Table 7. M. smithii genes in the significantly enriched GO categories listed in Table 6

- member of GO category
- not a member of GO category

NDICHED COM	DARED TO SEC	QUENCED ARCHAEA AND/OR NON-GU	T METHA	NOCENS			
URFACE	M. smithii	Annotation	MEIIIA	NOGENS			
ARIATION	genes	Ailliotation	ell on s	ell on	. Ф	ell sis	٠. –
tiAllOlt	genes		GO:0007047 - cell wall organization and biogenesis	GO:0042545 - cell wall modification	GO:0030599 - pectinesterase activity	GO:0042546 - cell wall biosynthesis	GO:0009252 - peptidoglycan biosynthesis
			47 iizi en	GO:0042545 wall modifica	GO:0030599 pectinesteras activity	45 T	GO:0009252 peptidoglyca biosynthesis
			70 gar og	25 odi	:003059 tinester activity	25 Sy	1 6 8
			org org bi	§ ₹	itin ac	9 id	);0
			GO:0007047 wall organiz and biogen	0; =	၁၅	;; <u></u>	G G S S S S S S S S S S S S S S S S S S
			G( W.	ິ ອັ	<u> </u>	დ ≋	_
	MSM0052	adhesin-like protein					
	MSM0118	cell wall biosynthesis protein, MurD-like					
		peptide ligase family					
	MSM0266	adhesin-like protein					
	MSM0359	cell wall biosynthesis protein, MurD-like					
		peptide ligase family					
	MSM0360	cell wall biosynthesis protein, phospho-					
		N-acetylmuramoyl-pentapeptide-					
		transferase family					
	MSM1111	adhesin-like protein					
		adhesin-like protein					
	MSM1113	adhesin-like protein					
	MSM1190	cell wall biosynthesis protein, UDP-N-					
		acetylmuramate-alanine ligase family					
	110111101						
	MSM1191	cell wall biosynthesis protein, MurD-like					
	MCM4227	peptide ligase family predicted CDP-					
	MSM1327	glycerol:poly(glycerophosphate)					
		glycerophosphotransferase					
	MSM1585	adhesin-like protein					
	MSM1586	adhesin-like protein					
	MSM1587	adhesin-like protein					
	MSM1590	adhesin-like protein					
	MSM1594	glycosyltransferase/CDP-					
	WISW 1334	glycerol:poly(glycerophosphate)					
		glycerophosphotransferase, GT2 family					
		gryocrophoophotianoicrase, 312 ianimy					
	MSM1602	glycosyltransferase/CDP-					
		glycerol:poly(glycerophosphate)					
		glycerophosphotransferase, GT2 family					
NTRAL	M. smithii	Annotation		٩ <u>٦</u>	uo	Ø	
TABOLISM	genes		82 - cid sm	GO:0006730 - one- carbon compound metabolism	33 - iration	48 - nesis	21 - e sm
			3O:0006082 organic acid metabolism	:0006730 - o bon compou metabolism		94 en	3O:0019321 pentose metabolism
			GO:000608 organic a metabolis	GO:0006730 carbon com metaboli	GO:00453; cellular respi	GO:00159. methanoge	GO:00193 pentose metabolis
			):0( gal eta	006 on c	):0	): 0 an	per eta
			90 Ori	9. 5 E	69 E 69	et 8	ල <sup>–</sup> දි
			_	G G	) le	Ξ	
	MSM0027	glutamate synthase, domain 2 with					
		rubredoxin					
	MSM0071	methionyl-tRNA synthetase, MetG					
	MSM0082	heterodisulfide reductase, subunit A,					
		HdrA					
	MSM0089	pyrroline-5-carboxylate reductase				<u>-</u>	
		(NADP oxidoreductase, coenzyme F420					
		dependent), ProC					
	MSM0102	cobalamin-independent methionine					
		synthase, MetE					
	MSM0154	homoserine dehydrogenase, ThrA			i		1

	· · · · · · · · · · · · · · · · · · ·	1	1	T
MSM0160	asparagine synthetase, AsnB			
MSM0174	O-acetylhomoserine sulfhydrylase (PLP-			
	dependent), MET17			
MSM0175	homoserine O-acetyltransferase, MetX			
MSM0214	threonine synthase (pyridoxal-			
	phosphate dependent), ThrC			
MSM0216	tryptophanyl-tRNA synthetase, TrpS			
MSM0231	3-dehydroquinate dehydratase			
MSM0265	O-acetylhomoserine sulfhydrylase			
MSM0268	cysteinyl-tRNA synthetase, CysS			
MSM0270	serine acetyltransferase, CysE			
MSM0271	cysteine synthase, CysK			
MSM0273	EPSP synthase (3-phosphoshikimate 1-			
MCMOSTE	carboxyvinyltransferase) valyl-tRNA synthetase, ValS	+		
MSM0275 MSM0277		+		
IVISIVIU2//	phenylalanyl-tRNA synthetase, beta subunit, PheT			
MSM0286	glycerol 1-phosphate dehydrogenase	1		
14101410700	(Dehydroquinate synthase-like family)			
MSM0287	prolyl-tRNA synthetase, ProS			
MSM0307	sugar kinase (ribokinase/pfkB			
	superfamily)			
MSM0308	formylmethanofuran:tetrahydromethano			
	pterin formyltransferase, FtrC			
MSM0334	L-asparaginase, GatD,			
MSM0343	GMP synthase (glutamine-hydrolysing),			
	subunit A. GuaA			
MSM0350	2-isopropylmalate synthase, LeuA			
MSM0368	glutamate synthase (NADPH), subunit 2			
	,,			
MSM0371	predicted glutamine amidotransferase			
	involved in pyridoxine biosynthesis,			
	Pdx2			
MSM0373	isocitrate/isopropylmalate			
	dehydrogenase, LeuB			
MSM0375	acetylglutamate kinase, ArgB			
MSM0379	glutamate N-acetyltransferase, ArgJ			
MSM0388	amino acid regulator			
MSM0393	fumarate reductase, iron-sulfur protein			
MSM0403	glycyl-tRNA synthetase			
MSM0415	uridylate kinase, PyrH			
MSM0457	D-3-phosphoglycerate dehydrogenase,			
MCM0400	SerA			
MSM0488	carbamoylphosphate synthase, large subunit, CarB			
MSM0489	carbamoylphosphate synthase, small			
14101410403	subunit, CarA			
MSM0513	tyrosyl-tRNA synthetase, TyrS			
MSM0516	corrinoid protein (methionine synthase-			
	related), MtaC			
MSM0518	methylcobalamin:coenzyme M		<b>†</b>	
	methyltransferase, MtaA			
MSM0556	dihydropteroate synthase			
MSM0572	H(2)-forming N5,N10-			
	methylenetetrahydromethanopterin			
	dehydrogenase (coenzyme F420-			
	dependent), Mth			
MSM0573	biotin synthetase, BioB			
MSM0604	predicted archaeal			
	aspartate/glutamate/uridylate kinase		<u> </u>	<u></u>
MSM0619	alanyl-tRNA synthetase, AlaS			
MSM0627	tetrahydromethanopterin S-			
	methyltransferase, subunit H, MtrH		<u> </u>	<u> </u>
MSM0641	prephenate dehydrogenase (NADP+)			

MSM0653	histidinol-phosphate aminotransferase,			
	HisC			
MSM0719	phosphoserine phosphatase, HAD			
	family, SerB			
MSM0722	2-isopropylmalate synthase, LeuA			
MSM0723	3-isopropylmalate dehydratase, LeuC			
MSM0727	S-adenosylhomocysteine hydrolase			
	(adenosylhomocysteinase), AhcY			
MSM0829	aspartate-semialdehyde			
	dehydrogenase, Asd			
MSM0830	dihydrodipicolinate reductas, DapB			
MSM0832	aspartokinase, alpha subunit			
MSM0834	chorismate mutase			
MSM0835	archaeal shikimate kinase			
MSM0847	archaeal 3-isopropylmalate			
	dehydratase, small subunit, LeuD			
MSM0858	phosphoribosylformimino-5-			
	aminoimidazole carboxamide ribotide			
	(ProFAR) isomerase, HisA			
MSM0860	aspartate-semialdehyde			
	dehydrogenase, ArgC			
MSM0878	pyruvoyl-dependent arginine			
	decarboxylase, PdaD			
MSM0888	glutamate dehydrogenase (NADP+),			
	GdhA			
MSM0902	methyl-coenzyme M reductase, alpha			
	subunit, McrA			
MSM0903	methyl-coenzyme M reductase, gamma			
	subunit, McrG			
MSM0904	methyl-coenzyme M reductase, D			
	subunit, McrD			
MSM0905	methyl-coenzyme M reductase, beta			
	subunit, McrB			
MSM0939	pyruvate carboxylase, subunit B, PycB			
MSM0965	3-hydroxyacyl-CoA dehydrogenase,			
	FadB			
MSM0967	glutamyl-tRNA reductase, HemA			
MSM0987	tyrosine decarboxylase, MfnA			
MSM0988	phosphoenolpyruvate synthase, PpsA			
MSM1001	methyl viologen-reducing hydrogenase,			
	delta subunit, MvhD			
MSM1007	N5-methyl-			
ĺ	tetrahydromethanopterin:coenzyme M			
	methyltransferase, subunit H, MtrH			
MSM1008	N5-methyl-			
	tetrahydromethanopterin:coenzyme M			
MONAGAA	methyltransferase, subunit G, MtrG			
MSM1011	N5-methyl-			
	tetrahydromethanopterin:coenzyme M			
MONAGAG	methyltransferase, subunit B, MtrB			
MSM1012	N5-methyl-			
	tetrahydromethanopterin:coenzyme M			
MeManar	methyltransferase, subunit C, MtrC			
MSM1015	methyl-coenzyme M reductase, alpha			
MSM1016	subunit, McrA methyl-coenzyme M reductase, gamma			
1410111010	subunit, McrG			
MSM1017	methyl-coenzyme M reductase, C			
14131411017	subunit, McrC			
MSM1018	methyl-coenzyme M reductase, D			
1410141010	subunit, McrD			
MSM1019	methyl-coenzyme M reductase, beta			
1.7.0.11.10.19	subunit, McrB			
MSM1052	prephenate dehydratase, PheA			
MSM1032	argininosuccinate synthase, ArgG			
141014111004	jargiiiiiosucciiiaic syllilasc, Alyc			

MSM1092	formylmethanofuran:tetrahydromethano			
	pterin formyltransferase, Ftr			
MSM1103	phosphoribosyl-ATP			
	pyrophosphohydrolase, HisE			
MSM1141	tryptophan synthase, alpha subunit,			
	TrpA			
MSM1142	tryptophan synthase, beta subunit, TrpB			
WISWI1142	li yptoprian synthase, beta subunit, mpb			
MCM4442	in data 2 attraces in base bate at with an			
MSM1143	indole-3-glycerol phosphate synthase,			
	TrpC	_		
MSM1144	anthranilate phosphoribosyltransferase,			
	TrpD			
MSM1145	anthranilate/para-aminobenzoate			
	synthase component II, TrpG			
MSM1159	glutamine amidotransferase, HisH			
MSM1172	leucyl-tRNA synthetase, LeuS			
MSM1179	shikimate 5-dehydrogenase, AroE			
MSM1181	histidyl-tRNA synthetase, HisS			
MSM1182	phosphoribosyl-AMP cyclohydrolase,			
	Hisl			
MSM1202	branched-chain-amino-acid			
	aminotransferase, IIvE			
MSM1204	coenzyme F420-dependent			
	methylenetetrahydromethanopterin			
	dehydrogenase, Mtd			
MSM1206	imidazoleglycerol-phosphate			
1	dehydrogenase, HisB			
MSM1214	threonyl-tRNA synthetase, ThrS			
MSM1222	ketol-acid reductoisomerase, IIvC			
MSM1224	acetolactate synthase, small subunit			
WISWI1224				
MCM400C	(regulatory), IIvH	-		
MSM1226	ornithine carbamoyltransferase, ArgF	-		
MSM1231	arginyl-tRNA synthetase, ArgS			
MSM1236	aspartyl-tRNA synthetase, AspS			
MSM1237	dihydroxy-acid dehydratase, IIvD			
MSM1238	histidinol dehydrogenase, HisD			
MSM1242	tryptophan synthase, beta subunit, TrpB			
MSM1246	isopropylmalate synthase, LeuA			
MSM1261	ATP phosphoribosyltransferase, HisG			
MSM1263	aspartate carbamoyltransferase, PyrB			
MSM1298	3-isopropylmalate dehydrogenase,			
	LeuB			
MSM1299	3-isopropylmalate dehydratase, small			
	subunit, LeuD			
MSM1300	3-isopropylmalate dehydratase, large			
	subunit, LeuC			
MSM1327	predicted CDP-			
	glycerol:poly(glycerophosphate)			
	glycerophosphotransferase			
MSM1337	glycine hydroxymethyltransferase, GlyA			
MSM1340	archaeal S-adenosylmethionine			
1	synthetase, MetK			
MSM1341	isoleucyl-tRNA synthetase, IleS			
MSM1364	imidazoleglycerol-phosphate synthase,			
1	HisF			
MSM1368	N-acetylornithine aminotransferase,			
1	AraD			
MSM1371	diaminopimelate decarboxylase, LysA			
	alaminopiniolate decarboxylase, LysA			
MSM1372	diaminopimelate epimerase, DapF			
MSM1372	lysyl-tRNA synthetase (class I), LysS			
MSM1387	sugar kinase, ribokinase/pfkB			
INICINITION				
MCM420C	superfamily			
MSM1396	tungsten formylmethanofuran			
<u> </u>	dehydrogenase, subunit E, FwdE			

	MSM1404	formate dehydrogenase, alpha subunit,						
		FdhA						]
	MSM1414	tungsten formylmethanofuran						
		dehydrogenase, subunit C, FwdC						]
	MSM1418	glutamine synthetase, GlnA						l
	MSM1440	predicted archaeal kinase						]
	MSM1452	glutamyl-tRNA synthetase, GltX						]
	MSM1461	methyl viologen-reducing hydrogenase,						
		delta subunit, MvhD						
	MSM1474	chorismate synthase, AroC						
		phenylalanyl-tRNA synthetase, PheS						
	MSM1594	glycosyltransferase/CDP-						
		glycerol:poly(glycerophosphate)						
		glycerophosphotransferase, GT2 family						
	MSM1602	glycosyltransferase/CDP-						
		glycerol:poly(glycerophosphate)						
		glycerophosphotransferase, GT2 family						
	MSM1636	ProFAR isomerase-related protein						I
	MSM1710	seryl-tRNA synthetase, SerS						J
	MSM1713	predicted regulatory protein, amino acid-						
	<u> </u>	binding ACT domain family				<u> </u>		
COFACTOR/	M. smithii	Annotation	al	_	Ъ	er		i a
VITAMIN	genes		iet	ē	₽	in at	ים י	5- lan tas
METABOLISM	ľ		0046872 - m ion binding	GO:0005506 - iron ion binding	Ž	D:0006767 - water soluble vitamin metabolism	GO:0042727 - riboflavin and derivative biosynthesis	GO:0008703 - { amino-6-(5- nosphoribosyla )uracil reducti
			ig 5	<u>ā</u> 8	50661 -   binding		GO:0042727 riboflavin an derivative biosynthesi	9 9 Pa
			387 nic	55 oin	66 Jdi	97.9 e v	avi iva	8 or ir r
			946 n b	8 -	50 bir	oo oo oo eta	eri Sc	is is 30
			00 ℃	은 은	8	3 6 5	15 d b 3	O: ar osp
			GO:0046872 - metal ion binding	9	GO:0050661 - NADP binding	GO:0006767 soluble vit metaboli	_	GO:0008703 - 5- amino-6-(5- phosphoribosylami no)uracil reductase
	MSM0027	alutanasta avinthasa damasin Ovith	U	_	U	U		0.2
	IVISIVIUUZI	glutamate synthase, domain 2 with rubredoxin						
	MSM0029							
		putative calcium-binding protein adhesin-like protein						
	MSM0065							
	MSM0079	CofH protein (7,8-didemethyl-8-hydroxy-						
	INISINIOU79							
		5-deazariboflavin (FO)/F420						
	MCMOOOO	biosynthesis) heterodisulfide reductase, subunit A,						
	MSM0082							
	MSM0084	heterodisulfide reductase, subunit C,						
	IVISIVIUU64	HdrC						
	MCMOOSE	putative ferredoxin						
	MSM0101	precorrin-3 methylase, CbiF						
				<u> </u>				
	MSM0107	hydrogenase expression/formation protein, HypB		ĺ				
	MSM0108	hydrogenase nickel incorporation						
	14101410100	protein, HypA		ĺ				
	MSM0129	nicotinamide mononucleotide						
		adenylyltransferase, NadR						
	MSM0131	molybdenum-binding protein, Mopl						
	MSM0135	coenzyme F420-reducing hydrogenase,						
		beta subunit						
	MSM0136	putative ferredoxin						
	MSM0148	predicted oxidoreductase, aldo/keto						
		reductase family						
	MSM0153	predicted phosphoglycerate mutase						
	MSM0187	rubredoxin						
	MSM0188							
		inorganic pyrophosphatase						
		nucleoside diphosphate kinase, Ndk						
	MSM0209	ferredoxin						
		iron dependent transcriptional regulator						
		(Fe2+-binding)						
	MSM0238	precorrin-6B methylase, CbiT						

MSM0262 desulfoferrodoxin (dr.) MSM0265 adhesin-like protein MSM0277 denoruclease III MSM0284 ribose 5-ptosphate isomerase, RpIA MSM0288 denoruclease III MSM0288 protein in in in in in in in its protein in in its protein in its pro					
MSM03272 domounclease III MSM03284 fibose 5-phosphate isomerase, RpIA MSM0289 by Oberreadoxin, iron-sulfur binding MSM03010 polyferreadoxin, iron-sulfur binding MSM0311 polyferreadoxin, iron-sulfur binding MSM0312 [NiFe]-hydrogenase-3-type complex, large subunit/NADH-cuinorne oxidoreductase (complex I), subunit 4 MSM0331 2-oxolsovalerate ferredoxin oxidoreductase (etale subunit MSM0357 conserved hypothetical membrane protein (possible Zinc-binding) MSM0368 glutamate synthase (NADPH), subunit 2 MSM0376 alcohol dehydrogenase (Zinc-binding). GroE3-like MSM0381 anaerobic magnesium-protoporphyrin IX momomethyl ester cyclase, Elongator protein 3MilaB/Niff family MSM0382 manerobic magnesium-protoporphyrin IX momomethyl ester cyclase, Elongator protein 3MilaB/Niff family MSM0393 tranate reductase, iron-sulfur protein MSM0393 ferredoxin, iron-sulfur binding MSM04941 (citopia) (					
MSM0227 endonuclease III MSM0288 by hosphomethylpyrimidine kinase (HMP-Kinase), ThiD MSM0306 polyferredoxin, iron-sulfur binding MSM0310 polyferredoxin, iron-sulfur binding MSM0311 polyferredoxin, iron-sulfur binding MSM0312 polyferredoxin, iron-sulfur binding MSM0313 (application oxidereduclase, delta subunit MSM0357 polyferredoxin polyferr		desulfoferrodoxin (dfx)			
MSM0288 biosphosphosphosphosphosphosphosphosphosph	MSM0266	adhesin-like protein			
MSM0328 phosphomethylpyrimidine kinase (HMP-kinase), Thili D MSM0306 polyferredoxin, Iron-sulfur binding MSM0311 polyferredoxin, Iron-sulfur binding MSM0311 polyferredoxin, Iron-sulfur binding MSM0312 polyferredoxin, Iron-sulfur binding MSM0312 polyferredoxin, Iron-sulfur binding MSM0311 polyferredoxin, Iron-sulfur binding MSM0312 polyferredoxin, Iron-sulfur binding MSM0313 polyferredoxin, Iron-sulfur binding PK/Ndh1/Nx00 2-xxxisovalerate ferredoxin xidoreductase, delfa subunit xidoreductase, xidoreductase, expension y xidoreductase, xidoreductase	MSM0272	endonuclease III			
MSM0306 polyFerredoxin, iron-sulfur binding MSM0310 polyFerredoxin, iron-sulfur binding MSM0311 polyFerredoxin, iron-sulfur binding MSM0311 polyFerredoxin, iron-sulfur binding MSM0312 polyFerredoxin, iron-sulfur binding MSM0311 polyFerredoxin, iron-sulfur binding with a substantial polyFerredoxin, iron-sulfur binding with a substantial polyFerredoxin possible Zinc-binding) mxM0331 polyFerredoxin possible Zinc-binding) mxM0333 glutamate synthase (NADFH), subunit 2 mxM0333 glutamate synthase (NaDFH), subunit 3 mxM0334 glutamate synthase (NaDFH), subunit 4 mxM0334 marerobic magnesium-protoporphyrin IX monomethyl ester cyclase, Elongator protein 3/MisB/MisB/MisB family indolepyruvate ferredoxin indolepyruvate fer	MSM0284	ribose 5-phosphate isomerase, RpiA			
MSM0306 polyferredoxin, iron-sulfur binding MSM0310 polyferredoxin, iron-sulfur binding MSM0311 polyferredoxin, iron-sulfur binding MSM0312 polyferredoxin, iron-sulfur binding MSM0313 polyferredoxin, iron-sulfur binding MSM0311 polyferredoxin, iron-sulfur binding MSM0314 polyferredoxin, iron-sulfur binding MSM0314 polyferredoxin, iron-sulfur binding MSM0315 polyferredoxin, iron-sulfur binding MSM0386 glutamate synthase (NADPH), subunit 2 polyferredoxin, iron-sulfur binding MSM0386 glutamate synthase (NADPH), subunit 2 polyferredoxin, iron-sulfur binding MSM0386 glutamate synthase (NADPH), subunit 2 polyferredoxin, iron-sulfur binding MSM0386 glutamate synthase (NADPH), subunit 2 polyferredoxin protein 3/MiaB/MIB family iron-sulfur binding MSM0393 polyferredoxin, iron-sulfur binding MSM0393 polyferredoxin, iron-sulfur binding MSM0393 polyferredoxin, iron-sulfur binding MSM0494 glutionitate-in-ucleotide pyrophosphorylase (carboxylating), NadC mSM0494 quinolinate synthase, subunit A, NadA mSM0494 quinolinate synthase, subunit A, NadA mSM0494 quinolinate synthase, subunit A, NadA mSM0494 glutionitate-in-ucleotide pyrophosphorylase (carboxylating), NadC methyltransferase activation protein, MapA methyltransferase activation protein, MapA methyltransferase activation glution protein, MapA methyltransferase activation protein, MapA mSM0494 predicted Fe's Oxidoreductase pyruvate ferredoxin, iron-sulfur binding mSM0496 proteited Fe's Oxidoreductase pyruvate ferredoxin, iron-sulfur binding mSM0593 polyferredoxin, iron-sulfur binding mSM0595 polyferredoxin, iron-sulfur binding mSM05050 polyferredoxin, iron-sulfur binding mSM0505	MSM0289	phosphomethylpyrimidine kinase			
MSM0306 polyferredoxin, iron-sulfur binding MSM0310 polyferredoxin, iron-sulfur binding MSM0311 polyferredoxin, iron-sulfur binding MSM0312 polyferredoxin, iron-sulfur binding MSM0313 polyferredoxin, iron-sulfur binding MSM0311 polyferredoxin, iron-sulfur binding MSM0314 polyferredoxin, iron-sulfur binding MSM0314 polyferredoxin, iron-sulfur binding MSM0315 polyferredoxin, iron-sulfur binding MSM0386 glutamate synthase (NADPH), subunit 2 polyferredoxin, iron-sulfur binding MSM0386 glutamate synthase (NADPH), subunit 2 polyferredoxin, iron-sulfur binding MSM0386 glutamate synthase (NADPH), subunit 2 polyferredoxin, iron-sulfur binding MSM0386 glutamate synthase (NADPH), subunit 2 polyferredoxin protein 3/MiaB/MIB family iron-sulfur binding MSM0393 polyferredoxin, iron-sulfur binding MSM0393 polyferredoxin, iron-sulfur binding MSM0393 polyferredoxin, iron-sulfur binding MSM0494 glutionitate-in-ucleotide pyrophosphorylase (carboxylating), NadC mSM0494 quinolinate synthase, subunit A, NadA mSM0494 quinolinate synthase, subunit A, NadA mSM0494 quinolinate synthase, subunit A, NadA mSM0494 glutionitate-in-ucleotide pyrophosphorylase (carboxylating), NadC methyltransferase activation protein, MapA methyltransferase activation protein, MapA methyltransferase activation glution protein, MapA methyltransferase activation protein, MapA mSM0494 predicted Fe's Oxidoreductase pyruvate ferredoxin, iron-sulfur binding mSM0496 proteited Fe's Oxidoreductase pyruvate ferredoxin, iron-sulfur binding mSM0593 polyferredoxin, iron-sulfur binding mSM0595 polyferredoxin, iron-sulfur binding mSM05050 polyferredoxin, iron-sulfur binding mSM0505		(HMPP-kinase), ThiD			
MSM0310 polyferedoxin, iron-sulfur binding MSM0311 polyferedoxin, iron-sulfur binding MSM0312   NiFe]-hydrogenase-3-type complex, large subunit/NADH-tyunone oxidoreductase (complex I), subunit 49K/Ndh/HvluoD   Avoisovalerate ferredoxin oxidoreductase, delta subunit polyferedoxin, iron-sulfur binding   Avoisovalerate ferredoxin oxidoreductase, delta subunit   Avoisovalerate ferredoxin oxidoreductase, delta subunit   Avoisovalerate ferredoxin   Avo	MSM0306				
MSM0312   Dolyferredoxin, iron-sulfur binding   MSM0312   Initie-Phytrogenases-3-type complex, large subunit/NADH; quinone oxidoreductase (complex I), subunit   49K/NdhH/NuoD   2-xxxisovalerate ferredoxin   xodioreductase, delta subunit   2-xxisovalerate ferredoxin   xodioreductase, ficin-binding)   xodioreductase, ficin-binding)   xodioreductase, ficin-binding   xodioreductase, alpha subunit   xodioreductase, alpha subunit   xodioreductase, alpha subunit   xodioreductase, alpha subunit   xodioreductase, inon-sulfur protein   xodioreductase, alpha subunit   xodioreductase, xo		polyferredoxin, iron-sulfur binding			
MSM0312 [NIFe]-hydrogenase-3-type complex, large subunit/NDD1-quinone oxidoreductase (complex I), subunit 44K/Ndh1-NuoD oxidoreductase, delta subunit conserved hypothetical membrane protein (possible Zinc-binding) distantes synthase (NADP1), subunit 2 glutamate synthase (NADP1), subunit 3 glutamate yellogical synthase (NADP1), subunit 4 glutamate yellogical synthase (NADP1), subunit 5 glutamate yellogical synthase (NADP1)	MSM0311				
iarge subunit/NADH:quinone oxidoreductase (complex I), subunit 49(K/NdhH/Nuo) 20					
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MSM0393 fumarate reductase, iron-sulfur protein  MSM0495 ferredoxin, iron-sulfur binding  MSM0409 C4-type Zinc-finger protein  MSM0424 transcription initiation factor TFIIB (zinc-binding)  MSM0491 nicotinate-nucleotide pyrophosphorylase (carboxylating), NadC  MSM0494 quinolinate synthetase, subunit A, NadA  MSM0516 corrinoid protein (methionine synthase-related), MtaC  methyltransferase activation protein, MapA  MSM0517 methyltransferase activation protein, MapA  MSM0518 pyruvate formate-lyase activating enzyme, PflA  MSM0540 pyruvate formate-lyase activating enzyme, PflA  MSM0541 predicted Fe-S oxidoreductase MSM0558 pyruvate-ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0563 cobalt ABC transporter, permease component, CbiM  MSM0565 cobalt ABC transporter, permease component, CbiQ  MSM0567 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding  MSM0609 ferredoxin, iron-sulfur binding  MSM0609 ferredoxin, iron-sulfur binding  MSM0609 ferredoxin, iron-sulfur binding	11101110002				
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MSM0424       transcription initiation factor TFIIB (zincbinding)         MSM0491       nicotinate-nucleotide pyrophosphorylase (carboxylating), NadC         MSM0494       quinolinate synthetase, subunit A, NadA         MSM0516       corrinoid protein (methionine synthase-related), MtaC         MSM0517       methyltransferase activation protein, MapA         MSM0517       methyltransferase activation protein, MapA         MSM0538       pyruvate formate-lyase activating enzyme, PflA         MSM0540       predicted Fe-S oxidoreductase         MSM0541       predicted Fe-S oxidoreductase, delta subunit, PorD         MSM0558       pyruvate-ferredoxin oxidoreductase, delta subunit, PorD         MSM0561       formate dehydrogenase, iron-sulfur subunit         MSM0573       biotin synthetase, BioB         MSM0573       biotin synthetase, BioB         MSM0579       polyferredoxin, iron-sulfur binding         MSM0581       cobalt ABC transporter, permease component, CbiQ         MSM0585       cobalt ABC transporter, permease component, CbiQ         MSM0607       predicted ATPase, RNase L inhibitor family         MSM0609       ferredoxin, iron-sulfur binding					
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MSM0494 quinolinate synthetase, subunit A, NadA  MSM0516 corrinoid protein (methionine synthase-related), MtaC  methyltransferase activation protein, MapA  MSM0517 methyltransferase activation protein, MapA  MSM0538 pyruvate formate-lyase activating enzyme, PflA  MSM0543 DNA repair photolyase, SplB  MSM0544 predicted Fe-S oxidoreductase MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit MSM0573 biotin synthetase, BioB MSM0573 biotin synthetase, BioB MSM0573 cobalt ABC transporter, permease component, CbiM MSM0585 cobalt ABC transporter, permease component, CbiQ MSM0607 predicted ATPase, RNase L inhibitor family MSM0609 ferredoxin, iron-sulfur binding MSM0609 ferredoxin, iron-sulfur binding					
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MSM0516 corrinoid protein (methionine synthase-related), MtaC  MSM0517 methyltransferase activation protein, MapA  MSM0518 methyltransferase activation protein, MapA  MSM0538 pyruvate formate-lyase activating enzyme, PflA  MSM0543 DNA repair photolyase, SplB predicted Fe-S oxidoreductase  MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB MSM0579 polyferredoxin, iron-sulfur binding MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ MSM0607 predicted ATPase, RNase L inhibitor family MSM0607 ferredoxin, iron-sulfur binding  MSM0607 ferredoxin, iron-sulfur binding  MSM0607 predicted ATPase, RNase L inhibitor family MSM0609 ferredoxin, iron-sulfur binding	MSM0494	quinolinate synthetase, subunit A. NadA			
related), MtaC methyltransferase activation protein, MapA  MSM0517 methyltransferase activation protein, MapA  MSM0538 pyruvate formate-lyase activating enzyme, PflA  MSM0543 DNA repair photolyase, SplB  MSM0544 predicted Fe-S oxidoreductase MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB MSM0579 polyferredoxin, iron-sulfur binding MSM0585 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding		, , , , , , , , , , , , , , , , , , , ,			
related), MtaC methyltransferase activation protein, MapA  MSM0517 methyltransferase activation protein, MapA  MSM0538 pyruvate formate-lyase activating enzyme, PflA  MSM0543 DNA repair photolyase, SplB  MSM0544 predicted Fe-S oxidoreductase MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB MSM0579 polyferredoxin, iron-sulfur binding MSM0585 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding	MSM0516	corrinoid protein (methionine synthase-			
MSM0517 methyltransferase activation protein, MapA  MSM0518 pyruvate formate-lyase activating enzyme, PflA  MSM0543 DNA repair photolyase, SplB  MSM0544 predicted Fe-S oxidoreductase pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0558 formate dehydrogenase, iron-sulfur subunit  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB  MSM0573 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding  MSM0609 ferredoxin, iron-sulfur binding  MSM0609 ferredoxin, iron-sulfur binding					
MSM0517 methyltransferase activation protein, MapA  MSM0538 pyruvate formate-lyase activating enzyme, PflA  MSM0543 DNA repair photolyase, SplB  MSM0544 predicted Fe-S oxidoreductase MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding  MSM0609 ferredoxin, iron-sulfur binding	MSM0517				
MSM0517 methyltransferase activation protein, MapA  MSM0538 pyruvate formate-lyase activating enzyme, PflA  MSM0543 DNA repair photolyase, SpIB  MSM0544 predicted Fe-S oxidoreductase  MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding  MSM0609 ferredoxin, iron-sulfur binding					
MSM0538 pyruvate formate-lyase activating enzyme, PflA  MSM0543 DNA repair photolyase, SplB MSM0544 predicted Fe-S oxidoreductase MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD MSM0561 formate dehydrogenase, iron-sulfur subunit MSM0562 formate dehydrogenase, iron-sulfur subunit MSM0573 biotin synthetase, BioB MSM0579 polyferredoxin, iron-sulfur binding Cobalt ABC transporter, permease component, CbiM MSM0585 cobalt ABC transporter, permease component, CbiQ MSM0607 predicted ATPase, RNase L inhibitor family MSM0609 ferredoxin, iron-sulfur binding MSM0609 ferredoxin, iron-sulfur binding	MSM0517				
MSM0538 pyruvate formate-lyase activating enzyme, PfIA  MSM0544 DNA repair photolyase, SpIB predicted Fe-S oxidoreductase  MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding					
enzyme, PfIA  MSM0543 DNA repair photolyase, SpIB  MSM0544 predicted Fe-S oxidoreductase  MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding	MSM0538				
MSM0543 DNA repair photolyase, SpIB MSM0544 predicted Fe-S oxidoreductase MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD MSM0561 formate dehydrogenase, iron-sulfur subunit MSM0562 formate dehydrogenase, iron-sulfur subunit MSM0573 biotin synthetase, BioB MSM0579 polyferredoxin, iron-sulfur binding MSM0583 cobalt ABC transporter, permease component, CbiM MSM0585 cobalt ABC transporter, permease component, CbiQ MSM0607 predicted ATPase, RNase L inhibitor family MSM0607 ferredoxin, iron-sulfur binding MSM0609 ferredoxin, iron-sulfur binding					
MSM0554 predicted Fe-S oxidoreductase MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD MSM0561 formate dehydrogenase, iron-sulfur subunit MSM0562 formate dehydrogenase, iron-sulfur subunit MSM0573 biotin synthetase, BioB MSM0579 polyferredoxin, iron-sulfur binding MSM0583 cobalt ABC transporter, permease component, CbiM MSM0585 cobalt ABC transporter, permease component, CbiQ MSM0607 predicted ATPase, RNase L inhibitor family MSM0609 ferredoxin, iron-sulfur binding	MSM0543				
MSM0558 pyruvate:ferredoxin oxidoreductase, delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding		predicted Fe-S oxidoreductase			
delta subunit, PorD  MSM0561 formate dehydrogenase, iron-sulfur subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding	MSM0558				
subunit  MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding		delta subunit, PorD			
MSM0562 formate dehydrogenase, iron-sulfur subunit  MSM0573 biotin synthetase, BioB  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding	MSM0561	formate dehydrogenase, iron-sulfur		 	
subunit  MSM0573 biotin synthetase, BioB  MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding				 	
MSM0573 biotin synthetase, BioB MSM0579 polyferredoxin, iron-sulfur binding MSM0583 cobalt ABC transporter, permease component, CbiM MSM0585 cobalt ABC transporter, permease component, CbiQ MSM0607 predicted ATPase, RNase L inhibitor family MSM0607 predicted ATPase, RNase L inhibitor family MSM0609 ferredoxin, iron-sulfur binding	MSM0562	formate dehydrogenase, iron-sulfur		 	
MSM0579 polyferredoxin, iron-sulfur binding  MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding					
MSM0583 cobalt ABC transporter, permease component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding		biotin synthetase, BioB			
component, CbiM  MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding	MSM0579				
MSM0585 cobalt ABC transporter, permease component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding	MSM0583				
component, CbiQ  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding		component, CbiM			
MSM0607 predicted ATPase, RNase L inhibitor family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding	MSM0585				
family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding		component, CbiQ			
family  MSM0607 predicted ATPase, RNase L inhibitor family  MSM0609 ferredoxin, iron-sulfur binding	MSM0607	predicted ATPase, RNase L inhibitor			]
family  MSM0609 ferredoxin, iron-sulfur binding		family			
MSM0609 ferredoxin, iron-sulfur binding	MSM0607	predicted ATPase, RNase L inhibitor			
		family			
MSM0616  adhesin-like protein					

MSM0617	thiamine biosynthesis ATP				
	pyrophosphatase, Thil				
MSM0644	thiamine biosynthesis protein, ThiC				
MSM0652	pyruvate formate-lyase activating				
	enzyme, PflA				
MSM0657	phosphoglycerate mutase, AP				
	superfamily				
MSM0696	Fe-S oxidoreductase				
MSM0723	3-isopropylmalate dehydratase, LeuC				
MSM0723	3-isopropylmalate dehydratase, LeuC				
MSM0728	predicted oxidoreductase, aldo/keto				
14131410720	reductase family				
MSM0771	cobalt ABC transporter, permease	ĺ			
IVISIVIOTTI					
MCMOZOS	component, CbiQ				
MSM0783	tungsten formylmethanofuran				
140140704	dehydrogenase, subunit F, FwdF				
	ferredoxin				
MSM0787	Fe-S oxidoreductase				
MSM0796	heterodisulfide reductase, subunit C,				
	HdrC				
MSM0808	nitrogenase iron-molybdenum cofactor				
	biosynthesis protein, NifB				
MSM0829	aspartate-semialdehyde				
	dehydrogenase, Asd				
MSM0837	cobalamin biosynthesis protein D, CbiD				
<u> </u>		<u></u>	<u></u>		
MSM0842	histone acetyltransferase, radical SAM				
	superfamily				
MSM0845	2-methylthioadenine synthetase, MiaB				
	, , , , , , , , , , , , , , , , , , , ,				
MSM0849	molybdenum cofactor biosynthesis-				
	related protein, MoaA				
MSM0865	putative glucose-methanol-choline				
MOMOOO	oxidoreductase (FAD-dependent)				
MSM0892	putative zinc-binding protein				
MSM0895	cation transport ATPase, HAD family				
MSM0896	precorrin-6X reductase, CbiJ				
MSM0916	hydroxyethylthiazole kinase, ThiM				
MSM0917					
INISINIO917	thiamine monophosphate synthase,				
MSM0922	ThiE				
	Fe-S oxidoreductase				
MSM0928	2-oxoglutarate ferredoxin				
140140000	oxidoreductase, delta subunit, KorD				
MSM0933	cobalamin-5-phosphate synthase, CobS				
	"				
MSM0960	cation transport ATPase, HAD family				
MSM0961	heavy-metal cation transporting ATPase				
MSM0962	glyceraldehyde 3-phosphate				
	dehydrogenase, GapA				
MSM0998	polyferredoxin, MvhB				
MSM0999	methyl viologen-reducing hydrogenase,				
	alpha subunit, MvhA				
MSM1020	Fe-S oxidoreductase, Radical SAM				
	family				
MSM1035	FO synthase subunit 1 (SAM-				
	dependent), CofG (F420 biosynthesis)				
MSM1043	dihydroorotate dehydrogenase electron				
	transfer subunit, PyrK				
MSM1055	coenzyme PQQ synthesis protein, SAM				
1	family				
MSM1063	energy-converting hydrogenase B,				
1	subunit N, EhbN				
MSM1065	energy-converting hydrogenase B,				
14121411063					
MSM4066	subunit L, EhbL				
MSM1066	energy-converting hydrogenase B,				
L	subunit K, EhbK				

MSM1099	biotin synthase related protein					
MSM1106	hydrogenase maturation factor, HypF					
MSM1111	adhesin-like protein					
MSM1112	adhesin-like protein					
MSM1122	coenzyme F420-reducing hydrogenase,					
WISWITIZZ						
MCM4400	gamma subunit, FrhG					
MSM1123	coenzyme F420-reducing hydrogenase,					
	delta subunit, FrhD					
MSM1124	coenzyme F420-reducing hydrogenase,					
	alpha subunit, FrhA					
MSM1127	cation transport ATPase, HAD family					
MSM1138	predicted glutamine amidotransferase,					
	CobB/CobQ-like family					
	CODE/CODQ IIIC Idillily					
MSM1153	ection transport ATPage HAD family					
	cation transport ATPase, HAD family					
MSM1167	cobalt precorrin-6Y C5,15-					
	methyltransferase, CbiE					
MSM1171	ammonia-dependent NAD+ synthetase,					
	NadE					
MSM1174	heat shock protein HtpX (Zn-dependent)					
MSM1179	shikimate 5-dehydrogenase, AroE					
MSM1198	O-sialoglycoprotein endopeptidase					
MSM1200	phosphoribosyltransferase, CobT					
MSM1215	cobyrinic acid a,c-diamide synthase,					
IVISIVI 12 15						
140144000	CbiA					
MSM1223	carbonic anhydrase					
MSM1230	transcriptional regulator, MarR family		1			
MSM1234	cobalt-precorrin-8X methylmutase, CbiC					
MSM1238	histidinol dehydrogenase, HisD					
MSM1239	predicted DNA-binding protein					
MSM1241	chromosome partitioning ATPase					
MSM1254	cobyric acid synthase					
MSM1256	3,4-dihydroxy-2-butanone 4-phosphate					
14101411200						
MCM40CC	synthase, RibB cobalamin biosynthesis protein D, CobD					
MSM1266	Cobalamin biosynthesis protein D, Cobb					
MSM1267	cobalamin biosynthesis protein G, CbiG					
MSM1273	cobalt precorrin-3B C17-					
	methyltransferase, CbiH					
MSM1283	thiamine monphosphate kinase, ThiL					
MSM1284	pyruvate formate-lyase activating					
	enzyme, PfIA					
MSM1296	riboflavin synthase, beta subunit, RibH					
MSM1300	3-isopropylmalate dehydratase, large					
1	subunit, LeuC					
MSM1301	predicted Fe-S oxidoreductase					
MSM1336	heterodisulfide reductase, subunit A,					
	HdrA					
MSM1338	archaeal flavoprotein					
MSM1348	rubrerythrin					
MSM1351	precorrin-2 C20-methyltransferase, CbiL				-	
		Í				
MSM1354	DNA-directed RNA polymerase subunit					
	M. RpoM					
MSM1380	NADP-dependent alcohol					
1.110.1111300						
MONAGOO	dehydrogenase					
MSM1386	cytosine deaminase					
MSM1388	thiamine biosynthesis protein, ThiC					
MSM1404	formate dehydrogenase, alpha subunit,					
	FdhA					
MSM1405	formate dehydrogenase, beta subunit,					1
	FdhB					

ı	MOM4 400	module double in a section bit and the section is					1	1
	MSM1406	molybdopterin cofactor biosynthesis						
	MON4 400	protein A, MoaA				1		
	MSM1408	tungsten formylmethanofuran						
	MCM4 400	dehydrogenase, subunit E, FwdE						
	MSM1409	tungsten formylmethanofuran dehydrogenase, subunit F, FwdF						
	MSM1410	tungsten formylmethanofuran						
	INISINI 14 IU	dehydrogenase, subunit G, FwdG						
	MSM1411	tungsten formylmethanofuran						
	INISINI 1411	dehydrogenase, subunit D, FwdD						
	MSM1436	ferredoxin						
	MSM1446	predicted hydroxylamine reductase, Hcp						
	INION 1440							
	MSM1450	predicted oxidoreductase, aldo/keto						
	1	reductase family						
	MSM1460	energy-converting hydrogenase B,						
	1	subunit K, EhbK						
	MSM1462	formate dehydrogenase, beta subunit,						
		FdhB						
	MSM1488	cobalt ABC transporter, permease						
		component, CbiM						
	MSM1497	predicted coenzyme PQQ synthesis		•				
		protein						
	MSM1565	cobyric acid synthase, CobQ						
	MSM1567	adhesin-like protein						
	MSM1590	adhesin-like protein						
	MSM1606	arylsulfatase regulator, AsIB						
	MSM1608	predicted oxidoreductase, aldo/keto						
		reductase family						
	MSM1618	cobalamin biosynthesis protein M, CbiM						
	MSM1619	cobalt ABC transporter, substrate-						
		binding component, CbiN						
	MSM1620	cobalt ABC transporter, permease						
		component, CbiQ						
		archaeal riboflavin synthase, RibC						
		predicted fumarate reductase						
		hypothetical protein (phage)						
		predicted ferredoxin						
		predicted ferritin						
	MSM1720	DNA-directed RNA polymerase, subunit						
	140144700	M, RpoM						
		rubrerythrin						
AMINO ACID	Ť	nicotinate phosphoribosyltransferase						
AMINO ACID	M. smithii	Annotation	. 13					
METABOLISM	genes		and	= 2 = is				
			51 d 2 ive	65 aci				
			GO:0006519 amino acid ar derivative	GO:0008652 amino acid biosynthesis				
			:00 of eri	S in S				
			O 는 한 함	를 잃 들 응				
			a a					
	14014222			1	ł			
	MSM0027	glutamate synthase, domain 2 with						
	MONIOSTA	rubredoxin						
	MSM0071 MSM0089	methionyl-tRNA synthetase, MetG			ł			
	INISINIOOS	pyrroline-5-carboxylate reductase (NADP oxidoreductase, coenzyme F420						
	MSM0102	dependent), ProC cobalamin-independent methionine						
	IVISIVIU IUZ	synthase, MetE						
	MSM0154	homoserine dehydrogenase, ThrA						
	MSM0160	asparagine synthetase, AsnB						
	MSM0174	O-acetylhomoserine sulfhydrylase (PLP-			1			
	1.7.5.1.0174	dependent), MET17						
	MSM0175	homoserine O-acetyltransferase, MetX						
•		1						

MCMOOAA	there are a company of the second of the sec	
MSM0214	threonine synthase (pyridoxal-	
MCMOOAC	phosphate dependent), ThrC	
MSM0216 MSM0231	tryptophanyl-tRNA synthetase, TrpS	
MSM0265	3-dehydroquinate dehydratase O-acetylhomoserine sulfhydrylase	
MSM0268	cysteinyl-tRNA synthetase, CysS	
MSM0270	serine acetyltransferase, CysE	
MSM0270	cysteine synthase, CysK	
MSM0271	EPSP synthase (3-phosphoshikimate 1-	
WISWIDZIS	carboxyvinyltransferase)	
MSM0275	valyl-tRNA synthetase, ValS	
MSM0277	phenylalanyl-tRNA synthetase, beta	
IIIOIIIOZ77	subunit, PheT	
MSM0286	glycerol 1-phosphate dehydrogenase	
	(Dehydroquinate synthase-like family)	
MSM0287	prolyl-tRNA synthetase, ProS	
MSM0334	L-asparaginase, GatD	
MSM0343	GMP synthase (glutamine-hydrolysing),	
	subunit A, GuaA	
MSM0368	glutamate synthase (NADPH), subunit 2	
	5 · · · · · · · · · · · · · · · · · · ·	
MSM0371	predicted glutamine amidotransferase	
	involved in pyridoxine biosynthesis,	
Ī	Pdx2	
MSM0373	isocitrate/isopropylmalate	
	dehydrogenase, LeuB	
MSM0375	acetylglutamate kinase, ArgB	
MSM0379	glutamate N-acetyltransferase, ArgJ	
MSM0388	amino acid regulator	
MSM0403	glycyl-tRNA synthetase	
MSM0415	uridylate kinase, PyrH	
MSM0457	D-3-phosphoglycerate dehydrogenase,	
	SerA	
MSM0488	carbamoylphosphate synthase, large	
	subunit, CarB	
MSM0489	carbamoylphosphate synthase, small	
	subunit, CarA	
MSM0513	tyrosyl-tRNA synthetase, TyrS	
MSM0516	corrinoid protein (methionine synthase-	
	related), MtaC	
MSM0604	predicted archaeal	
	aspartate/glutamate/uridylate kinase	
MSM0619	alanyl-tRNA synthetase, AlaS	
MSM0641	prephenate dehydrogenase (NADP+)	
MSM0653	histidinol-phosphate aminotransferase,	
	HisC	
MSM0719	phosphoserine phosphatase, HAD	
MONOTOR	family, SerB	
MSM0723 MSM0829	3-isopropylmalate dehydratase, LeuC	
IVI SIVIU 629	aspartate-semialdehyde	
MSM0830	dehydrogenase, Asd dihydrodipicolinate reductas, DapB	
MSM0830	aspartokinase, alpha subunit	
MSM0834	chorismate mutase	
MSM0835	archaeal shikimate kinase	
MSM0847	archaeal 3-isopropylmalate	
	dehydratase, small subunit, LeuD	
MSM0858	phosphoribosylformimino-5-	
	aminoimidazole carboxamide ribotide	
	(ProFAR) isomerase, HisA	
MSM0860	aspartate-semialdehyde	
11101110000	dehydrogenase, ArgC	
MSM0876	arginase/agmatinase/formimionoglutam	
	ate hydrolase, SpeB	
MSM0878	pyruvoyl-dependent arginine	
1	decarboxylase, PdaD	
	accarbonylace, i dab	

MSM0888	glutamate dehydrogenase (NADP+),	
MCMOOCZ	GdhA	
MSM0967 MSM1052	glutamyl-tRNA reductase, HemA prephenate dehydratase, PheA	
MSM1032	argininosuccinate synthase, ArgG	
MSM1103	phosphoribosyl-ATP	
WISWITIOS	pyrophosphohydrolase, HisE	
MSM1141	tryptophan synthase, alpha subunit,	
WOWITH	TrpA	
MSM1142	tryptophan synthase, beta subunit, TrpB	
1010111142	li yptoprian synthase, beta subunit, mpb	
MSM1143	indole-3-glycerol phosphate synthase,	
	TrpC	
MSM1144	anthranilate phosphoribosyltransferase,	
	TrpD	
MSM1145	anthranilate/para-aminobenzoate	
	synthase component II, TrpG	
MSM1159	glutamine amidotransferase, HisH	
MSM1172	leucyl-tRNA synthetase, LeuS	
MSM1179	shikimate 5-dehydrogenase, AroE	
MSM1181	histidyl-tRNA synthetase, HisS	
MSM1182	phosphoribosyl-AMP cyclohydrolase,	
	Hisl	
MSM1202	branched-chain-amino-acid	
	aminotransferase, IIvE	
MSM1206	imidazoleglycerol-phosphate	
	dehydrogenase, HisB	
MSM1214	threonyl-tRNA synthetase, ThrS	
MSM1222	ketol-acid reductoisomerase, IlvC	
MSM1224	acetolactate synthase, small subunit	
140144000	(regulatory), IIvH	
MSM1226	ornithine carbamoyltransferase, ArgF	
MSM1231	arginyl-tRNA synthetase, ArgS	
MSM1236 MSM1237	aspartyl-tRNA synthetase, AspS	
MSM1238	dihydroxy-acid dehydratase, IIvD histidinol dehydrogenase, HisD	
MSM1242	tryptophan synthase, beta subunit, TrpB	
IVIOIVI 1242	li yptoprian synthase, beta subunit, mpb	
MSM1261	ATP phosphoribosyltransferase, HisG	
MSM1263	aspartate carbamoyltransferase, PyrB	
MSM1298	3-isopropylmalate dehydrogenase,	
	LeuB	
MSM1299	3-isopropylmalate dehydratase, small	
	subunit, LeuD	
MSM1300	3-isopropylmalate dehydratase, large	
	subunit, LeuC	
MSM1337	glycine hydroxymethyltransferase, GlyA	
MSM1341	isoleucyl-tRNA synthetase, IleS	
MSM1364	imidazoleglycerol-phosphate synthase,	
MOM4000	HisF	
MSM1368	N-acetylornithine aminotransferase,	
MSM1371	ArgD diaminopimelate decarboxylase, LysA	
IVISIVI 1371	diaminopimerate decarboxyrase, LysA	
MSM1372	diaminopimelate epimerase, DapF	
MSM1372	lysyl-tRNA synthetase (class I), LysS	
MSM1418	glutamine synthetase, GlnA	
MSM1440	predicted archaeal kinase	
MSM1452	glutamyl-tRNA synthetase, GltX	
MSM1474	chorismate synthase, AroC	
MSM1478	phenylalanyl-tRNA synthetase, PheS	
MSM1615	deoxyhypusine synthase, Dys	
MSM1636	ProFAR isomerase-related protein	
MSM1710	seryl-tRNA synthetase, SerS	
MSM1713	predicted regulatory protein, amino acid-	
	binding ACT domain family	

DEPLETED COMPARED TO	SEQUENCED ARCHAEA AND/OR NON-GL	T METHA	NOGENS	
ENVIRONMENTAL M. smi				- t
SENSING gene	5	GO:0004672 - protein kinase activity	GO:0007165 - signal transduction	GO:0000160 - two-component signal transduction
		GO:0004672 protein kinas activity	:000710 signal nsduct	po po lar
		∯ ⊒ 0	og igr	:00001 compo signal nsduct
		ote of	O:C s ans	S s
		S g	9 5	E S G
MSM04	universal stress protein, UspA			_
MSM05				
	ubiquinone biosynthesis protein-related,			
	AarF			
MSM08				
MSM08				
MSM09				
MCM444	family			
MSM119 TRANSCRIPTIONAL M. smi	9 1 1			
TRANSCRIPTIONAL M. smi CONTROL gene		- z	3 of -	of of
CONTROL	•	35.	SO:0019222 regulation of metabolism	3O:0045449 - regulation of transcription
		oe iri	atic bo	atic
		) 0: Sr	) <u> </u>	)
]		GO:0006350 transcription	GO:0019222 regulation or metabolism	GO:0045449 - regulation of transcription
1401400	27		L	
MSM00 MSM00				
MSM00				
Wisiwioo	family)			
MSM01				
	polymerase, subunit E, RpoE			
MSM01				
	polymerase, subunit E, RpoE			
MSM02	1			
	(Fe2+-binding)			
MSM02				
MSM02	conserved hypothetical protein (DUF121 daomain)			
MSM03				
MSM03				
linemee	responsive), NikR			
MSM04				
MSM04				
	binding)			
MSM06				
MSM06				
MSM06				
MSM06	subunit   50   transcriptional regulator, TetR/AcrR			
Wisiwioo	family			
MSM07	- 1			
	binding protein			
MSM07	selenocysteine synthase, SelA			
MSM07				
MSM08				
MSM08				
MSM09	DNA-dependent RNA polymerase, subunit A. RpoA			
MSM09				
IVISIVIOS	subunit A', RpoA			
MSM09				
	subunit B', RpoB			
MSM09				
	subunit B. RpoB			
MSM09				
_	Laudermittle Docald			
MSM10	subunit H, RpoH transcriptional regulator, Lrp family			

	MSM1087	NAD-dependent protein deacetylase,		
		SIR2 family		
	MSM1107	predicted transcriptional regulator		
	MSM1126	predicted transcriptional regulator, ArsR		
	MCM4427	family		
	MSM1137	DNA polymerase sliding clamp subunit, PCNA family, Pcn		
	MSM1207	molybdate transport system regulatory		
	WISW1201	protein		
	MSM1230	transcriptional regulator, MarR family		
	MSM1315	predicted transcriptional regulator		
	MSM1350	predicted transcriptional regulator, ArsR		
		family		
	MSM1354	DNA-directed RNA polymerase subunit		
		M, RpoM		
	MSM1356	DNA-directed RNA polymerase, subunit		
		L, RpoL		
	MSM1376	DNA-directed RNA polymerase subunit		
	MSM1390	transcriptional regulator, LysR family		
	MSM1408	tungsten formylmethanofuran		
		dehydrogenase, subunit E, FwdE		
	MSM1428	DNA-directed RNA polymerase, subunit		
	140144 : 22	D, RpoD		
	MSM1432	DNA-directed RNA polymerase, subunit		
	MSM1433	N, RpoN DNA-directed RNA polymerase, subunit		
	IVISIVI 1433	K, RpoK		
	MSM1499	predicted transcriptional regulator		
	MSM1631	predicted DNA-directed RNA		
		polymerase II, subunit RPC10		
	MSM1720	DNA-directed RNA polymerase, subunit		
		M, RpoM		
	MSM1763	predicted DNA-directed RNA		
		polymerase, subunit M, RpoM		
	MSM1764	polymerase, subunit M, RpoM conserved hypothetical protein		
DUOCDUATE	MSM1764 MSM1765	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein		
PHOSPHATE METAROLISM	MSM1764 MSM1765 <i>M. smithii</i>	polymerase, subunit M, RpoM conserved hypothetical protein	96 - te sm	
PHOSPHATE METABOLISM	MSM1764 MSM1765	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein	6796 - hate olism	
	MSM1764 MSM1765 <i>M. smithii</i>	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein	006796 - sphate abolism	
	MSM1764 MSM1765 <i>M. smithii</i>	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein	D:0006796 - ohosphate netabolism	
	MSM1764 MSM1765 <i>M. smithii</i>	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i>	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  predicted archaeal kinase (GHMP kinase family)	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex,	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 M. smithii genes MSM0060 MSM0198 MSM0313	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 M. smithii genes MSM0060 MSM0198 MSM0313	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198 MSM0313	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198 MSM0313	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198 MSM0313 MSM0433 MSM0434	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit B	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198 MSM0313 MSM0434	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 M. smithii genes MSM0060 MSM0198 MSM0313 MSM0433 MSM0434 MSM0435	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit A	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198 MSM0313 MSM0433 MSM0434	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 M. smithii genes MSM0060 MSM0198 MSM0313 MSM0434 MSM0435 MSM0436 MSM0437	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit F	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 M. smithii genes MSM0060 MSM0198 MSM0313 MSM0433 MSM0434 MSM0435	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit C archaeal/vacuolar-type H+-transporting	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 M. smithii genes MSM0060 MSM0198 MSM0313 MSM0434 MSM0435 MSM0436 MSM0437	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit C archaeal/vacuolar-type H+-transporting ATP synthase, subunit C archaeal/vacuolar-type H+-transporting ATP synthase, subunit C	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 M. smithii genes MSM0060 MSM0198 MSM0313 MSM0434 MSM0435 MSM0436 MSM0437	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit C archaeal/vacuolar-type H+-transporting	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 M. smithii genes MSM0060 MSM0198 MSM0313 MSM0434 MSM0435 MSM0436 MSM0437	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit C archaeal/vacuolar-type H+-transporting ATP synthase, subunit E archaeal/vacuolar-type H+-transporting ATP synthase, subunit E archaeal/vacuolar-type H+-transporting ATP synthase, subunit E archaeal/vacuolar-type H+-transporting ATP synthase, subunit K predicted unusual protein kinase,	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198 MSM0313 MSM0434 MSM0435 MSM0435 MSM0436 MSM0437 MSM0438	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit C archaeal/vacuolar-type H+-transporting ATP synthase, subunit E archaeal/vacuolar-type H+-transporting ATP synthase, subunit E archaeal/vacuolar-type H+-transporting ATP synthase, subunit K predicted unusual protein kinase, ubiquinone biosynthesis protein-related,	GO:0006796 - phosphate metabolism	
	MSM1764 MSM1765 <i>M. smithii</i> genes MSM0060 MSM0198 MSM0313 MSM0434 MSM0435 MSM0435 MSM0436 MSM0437 MSM0438	polymerase, subunit M, RpoM conserved hypothetical protein conserved hypothetical protein  Annotation  Annotation  predicted archaeal kinase (GHMP kinase family) inorganic pyrophosphatase [NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB archaeal/vacuolar-type H+-transporting ATP synthase, subunit D archaeal/vacuolar-type H+-transporting ATP synthase, subunit B archaeal/vacuolar-type H+-transporting ATP synthase, subunit A archaeal/vacuolar-type H+-transporting ATP synthase, subunit F archaeal/vacuolar-type H+-transporting ATP synthase, subunit C archaeal/vacuolar-type H+-transporting ATP synthase, subunit E archaeal/vacuolar-type H+-transporting ATP synthase, subunit E archaeal/vacuolar-type H+-transporting ATP synthase, subunit E archaeal/vacuolar-type H+-transporting ATP synthase, subunit K predicted unusual protein kinase,	GO:0006796 - phosphate metabolism	

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	MSM0835	archaeal shikimate kinase	
	MSM0842	histone acetyltransferase, radical SAM	
		superfamily	
	MSM0848	predicted archaeal sugar kinase, GHMP	
		kinase family	
	MSM0952	serine/threonine protein kinase, RIO1	
		family	
	MSM0988	phosphoenolpyruvate synthase, PpsA	
	MSM1000	methyl viologen-reducing hydrogenase,	
		gamma subunit, MvhG	
	MSM1064	energy-converting hydrogenase B,	
		subunit M, EhbM	
	MSM1071	energy-converting hydrogenase B,	
	140144070	subunit F, EhbF	
	MSM1072	energy-converting hydrogenase B,	
	140144400	subunit E, EhbE	
	MSM1122	coenzyme F420-reducing hydrogenase,	
	MSM1198	gamma subunit, FrhG O-sialoglycoprotein endopeptidase	
	IIVIOIVI I 190	IO-sialogiveobrolein engobebligase	
	MSM1424	polyphosphate kinase, ppk	
DECOMPINATION	MSM1424 MSM1439	polyphosphate kinase, ppk mevalonate kinase	
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i>	polyphosphate kinase, ppk	0 - ion
RECOMBINATION	MSM1424 MSM1439	polyphosphate kinase, ppk mevalonate kinase	310 - , iation
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i>	polyphosphate kinase, ppk mevalonate kinase	06310 - NA bination
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i>	polyphosphate kinase, ppk mevalonate kinase	:0006310 - DNA mbination
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i>	polyphosphate kinase, ppk mevalonate kinase	3O:0006310 - DNA combination
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i> genes	polyphosphate kinase, ppk mevalonate kinase Annotation	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 M. smithii genes	polyphosphate kinase, ppk mevalonate kinase Annotation  integrase-recombinase protein	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i> genes	polyphosphate kinase, ppk mevalonate kinase Annotation  integrase-recombinase protein integrase-recombinase protein, phage	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 M. smithii genes MSM0002 MSM0428	polyphosphate kinase, ppk mevalonate kinase  Annotation  integrase-recombinase protein integrase-recombinase protein, phage integrase family	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 M. smithii genes MSM0002 MSM0428 MSM0611	polyphosphate kinase, ppk mevalonate kinase  Annotation  integrase-recombinase protein integrase-recombinase protein, phage integrase family DNA repair protein, RadB	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 M. smithii genes MSM0002 MSM0428 MSM0611 MSM0645	polyphosphate kinase, ppk mevalonate kinase  Annotation  integrase-recombinase protein integrase-recombinase protein, phage integrase family DNA repair protein, RadB ATP-dependent DNA ligase, Cdc9	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 <b>M. smithii</b> genes MSM0002 MSM0428 MSM0641 MSM0645 MSM1333	polyphosphate kinase, ppk mevalonate kinase  Annotation  integrase-recombinase protein integrase-recombinase protein, phage integrase family DNA repair protein, RadB ATP-dependent DNA ligase, Cdc9 DNA repair protein RadA, RadA	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i> genes MSM0002 MSM0428 MSM0641 MSM0645 MSM1333 MSM1523	polyphosphate kinase, ppk mevalonate kinase  Annotation  integrase-recombinase protein integrase-recombinase protein, phage integrase family DNA repair protein, RadB ATP-dependent DNA ligase, Cdc9 DNA repair protein RadA, RadA transposase	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 <b>M. smithii</b> genes MSM0002 MSM0428 MSM0641 MSM0645 MSM1333	polyphosphate kinase, ppk mevalonate kinase  Annotation  integrase-recombinase protein integrase-recombinase protein, phage integrase family DNA repair protein, RadB ATP-dependent DNA ligase, Cdc9 DNA repair protein RadA, RadA transposase DNA intergrase/recombinase, phage	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i> genes MSM0002 MSM0428 MSM0641 MSM0645 MSM1333 MSM1523 MSM1640	polyphosphate kinase, ppk mevalonate kinase  Annotation  integrase-recombinase protein integrase-recombinase protein, phage integrase family  DNA repair protein, RadB  ATP-dependent DNA ligase, Cdc9  DNA repair protein RadA, RadA transposase  DNA intergrase/recombinase, phage integrase family	GO:0006310 - DNA recombination
RECOMBINATION	MSM1424 MSM1439 <i>M. smithii</i> genes MSM0002 MSM0428 MSM0641 MSM0645 MSM1333 MSM1523	polyphosphate kinase, ppk mevalonate kinase  Annotation  integrase-recombinase protein integrase-recombinase protein, phage integrase family DNA repair protein, RadB ATP-dependent DNA ligase, Cdc9 DNA repair protein RadA, RadA transposase DNA intergrase/recombinase, phage	GO:0006310 - DNA recombination