9E-29
MSM1585	Msp_0983	member of asn/thr-rich large protein family	5.5E-38	MTH_911	probable surface protein	9.9E-06
MSM1586	Msp_0713	member of asn/thr-rich large protein family	1.8E-52	MTH_911	probable surface protein	3.7E-14
MSM1587	Msp_0590	member of asn/thr-rich large protein family	6.0E-44	MTH_716	cell surface glycoprotein (s-layer protein)	1.2E-06
MSM1588	NONE			NONE		
MSM1589	NONE			NONE		
MSM1590	Msp_0619	member of asn/thr-rich large protein family	2.5E-48	MTH_716	cell surface glycoprotein (s-layer protein)	1.3E-07
MSM1591	Msp_1118	conserved hypothetical protein	1.0E-37	MTH_639	conserved protein	5.6E-42
MSM1592	Msp_0205	predicted ABC-type polysaccharide/polyol phosphate export system, ATP-binding protein	9.8E-72	MTH_1370	ABC transporter (ATP-binding protein)	1.5E-20
MSM1593	Msp_0204	predicted ABC-type polysaccharide/polyol phosphate export system, permease protein	1.3E-53	MTH_1092	putative membrane protein	5.7E-11
MSM1594	Msp_0442	predicted glycosyltransferase	4.4E-60	MTH_884	teichoic acid biosynthesis related protein	1.5E-07
MSM1595	Msp_0929	predicted helicase	6.7E-04	NONE		
MSM1596	Msp_0017	conserved hypothetical protein	1.7E-28	NONE		
MSM1597	NONE			NONE		
MSM1598	NONE			NONE		
MSM1599	NONE			NONE		
MSM1600	NONE			NONE		
MSM1601	Msp_0692	hypothetical membrane-spanning protein	1.3E-07	NONE		
MSM1602	Msp_0220	predicted glycosyltransferase	6.9E-20	MTH_361	teichoic acid biosynthesis protein RodC related protein	1.7E-04
MSM1603	NONE			MTH_637	conserved protein	1.1E-20
MSM1604	Msp_1101	predicted UDP-glucose pyrophosphorylase	1.2E-103	MTH_634	UTP--glucose-1-phosphate uridylyltransferase	7.6E-109
MSM1605	NONE			NONE		
MSM1606	Msp_0612	predicted arylsulfatase regulatory protein	4.8E-102	MTH_114	arylsulfatase regulatory protein	1.9E-64
MSM1607	Msp_1060	hypothetical protein	2.4E-13	MTH_121	unknown	1.2E-05
MSM1608	Msp_1350	putative oxidoreductase	5.9E-97	MTH_907	conserved protein	8.1E-50
MSM1609	NONE			MTH_924	molybdate-binding periplasmic protein	6.6E-23
MSM1610	Msp_0342	PstC	1.1E-15	MTH_921	anion transport system permease protein	6.4E-25
MSM1611	Msp_1000	predicted ABC-type nitrate/sulfonate/bicarbonate transport system, ATB-binding protein	1.7E-28	MTH_920	anion permease	2.4E-34
MSM1612	Msp_0210	predicted UDP-glucose 6-dehydrogenase	6.3E-93	MTH_836	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	5.4E-24
MSM1613	NONE			NONE		
MSM1614	Msp_0394	predicted transcriptional regulator	1.3E-74	MTH_126	inosine-5'-monophosphate dehydrogenase related protein VII	2.1E-97
MSM1615	Msp_0395	putative deoxyhypusine synthase	7.4E-106	MTH_127	deoxyhypusine synthase	4.6E-95
MSM1616	Msp_0396	hypothetical membrane-spanning protein	4.0E-27	MTH_128	unknown	6.2E-27
MSM1617	Msp_0397	PyrF	1.9E-66	MTH_129	orotidine 5' monophosphate decarboxylase	4.3E-67
MSM1618	Msp_0398	CbiM1	6.0E-72	MTH_130	cobalamin biosynthesis protein M	9.5E-79
MSM1619	Msp_0399	CbiN	3.0E-31	MTH_131	cobalt transport protein N	7.2E-26

MSM1620	Msp_0400	CbiQ1	3.0E-38	MTH_132	cobalt transport protein Q	3.4E-42
MSM1621	Msp_0401	CbiO1	6.0E-88	MTH_133	cobalt transport ATP-binding protein O	9.3E-88
MSM1622	Msp_1239	RibC	6.9E-55	MTH_134	riboflavin synthase	2.3E-61
MSM1623	Msp_0541	predicted glycosyltransferase	2.1E-46	MTH_136	dolichyl-phosphate mannose synthase	6.1E-52
MSM1624	Msp_0542	hypothetical membrane-spanning protein	9.4E-19	MTH_137	unknown	1.2E-18
MSM1625	Msp_1044	TfrB	3.2E-34	MTH_1850	fumarate reductase	7.6E-33
MSM1626	Msp_1044	TfrB	3.0E-07	MTH_140	conserved protein	4.8E-107
MSM1627	Msp_0989	predicted glycosyltransferase	9.5E-11	MTH_377	dolichyl-phosphate mannose synthase related protein	2.0E-11
MSM1628	Msp_0430	conserved hypothetical protein	1.9E-75	MTH_141	conserved protein	7.0E-99
MSM1629	Msp_0431	GuaB	2.1E-163	MTH_142	inosine-5'-monophosphate dehydrogenase	1.5E-174
MSM1630	Msp_1253	50S ribosomal protein L37Ae	6.0E-33	MTH_681	ribosomal protein L37a	1.1E-36
MSM1631	NONE			NONE		
MSM1632	Msp_1254	partially conserved hypothetical protein	1.0E-21	MTH_680	conserved protein	1.4E-15
MSM1633	Msp_1255	conserved hypothetical protein	1.0E-12	MTH_679	unknown	5.3E-14
MSM1634	Msp_1256	partially conserved hypothetical protein	2.5E-27	MTH_678	conserved protein	2.1E-35
MSM1635	NONE			MTH_677	unknown	1.7E-10
MSM1636	Msp_1257	conserved hypothetical protein	2.6E-39	MTH_669	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase related protein	1.3E-58
MSM1637	Msp_0173	hypothetical membrane-spanning protein	9.9E-08	NONE		
MSM1638	Msp_1259	hypothetical membrane-spanning protein	1.6E-09	MTH_667	unknown	3.0E-11
MSM1639	Msp_0519	predicted Co/Zn/Cd cation transporter	4.1E-16	MTH_1893	cation efflux system protein (zinc/cadmium)	3.7E-17
MSM1640	Msp_0482	hypothetical membrane-spanning protein	1.8E-38	NONE		
MSM1641	NONE			NONE		
MSM1642	NONE			NONE		
MSM1643	NONE			NONE		
MSM1644	NONE			NONE		
MSM1645	NONE			NONE		
MSM1646	NONE			NONE		
MSM1647	NONE			NONE		
MSM1648	NONE			NONE		
MSM1649	NONE			NONE		
MSM1650	Msp_0260	hypothetical protein	7.9E-04	NONE		
MSM1651	NONE			NONE		
MSM1652	NONE			NONE		
MSM1653	NONE			NONE		
MSM1654	NONE			NONE		
MSM1655	Msp_1059	hypothetical protein	1.3E-05	NONE		
MSM1656	NONE			NONE		
MSM1657	Msp_0793	hypothetical protein	4.9E-06	NONE		
MSM1658	NONE			NONE		
MSM1659	NONE			NONE		
MSM1660	NONE			NONE		
MSM1661	NONE			NONE		
MSM1662	NONE			NONE		
MSM1663	NONE			NONE		
MSM1664	NONE			NONE		
MSM1665	NONE			NONE		
MSM1666	Msp_0946	conserved hypothetical protein	1.2E-05	NONE		
MSM1667	NONE			NONE		
MSM1668	NONE			NONE		
MSM1669	NONE			NONE		

MSM1670	Msp_0113	conserved hypothetical protein	1.8E-04	NONE		
MSM1671	NONE			NONE		
MSM1672	NONE			NONE		
MSM1673	Msp_0474	hypothetical protein	4.6E-04	NONE		
MSM1674	Msp_0822	hypothetical protein	2.5E-04	NONE		
MSM1675	NONE			NONE		
MSM1676	NONE			NONE		
MSM1677	NONE			NONE		
MSM1678	NONE			NONE		
MSM1679	NONE			NONE		
MSM1680	NONE			NONE		
MSM1681	NONE			NONE		
MSM1682	NONE			NONE		
MSM1683	NONE			NONE		
MSM1684	Msp_0912	member of asn/thr-rich large protein family	2.1E-06	MTH_412	conserved protein	4.7E-04
MSM1685	NONE			NONE		
MSM1686	NONE			NONE		
MSM1687	Msp_0658	hypothetical membrane-spanning protein	8.1E-07	MTH_1459	unknown	3.6E-07
MSM1688	NONE			NONE		
MSM1689	NONE			NONE		
MSM1690	NONE			NONE		
MSM1691	Msp_1039	partially conserved hypothetical membrane-spanning protein	1.5E-07	MTH_357	conserved protein	5.3E-08
MSM1692	NONE			NONE		
MSM1693	Msp_1258	predicted ribokinase	6.9E-39	MTH_668	unknown	1.8E-20
MSM1694	Msp_0929	predicted helicase	3.6E-193	MTH_487	DNA helicase related protein	4.9E-304
MSM1695	Msp_0572	UvrC	6.3E-164	MTH_441	excinuclease ABC subunit C	5.6E-161
MSM1696	Msp_1548	hypothetical protein	1.7E-08	NONE		
MSM1697	NONE			NONE		
MSM1698	Msp_0439	methyl-coenzyme M reductase, component A2-like protein	2.7E-147	NONE	methyl coenzyme M reductase system, component A2 homolog	5.4E-179
MSM1699	Msp_0438	predicted universal stress protein	2.1E-14	MTH_153	conserved protein	5.4E-21
MSM1700	Msp_1061	hypothetical protein	7.3E-12	MTH_278	ferredoxin	1.4E-20
MSM1701	Msp_1062	predicted dehydrogenase	4.0E-130	MTH_277	bacteriochlorophyll synthase 43 kDa subunit	8.8E-147
MSM1702	Msp_1088	ExoB	7.9E-102	MTH_631	UDP-glucose 4-epimerase	3.5E-97
MSM1703	NONE			MTH_647	unknown	5.0E-25
MSM1704	Msp_1122	PurF	1.4E-143	MTH_646	amidophosphoribosyltransferase	1.2E-156
MSM1705	Msp_1121	predicted peptidase	2.4E-100	MTH_645	collagenase	3.7E-100
MSM1706	Msp_1513	hypothetical membrane-spanning protein	2.9E-24	NONE		
MSM1707	Msp_1120	NifH	2.6E-96	MTH_643	nitrogenase NifH subunit	5.5E-99
MSM1708	NONE			NONE		
MSM1709	Msp_0440	member of asn/thr-rich large protein family	1.3E-35	MTH_716	cell surface glycoprotein (s-layer protein)	2.4E-04
MSM1710	Msp_1277	SerS	1.9E-187	MTH_1455	threonyl-tRNA synthetase	5.3E-06
MSM1711	Msp_0725	hypothetical protein	1.0E-08	NONE		
MSM1712	Msp_0852	predicted ferritin	8.4E-50	MTH_158	ferritin like protein (RsgA)	2.3E-59
MSM1713	Msp_1008	predicted regulatory protein	5.4E-32	MTH_162	unknown	1.5E-41
MSM1714	Msp_1040	coenzyme F390 synthetase II	6.3E-164	MTH_161	coenzyme F390 synthetase III	3.7E-164
MSM1715	Msp_1110	CobN	1.7E-68	MTH_714	magnesium chelatase subunit	0.0E+00
MSM1716	Msp_0590	member of asn/thr-rich large protein family	2.5E-16	MTH_717	unknown	3.9E-25
MSM1717	Msp_1105	predicted transporter	1.9E-52	MTH_672	unknown	2.3E-52
MSM1718	Msp_1106	conserved hypothetical membrane-spanning protein	2.0E-50	MTH_671	unknown	3.7E-61

MSM1719	Msp_1107	conserved hypothetical membrane-spanning protein	4.1E-25	MTH_670	unknown	1.2E-32
MSM1720	Msp_1533	RpoM1	7.3E-28	MTH_1314	transcription elongation factor TFIIS	8.6E-30
MSM1721	NONE			NONE		
MSM1722	Msp_0965	predicted nitroreductase	6.9E-16	MTH_120	NADPH-oxidoreductase	7.3E-33
MSM1723	Msp_1238	N(5),N(10)-methenyltetrahydromethanopterin cyclohydrolase	6.7E-105	NONE	N5,N10-methenyl-tetrahydromethanopterin cyclohydrolase	2.1E-138
MSM1724	Msp_0961	hypothetical membrane-spanning protein	3.1E-36	MTH_1192	conserved protein	9.2E-25
MSM1725	Msp_0961	hypothetical membrane-spanning protein	5.7E-28	MTH_1192	conserved protein	1.6E-30
MSM1726	Msp_0879	hypothetical membrane-spanning protein	9.0E-30	MTH_1192	conserved protein	1.3E-25
MSM1727	Msp_0844	predicted multimeric flavodoxin	1.2E-18	MTH_135	conserved protein	1.9E-18
MSM1728	NONE			NONE		
MSM1729	Msp_0587	hypothetical membrane-spanning protein	5.0E-29	MTH_520	unknown	3.9E-10
MSM1730	Msp_0607	hypothetical membrane-spanning protein	6.5E-20	MTH_1192	conserved protein	1.2E-26
MSM1731	Msp_0714	predicted short chain dehydrogenase	1.7E-115	NONE		
MSM1732	Msp_1548	hypothetical protein	8.2E-07	NONE		
MSM1733	Msp_0789	rubrerythrin	1.6E-39	MTH_756	rubrerythrin	3.3E-43
MSM1734	Msp_1237	ThyA	8.9E-28	MTH_774	thymidylate synthase	7.2E-26
MSM1735	Msp_0777	member of asn/thr-rich large protein family	7.4E-116	MTH_716	cell surface glycoprotein (s-layer protein)	1.4E-06
MSM1736	NONE			NONE		
MSM1737	NONE			NONE		
MSM1738	Msp_0154	member of asn/thr-rich large protein family	2.3E-06	NONE		
MSM1739	Msp_0987	hypothetical membrane-spanning protein	2.7E-07	MTH_521	unknown	1.4E-05
MSM1740	Msp_1323	conserved hypothetical protein	1.1E-16	MTH_83	O-linked GlcNAc transferase	4.7E-38
MSM1741	Msp_0113	conserved hypothetical protein	5.0E-05	NONE		
MSM1742	Msp_0482	hypothetical membrane-spanning protein	2.7E-76	NONE		
MSM1743	Msp_0113	conserved hypothetical protein	4.1E-06	NONE		
MSM1744	NONE			NONE		
MSM1745	Msp_0344	predicted phosphate uptake regulator	2.0E-04	NONE		
MSM1746	NONE			NONE		
MSM1747	Msp_0911	member of asn/thr-rich large protein family	8.1E-06	NONE		
MSM1748	NONE			NONE		
MSM1749	NONE			NONE		
MSM1750	NONE			NONE		
MSM1751	Msp_0113	conserved hypothetical protein	6.3E-15	NONE		
MSM1752	Msp_0702	conserved hypothetical protein	1.2E-59	MTH_1210	mrr restriction system related protein	3.4E-42
MSM1753	Msp_0465	conserved hypothetical membrane-spanning protein	6.7E-04	NONE		
MSM1754	Msp_1328	putative ATP-dependent protease La	3.6E-06	NONE		
MSM1755	Msp_0219	conserved hypothetical protein	6.7E-04	NONE		
MSM1756	Msp_0976	hypothetical protein	2.8E-05	NONE		
MSM1757	NONE			NONE		
MSM1758	NONE			NONE		
MSM1759	NONE			NONE		
MSM1760	NONE			NONE		
MSM1761	Msp_0113	conserved hypothetical protein	7.6E-07	MTH_540	intracellular protein transport protein	2.7E-05
MSM1762	NONE			NONE		
MSM1763	Msp_1533	RpoM1	4.6E-10	MTH_1314	transcription elongation factor TFIIS	3.1E-09
MSM1764	Msp_0226	hypothetical protein	8.9E-04	NONE		
MSM1765	NONE			NONE		
MSM1766	Msp_1323	conserved hypothetical protein	4.8E-15	MTH_83	O-linked GlcNAc transferase	3.4E-35
MSM1767	Msp_1548	hypothetical protein	1.3E-04	NONE		
MSM1768	NONE			NONE		

MSM1769	Msp_0724	hypothetical membrane-spanning protein	2.1E-08	MTH_1277	unknown	8.9E-05
MSM1770	Msp_0934	conserved hypothetical membrane-spanning protein	1.4E-17	MTH_518	conserved protein	3.4E-19
MSM1771	Msp_0128	predicted helicase	5.0E-19	MTH_511	DNA helicase II	1.1E-26
MSM1772	Msp_0725	hypothetical protein	4.0E-11	MTH_470	conserved protein	1.2E-04
MSM1773	Msp_1548	hypothetical protein	4.3E-07	MTH_521	unknown	7.7E-05
MSM1774	NONE			NONE		
MSM1775	NONE			NONE		
MSM1776	NONE			NONE		
MSM1777	Msp_0799	predicted transcriptional regulator	3.3E-05	MTH_671	unknown	2.6E-04
MSM1778	Msp_0726	hypothetical protein	2.7E-69	NONE		
MSM1779	Msp_0725	hypothetical protein	2.6E-119	NONE		
MSM1780	Msp_1055	hypothetical membrane-spanning protein	1.1E-10	MTH_1277	unknown	2.7E-06
MSM1781	Msp_0725	hypothetical protein	2.4E-13	MTH_470	conserved protein	1.4E-05
MSM1782	NONE			NONE		
MSM1783	NONE			NONE		
MSM1784	NONE			NONE		
MSM1785	NONE			NONE		
MSM1786	Msp_1323	conserved hypothetical protein	4.1E-07	MTH_83	O-linked GlcNAc transferase	6.9E-12
MSM1787	Msp_1323	conserved hypothetical protein	5.6E-09	MTH_72	O-linked GlcNAc transferase	3.6E-16
MSM1788	Msp_1323	conserved hypothetical protein	7.3E-11	MTH_83	O-linked GlcNAc transferase	2.0E-20
MSM1789	Msp_0757	predicted ATPase	2.5E-08	NONE		
MSM1790	Msp_0757	predicted ATPase	4.9E-08	NONE		
MSM1791	NONE			MTH_512	unknown	1.1E-25
MSM1792	Msp_0764	predicted nicotinate phosphoribosyltransferase	1.7E-193	NONE		
MSM1793	NONE			NONE		
MSM1794	Msp_1103	member of asn/thr-rich large protein family	1.5E-04	MTH_512	unknown	1.2E-24
MSM1795	Msp_0757	predicted ATPase	1.7E-99	NONE		