Table 2. Predicted proteome of *M. smithii* strain PS and conservation among other strains and in the fecal microbiome of two healthy adults.

- Present Absent Divergent **Human Gut** M. smithii strain genotyping Microbiome<sup>2</sup> Annotation F1 ALI B181 Gene MSM0001 exoribonuclease VII, large subunit, XseA MSM0002 integrase-recombinase protein MSM0003 conserved hypothetical membrane protein (putative heme utilization/adhesion related) MSM0004 predicted lysine decarboxylase MSM0005 conserved hypothetical protein MSM0006 conserved hypothetical protein MSM0007 SAM-dependent methyltransferase MSM0008 putative transposase MSM0009 conserved hypothetical protein MSM0010 N-acetyltransferase, GNAT family MSM0011 hypothetical protein MSM0012 conserved hypothetical protein MSM0013 hypothetical protein MSM0014 putative heat shock related protein hypothetical protein MSM0015 MSM0016 hypothetical protein MSM0017 hypothetical protein MSM0018 hypothetical protein MSM0019 hypothetical protein predicted O-linked GlnNAc transferase MSM0020 MSM0021 short chain dehydrogenase (7-alpha-hydroxysteroid dehydrogenase) MSM0022 hypothetical protein uncharacterized protein predicted to be involved in DNA repair MSM0023 MSM0024 hypothetical protein MSM0025 long-chain-fatty-acid-CoA ligase MSM0026 predicted transcriptional regulator MSM0027 glutamate synthase, domain 2 with rubredoxin MSM0028 SAM-dependent methyltransferase MSM0029 putative calcium-binding protein MSM0030 conserved hypothetical membrane protein MSM0031 adhesin-like protein MSM0032 hypothetical protein MSM0033 ketopantoate reductase, ApbA MSM0034 conserved hypothetical protein MSM0035 hypothetical protein MSM0036 hypothetical protein MSM0037 hypothetical protein MSM0038 hypothetical protein MSM0039 hypothetical protein MSM0040 conserved hypothetical protein MSM0041 hypothetical protein MSM0042 hypothetical protein peptide methionine sulfoxide reductase, PMSR MSM0043 MSM0044 PLP dependent aminotransferase (aspartate) MSM0045 nucleotide-binding protein (putative ATPase involved in chromosome partitioning) NADH oxidase MSM0046 MSM0047 Chloramphenicol O-acetyltransferase MSM0048 conserved hypothetical protein F420-dependent NADP oxidoreductase, fno MSM0049 MSM0050 predicted metal-binding protein MSM0051 adhesin-like protein MSM0052 adhesin-like protein MSM0053 tRNA nucleotidyltransferase (CCA-adding enzyme) MSM0054 2'-5' RNA ligase, LigT MSM0055 predicted alternative 3-dehydroquinate synthase archaeal fructose-1,6-bisphosphate aldolase MSM0056 MSM0057 adhesin-like protein MSM0058 DNA helicase II MSM0059 SAM-dependent methyltransferase MSM0060 predicted archaeal kinase (GHMP kinase family) MSM0061 predicted ATPase (AAA+ superfamily) MSM0062 flavodoxin amidohydrolase (PHP family) MSM0063 conserved hypothetical protein MSM0064 MSM0065 riboflavin-specific deaminase MSM0066 N-acetylglucosamine-1-phosphate transferase, GT4 family conserved hypothetical protein

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### AISMO108   hydrogenase nickel incorporation protein, HypA   ### AISMO109   conserved hypothetical membrane-spanning protein   ### AISMO1109   hypothetical protein   ### AIP-dependent RNA helicase, eIF-4A family   ### A	MSM0106	conserved hypothetical protein					
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### ASMO110 predicted transposase ### ASMO111 hypothetical protein ### ASMO113 DNA helicase ### ATP-dependent RNA helicase, eIF-4A family ### ASMO113 DNA helicase ### ATP-dependent RNA helicase, eIF-4A family ### ASMO114 hypothetical protein ### ASMO116 Conserved hypothetical protein ### ASMO117 conserved hypothetical membrane protein ### ASMO118 MobA-related protein ### ASMO119 predicted nuclease ### ASMO120 purine NTPase involved in DNA repair, Rad50 ### ASMO120 DNA repair exonuclease (SbcD/Mre11-family), Rad32 ### ASMO121 DNA repair exonuclease (SbcD/Mre11-family), Rad32 ### ASMO122 predicted ATPase ### ASMO123 uncharacterized protein conserved in archaea ### ASMO124 predicted phosphate-binding protein (PcrB family) ### ASMO125 ribosomal protein L40e ### ASMO126 conserved hypothetical protein ### ASMO127 inicotinamide mononucleotide adenylyltransferase, NadR ### ASMO128 conserved hypothetical protein ### ASMO129 molybdenum cofactor biosynthesis protein, MoaE ### ASMO131 molybdenum-binding protein, MopI ### ASMO132 conserved hypothetical protein ### ASMO133 molybdenum-binding protein, MopI ### ASMO134 molybdenum-binding protein, MopI ### ASMO135 conserved hypothetical protein ### ASMO136 predicted thioesterase, FcbC ### ASMO137 putative archaeal flagellar protein D/E ### ASMO138 predicted exonuclease ### ASMO138 predicted exonuclease ### ASMO139 hypothetical protein ### ASMO139 predicted exonuclease ### ASMO139 hypothetical protein ### ASMO139 hypothetical protein ### ASMO130 conserved hypothetical protein ### ASMO139 hypothetical protein ### ASMO130 conserved hypothetical protein ### ASMO139 hypothetical protein ### ASMO139 hypothetical protein ### ASMO130 conserved hypo	MSM0108	hydrogenase nickel incorporation protein, HypA					
### ATP-dependent RNA helicase, eIF-4A family ### ATP-dependent RNA helicase, eIF-4A family ### DNA helicase ### DNA helicase ### DNA helicase ### DNA helicase ### MobA-related protein NurD-like peptide ligase family ### MobA-related protein conserved in archaea ### MobM0123 uncharacterized protein (PcrB family) ### MobM0124 predicted phosphate-binding protein (PcrB family) ### MobA-related protein NurD-related protein ### MobA-related protein ### MobA-related protein NurD-related protein ### MobA-related protein ### MobA-related protein NurD-related protein ### MobA-related protein ### MobA-related protein ### MobA-related	MSM0109	conserved hypothetical membrane-spanning protein					
### ASM0112 ATP-dependent RNA helicase, eIF-4A family ### ASM0113 DNA helicase ### ASM0115 Conserved hypothetical protein ### ASM0115 Conserved hypothetical membrane protein ### ASM0116 MobA-related protein ### ASM0117 Conserved hypothetical membrane protein ### ASM0118 Cell wall biosynthesis protein, MurD-like peptide ligase family ### ASM0119 predicted nuclease ### ASM0120 DNA repair exonuclease (SbcD/Mre11-family), Rad32 ### ASM0121 DNA repair exonuclease (SbcD/Mre11-family), Rad32 ### ASM0122 predicted ATPase ### ASM0123 uncharacterized protein conserved in archaea ### ASM0124 predicted phosphate-binding protein (PcrB family) ### ASM0125 ribosomal protein L40e ### ASM0126 conserved hypothetical protein ### ASM0127 hypothetical protein ### ASM0128 conserved hypothetical protein ### ASM0129 nicotinamide mononucleotide adenylyltransferase, NadR ### MSM0131 molybdenum-binding protein, Mopl ### MSM0131 molybdenum cofactor biosynthesis protein, MoaE ### ASM0131 molybdenum cofactor biosynthesis protein, MoaE ### ASM0133 predicted thioesterase, FcbC ### ASM0134 M42 glutamyl aminopeptidase/endo-glucanase ### ASM0135 conserved hypothetical protein ### ASM0136 putative archaeal flagellar protein D/E ### ASM0138 predicted exonuclease ### ASM0139 hypothetical protein ### ASM0139 hypothetical protein ### ASM0139 hypothetical protein ### ASM0139 hypothetical protein ### ASM0130 conserved hypothetical protein ### ASM0130 hypothetical protein ### ASM0130 hypothetical protein ### ASM0131 hypothetical protein ### ASM0131 hypothetical protein ### ASM0131 hypothetical protein ### ASM0133 hypothetical protein ### ASM0130 hypothetical protein	MSM0110	predicted transposase					
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MSM0142	predicted ATPase (PP-loop superfamily)			
MSM0143	conserved hypothetical membrane protein			
MSM0144	hypothetical protein (putative ADP-ribosylation domain)			
MSM0145	conserved hypothetical protein			
MSM0146	type IV leader peptidase			
MSM0147	CTP synthase (UTP-ammonia lyase), PyrG			
MSM0148	predicted oxidoreductase, aldo/keto reductase family			
MSM0149	predicted acetylesterase			
MSM0150	hypothetical protein			
MSM0151	hypothetical protein			
NAON 404 50				
MSM0152	Na+-driven multidrug efflux pump (MATE family), NorM			
MSM0153	predicted phosphoglycerate mutase			
MSM0154	homoserine dehydrogenase, ThrA			
MSM0155	predicted allosteric regulator of homoserine dehydrogenase			
MSM0156	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase, C subunit			
MSM0157	predicted type I restriction-modification enzyme, subunit S			
MSM0158	type I restriction-modification system methylase, subunit S			
MSM0159	adhesin-like protein			
MSM0160	asparagine synthetase, AsnB			
MSM0161	hypothetical protein			
MSM0162	hypothetical protein			
MSM0163	conserved hypothetical proetin predicted to be involved in DNA repair			
MSM0164	conserved hypothetical protein predicted to be involved in DNA repair			
MSM0165	predicted exonuclease			
MSM0166	predicted helicase			
MSM0167	conserved hypothetical protein predicted to be involved in DNA repair			
IVICIVIO 107				
<u></u>	(RAMP superfamily)			
MSM0168	conserved hypothetical protein predicted to be involved in DNA repair			
MSM0169	predicted CRISPR-associated protein			
MSM0170	conserved hypothetical protein predicted to be involved in DNA repair			
IVISIVIOTI	71 1 1			
	(RAMP superfamily)			
MSM0171	conserved hypothetical membrane protein (invasin/intimin cell-			
	adhesion domain)			
MCM0470				
MSM0172	hypothetical protein			
MSM0173	adhesin-like protein			
MSM0174	O-acetylhomoserine sulfhydrylase (PLP-dependent), MET17			
MSM0175	homoserine O-acetyltransferase, MetX			
MSM0176	ribonuclease III (dsRNA-specific), Rnc			
MSM0177	hypothetical protein			
MSM0178	conserved hypothetical protein			
MSM0179	hypothetical protein			
MSM0180	hypothetical protein			
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MSM0183 MSM0184 MSM0185 MSM0186 MSM0187 MSM0188 MSM0190 MSM0191 MSM0192 MSM0193 MSM0194 MSM0195 MSM0196 MSM0199 MSM0199 MSM0201 MSM0200 MSM0201 MSM0200 MSM0201 MSM0205 MSM0206 MSM0207 MSM0208 MSM0209 MSM0209 MSM0209 MSM0209	snRNP Sm-like protein RNA-binding protein, PUA domain family creatinine amidohydrolase conserved hypothetical membrane protein conserved hypothetical protein rubredoxin rubredoxin rubredoxin acetyl/acyl transferase related protein predicted ATPase conserved hypothetical protein argininosuccinate lyase, ArgH ribosomal protein S27ae ribosomal protein S27ae ribosomal protein S24ae uncharacterized protein conserved in archaea archaeal DNA-dependent RNA polymerase, subunit E, RpoE archaeal DNA-dependent RNA polymerase, subunit E, RpoE inorganic pyrophosphatase conserved hypothetical protein (PilT N-term./Vapc superfamily) translation initiation factor alF-2, gamma subunit ribosomal protein S6e translation initiation factor alF-2, InfB nucleoside diphosphate kinase, Ndk ribosomal protein L24e ribosomal protein L7ae predicted DNA-binding protein predicted DNA-binding protein ferredoxin hypothetical protein			
MSM0183 MSM0184 MSM0184 MSM0186 MSM0186 MSM0188 MSM0189 MSM0190 MSM0191 MSM0193 MSM0194 MSM0195 MSM0196 MSM0197 MSM0197 MSM0199 MSM0200 MSM0201 MSM0202 MSM0203 MSM0204 MSM0205 MSM0205 MSM0207 MSM0207 MSM0209 MSM0209 MSM0209 MSM0201 MSM0209 MSM0201 MSM0211	snRNP Sm-like protein RNA-binding protein, PUA domain family creatinine amidohydrolase conserved hypothetical membrane protein conserved hypothetical protein rubredoxin rubredoxin acetyl/acyl transferase related protein predicted ATPase conserved hypothetical protein argininosuccinate lyase, ArgH ribosomal protein S27ae ribosomal protein S27ae ribosomal protein S24ae uncharacterized protein conserved in archaea archaeal DNA-dependent RNA polymerase, subunit E, RpoE archaeal DNA-dependent RNA polymerase, subunit E, RpoE inorganic pyrophosphatase conserved hypothetical protein (PilT N-term./Vapc superfamily) translation initiation factor alF-2, gamma subunit ribosomal protein S6e translation initiation factor alF-2, InfB nucleoside diphosphate kinase, Ndk ribosomal protein L24e ribosomal protein S28e ribosomal protein L7ae predicted DNA-binding protein predicted DNA-binding protein			
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MSM0183 MSM0184 MSM0184 MSM0186 MSM0186 MSM0188 MSM0190 MSM0190 MSM0191 MSM0193 MSM0194 MSM0195 MSM0196 MSM0199 MSM0200 MSM0201 MSM0202 MSM0203 MSM0204 MSM0205 MSM0205 MSM0205 MSM0206 MSM0207 MSM0208 MSM0208 MSM0209 MSM0201 MSM0201 MSM0201 MSM0201 MSM0202 MSM0201 MSM0211 MSM0211	snRNP Sm-like protein RNA-binding protein, PUA domain family creatinine amidohydrolase conserved hypothetical membrane protein conserved hypothetical protein rubredoxin rubredoxin acetyl/acyl transferase related protein predicted ATPase conserved hypothetical protein argininosuccinate lyase, ArgH ribosomal protein S27ae ribosomal protein S24ae uncharacterized protein conserved in archaea archaeal DNA-dependent RNA polymerase, subunit E, RpoE archaeal DNA-dependent RNA polymerase, subunit E, RpoE inorganic pyrophosphatase conserved hypothetical protein (PilT N-term./Vapc superfamily) translation initiation factor aIF-2, gamma subunit ribosomal protein S6e translation initiation factor aIF-2, InfB nucleoside diphosphate kinase, Ndk ribosomal protein L24e ribosomal protein L24e ribosomal protein S28e ribosomal protein L7ae predicted DNA-binding protein predicted DNA-binding protein ferredoxin hypothetical protein hypothetical protein			
MSM0183 MSM0184 MSM0185 MSM0186 MSM0188 MSM0189 MSM0190 MSM0191 MSM0192 MSM0193 MSM0194 MSM0195 MSM0196 MSM0197 MSM0198 MSM0199 MSM0200 MSM0201 MSM0202 MSM0203 MSM0204 MSM0205 MSM0205 MSM0205 MSM0206 MSM0207 MSM0208 MSM0209 MSM0209 MSM0210 MSM0211 MSM0211 MSM0212 MSM0213	snRNP Sm-like protein RNA-binding protein, PUA domain family creatinine amidohydrolase conserved hypothetical membrane protein cuserved hypothetical protein rubredoxin rubredoxin acetyl/acyl transferase related protein predicted ATPase conserved hypothetical protein argininosuccinate lyase, ArgH ribosomal protein S27ae ribosomal protein S27ae ribosomal protein S24ae uncharacterized protein conserved in archaea archaeal DNA-dependent RNA polymerase, subunit E, RpoE archaeal DNA-dependent RNA polymerase, subunit E, RpoE inorganic pyrophosphatase conserved hypothetical protein (PilT N-term./Vapc superfamily) translation initiation factor aIF-2, gamma subunit ribosomal protein S6 translation initiation factor aIF-2, InfB nucleoside diphosphate kinase, Ndk ribosomal protein L24e ribosomal protein L28e ribosomal protein L7ae predicted DNA-binding protein predicted DNA-binding protein ferredoxin hypothetical protein hypothetical protein conserved hypothetical protein archaeal histone, HMtA			
MSM0183 MSM0184 MSM0184 MSM0186 MSM0187 MSM0188 MSM0190 MSM0191 MSM0193 MSM0194 MSM0195 MSM0196 MSM0197 MSM0198 MSM0199 MSM0200 MSM0201 MSM0202 MSM0203 MSM0204 MSM0205 MSM0205 MSM0205 MSM0205 MSM0207 MSM0208 MSM0209 MSM0209 MSM0201 MSM0211 MSM0211	snRNP Sm-like protein RNA-binding protein, PUA domain family creatinine amidohydrolase conserved hypothetical membrane protein conserved hypothetical protein rubredoxin rubredoxin acetyl/acyl transferase related protein predicted ATPase conserved hypothetical protein argininosuccinate lyase, ArgH ribosomal protein S27ae ribosomal protein S24ae uncharacterized protein conserved in archaea archaeal DNA-dependent RNA polymerase, subunit E, RpoE archaeal DNA-dependent RNA polymerase, subunit E, RpoE inorganic pyrophosphatase conserved hypothetical protein (PilT N-term./Vapc superfamily) translation initiation factor aIF-2, gamma subunit ribosomal protein S6e translation initiation factor aIF-2, InfB nucleoside diphosphate kinase, Ndk ribosomal protein L24e ribosomal protein L24e ribosomal protein S28e ribosomal protein L7ae predicted DNA-binding protein predicted DNA-binding protein ferredoxin hypothetical protein hypothetical protein			

MSM0215	agreement by methodical integral membrane protein			
MSM0216	conserved hypothetical integral membrane protein tryptophanyl-tRNA synthetase, TrpS			
MSM0217	tRNA intron endonuclease, EndA			
MSM0218	iron dependent transcriptional regulator (Fe2+-binding)			
MSM0219	putative cysteine protease (transglutaminase-like superfamily)			
MSM0220	chaperonin (TCP-1/cpn60 family), alpha subunit			
MSM0221	adhesin-like protein			
MSM0222	flavoprotein (Metallo-beta-lactamase superfamily), FpaA			
MSM0223	conserved hypothetical protein			
MSM0224	conserved hypothetical protein			
MSM0225	conserved hypothetical protein			
MSM0226	hypothetical protein			
MSM0227	hydroxymethylglutaryl-CoA (HMG-CoA) reductase, HmgA			
MSM0228	succinyl-CoA synthetase, alpha subunit, SucD			
MSM0229	conserved hypothetical protein			
MSM0230	putative transposase	N	D	
MSM0231	3-dehydroquinate dehydratase			
MSM0232	signal peptidase I			
MSM0233	nitrogen regulatory protein P-II, GlnK			
MSM0234	ammonium transporter			
MSM0235	hypothetical protein			
MSM0236	phosphohydrolase (HD superfamily)			
MSM0237	3-polyprenyl-4-hydroxybenzoate decarboxylase, UbiX			
MSM0238	precorrin-6B methylase, CbiT			
MSM0239	conserved hypothetical protein			
MSM0240	molybdopterin-guanine dinucleotide biosynthesis protein A, MobA			
MSM0241	ribonuclease PH-related protein			
MSM0242	ribonuclease PH, Rph			
MSM0243	RNA-binding protein Rrp4			
MSM0244	predicted exosome subunit			
MSM0245	proteasome, alpha subunit, PsmA			
MSM0246	ribonuclease P, subunit Rpp14			
MSM0247	ribonuclease P, subunit p30			
MSM0248	hypothetical protein			
MSM0249	conserved hypothetical protein			
MSM0250	conserved hypothetical membrane protein (putative zinc-finger domain,			
MCMOOF4	Znf265)			
MSM0251	hypothetical protein Na+-driven multidrug efflux pump, NorM			
MSM0252 MSM0253	conserved hypothetical protein			
MSM0254	hypothetical protein			
MSM0255	putative transcription regulator (winged helix DNA-binding domain)			
MSM0256	putative transposase			
MSM0257	conserved hypothetical membrane protein			
MSM0258	hypothetical protein (putative zinc-finger domain, Znf265)			
MSM0259	hypothetical protein (putative zinc beta-ribbon superfamily)			
MSM0260	archaea-specific RecJ-like exonuclease			
MSM0261	conserved hypothetical protein			
MSM0262	desulfoferrodoxin (dfx)			
MSM0263	nitrogen fixation protein, NifU			
MSM0264	cysteine desulfurase, NifS			
MSM0265	O-acetylhomoserine sulfhydrylase			
	adhesin-like protein			
MSM0267	NAD(P)H-dependent FMN reductase (multimeric flavodoxin)			
MSM0268	cysteinyl-tRNA synthetase, CysS			
MSM0269	predicted transcriptional regulator (lambda repressor-like)			
MSM0270	serine acetyltransferase, CysE			
MSM0271	cysteine synthase, CysK			
MSM0272	endonuclease III			
MSM0273	EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)			
MSM0274	SAM-dependent methyltransferase (cyclopropane fatty acid synthase-			
MOMOOTE	related)			
MSM0275	valyl-tRNA synthetase, ValS			
MSM0276	conserved hypothetical protein			
MSM0277	phenylalanyl-tRNA synthetase, beta subunit, PheT			
MSM0278	hypothetical protein conserved hypothetical protein (UPF0047 family)			
MSM0279 MSM0280	predicted archaeal ATPase (AAA+ superfamily)			
	putative adhesin-like protein			
MSM0281				
MSM0282 MSM0283	adhesin-like protein hypothetical protein			
MSM0283 MSM0284	ribose 5-phosphate isomerase, RpiA			
MSM0285	conserved hypothetical protein (UPF0179 family)			
MSM0286	glycerol 1-phosphate dehydrogenase (Dehydroquinate synthase-like			
WICIVIOZOU	family)			
MSM0287	prolyl-tRNA synthetase, ProS			
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MSM0288	conserved hypothetical protein (DUF121 daomain)				
MSM0289	phosphomethylpyrimidine kinase (HMPP-kinase), ThiD				
MSM0290	nitrate/sulfonate/bicarbonate ABC transporter, ATPase component,				
	TauB				
MSM0291	nitrate/sulfonate/bicarbonate ABC transporter, permease component,				
WOW OZO					
	TauC				
MSM0292	predicted metal-dependent membrane protease				
MSM0293	cation transport ATPase, HAD family				
MSM0294	conserved hypothetical protein				
10101010294					
MSM0295	formate dehydrogenase accessory protein, FdhD				
MSM0296	putative carboxymuconolactone decarboxylase				
MSM0297	predicted exosome subunit				
MSM0298	ribosomal protein L15e				
MSM0299	conserved hypothetical protein				
MSM0300	peptide/nickel ABC transporter, solute-binding component				
MSM0301	peptide/nickel ABC transporter, permease component, DppB				
MSM0302	peptide/nickel ABC transporter, permease component, DppC				
MSM0303	peptide/nickel ABC transporter, ATP-binding component, DppD				
MSM0304	peptide/nickel ABC transporter, ATP-binding component, DppF				
MSM0305	conserved hypothetical membrane protein (IMP dehydrogenase				
IVIOIVIOOOO					
	related)				
MSM0306	polyferredoxin, iron-sulfur binding				
MSM0307	sugar kinase (ribokinase/pfkB superfamily)				
MSM0308	formylmethanofuran:tetrahydromethanopterin formyltransferase, FtrC			الكالي ال	
IVIOIVIOSOS	iomymemanoruran.tetranyuromethanoptenin iomyttanisierase, Ftio				
MSM0309	conserved hypothetical membrane protein				
MSM0310	polyferredoxin, iron-sulfur binding				
MSM0311	polyferredoxin, iron-sulfur binding				
MSM0312	[NiFe]-hydrogenase-3-type complex, large subunit/NADH:quinone				
	oxidoreductase (complex I), subunit 49K/NdhH/NuoD				
MSM0313	[NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone				
WICHWIOOTO					
	oxidoreductase (complex I), subunit PSST/NdhK/NuoB				
MSM0314	conserved hypothetical protein				
MSM0315	predicted [NiFe]-hydrogenase-3-type complex Eha, membrane protein				
	EhaL				
140140040					
MSM0316	hypothetical protein				
MSM0317	NADH dehydrogenase (ubiquinone), subunit 1				
MSM0318	conserved hypothetical membrane protein				
MSM0319	NADH dehydrogenase I, subunit N related				
MSM0320	predicted [NiFe]-hydrogenase-3-type complex Eha, membrane protein				
	EhaG				
MSM0321	conserved hypothetical membrane protein				
MSM0322	predicted [NiFe]-hydrogenase-3-type complex Eha, membrane protein				
MOMOSZZ					
	EhaE				
MSM0323	conserved hypothetical membrane protein				
MSM0324	conserved hypothetical membrane protein				
MSM0325	conserved hypothetical membrane protein				
MSM0326	conserved hypothetical membrane protein				
MSM0327	UDP-glucose 4-epimerase (NAD dependent)				
MSM0328	conserved hypothetical protein				
MSM0329	DNA binding protein (regulator), xenobiotic response element family				
MSM0330	acetyl-CoA synthetase, AMP-forming-related, Acs				
MSM0331	2-oxoisovalerate ferredoxin oxidoreductase, delta subunit				
	2-oxoisovalerate ferredoxin oxidoreductase, alpha subunit				
MSM0333	2-oxoisovalerate ferredoxin oxidoreductase, beta subunit				
MSM0334	L-asparaginase, GatD,			الساوي و	
MSM0335	archaeal glutamyl-tRNA(Gln) amidotransferase, subunit E, GatE				
MSM0336	hypothetical protein				
MSM0337	putative adhesin-like protein				
MSM0338	hypothetical protein				
MSM0339	hypothetical protein				
MSM0340	thioredoxin reductase (NADPH), TrxB				
MSM0341	hypothetical protein				
MSM0342	putative transposase		ND		
			ואַט		
MSM0343	GMP synthase (glutamine-hydrolysing), subunit A, GuaA				
MSM0344	hypothetical protein				
MSM0345					
	IGNP synthase (diutamine-nydrolysing) PP-ATPase domain/silbitinit				
10131010343	GMP synthase (glutamine-hydrolysing), PP-ATPase domain/subunit,				
	GuaA				
MSM0346					
	GuaA				
MSM0346 MSM0347	GuaA conserved hypothetical protein putative pyridoxal phosphate-dependent enzyme				
MSM0346 MSM0347 MSM0348	GuaA conserved hypothetical protein putative pyridoxal phosphate-dependent enzyme conserved hypothetical protein				
MSM0346 MSM0347 MSM0348 MSM0349	GuaA conserved hypothetical protein putative pyridoxal phosphate-dependent enzyme conserved hypothetical protein hypothetical protein				
MSM0346 MSM0347 MSM0348	GuaA conserved hypothetical protein putative pyridoxal phosphate-dependent enzyme conserved hypothetical protein				
MSM0346 MSM0347 MSM0348 MSM0349 MSM0350	GuaA conserved hypothetical protein putative pyridoxal phosphate-dependent enzyme conserved hypothetical protein hypothetical protein	•			
MSM0346 MSM0347 MSM0348 MSM0349 MSM0350 MSM0351	GuaA  conserved hypothetical protein putative pyridoxal phosphate-dependent enzyme conserved hypothetical protein hypothetical protein 2-isopropylmalate synthase, LeuA conserved hypothetical protein				
MSM0346 MSM0347 MSM0348 MSM0349 MSM0350 MSM0351 MSM0352	GuaA  conserved hypothetical protein putative pyridoxal phosphate-dependent enzyme conserved hypothetical protein hypothetical protein 2-isopropylmalate synthase, LeuA conserved hypothetical protein predicted DNA modification methylase				
MSM0346 MSM0347 MSM0348 MSM0349 MSM0350 MSM0351	GuaA  conserved hypothetical protein putative pyridoxal phosphate-dependent enzyme conserved hypothetical protein hypothetical protein 2-isopropylmalate synthase, LeuA conserved hypothetical protein				

MSM0354	ATP-dependent 26S proteasome regulatory subunit, RPT1		
MSM0355	predicted transcription factor (eukaryotic MBF1 related)		
MSM0356	conserved hypothetical protein		
MSM0357	conserved hypothetical membrane protein (possible Zinc-binding)		
MSM0358	conserved hypothetical membrane protein		
MSM0359	cell wall biosynthesis protein, MurD-like peptide ligase family		
MSM0360	cell wall biosynthesis protein, phospho-N-acetylmuramoyl-pentapeptide-		
	transferase family		
MSM0361	carbamoyl-phosphate synthase, large subunit, CarB		
MSM0362	coenzyme F420-reducing hydrogenase (Ni,Fe-hydrogenase maturation		
	protease), delta subunit		
MSM0363	predicted RNA methylase		
MSM0364	transcriptional regulator (nickel-responsive), NikR		
MSM0365	conserved hypothetical protein		
MSM0366	hypothetical protein		
MSM0367	conserved hypothetical protein		
MSM0368	glutamate synthase (NADPH), subunit 2		
MSM0369	glutamate synthase, subunit 3		
MSM0370	glutamate synthase, subunit 1		
MSM0371	predicted glutamine amidotransferase involved in pyridoxine		
VIOIVIOO7 I	biosynthesis, Pdx2		
MSM0372	phycobiliprotein (PBS) lyase (HEAT repeat)		
MSM0373			
MSM0374	isocitrate/isopropylmalate dehydrogenase, LeuB long-chain fatty-acid-CoA ligase (AMP-forming), CaiC		
MSM0374 MSM0375	acetylglutamate kinase, ArgB		
MSM0376	alcohol dehydrogenase (zinc-binding), GroES-like		
MSM0376 MSM0377	4-diphosphocytidyl-2-methyl-D-erithritol synthase, IspD		
MSM0378	SAM-dependent methyltransferase		
MSM0379	glutamate N-acetyltransferase, ArgJ		
MSM0380	hypothetical protein		
MSM0381	conserved hypothetical protein		
MSM0382	conserved hypothetical protein (PIN domain-like)		
MSM0383	predicted phosphohydrolase, calcineurin-like superfamily		
MSM0384	transcription factor, NACalpha-BTF3 related		
MSM0385	anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase,		
	Elongator protein 3/MiaB/NifB family		
MSM0386	sodium/proline symporter (proline permease), PutP		
MSM0387	coenzyme F390 synthetase, PaaK		
MSM0388	amino acid regulator		
MSM0389	hypothetical protein		
MSM0390	hypothetical protein		
MSM0391	indolepyruvate ferredoxin oxidoreductase, beta subunit		
MSM0392	indolepyruvate ferredoxin oxidoreductase, alpha subunit		
MSM0393	fumarate reductase, iron-sulfur protein		
MSM0394	rRNA methylase, SpoU family		
MSM0395	ferredoxin, iron-sulfur binding		
MSM0396	putative transposase		
MSM0397			
	xanthine/uracil permease, UraA		
MSM0398	uracil phosphoribosyltransferase, Upp		
MSM0398 MSM0399	uracil phosphoribosyltransferase, Upp hypothetical protein		
MSM0398 MSM0399 MSM0400	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein		
MSM0398 MSM0399 MSM0400 MSM0401	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlycyl-tRNA synthetase		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlycyl-tRNA synthetase predicted transcriptional regulator		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlvcyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlvcyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0404 MSM0405 MSM0406 MSM0407	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406 MSM0407 MSM0408 MSM0408	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family glycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein P-loop containing nucleoside triphosphate hydrolase (NAD(P)-binding)  2-phosphoglycerate kinase/small-molecule binding protein C4-type Zinc-finger protein		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406 MSM0407 MSM0408 MSM0408 MSM0409 MSM0409	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family glycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein P-loop containing nucleoside triphosphate hydrolase (NAD(P)-binding) 2-phosphoglycerate kinase/small-molecule binding protein		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406 MSM0407 MSM0408 MSM0408 MSM0409 MSM0409	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlvcyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein P-loop containing nucleoside triphosphate hydrolase (NAD(P)-binding)  2-phosphoglycerate kinase/small-molecule binding protein C4-type Zinc-finger protein conserved hypothetical protein, histone-fold superfamily adhesin-like protein		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406 MSM0407 MSM0408 MSM0409 MSM0409 MSM0410 MSM0411	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein P-loop containing nucleoside triphosphate hydrolase (NAD(P)-binding)  2-phosphoglycerate kinase/small-molecule binding protein C4-type Zinc-finger protein conserved hypothetical protein, histone-fold superfamily		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406 MSM0407 MSM0408 MSM0408 MSM0410 MSM0411 MSM0411	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family qlvcyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein P-loop containing nucleoside triphosphate hydrolase (NAD(P)-binding)  2-phosphoglycerate kinase/small-molecule binding protein C4-type Zinc-finger protein conserved hypothetical protein, histone-fold superfamily adhesin-like protein		
MSM0398 MSM0399 MSM04001 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406 MSM0407 MSM0408 MSM0409 MSM0410 MSM0411 MSM0411 MSM0412 MSM0413	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family glycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein P-loop containing nucleoside triphosphate hydrolase (NAD(P)-binding) 2-phosphoglycerate kinase/small-molecule binding protein C4-type Zinc-finger protein conserved hypothetical protein, histone-fold superfamily adhesin-like protein putative adhesin-like protein		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406 MSM0407 MSM0408 MSM0409 MSM0410 MSM0411 MSM0411 MSM0413 MSM0413 MSM0414	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family glycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein P-loop containing nucleoside triphosphate hydrolase (NAD(P)-binding)  2-phosphoglycerate kinase/small-molecule binding protein C4-type Zinc-finger protein conserved hypothetical protein, histone-fold superfamily adhesin-like protein putative adhesin-like protein transcriptional regulator, MarR family		
MSM0398 MSM0399 MSM0400 MSM0401 MSM0402 MSM0403 MSM0404 MSM0405 MSM0406 MSM0407 MSM0408 MSM0409 MSM0410 MSM0411 MSM0411 MSM0413 MSM0413 MSM0414 MSM0414 MSM0414	uracil phosphoribosyltransferase, Upp hypothetical protein hypothetical protein predicted surface protease dCTP deaminase, dUTPase family glycyl-tRNA synthetase predicted transcriptional regulator predicted metal-dependent DNase, TatD-related family conserved hypothetical protein P-loop containing nucleoside triphosphate hydrolase (NAD(P)-binding)  2-phosphoglycerate kinase/small-molecule binding protein C4-type Zinc-finger protein conserved hypothetical protein, histone-fold superfamily adhesin-like protein putative adhesin-like protein transcriptional regulator, MarR family Na+-driven multidrug efflux pump, NorM uridylate kinase, PyrH		
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MSM0424	transcription initiation factor TFIIB (zinc-binding)				
MSM0425					
	predicted RNA-binding protein involved in rRNA processing				
MSM0426	demethylmenaguinone methyltransferase				
MSM0427	DNA primase (bacterial type), DnaG				
MSM0428	integrase-recombinase protein, phage integrase family				
MSM0429	biotin biosynthesis protein, BioY				
MSM0430	conserved hypothetical protein, predicted metal-binding				
MSM0431	predicted ATP-dependent carboligase, biotin carboxylase-related				
MSM0432	conserved hypothetical protein				
MSM0433	archaeal/vacuolar-type H+-transporting ATP synthase, subunit D				
MSM0434	archaeal/vacuolar-type H+-transporting ATP synthase, subunit B				
MSM0435	archaeal/vacuolar-type H+-transporting ATP synthase, subunit A				
MSM0436					
	archaeal/vacuolar-type H+-transporting ATP synthase, subunit F				
MSM0437	archaeal/vacuolar-type H+-transporting ATP synthase, subunit C				
MSM0438	archaeal/vacuolar-type H+-transporting ATP synthase, subunit E				
MSM0439	archaeal/vacuolar-type H+-transporting ATP synthase, subunit K				
MSM0440	archaeal/vacuolar-type H+-transporting ATP synthase, subunit I				
MSM0441	archaeal/vacuolar-type H+-transporting ATP synthase, subunit H				
MSM0442	hypothetical protein				
MSM0443	hypothetical protein				
MSM0444	hypothetical protein				
MSM0445	NADH dehydrogenase/NAD(P)H nitroreductase				
MSM0446	citrate synthase, GltA				
MSM0447	fumarate hydratase, alpha subunit				
MSM0448	conserved hypothetical protein				
MSM0449	2-methylcitrate dehydratase, MmgE/PrpD family				
MSM0450	conserved hypothetical membrane protein				
MSM0451	conserved hypothetical membrane protein				
	predicted DNA-binding protein				
MSM0452					
MSM0453	predicted transcriptional regulator				
MSM0454	hypothetical protein				
MSM0455	conserved hypothetical protein				
MSM0456	conserved hypothetical protein				
MSM0457	D-3-phosphoglycerate dehydrogenase, SerA				
MSM0458	transposase, homeodomain-like superfamily	N	ID		
MSM0459	hypothetical protein				
MSM0460	predicted transposase				
MSM0461	adhesin-like protein				
IMSM0462	predicted metal-dependent protease PAD1/JAB1 superfamily				
MSM0462	predicted metal-dependent protease, PAD1/JAB1 superfamily				
MSM0463	predicted tRNA(His) guanylyltransferase				
MSM0463	predicted tRNA(His) guanylyltransferase				
	predicted tRNA(His) guanylyltransferase homoserine/aspartate dehydrogenase (NAD binding), glyceraldehyde-3				
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MSM0463 MSM0464 MSM0465	predicted tRNA(His) guanylyltransferase homoserine/aspartate dehydrogenase (NAD binding), glyceraldehyde-3- phosphate dehydrogenase-like superfamily conserved hypothetical protein		Ę		
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MSM0463 MSM0464 MSM0465 MSM0466 MSM0467 MSM0468 MSM0469	predicted tRNA(His) guanylyltransferase homoserine/aspartate dehydrogenase (NAD binding), glyceraldehyde-3 phosphate dehydrogenase-like superfamily conserved hypothetical protein predicted tRNA-binding protein NADP-dependent glyceraldehyde-3-phosphate dehydrogenase conserved hypothetical membrane protein conserved hypothetical membrane protein				
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MSM0497	predicted nuclease, RecB family				
MSM0498	hypothetical protein				
MSM0499	conserved hypothetical protein				
MSM0500	N-carbamoyl-D-amino acid amidohydrolase				
MSM0501	phycocyanin alpha phycocyanobilin Iyase, CpcE				
MSM0502	ATP-dependent helicase, Lhr-like				
MSM0503	flavodoxin, FldA				
MSM0504	conserved hypothetical protein				
MSM0505	hypothetical protein				
MSM0506	ATP-utilizing enzyme, ATP-grasp superfamily				
MSM0507	predicted phosphoesterase, YfcE				
MSM0508	cell division protein J (23S rRNA methylase), FtsJ				
MSM0509	conserved hypothetical protein				
MSM0510	predicted ATPase involved in DNA replication control, MCM2/3/5 family				
INISINIOSTU	predicted ATPase involved in DNA replication control, MCM2/3/5 family				
MSM0511	translation initiation factor 2, beta subunit (aIF-2beta)				
MSM0512	NMD3-related protein (nonsense mediated mRNA decay)				
MSM0513	tyrosyl-tRNA synthetase, TyrS				
MSM0514	conserved hypothetical protein				
MSM0515					
	methanol:cobalamin methyltransferase, MtaB				
MSM0516	corrinoid protein (methionine synthase-related), MtaC				
MSM0517	methyltransferase activation protein, MapA				
MSM0518	methylcobalamin:coenzyme M methyltransferase, MtaA				
MSM0519	conserved hypothetical protein				
MSM0520	thymidylate kinase, Tmk				
MSM0521	conserved hypothetical membrane protein				
MSM0522	collagenase, peptidase family U32				
MSM0523	collagenase, peptidase family U32				
MSM0524	DNA mismatch repair ATPase, MutS				
MSM0525	predicted unusual protein kinase, ubiquinone biosynthesis protein-				
	related, AarF				
MCMOEOG	conserved hypothetical protein			'	
MSM0526					
MSM0527	IS element ISM1 (ICSNY family)				
MSM0528	IS element ISM1 (ICSNY family)				
MSM0529	hypothetical protein				
MSM0530	predicted O-linked GlcNAc transferase				
MSM0531	adenine/cytosine DNA methyltransferase				
MSM0532	IS element ISM1 (ICSNY family)				
MSM0533	IS element ISM1 (ICSNY family)				
MSM0534	IS element ISM1 (ICSNY family)				
MSM0535					
	hypothetical protein				
MSM0536	hypothetical protein hypothetical protein				
MSM0536	hypothetical protein				
MSM0536 MSM0537	hypothetical protein TPR-repeat protein				
MSM0536 MSM0537 MSM0538	hypothetical protein TPR-repeat protein pyruvate formate-lyase activating enzyme, PflA				
MSM0536 MSM0537 MSM0538 MSM0539	hypothetical protein TPR-repeat protein pyruvate formate-lyase activating enzyme, PflA putative DNA-directed DNA polymerase				
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MSM0536 MSM0537 MSM0538 MSM0539 MSM0540 MSM0541 MSM0542 MSM0543 MSM0544 MSM0545 MSM0546 MSM0547 MSM0548 MSM0550 MSM0551 MSM0551 MSM0552 MSM0553	hypothetical protein TPR-repeat protein pyruvate formate-lyase activating enzyme, PflA putative DNA-directed DNA polymerase predicted transcriptional regulator hypothetical protein coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase, Mer DNA repair photolyase, SplB predicted Fe-S oxidoreductase conserved hypothetical protein conserved hypothetical protein predicted nucleotidyltransferase, cytidyltransferase-related 6-phosphogluconate dehydrogenase, beta-hydroxyacid dehydrogenase related, MmsB cytochrome C-type biogenesis protein, DsbD protein disulfide-isomerase, thioredoxin-related conserved hypothetical protein sulfur transfer protein involved in thiamine biosynthesis ATPase, PP-loop superfamily	N	D		
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	MSM0606 MSM0607 MSM0608 MSM0609 MSM0609 MSM0610 MSM0611 MSM0611 MSM0612 MSM0613 MSM0615 MSM0615 MSM0616 MSM0617 MSM0618 MSM0617 MSM0618 MSM0620 MSM0621 MSM0620 MSM0621 MSM0622 MSM0623 MSM0624 MSM0625 MSM0625 MSM0625 MSM0625 MSM0626 MSM0627 MSM0628 MSM0627 MSM0628 MSM0629 MSM0630 MSM0631 MSM0631 MSM0631 MSM0633 MSM0634 MSM0635 MSM0636 MSM0637 MSM0638	hypothetical protein predicted ATPase, RNase L inhibitor family putative metal-binding protein ferredoxin, iron-sulfur binding aspartate aminotransferase DNA repair protein, RadB putative translation factor, Sua5/YciO/YrdC/YwlC family phosphatidylglycerophosphate synthase, PgsA conserved hypothetical protein archaeal fructose 1,6-bisphosphatase adhesin-like protein thiamine biosynthesis ATP pyrophosphatase, Thil pH regulator (monovalent cation:H+ antiporter) alanyl-tRNA synthetase, AlaS ribosomal protein L12p ribosomal protein L10p ribosomal protein L10p ribosomal protein L10p ribosomal protein L11 transcription antiterminator, NusG protein translocation complex sec61, gamma subunit cell division protein, FtsZ tetrahydromethanopterin S-methyltransferase, subunit H, MtrH conserved hypothetical protein putative transposase conserved hypothetical protein transcription initiation factor IIE, alpha subunit predicted hydrolase, HD superfamily archaeosine tRNA-ribosyltransferase predicted metal-sulfur cluster biosynthetic enzyme predicted regulator of amino acid metabolism hydrogenase expression/formation protein, HypC dihydrolipoamide dehydrogenase pfam match to MurG; not predicted to be a carbohydrate active enzyme by CAZy putative cell wall biosynthesis protein cell division protein (RNA-binding), PelA	N	ID.	

MSM0643	conserved hypothetical protein			
MSM0644	thiamine biosynthesis protein, ThiC			
MSM0645	ATP-dependent DNA ligase, Cdc9			
MSM0646	conserved hypothetical protein			
MSM0647	predicted RNA-binding protein, contains TRAM domain			
MSM0648	phosphomannomutase, ManB			
MSM0649	conserved hypothetical protein			
MSM0650	transcriptional regulator, TetR/AcrR family			
MSM0651	best blast hit to MTH_1585; not predicted to be a carbohydrate active			
INSINIOS I				
	enzyme by CAZy			
MSM0652	pyruvate formate-lyase activating enzyme, PflA			
MSM0653	histidinol-phosphate aminotransferase, HisC			
MSM0654	carbonic anhydrase, Cab			
MSM0655	glucose-1-phosphate thymidylyltransferase			
MSM0656	phosphomannomutase, ManB			
MSM0657	phosphoglycerate mutase, AP superfamily			
MSM0658	hypothetical protein			
MSM0659	conserved hypothetical membrane protein			
MSM0660				
	LemA protein			
MSM0661	small subunit ribosomal protein S3Ae			
MSM0662	putative flagellar protein, FliL			
MSM0663	dinitrogenase iron-molybdenum cofactor biosynthesis protein,			
	NifX NifB family			
MSMOSSA	multimeric flavodoxin, NADPH-dependent FMN reductase family			
MSM0664				
MSM0665	5'-methylthioadenosine phosphorylase			
MSM0666	conserved hypothetical protein			
MSM0667	conserved hypothetical protein			
MSM0668	conserved hypothetical protein			
MSM0669	hypothetical protein			
MSM0670	conserved hypothetical protein			
MSM0671	cell division control protein Cdc6-related, AAA+ ATPase superfamily			
MSM0672	thiamine pyrophosphokinase			
MSM0673	conserved hypothetical membrane protein			
MSM0674	hypothetical protein			
MSM0675	hypothetical protein			
MSM0676	conserved hypothetical membrane protein			
MSM0677	archaeal aspartate aminotransferase			
MSM0678	conserved hypothetical membrane protein			
MSM0679				
	conserved hypothetical membrane protein			1
MSM0680	predicted ATPase, AAA+ superfamily			
MSM0681	conserved hypothetical protein			
MSM0682	hypothetical protein			
MSM0683	conserved hypothetical protein			
MSM0684	conserved hypothetical protein			
MSM0685	hypothetical protein			
MSM0686	acetolactate synthase (TPP-requiring), large subunit, IIvB			
MSM0687	deoxycytidine-triphosphate deaminase, Dcd			
MSM0688	4-oxalocrotonate tautomerase			
MSM0689	hypothetical protein			
MSM0690	helicase			
MSM0691	mutator mutT protein (NUDIX domain)			
MSM0692	conserved hypothetical protein			
MSM0693	ATPase involved in DNA repair, SbcC			
MSM0694	hypothetical protein			
MSM0695	DNA repair helicase			
MSM0696	Fe-S oxidoreductase			
MSM0697	hypothetical protein			
MSM0698	hypothetical protein			
MSM0699	Na+-dependent transporter, SNF family			
MSM0700	putative poly-gamma-glutamate synthesis protein, PgsA			
MSM0701	signal recognition particle GTPase SRP54			
MSM0702	predicted prefoldin, alpha subunit			
MSM0703	ribosomal protein LX			
MSM0704	translation initiation factor 6 (aIF-6)			
MSM0705	ribosomal protein L31a			
MSM0706	ribosomal protein L39a			
MSM0707	predicted subunit of tRNA methyltransferase			
MSM0708	dsDNA-binding protein			
MSM0709	ribosomal protein S16a			
MSM0710	RNA-binding protein, CRS1/YhbY family			
MSM0711	ribonuclease P, subunit RPR2			
MSM0712	conserved hypothetical protein (DUF1696 domain)			
MSM0713	predicted nucleotide kinase			
MSM0714	predicted GTPase			
MSM0715	predicted GTPase			
MSM0716	oligosaccharyl transferase, STT3 subunit			

MSM0717	DNA tanaisamarasa I. TanA				
MSM0717	DNA topoisomerase I, TopA conserved hypothetical protein				
MSM0719	phosphoserine phosphatase, HAD family, SerB				
MSM0720	transcription initiation factor TFIID TATA binding protein				
MSM0721	adenylate cyclase, class 2				
MSM0722	2-isopropylmalate synthase, LeuA				
MSM0723	3-isopropylmalate dehydratase, LeuC				
MSM0724	4-hydroxybenzoate synthetase (chorismate lyase)				
MSM0725	DNA repair flap structure-specific 5'-3' endonuclease				
MSM0726	conserved hypothetical protein				
MSM0727	S-adenosylhomocysteine hydrolase (adenosylhomocysteinase), AhcY				
WIGWIOT ZT	ductiosymomocysteme flydrolase (adenosymomocystemase), 7 me f				
MSM0728	predicted oxidoreductase, aldo/keto reductase family				
MSM0729	molybdopterin biosynthesis protein, MoeB				
MSM0730	putative transposase	N	D	l	
MSM0731	putative DNA helicase II, UvrD				
MSM0732	tRNA pseudouridine synthase B, TruB				
MSM0733	ribosomal protein L14e				
MSM0734	cytidylate kinase, Cmk				
MSM0735	ribosomal protein L34e				
MSM0736	conserved hypothetical membrane protein				
MSM0737	archaeal adenylate kinase, AdkA				
MSM0738	preprotein translocase, SecY subunit, SecY				
MSM0739	ribosomal protein L15p				
MSM0740	ribosomal protein L30p				
MSM0741	ribosomal protein S5p, RpsE				
MSM0742	ribosomal protein L18p, RpIR				
MSM0743	ribosomal protein L19e				
MSM0744	ribosomal protein L32e				
MSM0745	ribosomal protein L6p, RpIF				
MSM0746	ribosomal protein S8p				
MSM0747	ribosomal protein S14p				
MSM0748	ribosomal protein L5p				
MSM0749	ribosomal protein S4e				
MSM0750	ribosomal protein L24p				
MSM0751	ribosomal protein L14p				
MSM0752	ribosomal protein S17p				
MSM0753	ribonuclease P, subunit P29				
MSM0754	translation initiation factor SUI1				
MSM0755	ribosomal protein L29p				
MSM0756	ribosomal protein S3p				
MSM0757	ribosomal protein L22p				
MSM0758	ribosomal protein S19p				
MSM0759	ribosomal protein L2p				
MSM0760	ribosomal protein L23p				
MSM0761	ribosomal protein L1e				
MSM0762	ribosomal protein L3p				
MSM0763	conserved hypothetical protein				
MSM0764	ribosomal L11 RNA methyltransferase (SAM-dependent)				
MSM0765	pyruvate carboxylase (acetyl-CoA/biotin carboxylase), subunit A, PycA				
MSM0766	biotin-[acetyl-CoA-carboxylase] ligase/biotin operon regulator				
	bifunctional protein, BirA				
MSM0767	selenocysteine synthase, SelA				
MSM0768	conserved hypothetical protein				
MSM0769	fumarate hydratase, class I				
MSM0770	cobalt ABC transporter, ATPase component, CbiO				
MSM0771	cobalt ABC transporter, permease component, CbiQ				
MSM0772	predicted permease, major facilitator superfamily				
MSM0773	multidrug ABC transporter, ATPase component				
MSM0774	multidrug ABC transporter, ATPase component				
MSM0775	transcriptional regulator, AraC family				
MSM0776	conserved hypothetical membrane protein				
MSM0777	conserved hypothetical protein				
MSM0778	predicted RNA-binding protein, eukaryotic snRNP-like				
MSM0779	predicted Zn-dependent hydrolase, metallo-beta-lactamase superfamily				
MSM0780	conserved hypothetical protein				
MSM0781	conserved hypothetical protein				
MSM0782	hypothetical protein				
MSM0783	tungsten formylmethanofuran dehydrogenase, subunit F, FwdF				
MSM0784	ferredoxin				
MSM0785	predicted phosphopantetheine adenylyltransferase (PPAT)				
MSM0786	transglutaminase-like protein, putative cysteine protease				
MSM0787	Fe-S oxidoreductase				
MSM0788	aspartate aminotransferase				
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MSM0789	cation efflux system protein (zinc/cadmium/cobalt)		
MSM0790	CBS-domain-containing protein		
MSM0791	2-phosphoglycerate kinase		
MSM0792	predicted calcineurin-like phosphoesterase		
MSM0793	conserved hypothetical protein		
MSM0794	conserved hypothetical protein		
MSM0795	heterodisulfide reductase, subunit B, HdrB		
MSM0796	heterodisulfide reductase, subunit C, HdrC		
MSM0797			
	archaeosine tRNA-ribosyltransferase		
MSM0798	hypothetical protein		
MSM0799	conserved hypothetical protein		
MSM0800	hypothetical protein		
MSM0801	diphthine synthase, DphB		
MSM0802	methyltransferase		
MSM0803	predicted metal-dependent membrane protease, CAAX amino terminal		
	protease family		
MSM0804	translation initiation factor aIF-2B, alpha subunit		
MSM0805	polar amino acid ABC transporter, ATPase component		
MSM0806	polar amino acid ABC transporter, permease component		
MSM0807	polar amino acid ABC transporter, substrate-binding component		
MSM0808	nitrogenase iron-molybdenum cofactor biosynthesis protein, NifB		
MSM0809	conserved hypothetical protein		
MSM0810	activator of (R)-2-hydroxyglutaryl-CoA dehydratase		
MSM0811	conserved hypothetical protein		
MSM0812	conserved hypothetical protein		
MSM0813	predicted peptidyl-prolyl cis-trans isomerase		
MSM0814	phosphoribosylformylglycinamidine synthase-related protein		
	(selenophosphate synthetase)		
MSM0815	conserved hypothetical protein		
MSM0816	predicted nucleic acid-binding protein, PIN domain-like family		
MSM0817	predicted transcriptional regulator		
MSM0818	predicted transcriptional regulator		
MSM0819	putative transcription regulator, ArsR family		
MSM0820	molybdenum cofactor biosynthesis protein, MoaB		
MSM0821	orotate phosphoribosyltransferase, PyrE		
MSM0822	photosynthetic reaction centre cytoplasmic domain-containing protein		
IVISIVIUOZZ	photosynthetic reaction centre cytopiasmic domain-containing protein		
MCMOOOO	phoophoopologicute outthooplogicute phoophoto dikinggo DogA		
MSM0823	phosphoenolpyruvate synthase/pyruvate phosphate dikinase, PpsA		
MSM0824	putative N-acetyltransferase, GNAT family		
MSM0824 MSM0825	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ		
MSM0824 MSM0825 MSM0826	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL		
MSM0824 MSM0825 MSM0826 MSM0827	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family		
MSM0824 MSM0825 MSM0826	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830 MSM0831	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830 MSM0831 MSM0832	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0827 MSM0829 MSM0830 MSM0831 MSM0831 MSM0832 MSM0833	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830 MSM0831 MSM0833 MSM0833	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830 MSM0831 MSM0832 MSM0833 MSM0834 MSM0834	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830 MSM0831 MSM0831 MSM0833 MSM0834 MSM0835 MSM0836	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase related to alpha-glycosyltransferases, GT4 family		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0830 MSM0831 MSM0831 MSM0833 MSM0833 MSM0834 MSM0835 MSM0836 MSM0837	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase related to alpha-glycosyltransferases, GT4 family cobalamin biosynthesis protein D, CbiD		
MSM0824 MSM0825 MSM0825 MSM0827 MSM0827 MSM0829 MSM0830 MSM0831 MSM0832 MSM0833 MSM0834 MSM0835 MSM0836 MSM0837 MSM0837	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase related to alpha-glycosyltransferases, GT4 family cobalamin biosynthesis protein D, CbiD putative thioredoxin/glutaredoxin		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830 MSM0831 MSM0832 MSM0834 MSM0835 MSM0836 MSM0836 MSM0836 MSM0837 MSM0838	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase related to alpha-glycosyltransferases, GT4 family cobalamin biosynthesis protein D, CbiD putative thioredoxin/glutaredoxin ATP-dependent helicase		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830 MSM0831 MSM0833 MSM0834 MSM0835 MSM0835 MSM0836 MSM0837 MSM0838 MSM0839 MSM0839	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase related to alpha-glycosyltransferases, GT4 family cobalamin biosynthesis protein D, CbiD putative thioredoxin/glutaredoxin ATP-dependent helicase conserved hypothetical protein		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0829 MSM0830 MSM0831 MSM0832 MSM0834 MSM0835 MSM0836 MSM0836 MSM0836 MSM0837 MSM0838	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase related to alpha-glycosyltransferases, GT4 family cobalamin biosynthesis protein D, CbiD putative thioredoxin/glutaredoxin ATP-dependent helicase		
MSM0824 MSM0825 MSM0825 MSM0827 MSM0827 MSM0829 MSM0830 MSM0831 MSM0831 MSM0834 MSM0835 MSM0835 MSM0836 MSM0837 MSM0838 MSM0837 MSM0838 MSM0839 MSM0840 MSM0841	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase related to alpha-glycosyltransferases, GT4 family cobalamin biosynthesis protein D, CbiD putative thioredoxin/glutaredoxin ATP-dependent helicase conserved hypothetical protein photosynthetic reaction centre cytoplasmic domain containing protein		
MSM0824 MSM0825 MSM0826 MSM0827 MSM0828 MSM0830 MSM0831 MSM0831 MSM0833 MSM0834 MSM0835 MSM0835 MSM0836 MSM0837 MSM0838 MSM0839 MSM0840 MSM0841	putative N-acetyltransferase, GNAT family adenosylcobinamide amidohydrolase, CbiZ chaperonin, Cpn60/TCP-1/thermosome family, GroL predicted metal-dependent hydrolase, cyclase family best blast hit to Msp_0220; not predicted to be a carbohydrate active enzyme by CAZy aspartate-semialdehyde dehydrogenase, Asd dihydrodipicolinate reductas, DapB dihydrodipicolinate synthase, DapA aspartokinase, alpha subunit ribosomal protein S17a chorismate mutase archaeal shikimate kinase related to alpha-glycosyltransferases, GT4 family cobalamin biosynthesis protein D, CbiD putative thioredoxin/glutaredoxin ATP-dependent helicase conserved hypothetical protein photosynthetic reaction centre cytoplasmic domain containing protein		
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MSM0859	glycerol-3-phosphate cytidylyltransferase				
MSM0860	aspartate-semialdehyde dehydrogenase, ArgC				
MSM0861	flavodoxin				
MSM0862	aspartate carbamoyltransferase regulatory chain, Pyrl				
MSM0863	pyridoxamine-phosphate oxidase (FMN-binding)				
MSM0864	predicted transcriptional regulator				
MSM0865	putative glucose-methanol-choline oxidoreductase (FAD-dependent)				
MSM0866	Zn metalloprotease, TldD				
MSM0867	AMMECR1-related protein				
MSM0868	hypothetical protein				
MSM0869	GTPase, GTP1/OBG family				
MSM0870	molecular chaperone (small heat shock protein), HSP20/alpha				
	crystallin family				
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MSM0871	putative transposase	N	ID .	1	
MSM0872	glucosamine:fructose-6-phosphate aminotransferase (isomerizing),				
	AgaS				
MSM0873	conserved hypothetical protein				
MSM0874	adenine deaminase, AdeC				
MSM0875	lysine-oxoglutarate reductase/Saccharopine dehydrogenase				
	(LOR/SDH) bifunctional enzyme				
MSM0876	arginase/agmatinase/formimionoglutamate hydrolase, SpeB				
MSM0877	translation initiation factor 5A (aIF-5A)				
MSM0878	pyruvoyl-dependent arginine decarboxylase, PdaD				
MSM0879	Poly(P)/ATP NAD kinase, inositol monophosphatase family, PpnK				
MSM0880	UDP-N-acetylmuramyl tripeptide synthetase (Mur ligase)				
MSM0881	porphobilinogen deaminase				
MSM0882	3-chlorobenzoate-3,4-dioxygenase dyhydrogenase				
MSM0883	orotate phosphoribosyltransferase				
MSM0884	adhesin-like protein				
MSM0885					
	adhesin-like protein				
MSM0886	hypothetical protein				
MSM0887	universal stress protein, adenine nucleotide alpha hydrolase-like family				
MSM0888	glutamate dehydrogenase (NADP+), GdhA				
MSM0889	hypothetical protein				
MSM0890	hypothetical protein				
MSM0891	peptide chain release factor eRF, subunit 1				
MSM0892	putative zinc-binding protein				
MSM0893	acetyltransferase				
MSM0893 MSM0894					
MSM0894	conserved hypothetical protein				
MSM0894 MSM0895	conserved hypothetical protein cation transport ATPase, HAD family				
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MSM0932	conserved hypothetical protein			
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MSM0934	predicted phosphatidylglycerophosphatase A-related protein			
MSM0935	conserved hypothetical protein			
MSM0936	transcription regulator-related ATPase, ExsB			
MSM0937	HD superfamily hydrolase			
MSM0938	hypothetical protein			
MSM0939	pyruvate carboxylase, subunit B, PycB			
MSM0940	myo-inositol-1-phosphate synthase			
MSM0941	prenyltransferase, UbiA			
MSM0942	conserved hypothetical membrane protein			
MSM0943	conserved hypothetical protein			
MSM0944	CMP-N-acetylneuraminic acid synthetase, NeuA			
MSM0945	hydrogenase expression/formation protein, HypD			
MSM0946 MSM0947	archaeal sucrose-phosphate phosphatase (SPP-like), HAD family predicted zinc metalloprotease, modulator of DNA gyrase			
	hypothetical protein			
MSM0948 MSM0949	transcriptional activator			
MSM0950	molybdopterin biosynthesis protein, MoeA			
MSM0951	translation initiation factor aIF-1A			
MSM0952 MSM0953	serine/threonine protein kinase, RIO1 family conserved hypothetical membrane protein			
MSM0954	predicted RNA-binding protein			
MSM0955	type II DNA topoisomerase VI, subunit B			
MSM0956	type II DNA topoisomerase VI, subunit A			
MSM0957	adhesin-like protein			
MSM0958 MSM0959	predicted 1,4-beta-cellobiosidase conserved hypothetical protein			
MSM0960	cation transport ATPase, HAD family			
MSM0961	heavy-metal cation transporting ATPase			
MSM0962	glyceraldehyde 3-phosphate dehydrogenase, GapA			
MSM0963				
MSM0964	endonuclease IV, xylose isomerase-like TIM barrel family, Nfo calcineurin-like phosphoesterase			
MSM0965	3-hydroxyacyl-CoA dehydrogenase, FadB			
MSM0966	predicted 26S protease regulatory subunit (ATP-dependent), AAA+			
MSMOSO	family ATPase			
MSM0967	glutamyl-tRNA reductase, HemA			
MSM0968	bifunctional precorrin-2 oxidase/chelatase (siroheme synthase), CysG			
MSMOSO	bilufictional preconfir-2 oxidase/chelatase (siloneme synthase), Cyso			
MSM0969	predicted metal-binding transcription factor			
MSM0970	conserved hypothetical protein			
MSM0971	methyl-coenzyme M reductase, component A2			
MSM0972	tRNA-dihydrouridine synthase			
MSM0973	GTP cyclohydrolase III, GGDN family			
MSM0974	LPPG:FO 2-phospho-L-lactate transferase, CofD			
MSM0975	F420-0:gamma-glutamyl ligase, CofE			
MSM0976	archaeal IMP cyclohydrolase, PurO			
MSM0977	putative biopolymer transport protein, ExbD/ToIR family			
MSM0978	biopolymer transport protein, MotA/ToIQ/ExbB proton channel family			
MSM0979	ribonuclease HII, RnhB			
MSM0980	rod shape-determining protein, MreB/Mrl family			
MSM0981	conserved hypothetical protein			
MSM0982	phosphatidylserine synthase, PssA			
MSM0983	conserved hypothetical protein			
MSM0984	sortase (surface protein transpeptidase), SrtA			
MSM0985	conserved hypothetical protein			
MSM0986	conjugated bile acid hydrolase (CBAH)			
MSM0987	tyrosine decarboxylase, MfnA			
MSM0988	phosphoenolpyruvate synthase, PpsA			
MSM0989	ribosomal protein L10e			
MSM0990	nitrate/sulfonate/bicarbonate ABC transporter, ATPase component			
MSM0991	nitrate/sulfonate/bicarbonate ABC transporter, substrate-binding			
	component			
MSM0992	conserved hypothetical protein			
MSM0993	putative ATPase, glucocorticoid receptor-like (DNA-binding domain)			
	family			
MSM0994	predicted nucleotidyltransferase			
MSM0995	adhesin-like protein			
MSM0996	adhesin-like protein			
MSM0997	dihydroorotase, PyrC			
MSM0998	polyferredoxin, MvhB			
MSM0999	methyl viologen-reducing hydrogenase, alpha subunit, MvhA			
	methyl viologen-reducing hydrogenase, gamma subunit, MvhG			
MSM1000				
MSM1000	methyl viologen-reducing hydrogenase, delta subunit, MvhD			

MSM1002			
	ABC transporter involved in Fe-S cluster assembly, permease component		
MSM1003	ABC transporter involved in Fe-S cluster assembly, ATPase component		
MSM1004	photosynthetic reaction centre cytoplasmic domain containing protein		
MSM1005	GTP:adenosylcobinamide-phosphate guanylyltransferase		
MSM1006	conserved hypothetical protein		
MSM1007	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase,		
MSM1008	subunit H, MtrH N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase,		
MSM1009	subunit G, MtrG N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase,		
	subunit F, MtrF		
MSM1010	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit A, MtrA		
MSM1011	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit B, MtrB		
MSM1012	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase,		
MSM1013	subunit C, MtrC N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase,		
	subunit D, MtrD		
MSM1014	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit E, MtrE		
MSM1015	methyl-coenzyme M reductase, alpha subunit, McrA		
MSM1016	methyl-coenzyme M reductase, gamma subunit, McrG		
MSM1017	methyl-coenzyme M reductase, C subunit, McrC		
MSM1018	methyl-coenzyme M reductase, D subunit, McrD		
MSM1019	methyl-coenzyme M reductase, beta subunit, McrB		
MSM1020 MSM1021	Fe-S oxidoreductase, Radical SAM family		
IVIOIVI IUZ I	uncharacterized protein related to methyl coenzyme M reductase subunit C (McrC)		
MSM1022	conserved hypothetical protein		
MSM1022	2-phosphosulpholactate phosphatase, ComB, (coenzyme M		
	biosynthesis)		
MSM1024	pheromone shutdown protein, TraB family		
MSM1025	conserved hypothetical protein		
MSM1026	hemolysin-related protein, transporter-associated family, TlyC		
MSM1027	Ca2+/Na+ antiporter (K+-dependent)		
MSM1028	predicted ATPase, PP-loop family		
MSM1029	conserved hypothetical protein		
MSM1030	predicted pyridoxal phosphate-dependent enzyme		
MSM1031 MSM1032	N2,N2-dimethylguanosine tRNA methyltransferase, Trm1 transcriptional regulator, Lrp family		
MSM1032 MSM1033	conserved hypothetical protein		
MSM1033	conserved hypothetical protein		
MSM1034	FO synthase subunit 1 (SAM-dependent), CofG (F420 biosynthesis)		
MSM1036	predicted methyltransferase		
MSM1037	proteasome, beta subunit		
MSM1038	predicted metal-dependent RNase		
	phosphoribosylformylglycinamidine cyclo-ligase (AIRS), PurM		
MSM1040	malate/L-lactate dehydrogenase		
MSM1040 MSM1041	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1		
MSM1040 MSM1041 MSM1042	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease		
MSM1040 MSM1041 MSM1042 MSM1043	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK		
MSM1040 MSM1041 MSM1042 MSM1043 MSM1044	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease		
MSM1040 MSM1041 MSM1042 MSM1043 MSM1044 MSM1045 MSM1046	malate/L-lactate dehydrogenase  DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK dihydroorotate dehydrogenase, PyrD possible glycosyltransferase pre-mRNA splicing ribonucleoprotein PRP31		
MSM1040 MSM1041 MSM1042 MSM1043 MSM1044 MSM1045 MSM1046 MSM1047	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK dihydroorotate dehydrogenase, PyrD possible glycosyltransferase pre-mRNA splicing ribonucleoprotein PRP31 fibrillarin-like pre-rRNA processing protein, FlpA		
MSM1040 MSM1041 MSM1042 MSM1043 MSM1044 MSM1045 MSM1046 MSM1047 MSM1048	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK dihydroorotate dehydrogenase, PyrD possible glycosyltransferase pre-mRNA splicing ribonucleoprotein PRP31 fibrillarin-like pre-rRNA processing protein, FlpA phosphopantothenoylcysteine synthetase/decarboxylase		
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MSM1040 MSM1041 MSM1042 MSM1043 MSM1044 MSM1045 MSM1046 MSM1047 MSM1048 MSM1049 MSM1050 MSM1051 MSM1051 MSM1052 MSM1053	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK dihydroorotate dehydrogenase, PyrD possible glycosyltransferase pre-mRNA splicing ribonucleoprotein PRP31 fibrillarin-like pre-rRNA processing protein, FlpA phosphopantothenoylcysteine synthetase/decarboxylase phosphopantothenoylcysteine synthetase/decarboxylase conserved hypothetical protein putative endoglucanase prephenate dehydratase, PheA IMP dehydrogenase related protein		
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MSM1040 MSM1041 MSM1042 MSM1043 MSM1044 MSM1045 MSM1046 MSM1047 MSM1047 MSM1050 MSM1051 MSM1051 MSM1052 MSM1053 MSM1053 MSM1054 MSM1055 MSM1055 MSM1055 MSM1056 MSM1056 MSM1056	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK dihydroorotate dehydrogenase, PyrD possible glycosyltransferase pre-mRNA splicing ribonucleoprotein PRP31 fibrillarin-like pre-rRNA processing protein, FlpA phosphopantothenoylcysteine synthetase/decarboxylase phosphopantothenoylcysteine synthetase/decarboxylase conserved hypothetical protein putative endoglucanase prephenate dehydratase, PheA IMP dehydrogenase related protein IMP dehydrogenase related protein coenzyme PQQ synthesis protein, SAM family		
MSM1040 MSM1041 MSM1042 MSM1043 MSM1044 MSM1045 MSM1046 MSM1047 MSM1048 MSM1050 MSM1050 MSM1051 MSM1052 MSM1053 MSM1053 MSM1055 MSM1055 MSM1055 MSM1055 MSM1055 MSM1056 MSM1056 MSM1057 MSM1056	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK dihydroorotate dehydrogenase, PyrD possible glycosyltransferase pre-mRNA splicing ribonucleoprotein PRP31 fibrillarin-like pre-rRNA processing protein, FlpA phosphopantothenoylcysteine synthetase/decarboxylase phosphopantothenoylcysteine synthetase/decarboxylase conserved hypothetical protein putative endoglucanase prephenate dehydratase, PheA IMP dehydrogenase related protein IMP dehydrogenase related protein coenzyme PQQ synthesis protein, SAM family 6-pyruvoyl-tetrahydropterin synthase conserved hypothetical protein coenserved hypothetical protein		
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MSM1040 MSM1041 MSM1043 MSM1043 MSM1044 MSM1045 MSM1046 MSM1047 MSM1049 MSM1050 MSM1051 MSM1052 MSM1053 MSM1054 MSM1055 MSM1055 MSM1056 MSM1057 MSM1057 MSM1058 MSM1058 MSM1058 MSM1059 MSM1050 MSM1050 MSM1051 MSM1050 MSM1051 MSM1050 MSM1051 MSM1050	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK dihydroorotate dehydrogenase, PyrD possible glycosyltransferase pre-mRNA splicing ribonucleoprotein PRP31 fibrillarin-like pre-rRNA processing protein, FlpA phosphopantothenoylcysteine synthetase/decarboxylase phosphopantothenoylcysteine synthetase/decarboxylase phosphopantothenoylcysteine synthetase/decarboxylase conserved hypothetical protein putative endoglucanase prephenate dehydratase, PheA IMP dehydrogenase related protein IMP dehydrogenase related protein coenzyme PQQ synthesis protein, SAM family 6-pyruvoyl-tetrahydropterin synthase conserved hypothetical protein conserved hypothetical protein predicted RecB family exonuclease energy-converting hydrogenase B, subunit Q, EhbQ energy-converting hydrogenase B, subunit P, EhbP energy-converting hydrogenase B, subunit O, EhbO		
MSM1040 MSM1041 MSM1041 MSM1043 MSM1044 MSM1045 MSM1046 MSM1047 MSM1049 MSM1050 MSM1051 MSM1052 MSM1053 MSM1054 MSM1055 MSM1055 MSM1055 MSM1057 MSM1057 MSM1058 MSM1058 MSM1059 MSM1059 MSM1050 MSM1051 MSM1050 MSM1051 MSM1051 MSM1051 MSM1051 MSM1050 MSM1051 MSM1050 MSM1051 MSM1050 MSM1060 MSM1060 MSM1060 MSM1060	malate/L-lactate dehydrogenase DNA-dependent DNA polymerase I, PolB1 predicted permease dihydroorotate dehydrogenase electron transfer subunit, PyrK dihydroorotate dehydrogenase, PyrD possible glycosyltransferase pre-mRNA splicing ribonucleoprotein PRP31 fibrillarin-like pre-rRNA processing protein, FlpA phosphopantothenoylcysteine synthetase/decarboxylase phosphopantothenoylcysteine synthetase/decarboxylase conserved hypothetical protein putative endoglucanase prephenate dehydratase, PheA IMP dehydrogenase related protein IMP dehydrogenase related protein coenzyme PQQ synthesis protein, SAM family 6-pyruvoyl-tetrahydropterin synthase conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein predicted RecB family exonuclease energy-converting hydrogenase B, subunit Q, EhbQ energy-converting hydrogenase B, subunit P, EhbP		

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MSM1065	energy-converting hydrogenase B, subunit L, EhbL				
MSM1066	energy-converting hydrogenase B, subunit K, EhbK				
MSM1067	energy-converting hydrogenase B, subunit J, EhbJ				
MSM1068	energy-converting hydrogenase B, subunit I, Ehbl				
MSM1069	energy-converting hydrogenase B, subunit H, EhbH				
MSM1070	energy-converting hydrogenase B, subunit G, EhbG				
MSM1071	energy-converting hydrogenase B, subunit F, EhbF				
MSM1072	energy-converting hydrogenase B, subunit E, EhbE				
MSM1073	energy-converting hydrogenase B, subunit D, EhbD				
MSM1074	energy-converting hydrogenase B, subunit C, EhbC				
MSM1075	energy-converting hydrogenase B, subunit B, EhbB				
MSM1076	energy-converting hydrogenase B, subunit A, EhbA				
MSM1077	putative permease (transport)				
MSM1078	predicted bile acid/sodium symporter				
MSM1079	predicted membrane-bound metal-dependent hydrolase, NCS2 family				
MSM1080	predicted deacylase				
MSM1081	transcriptional regulator (enhancer-binding protein), DNA2/NAM7				
	helicase family				
MSM1082	hypothetical protein				
MSM1083	conserved hypothetical membrane protein				
MSM1084	argininosuccinate synthase, ArgG				
MSM1085	aquaporin, MIP superfamily, AqpM				
MSM1086	conserved hypothetical protein				
MSM1087	NAD-dependent protein deacetylase, SIR2 family				
MSM1088	hypothetical protein				
MSM1089	hypothetical protein				
MSM1090	sugar fermentation stimulation protein, SfsA				
MSM1091	sugar kinase, YjeF-related protein family				
MSM1092	formylmethanofuran:tetrahydromethanopterin formyltransferase, Ftr				
MSM1093	putative transposase	N	D		
MSM1094	conserved hypothetical integral membrane protein				
MSM1095	Trk-type potassium transport system, membrane component, TrkH				
MSM1096	Trk-type potassium transport system, NAD-binding component, TrkA				
MSM1097	Zn-dependent hydrolase				
MSM1098	archaeal holliday junction resolvase				
MSM1099	biotin synthase related protein				
MSM1100	conserved hypothetical protein				
MSM1101	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase, B subunit, GatB				
MSM1102	IMP dehydrogenase related protein				
MSM1103	phosphoribosyl-ATP pyrophosphohydrolase, HisE				
MSM1104	acetyltransferase, GNAT family				
MSM1105	NCAIR mutase related protein, PurE				
MSM1106	hydrogenase maturation factor, HypF				
MSM1107	predicted transcriptional regulator				
MSM1108	molecular chaperone GrpE				
MSM1109	molecular chaperone OnaK				
MSM1110	molecular chaperone DnaJ				
MSM1111	adhesin-like protein				
MSM1112	adhesin-like protein				
MSM1113	adhesin-like protein				
MSM1114	adhesin-like protein	N I	D		
MSM1115	putative transposase	N	D		
MSM1116	adhesin-like protein				
MSM1117	cobalamin biosynthesis protein N, CobN				
MSM1118	conserved hypothetical protein				
MSM1119	conserved hypothetical protein				
MSM1120	methionine aminopeptidase, Map				
MSM1121	coenzyme F420-reducing hydrogenase, beta subunit, FrhB				
MSM1122	coenzyme F420-reducing hydrogenase, gamma subunit, FrhG				
MSM1123	coenzyme F420-reducing hydrogenase, delta subunit, FrhD				
MSM1124	coenzyme F420-reducing hydrogenase, alpha subunit, FrhA				
MSM1125	predicted endoglucanase (CobN-related)				
MSM1126	predicted transcriptional regulator, ArsR family				
MSM1127	cation transport ATPase, HAD family				
MSM1128	hypothetical protein				
MSM1129	conserved hypothetical protein				
MSM1130	conserved hypothetical protein				
MSM1131	conserved hypothetical protein				
MSM1132	ribosome biogenesis protein Nop10				
MSM1133	translation initiation factor aIF-2, alpha subunit				
MSM1134	ribosomal protein S27e				
MSM1135	ribosomal protein L44e				
MSM1136	conserved hypothetical protein				
MSM1137	DNA polymerase sliding clamp subunit, PCNA family, Pcn				
MACMAAAA	prodicted alutaming amidetraneforage CabD/CabO like familie				
MSM1138	predicted glutamine amidotransferase, CobB/CobQ-like family				

MSMI1101 protochen swithses, alpha subunit, TrpA MSMI1121 protochen swithses, alpha subunit, TrpA MSMI1122 brytopchan swithses, beta subunit, TrpA MSMI1123 protochen swithses, beta subunit, TrpA MSMI1123 protochen swithses, beta subunit, TrpA MSMI1243 protochen swithses, beta subunit, TrpA MSMI1243 protochen swithses, beta subunit, TrpA MSMI1243 protochen swithses component II, TrpG MSMI1243 protochen swithses component II, TrpG MSMI1240 conserved hypothetical membrane protein MSMI1250 conserved hypothetical membrane protein MSMI1250 conserved hypothetical membrane protein MSMI1250 conserved hypothetical membrane protein MSMI1251 conserved hypothetical membrane protein MSMI1251 conserved hypothetical membrane protein MSMI1251 conserved hypothetical protein MSMI1252 conserved hypothetical protein MSMI1251 conserved hypothetical protein MSMI1252 conserved hypothetical protein MSMI1252 conserved hypothetical protein MSMI1253 protochen served hypothetical protein MSMI1251 conserved hypothetical protein MSMI1252 conserved hypothetical protein MSMI1253 protein MSMI1253 conserved hypothetical protein MSMI1251 conserved hypothetical protein MSMI1252 conserved hypothetical protein MSMI1253 protochen served hypothetical protein MSMI1251 conserved hypothetical protein MSMI1252 conserved hypothetical membrane protein MSMI1252 conserved hypothetical membrane protein MSMI1253 conserved hypothetical membrane protein MSMI1253 conserved hypothetical membrane protein MSMI1253 conserved hypothetical membrane protein MSMI1254 conserved hypothetical membrane protein MSMI1254 conserved hypothetical membrane protein MSMI1254 conserved hypothetical membrane protein MSMI1255 conserved hypothetical m	100001139	and well bine with a in westein Mark Blue moutide linear family.			
Institution		cell wall biosynthesis protein, MurD-like peptide ligase family			
MSMI113 indices—general phosphate synthase, TrpC MSMI114 anthranilate phosphorobosyltransferase, TrpC MSMI114 anthranilate phosphorobosyltransferase, TrpC MSMI114 anthranilate phosphorobosyltransferase, TrpC MSMI114 anthranilate phosphorobosyltransferase, TrpC MSMI115 produced in the phosphorobosyltransferase component II. TrpC MSMI117 lyouthelical orderin MSMI118 produced metal-dependent membrane protein MSMI119 conserved hypothelical membrane protein MSMI119 adenylosuconate lyase, Purß MSMI110 adenylosuconate lyase, Purß MSMI110 adenylosuconate lyase, Purß MSMI110 anthranilate phosphorobosyltransferase, Purß MSMI110 produced in the protein and					
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MSMM116 antimaliate/para-aminoberozate swithses component II, TrpG MSM117 hypothetical protein MSM117 hypothetical protein MSM118 proteided metal-dependent membrane protease MSM119 proteided metal-dependent membrane protease MSM119 proteided metal-dependent membrane protein MSM119 proteided metal-dependent amidohydrolase MSM119 proteided membrane protein MSM119 proteided protein MSM119 protein MSM119 proteided protein MSM1119 proteided protein MSM119	MSM1143	indole-3-glycerol phosphate synthase, TrpC			
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MSM1288 cor MSM1289 Gtr			
MSM1288 coi MSM1289 Gti	nosphoribosylaminoimidazole carboxylase (NCAIR mutase), PurE		
MSM1289 Gti	onserved hypothetical membrane protein		
	trA-like surface polysaccharide biosynthesis protein, GtrA		
1M2M1580 1917			
, <u>-</u> giy	ycosyltransferase (related to beta-glycosidases), GT2 family [CAZy]		
MSM1291 co	onserved hypothetical membrane protein		
MSM1292 tra	anscriptional accessory protein, S1 RNA binding family, Tex		
	troreductase, NADH oxidase/flavin reductase family		
	ycosyltransferase, GT2 family		
	redicted DNA-binding protein		
MSM1296 rib	poflavin synthase, beta subunit, RibH		
MSM1297 gly	ycosyltransferase, GT2 family		
	isopropylmalate dehydrogenase, LeuB		
	isopropylmalate dehydratase, small subunit, LeuD		
	isopropylmalate dehydratase, large subunit, LeuC		
	redicted Fe-S oxidoreductase		
	onserved hypothetical protein		
MSM1303 UE	DP-N-acetyl-D-mannosaminuronate dehydrogenase		
	TDP-4-dehydrorhamnose reductase, RfbD		
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	TDP-glucose pyrophosphorylase, RfbA	الصور	
MSM1308 dT	ΓDP-4-dehydrorhamnose 3,5-epimerase		
MSM1309 dT	FDP-D-glucose 4,6-dehydratase, RfbB	الصور	
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	ycosyltransferase, GT2 family		
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	ycosyltransferase, GT2 family		
	stantly related to glycosyltransferases, GT4 family	المهرور	
	pothetical protein		
MSM1315 pre	redicted transcriptional regulator	الصور	
	ycosyltransferase, GT2 family	المهرور	
	stantly related to glycosyltransferases, GT4 family	الصور	
		الصور	
MSM1318 co	onserved hypothetical protein		
	onserved hypothetical protein		
	ossible glycosyltransferase		
MSM1321 pre	redicted glycosyltransferase, GT2 family		
MSM1322 dis	stantly related to alpha-glycosyltransferases, GT4 family		
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1	redicted polysaccharide/polyol phosphate ABC transporter, permease		
	omponent		
MSM1326 po	olysaccharide/polyol phosphate ABC transporter, ATPase component		
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	ycosyltransferase, GT2 family		
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MSM1359	adenine phosphoribosyltransferase, Apt				
MSM1360	signal recognition particle GTPase SRP54				
MSM1361	predicted pseudouridylate synthase				
MSM1362	molybdenum cofactor biosynthesis protein C, MoaC				
MSM1363	preprotein translocase, SecG subunit, SecG				
MSM1364	imidazoleglycerol-phosphate synthase, HisF				
MSM1365	3-methyladenine DNA glycosylase/8-oxoguanine DNA glycosylase				
MSM1366	lactoylglutathione lyase, LqlU				
MSM1367	peptidyl-prolyl cis-trans isomerase, PpiB				
MSM1368	N-acetylornithine aminotransferase, ArgD				
MSM1369	MutT-related protein, NUDIX family				
MSM1370	conserved hypothetical membrane protein				
MSM1371	diaminopimelate decarboxylase, LysA				
MSM1372	diaminopimelate decarboxylase, LysA diaminopimelate epimerase, DapF				
MSM1373					
	methyltransferase, HemK				
MSM1374	dimethyladenosine transferase, KsgA				
MSM1375	predicted RNA-binding protein				
MSM1376	DNA-directed RNA polymerase subunit F				
MSM1377	ribosomal protein L21e				
MSM1378	putative monooxygenase, ABM family				
MSM1379	predicted NADP-dependent alcohol dehydrogenase				
MSM1380	NADP-dependent alcohol dehydrogenase				
MSM1381	putative NADP-dependent alcohol dehydrogenase				
MSM1382	conserved hypothetical membrane protein				
MSM1383	anaerobic ribonucleoside-triphosphate reductase, NrdD				
MSM1384	archaeal DNA polymerase II, large subunit, PolC				
MSM1385	predicted acyltransferase				
MSM1386	cytosine deaminase				
MSM1387	lysyl-tRNA synthetase (class I), LysS				
MSM1388	thiamine biosynthesis protein, ThiC				
MSM1389	sugar kinase, ribokinase/pfkB superfamily				
MSM1390	transcriptional regulator, LysR family				
MSM1391	predicted sugar phosphate isomerase involved in capsule formation,				
WIOWITOOT	GutQ				
MSM1392	formate dehydrogenase accessory protein FdhD, FdhD				
MSM1393	iron(III) ABC transporter, substrate-binding component				
MSM1394	iron(III) ABC transporter, permease component				
MSM1395	iron(III) ABC transporter, ATPase component				
MSM1396	tungsten formylmethanofuran dehydrogenase, subunit E, FwdE				
MSM1397	adhesin-like protein				
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NACNALAGE	analana		
MSM1435 MSM1436	enolase		
MSM1437	ferredoxin ribosomal protein S2p		
MSM1438	predicted dioxygenase		
MSM1439	mevalonate kinase		
MSM1440	predicted archaeal kinase		
MSM1441	isopentenyl-diphosphate delta-isomerase		
MSM1442	predicted RNA hydrolase, metallo-beta-lactamase superfamily		
MSM1443	bifunctional short chain isoprenyl diphosphate synthase, IdsA		
MSM1444	conserved hypothetical membrane protein		
MSM1445	predicted transcriptional regulator		
MSM1446	predicted hydroxylamine reductase, Hcp		
MSM1447	conserved hypothetical protein		
MSM1448	SAM-dependent methyltransferase		
MSM1449	putative O-linked GlcNAc transferase		
MSM1450	predicted oxidoreductase, aldo/keto reductase family		
MSM1451	best blast hit to TPR repeat protein (Mba); not predicted to be a		
	carbohydrate active enzyme by CAZy		
MSM1452	glutamyl-tRNA synthetase, GltX		
MSM1453	hypothetical protein		
MSM1454	predicted ATPase, AAA+ family		
MSM1455	aspartate/tyrosine/aromatic aminotransferase		
MSM1456	conserved hypothetical protein		
MSM1457	hypothetical protein		
MSM1458	hypothetical protein		
MSM1459	multidrug efflux permease, AraJ		
MSM1460	energy-converting hydrogenase B, subunit K, EhbK		
MSM1461	methyl viologen-reducing hydrogenase, delta subunit, MvhD		
MSM1462	formate dehydrogenase, beta subunit, FdhB		
MSM1463	formate dehydrogenase, alpha subunit, FdhA		
MSM1464	FlpE-related protein		
MSM1465	multidrug efflux permease, AraJ		
MSM1466	hypothetical protein		
MSM1467	hypothetical protein		
MSM1468	adenylosuccinate synthetase, PurA		
MSM1469	nitrate/sulfonate/bicarbonate ABC transporter, substrate-binding		
	component, TauA		
MSM1470	hypothetical protein		
MSM1471	acyl-CoA synthetase		
MSM1472	conserved hypothetical protein		
MSM1473	metal-dependent hydrolase, beta-lactamase superfamily		
MSM1474	chorismate synthase, AroC		
MSM1475	predicted endonuclease III-related protein		
MSM1476			
	porphobilinogen synthase, HemB		
MSM1477	ATP:dephospho-CoA triphosphoribosyl transferase		
MSM1478	ATP:dephospho-CoA triphosphoribosyl transferase phenylalanyl-tRNA synthetase, PheS		
MSM1478 MSM1479	ATP:dephospho-CoA triphosphoribosyl transferase phenylalanyl-tRNA synthetase, PheS exodeoxyribonuclease, XthA		
MSM1478 MSM1479 MSM1480	ATP:dephospho-CoA triphosphoribosyl transferase phenylalanyl-tRNA synthetase, PheS exodeoxyribonuclease, XthA predicted hydrolase, HAD superfamily		
MSM1478 MSM1479 MSM1480 MSM1481	ATP:dephospho-CoA triphosphoribosyl transferase phenylalanyl-tRNA synthetase, PheS exodeoxyribonuclease, XthA predicted hydrolase, HAD superfamily DNA-directed DNA polymerase, family B, PolB		
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MSM1518 IS element ISM1 (ICSNY family)	
MSM1519 IS element ISM1 (ICSNY family)	
MSM1520 IS element ISM1 (ICSNY family)	
MSM1521 hypothetical protein	
MSM1522 hypothetical protein	
MSM1523 transposase	
MSM1524 conserved hypothetical protein	
MSM1525 conserved hypothetical protein	
MSM1526 conserved hypothetical membrane protein	
MSM1527 predicted ATPase, AAA+ superfamily	
MSM1528   predicted transcriptional regulator, HTH XRE-like family	
MSM1529 putative Zn peptidase	
MSM1530 putative nucleic acid-binding protein	
MSM1531 Na+-dependent transporter, SNF family	
MSM1532 Na+-dependent transporter, SNF family	
MSM1533   adhesin-like protein	
MSM1534 adhesin-like protein	
MSM1535 predicted dTDP-D-glucose 4,6-dehydratase	
MSM1536   pleiotropic regulatory protein DegT (PLP-dependent)	
MSM1537 predicted acylneuraminate cytidylyltransferase, NeuS	
MSM1538 CMP-sialic acid synthetase, NeuA	
MSM1539 sialic acid synthase, NeuB	
MSM1540 glycerol-3-phosphate dehydrogenase (NAD)	
MSM1541 hypothetical protein	
MSM1542 4-diphosphocytidyl-2-methyl-D-erithritol synthase, lspD	
MSM1543 hypothetical protein	
MSM1544 lipopolysaccharide cholinephosphotransferase	
MSM1545 glycosyltransferase, GT2 family	
MSM1546 hypothetical protein	
MSM1547 phosphoribosylaminoimidazole-succinocarboxamide (SAICAR)	
synthase, PurC	
synthase, PurC  MSM1548 phosphoribosylformylglycinamidine (FGAM) synthase, PurS	
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synthase, PurC  MSM1548 phosphoribosylformylglycinamidine (FGAM) synthase, PurS  MSM1549 phosphoribosylformylglycinamidine (FGAM) synthase, PurQ  MSM1550 uroporphyrin-III C-methyltransferase, CobA  MSM1551 glucosaminefructose-6-phosphate aminotransferase, GlmS  MSM1552 hypothetical protein  MSM1553 hypothetical protein  MSM1554 putative adhesin-like protein  MSM1555 SAM-dependent methyltransferase  MSM1556 conserved hypothetical membrane protein  MSM1557 queuine/archaeosine tRNA-ribosyltransferase  MSM1558 SAM-dependent methyltransferase, UbiE family  MSM1559 polysaccharide biosynthesis protein, MviN-like family	
synthase, PurC  MSM1548 phosphoribosylformylglycinamidine (FGAM) synthase, PurS  MSM1549 phosphoribosylformylglycinamidine (FGAM) synthase, PurQ  MSM1550 uroporphyrin-III C-methyltransferase, CobA  MSM1551 glucosaminefructose-6-phosphate aminotransferase, GlmS  MSM1552 hypothetical protein  MSM1553 hypothetical protein  MSM1554 putative adhesin-like protein  MSM1555 SAM-dependent methyltransferase  MSM1556 conserved hypothetical membrane protein  MSM1557 queuine/archaeosine tRNA-ribosyltransferase  MSM1558 SAM-dependent methyltransferase, UbiE family  MSM1559 polysaccharide biosynthesis protein, MviN-like family  MSM1560 polysaccharide biosynthesis protein, MviN-like family	
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synthase, PurC  MSM1548 phosphoribosylformylglycinamidine (FGAM) synthase, PurS  MSM1549 phosphoribosylformylglycinamidine (FGAM) synthase, PurQ  MSM1550 uroporphyrin-III C-methyltransferase, CobA  MSM1551 glucosaminefructose-6-phosphate aminotransferase, GlmS  MSM1552 hypothetical protein  MSM1553 hypothetical protein  MSM1555 SAM-dependent methyltransferase  MSM1556 conserved hypothetical membrane protein  MSM1557 queuine/archaeosine tRNA-ribosyltransferase  MSM1558 SAM-dependent methyltransferase, UbiE family  MSM1559 polysaccharide biosynthesis protein, MviN-like family  MSM1560 polysaccharide biosynthesis protein, MviN-like family  MSM1561 3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) synthase  MSM1562 acetyl-CoA acyltransferase, SCP-type thiolase family	
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MSM1583	archaea-specific helicase	
MSM1584	predicted excinuclease ABC, C subunit, UvrC	
MSM1585	adhesin-like protein	
MSM1586	adhesin-like protein	
MSM1587	adhesin-like protein	
MSM1588	transposase	
MSM1589	transposase, RNaseH-like family	ND
MSM1590	adhesin-like protein	
MSM1591	conserved hypothetical protein	
MSM1592	polysaccharide/polyol phosphate ABC transporter, ATPase component	
IVISIVI 1392	polysacchande/polyor phosphate ADC transporter, ATF ase component	
MSM1593	polysaccharide/polyol phosphate ABC transporter, permease	
	component	
MSM1594	glycosyltransferase/CDP-glycerol:poly(glycerophosphate)	
WOW 1004		
	glycerophosphotransferase, GT2 family	
MSM1595	SAM-dependent methyltransferase, FkbM family	
MSM1596	putative transposase	ND
MSM1597	hypothetical protein	
MSM1598	SAM-dependent methyltransferase	
MSM1599	SAM-dependent methyltransferase	
MSM1600	putative acetyltransferase, trimeric LpxA-like family	
MSM1601	conserved hypothetical protein	
MSM1602	glycosyltransferase/CDP-glycerol:poly(glycerophosphate)	
I	glycerophosphotransferase, GT2 family	
MSM1603	conserved hypothetical protein	
MSM1604	UDP-glucose pyrophosphorylase, GalU	
MSM1605	hypothetical protein	
MSM1606	arylsulfatase regulator, AsiB	
MSM1607	conserved hypothetical protein	
MSM1608	predicted oxidoreductase, aldo/keto reductase family	
		-
MSM1609	molybdate ABC transporter, substrate-binding component, ModA	
MSM1610	molybdate ABC transporter, permease component, ModC	
MSM1611	molybdate ABC transporter, ATPase component, ModB	
MSM1612	predicted UDP-glucose 6-dehydrogenase	
MSM1613	predicted UDP-glucose/GDP-mannose dehydrogenase	
MSM1614	predicted transcriptional regulator	-
MSM1615	deoxyhypusine synthase, Dys	
MSM1616	conserved hypothetical membrane protein	
MSM1617	orotidine-5'-phosphate decarboxylase, PyrF	
MSM1618	cobalamin biosynthesis protein M, CbiM	
MSM1619	cobalt ABC transporter, substrate-binding component, CbiN	-
MSM1620	cobalt ABC transporter, permease component, CbiQ	
MSM1621	cobalt ABC transporter, ATPase component, CbiO	
MSM1622	archaeal riboflavin synthase, RibC	
MSM1623	glycosyltransferase/dolichyl-phosphate mannose synthase, GT2 family	
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MSM1624	conserved hypothetical protein	
MSM1625	thiol:fumarate reductase, subunit B, TfrB	
MSM1626	predicted fumarate reductase	
MSM1627	glycosyltransferase, GT2 family	
MSM1628	conserved hypothetical protein, aldolase family	
MSM1629	IMP dehydrogenase/GMP reductase, GuaB	-
MSM1630	ribosomal protein L37Ae	
MSM1631	predicted DNA-directed RNA polymerase II, subunit RPC10	
MSM1632	predicted brix-domain ribosomal biogenesis protein	
MSM1633	conserved hypothetical protein	
MSM1634	prefoldin, beta subunit	
MSM1635	conserved hypothetical protein	
MSM1636	ProFAR isomerase-related protein	
MSM1637	conserved hypothetical membrane protein	
MSM1638	conserved hypothetical membrane protein	
MSM1639	heavy metal cation (Co/Zn/Cd) efflux system protein, CzcD family	
MSM1640	DNA intergrase/recombinase, phage integrase family	
MSM1641	hypothetical protein	
MSM1642	conserved hypothetical protein	
MSM1643	hypothetical protein	
MSM1644	hypothetical protein	
MSM1645	virulence protein	
MSM1646	putative ATPase (AAA+ superfamily)	
MSM1647	hypothetical protein	
MSM1648	hypothetical protein	
MSM1649		
W3W1049	hypothetical protein	
MSM1650	hypothetical protein	
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<sup>&</sup>lt;sup>1</sup>GeneChip-based genotyping of *M. smithii* strains done in duplicate; 'present' or 'absent' calls were determined using a perfect match/mismatch (PM/MM) model in dChip (see *Methods*). Note that the term 'absent' is based on different criteria than those used for the human microbiome dataset (see footnote 2).

<sup>2</sup>Metagenomic datasets from the microbiomes of two healthy lean adults (Gill et al., 2006) were tested for identity to *M. smithii* PS ORFs; ORFs with reads that matched with >95% identity are called 'present', 80-95% identity are called 'divergent', and <80% identity are called 'absent'.

<sup>3</sup>Probeset for *M. smithii* gene not represented on GeneChip.