Supplementary Table 1. Similar MHC-I restricted BCG-Pasteur T cell epitopes and SARS-CoV-2 T cell epitopes.

HLA SUPERTYPE	BCG PROTEIN ID	BCG PROTEIN NAME	BCG PEPTIDE	%RANK	IDENTITY %	SARS2 PEPTIDE	SARS2 PROTEIN NAME
A02	WP_003405938.1	CPBP family intramembrane metalloprotease [Mycobacterium]	LLLAGIFGV	0,01	0,778	LLSAGIFGA	nsp03
A02	WP_003898761.1	RND transporter MmpL10 [Mycobacterium]	LLSAMIAGA	0,4	0,778	LLSAGIFGA	nsp03
A02	WP_003409205.1	TetR/AcrR family transcriptional regulator [Mycobacterium]	LLWAGVVGA	0,12	0,667	LLSAGIFGA	nsp03
A02	WP_003405320.1	potassium-transporting ATPase subunit KdpB [Mycobacterium]	ILSAVIFNA	0,15	0,667	LLSAGIFGA	nsp03
A02	WP_003898666.1	DUF5134 domain-containing protein [Mycobacterium]	LLAAVWFGA	0,25	0,667	LLSAGIFGA	nsp03
A02	WP_003404651.1	NAD(P)/FAD-dependent oxidoreductase [Mycobacterium]	LLSAGITDV	0,3	0,667	LLSAGIFGA	nsp03
A02	WP_011799295.1	MATE family efflux transporter [Mycobacterium]	LLAAGILAA	0,3	0,667	LLSAGIFGA	nsp03
A02	WP_011799269.1	LuxR family transcriptional regulator [Mycobacterium tuberculosis]	LLLADIEGA	0,5	0,667	LLSAGIFGA	nsp03
A02	WP_011799327.1	UPF0182 family protein [Mycobacterium]	LLSSLIVGA	0,5	0,667	LLSAGIFGA	nsp03
A02	WP_010950362.1	molybdopterin-dependent oxidoreductase [Mycobacterium]	YIFGFSFYT	0,03	0,667	YIFFASFYY	nsp03
A02	WP_010950933.1	radical SAM protein [Mycobacterium]	RLLNVEDYL	0,4	0,667	FLLNKEMYL	nsp04
A02	WP_003414826.1	DivIVA domain-containing protein [Mycobacterium]	FLNGTLRSV	0,17	0,667	FLNGSCGSV	nsp05
A02	WP_003900470.1	hypothetical protein [Mycobacterium]	ALDRFTTAL	0,5	0,667	FLNRFTTTL	nsp05
A02	WP_003404603.1	DUF2530 domain-containing protein [Mycobacterium]	ALAWLVAAV	0,1	0,778	VLAWLYAAV	nsp05
A02	WP_003404552.1	molybdenum cofactor biosynthesis protein MoaE [Mycobacterium]	VLADLVAEV	0,01	0,667	VLAWLYAAV	nsp05
A02	WP_003404690.1	response regulator transcription factor [Mycobacterium]	VLAELVARV	0,06	0,667	VLAWLYAAV	nsp05
A02	WP_010950935.1	ABC transporter substrate-binding protein [Mycobacterium]	GLAELNAAV	0,09	0,667	VLAWLYAAV	nsp05
A02	WP_010950412.1	hypothetical protein [Mycobacterium]	VLAALVVAV	0,09	0,667	VLAWLYAAV	nsp05
A02	WP_003904964.1	phthiocerol type I polyketide synthase PpsE [Mycobacterium]	TLASLTAAV	0,12	0,667	VLAWLYAAV	nsp05
A02	WP_011799239.1	DEAD/DEAH box helicase [Mycobacterium]	SLADDYAAV	0,12	0,667	VLAWLYAAV	nsp05
A02	WP_010950812.1	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA [Mycobacterium]	VLASFEAAV	0,15	0,667	VLAWLYAAV	nsp05

A02	WP_003419534.1	membrane protein [Mycobacterium]	VLLALWAAV	0,15	0,667	VLAWLYAAV	nsp05
A02	WP_010950811.1	sorbosone dehydrogenase family protein [Mycobacterium]	GLAALCAAV	0,15	0,667	VLAWLYAAV	nsp05
A02	WP_003408868.1	type VII secretion system ESX-5 AAA family ATPase EccA5 [Mycobacterium]	SLACAYAAV	0,2	0,667	VLAWLYAAV	nsp05
A02	WP_003418931.1	LppP/LprE family lipoprotein [Mycobacterium]	VLACVAAAV	0,25	0,667	VLAWLYAAV	nsp05
A02	WP_003405305.1	two-component system response regulator KdpE [Mycobacterium]	FLARLRAAV	0,3	0,667	VLAWLYAAV	nsp05
A02	WP_003900438.1	acyl-CoA dehydrogenase [Mycobacterium]	GLAWCYARV	0,3	0,667	VLAWLYAAV	nsp05
A02	WP_003417969.1	hypothetical protein [Mycobacterium]	NLADLYDAV	0,3	0,667	VLAWLYAAV	nsp05
A02	WP_003408868.1	type VII secretion system ESX-5 AAA family ATPase EccA5 [Mycobacterium]	VLAGAWAAV	0,4	0,667	VLAWLYAAV	nsp05
A02	WP_003899297.1	non-ribosomal peptide synthetase [Mycobacterium]	VLCELAAAV	0,4	0,667	VLAWLYAAV	nsp05
A02	WP_003899010.1	hypothetical protein [Mycobacterium]	VLLILLAAV	0,4	0,667	VLAWLYAAV	nsp05
A02	WP_003901785.1	UPF0182 family protein [Mycobacterium]	VLNWLFVAV	0,4	0,667	VLAWLYAAV	nsp05
A02	WP_003400368.1	serine/threonine phosphatase PstP [Mycobacterium]	LLAKLDAAV	0,5	0,667	VLAWLYAAV	nsp05
A02	WP_003401597.1	L,D-transpeptidase [Mycobacterium]	LLALLCAAV	0,5	0,667	VLAWLYAAV	nsp05
A02	WP_003419582.1	hypothetical protein [Mycobacterium]	LLAWLTAAA	0,5	0,667	VLAWLYAAV	nsp05
A02	WP_003401206.1	hypothetical protein [Mycobacterium]	VLARMAAAV	0,5	0,667	VLAWLYAAV	nsp05
A02	WP_003899696.1	arabinosyltransferase EmbA [Mycobacterium]	VLAVLVAMV	0,5	0,667	VLAWLYAAV	nsp05
A02	WP_003401224.1	acyl dehydratase [Mycobacterium]	RLLPNLATV	0,08	0,778	FLLPSLATV	nsp06
A02	WP_003419517.1	type III pantothenate kinase [Mycobacterium]	LLLPELHTV	0,03	0,667	FLLPSLATV	nsp06
A02	WP_003417121.1	carbonic anhydrase [Mycobacterium]	LLLPRLTTV	0,07	0,667	FLLPSLATV	nsp06
A02	WP_003419324.1	nitronate monooxygenase [Mycobacterium]	FLLTSDSTV	0,12	0,667	FLLPSLATV	nsp06
A02	WP_003898943.1	calcium:proton antiporter [Mycobacterium]	VVLPSLAFV	0,25	0,667	FLLPSLATV	nsp06
A02	WP_003408160.1	bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ [Mycobacterium]	MLAPSLATM	0,25	0,667	FLLPSLATV	nsp06
A02	WP_003405914.1	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Mycobacterium]	TLLGSAATV	0,5	0,667	FLLPSLATV	nsp06
A02	WP_003405914.1	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Mycobacterium]	TLLGSAATV	0,5	0,667	FLLPSLATV	nsp06

B27	WP_003405912.1	DUF3556 domain-containing protein [Mycobacterium]	FRAMNSHGR	0,25	0,667	FRYMNSQGL	nsp06
A03	WP_010950426.1	(3R)-hydroxyacyl-ACP dehydratase subunit HadB [Mycobacterium]	ALREFSSVK	0,08	0,667	ALRANSAVK	nsp08
A03	WP_003898564.1	signal peptide peptidase SppA [Mycobacterium]	AIAAFSAVK	0,15	0,667	ALRANSAVK	nsp08
A03	WP_003408360.1	alpha/beta fold hydrolase [Mycobacterium]	ALRANGIPK	0,2	0,667	ALRANSAVK	nsp08
A02	WP_003408148.1	phenylalanine--tRNA ligase subunit beta [Mycobacterium]	ALFAIAQVV	0,4	0,667	ALWEIQQVV	nsp08
A02	WP_003410018.1	Cd(II)/Pb(II)-sensing metalloregulatory transcriptional regulator CmtR [Mycobacterium]	ALGELVQVV	0,5	0,667	ALWEIQQVV	nsp08
A03	WP_011799303.1	AMP-binding protein [Mycobacterium]	ATVYVATSK	0,5	0,667	ATVVIGTSK	nsp12
A02	WP_010950383.1	isoniazid-induced protein IniA [Mycobacterium]	FVDDISFVV	0,03	0,667	FVDGVPFVV	nsp12
A01	WP_010950383.1	isoniazid-induced protein IniA [Mycobacterium]	FVDDISFVV	0,5	0,667	FVDGVPFVV	nsp12
A01	WP_003901660.1	acyl-CoA synthetase [Mycobacterium tuberculosis complex]	GSDQDYRRY	0,3	0,667	ISDYDYYRY	nsp12
A02	WP_003399771.1	hypothetical protein [Mycobacterium]	LLAPILTPV	0,01	0,667	LLMPILTLT	nsp12
A02	WP_003412229.1	HlyC/CorC family transporter [Mycobacterium]	LLMPISRLL	0,3	0,667	LLMPILTLT	nsp12
A02	WP_003900282.1	mannosyltransferase [Mycobacterium]	RILGWGWLV	0,1	0,667	RILGAGCFV	nsp12
A02	WP_003420798.1	UDP-galactopyranose mutase [Mycobacterium]	RTLDFEVEV	0,5	0,667	RQLLFVVEV	nsp12
A02	WP_003898943.1	calcium:proton antiporter [Mycobacterium]	VLFLFTQTV	0,25	0,667	ILGLPTQTV	nsp13
B07	WP_003405136.1	polyprenyl-diphosphate synthase GrcC [Mycobacterium]	QPRRALATL	0,02	0,667	IPRRNVATL	nsp13
B07	WP_003402286.1	DUF5078 domain-containing protein [Mycobacterium]	IPRRMIATT	0,17	0,667	IPRRNVATL	nsp13
B07	WP_010950351.1	PE-PPE domain-containing protein [Mycobacterium]	IPGLNVTTL	0,4	0,667	IPRRNVATL	nsp13
A02	WP_003419780.1	RDD family protein [Mycobacterium]	IIFTVLALV	0,3	0,667	IVDTVSALV	nsp13
A03	WP_003416363.1	two-component system sensor histidine kinase DevS [Mycobacterium]	RLVAAEALK	0,4	0,667	KLFAAETLK	nsp13
A03	WP_003416868.1	hypothetical protein [Mycobacterium]	VVYRVTGTK	0,02	0,667	VVYRGTTTY	nsp13
B58	WP_003413866.1	class I SAM-dependent methyltransferase [Mycobacterium]	ITYLGTTTY	0,4	0,667	VVYRGTTTY	nsp13
A02	WP_003916382.1	phospholipase C [Mycobacterium tuberculosis]	YLLADAFTV	0,01	0,667	ALLADKFPV	nsp14

A02	WP_011799332.1	phosphate signaling complex protein PhoU [Mycobacterium]	ALLALQHPV	0,03	0,667	ALLADKFPV	nsp14
A02	WP_010950533.1	SpoIIE family protein phosphatase [Mycobacterium]	ALLAASVPV	0,04	0,667	ALLADKFPV	nsp14
A02	WP_003418021.1	chaperonin GroEL [Mycobacterium]	ALLASATPV	0,06	0,667	ALLADKFPV	nsp14
A02	WP_003419701.1	ABC transporter permease [Mycobacterium]	AVLAHAFPV	0,12	0,667	ALLADKFPV	nsp14
A02	WP_003401260.1	acyltransferase [Mycobacterium]	AALAMVFPV	0,2	0,667	ALLADKFPV	nsp14
A02	WP_010950697.1	NAD-dependent malic enzyme [Mycobacterium]	ALLATGSPV	0,3	0,667	ALLADKFPV	nsp14
B58	WP_003400151.1	thioredoxin-disulfide reductase [Mycobacterium]	TTLPVTGVF	0,4	0,667	TTLPVNVAF	nsp15
B58	WP_011799375.1	polyketide synthase Pks13 [Mycobacterium]	VTLSVAVAF	0,4	0,667	TTLPVNVAF	nsp15
A03	WP_011799327.1	UPF0182 family protein [Mycobacterium]	KVQRMLLAK	0,17	0,778	KMQRMLLEK	nsp16
A02	WP_010950818.1	phosphoserine phosphatase SerB [Mycobacterium]	TLAGLPATV	0,3	0,667	TLIGDCATV	nsp16
A02	WP_003900824.1	dihydroxy-acid dehydratase [Mycobacterium]	LLHGDCLTV	0,5	0,667	TLIGDCATV	nsp16
A02	WP_003406937.1	DUF3817 domain-containing protein [Mycobacterium]	LLLTLNLAV	0,08	0,667	YLNTLTLAV	nsp16
A02	WP_071854213.1	thiol reductant ABC exporter subunit CydD [Mycobacterium]	YLPTLLLAA	0,25	0,667	YLNTLTLAV	nsp16
A02	WP_003409281.1	HlyC/CorC family transporter [Mycobacterium]	LLHTLSLAV	0,4	0,667	YLNTLTLAV	nsp16
A02	WP_003401670.1	glucose-1-phosphate thymidylyltransferase RfbA [Mycobacterium]	YLNQGRLAV	0,5	0,667	YLNTLTLAV	nsp16
B44	WP_003414292.1	type III-A CRISPR-associated RAMP protein Csm3 [Mycobacterium]	IEITGTLTV	0,2	0,667	SEETGTLIV	orf4
B44	WP_003407194.1	HNH endonuclease [Mycobacterium]	SEWRATLIV	0,5	0,667	SEETGTLIV	orf4
B44	WP_003416051.1	HNH endonuclease [Mycobacterium]	SEWRATLIV	0,5	0,667	SEETGTLIV	orf4
A24	WP_003409492.1	DUF4389 domain-containing protein [Mycobacterium]	RYPIGLYNL	0,06	0,667	RYRIGNYKL	orf5
A02	WP_003399839.1	type VII secretion system ESX-1 adaptor EspG1 [Mycobacterium]	HLVDFPVTL	0,4	0,778	HLVDFQVTI	orf6
A02	WP_003414861.1	phthiocerol dimycocerosate RND transporter MmpL7 [Mycobacterium]	SLVDSQVTV	0,2	0,667	HLVDFQVTI	orf6
A02	WP_011799123.1	arylsulfatase AtsA [Mycobacterium]	KLFCRMAEV	0,03	0,667	KLFIRQEEV	orf7a
A02	WP_010950867.1	arylsulfatase AtsB [Mycobacterium]	RLFARQMEV	0,09	0,667	KLFIRQEEV	orf7a
A02	WP_003403680.1	30S ribosomal protein S5 [Mycobacterium]	KLLQRPEEV	0,5	0,667	KLFIRQEEV	orf7a

A02	WP_003900222.1	alpha-keto acid decarboxylase family protein [Mycobacterium]	YLLDRLAEL	0,01	0,667	LLLDRLNQL	orf9
A02	WP_003413979.1	TerC/Alx family metal homeostasis membrane protein [Mycobacterium]	GLLDRLVYL	0,03	0,667	LLLDRLNQL	orf9
A02	WP_003899091.1	epoxide hydrolase EphB [Mycobacterium]	LLLDFLGGL	0,1	0,667	LLLDRLNQL	orf9
A02	WP_003402126.1	thiazole synthase [Mycobacterium]	GLLDLLNRL	0,12	0,667	LLLDRLNQL	orf9
A02	WP_003401905.1	ATP-dependent chaperone ClpB [Mycobacterium]	RLLDRLPQA	0,25	0,667	LLLDRLNQL	orf9
A02	WP_003406680.1	ATP synthase subunit I [Mycobacterium]	LLLGLLNAL	0,25	0,667	LLLDRLNQL	orf9
A02	WP_003417269.1	succinate dehydrogenase hydrophobic membrane anchor subunit [Mycobacterium]	LLLLWLAQL	0,4	0,667	LLLDRLNQL	orf9
A02	WP_011799223.1	NAD(P)/FAD-dependent oxidoreductase [Mycobacterium]	FIAWLIWLV	0,01	0,667	FIAGLIAIV	sg
A02	WP_003404792.1	phosphate ABC transporter permease subunit PstC [Mycobacterium]	FIAHHIAPV	0,01	0,667	FIAGLIAIV	sg
A02	WP_003417126.1	5-(carboxyamino)imidazole ribonucleotide synthase [Mycobacterium]	FIAPLVAMV	0,06	0,667	FIAGLIAIV	sg
A02	WP_010950360.1	AI-2E family transporter [Mycobacterium]	FIAGLPHLV	0,07	0,667	FIAGLIAIV	sg
A02	WP_003417121.1	carbonic anhydrase [Mycobacterium]	IIAGVIAAV	0,25	0,667	FIAGLIAIV	sg
A02	WP_003414049.1	ribonuclease J [Mycobacterium]	RLDDIEALV	0,1	0,667	RLDKVEAEV	sg
A02	WP_010950704.1	non-ribosomal peptide synthetase [Mycobacterium]	RLDAVLAAV	0,12	0,667	RLDKVEAEV	sg
A02	WP_003399801.1	PHP domain-containing protein [Mycobacterium]	RLDIVVASV	0,5	0,667	RLDKVEAEV	sg
A02	WP_003418013.1	sigma-70 family RNA polymerase sigma factor [Mycobacterium]	RLDAVVAEA	0,5	0,667	RLDKVEAEV	sg
A02	WP_003400124.1	NUDIX hydrolase [Mycobacterium]	RLAEVADEL	0,5	0,667	RLNEVAKNL	sg
A02	WP_010950939.1	arabinosyltransferase EmbB [Mycobacterium]	ALGSLVTYV	0,09	0,667	RLQSLQTYV	sg
A02	WP_003412516.1	glutamate-5-semialdehyde dehydrogenase [Mycobacterium]	RLASLPTTV	0,25	0,667	RLQSLQTYV	sg
A01	WP_003898438.1	glucose-6-phosphate dehydrogenase (coenzyme-F420) [Mycobacterium]	RVDFDGDYY	0,08	0,667	RVDFCGKGY	sg

Supplementary Table 2. Similar BCG-Pasteur B cell epitopes and SARS-CoV-2 B cell epitopes

BCG PROTEIN ID	BCG PROTEIN NAME	BCG PEPTIDE	IDENTITY %	SARS-CoV-2 PEPTIDE	SARS-CoV-2 PROTEIN
WP_003400657.1	winged helix-turn-helix transcriptional regulator [Mycobacterium]	DVGLESSN	0,625	DVNLHSSR	nsp12
WP_003402848.1	cytochrome c biogenesis protein [Mycobacterium]	DGTLLSSR	0,625	DVNLHSSR	nsp12
WP_003405138.1	hypothetical protein [Mycobacterium]	DVRLLGSR	0,625	DVNLHSSR	nsp12
WP_003407587.1	methylmalonyl-CoA mutase [Mycobacterium]	GVPLHSER	0,625	DVNLHSSR	nsp12
WP_003410763.1	RNA helicase [Mycobacterium]	DPELESSR	0,625	DVNLHSSR	nsp12
WP_003413852.1	N-acetyltransferase [Mycobacterium]	DANLSSAR	0,625	DVNLHSSR	nsp12
WP_003414837.1	phthiocerol type I polyketide synthase PpsC [Mycobacterium tuberculosis complex]	VVNLDSSG	0,625	DVNLHSSR	nsp12
WP_003898437.1	MBL fold metallo-hydrolase [Mycobacterium]	DVALRSWR	0,625	DVNLHSSR	nsp12
WP_003901219.1	phenylalanine--tRNA ligase subunit alpha [Mycobacterium]	DVTLPSTR	0,625	DVNLHSSR	nsp12
WP_011799224.1	NAD(P)H-binding protein [Mycobacterium]	DGNLASIR	0,625	DVNLHSSR	nsp12
WP_010950852.1	sensor histidine kinase [Mycobacterium tuberculosis]	RVKN	1	RVKN	orf4
WP_010950950.1	type VII secretion system ESX-1 AAA family ATPase EccA1 [Mycobacterium]	RVKN	1	RVKN	orf4
WP_003400000.1	type VII secretion system ESX-1 subunit EccE1 [Mycobacterium]	RVGN	0,75	RVKN	orf4
WP_003400344.1	cell division protein CrgA [Mycobacterium]	RKKN	0,75	RVKN	orf4
WP_003400514.1	DUF2029 domain-containing protein [Mycobacterium]	RVAN	0,75	RVKN	orf4
WP_003400665.1	class I SAM-dependent methyltransferase [Mycobacterium]	RVKG	0,75	RVKN	orf4
WP_003400974.1	aldehyde dehydrogenase family protein [Mycobacterium]	RVKA	0,75	RVKN	orf4
WP_003401230.1	hypothetical protein [Mycobacterium]	RFKN	0,75	RVKN	orf4
WP_003401858.1	hypothetical protein [Mycobacterium]	RVRN	0,75	RVKN	orf4
WP_003401912.1	LuxR family transcriptional regulator [Mycobacterium]	RVAN	0,75	RVKN	orf4
WP_003401912.1	LuxR family transcriptional regulator [Mycobacterium]	RVDN	0,75	RVKN	orf4
WP_003402272.1	membrane protein [Mycobacterium]	RVSN	0,75	RVKN	orf4
WP_003402316.1	isocitrate lyase [Mycobacterium]	RTKN	0,75	RVKN	orf4
WP_003402886.1	DUF2064 domain-containing protein [Mycobacterium]	RVKT	0,75	RVKN	orf4
WP_003403453.1	30S ribosomal protein S12 [Mycobacterium]	RVKD	0,75	RVKN	orf4
WP_003403453.1	30S ribosomal protein S12 [Mycobacterium]	GVKN	0,75	RVKN	orf4
WP_003403827.1	helix-turn-helix domain-containing protein [Mycobacterium]	RVLN	0,75	RVKN	orf4
WP_003404293.1	sulfurtransferase [Mycobacterium tuberculosis complex]	NVKN	0,75	RVKN	orf4
WP_003404631.1	FAD-dependent oxidoreductase [Mycobacterium]	RVRN	0,75	RVKN	orf4
WP_003405183.1	methionine--tRNA ligase [Mycobacterium]	RVPN	0,75	RVKN	orf4
WP_003405263.1	ribose-phosphate diphosphokinase [Mycobacterium]	RVPN	0,75	RVKN	orf4
WP_003405328.1	response regulator transcription factor [Mycobacterium]	RVWN	0,75	RVKN	orf4

WP_003406182.1	PadR family transcriptional regulator [Mycobacterium]	RVKS	0,75	RVKN	orf4
WP_003406196.1	AMP-binding protein [Mycobacterium]	RVKD	0,75	RVKN	orf4
WP_003406257.1	RNA polymerase sigma factor SigE [Mycobacterium]	RVGN	0,75	RVKN	orf4
WP_003406553.1	response regulator transcription factor EmbR [Mycobacterium]	RVKT	0,75	RVKN	orf4
WP_003406598.1	oxidoreductase [Mycobacterium]	RDKN	0,75	RVKN	orf4
WP_003406602.1	ABC transporter ATP-binding protein [Mycobacterium]	RVKT	0,75	RVKN	orf4
WP_003406621.1	adenylyl-sulfate kinase [Mycobacterium]	RPKN	0,75	RVKN	orf4
WP_003406897.1	alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase [Mycobacterium]	RVKP	0,75	RVKN	orf4
WP_003407308.1	bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD [Mycobacterium]	RVLN	0,75	RVKN	orf4
WP_003408165.1	ornithine carbamoyltransferase [Mycobacterium]	RVKP	0,75	RVKN	orf4
WP_003409271.1	malate synthase G [Mycobacterium]	RVLN	0,75	RVKN	orf4
WP_003409667.1	serine hydrolase [Mycobacterium]	RVGN	0,75	RVKN	orf4
WP_003410042.1	NAD(P)/FAD-dependent oxidoreductase [Mycobacterium]	AVKN	0,75	RVKN	orf4
WP_003410624.1	30S ribosomal protein S14 [Mycobacterium]	IVKN	0,75	RVKN	orf4
WP_003410735.1	protein kinase [Mycobacterium tuberculosis complex]	DVKN	0,75	RVKN	orf4
WP_003410775.1	YafY family transcriptional regulator [Mycobacterium]	RDKN	0,75	RVKN	orf4
WP_003411124.1	type II toxin-antitoxin system RelE/ParE family toxin [Mycobacterium]	RVHN	0,75	RVKN	orf4
WP_003412005.1	ThiF family adenylyltransferase [Mycobacterium]	RVKE	0,75	RVKN	orf4
WP_003412005.1	ThiF family adenylyltransferase [Mycobacterium]	RVKR	0,75	RVKN	orf4
WP_003412298.1	nitrite/sulfite reductase [Mycobacterium]	RLKN	0,75	RVKN	orf4
WP_003412557.1	HAMP domain-containing protein [Mycobacterium]	RHKN	0,75	RVKN	orf4
WP_003412717.1	wax ester/triacylglycerol synthase family O-acyltransferase [Mycobacterium]	RVLN	0,75	RVKN	orf4
WP_003413373.1	lipoprotein [Mycobacterium]	RVNN	0,75	RVKN	orf4
WP_003414006.1	intein-containing recombinase RecA [Mycobacterium]	RVKV	0,75	RVKN	orf4
WP_003414006.1	intein-containing recombinase RecA [Mycobacterium]	VVKN	0,75	RVKN	orf4
WP_003414919.1	rhamnosyl O-methyltransferase [Mycobacterium]	RLKN	0,75	RVKN	orf4
WP_003415170.1	PH domain-containing protein [Mycobacterium]	RVPN	0,75	RVKN	orf4
WP_003416369.1	two-component system response regulator DevR [Bacteria]	TVKN	0,75	RVKN	orf4
WP_003416607.1	flavin monoamine oxidase family protein [Mycobacterium]	DVKN	0,75	RVKN	orf4
WP_003417288.1	class I SAM-dependent methyltransferase [Mycobacterium]	RVKP	0,75	RVKN	orf4
WP_003419304.1	steroid C26-monooxygenase Cyp125 [Mycobacterium]	RFKN	0,75	RVKN	orf4

WP_003420624.1	nucleoside diphosphate kinase regulator [Mycobacterium]	EVKN	0,75	RVKN	orf4
WP_003898475.1	DUF2993 domain-containing protein [Mycobacterium]	RLKN	0,75	RVKN	orf4
WP_003898507.1	hypothetical protein [Mycobacterium]	REKN	0,75	RVKN	orf4
WP_003898557.1	mycofactocin biosynthesis FMN-dependent deaminase MftD [Mycobacterium]	RVPN	0,75	RVKN	orf4
WP_003898651.1	phosphate ABC transporter permease PstA [Mycobacterium]	RIKN	0,75	RVKN	orf4
WP_003898655.1	ATP-dependent DNA ligase [Mycobacterium]	RLKN	0,75	RVKN	orf4
WP_003898889.1	iron-regulated aconitate hydratase Acn [Mycobacterium]	RVSN	0,75	RVKN	orf4
WP_003898889.1	iron-regulated aconitate hydratase Acn [Mycobacterium]	RVKS	0,75	RVKN	orf4
WP_003898998.1	protein kinase [Mycobacterium]	RVLN	0,75	RVKN	orf4
WP_003899482.1	transposase [Mycobacterium]	TVKN	0,75	RVKN	orf4
WP_003899505.1	translation initiation factor IF-2 [Mycobacterium]	RVGN	0,75	RVKN	orf4
WP_003899528.1	30S ribosomal protein S2 [Mycobacterium]	REKN	0,75	RVKN	orf4
WP_003899536.1	amidohydrolase family protein [Mycobacterium]	RVLN	0,75	RVKN	orf4
WP_003899637.1	metallophosphoesterase [Mycobacterium]	RLKN	0,75	RVKN	orf4
WP_003899711.1	acyltransferase PapA1 [Mycobacterium]	RVGN	0,75	RVKN	orf4
WP_003900225.1	MFS transporter [Mycobacterium]	EVKN	0,75	RVKN	orf4
WP_003900449.1	type II toxin-antitoxin system RelE/ParE family toxin [Mycobacterium]	RHKN	0,75	RVKN	orf4
WP_003900487.1	acyl-CoA carboxylase subunit beta [Mycobacterium]	RHKN	0,75	RVKN	orf4
WP_003900516.1	elongation factor 4 [Mycobacterium]	RVTN	0,75	RVKN	orf4
WP_003900556.1	Si-specific NAD(P)(+) transhydrogenase [Mycobacterium]	RVKD	0,75	RVKN	orf4
WP_003900633.1	GTP 3',8-cyclase MoaA [Mycobacterium]	RVKD	0,75	RVKN	orf4
WP_003900842.1	PecA family PE domain-processing aspartic protease [Mycobacterium]	RVEN	0,75	RVKN	orf4
WP_003900945.1	exopolyphosphatase Ppx1 [Mycobacterium]	RVKR	0,75	RVKN	orf4
WP_003901420.1	type I polyketide synthase [Mycobacterium]	RVKL	0,75	RVKN	orf4
WP_003901420.1	type I polyketide synthase [Mycobacterium]	RVKK	0,75	RVKN	orf4
WP_003909568.1	cobalt-precorrin-6A reductase [Mycobacterium]	RVPN	0,75	RVKN	orf4
WP_003909645.1	hypothetical protein [Mycobacterium]	RRKN	0,75	RVKN	orf4
WP_003910893.1	Pup--protein ligase [Mycobacterium tuberculosis complex]	RVKR	0,75	RVKN	orf4
WP_010950580.1	biotin carboxylase [Mycobacterium]	RVLN	0,75	RVKN	orf4
WP_010950586.1	hypothetical protein [Mycobacterium]	RVGN	0,75	RVKN	orf4
WP_010950675.1	DUF4191 domain-containing protein [Mycobacterium]	RVKP	0,75	RVKN	orf4
WP_010950826.1	ferredoxin--NADP(+) reductase FprA [Mycobacterium]	RVKL	0,75	RVKN	orf4
WP_010950934.1	wax ester/triacylglycerol synthase family O-acyltransferase [Mycobacterium]	RVKA	0,75	RVKN	orf4

WP_010950955.1	type VII secretion system ESX-2 subunit EccE2 [Mycobacterium]	RRKN	0,75	RVKN	orf4
WP_011799147.1	sensor histidine kinase KdpD [Mycobacterium]	RVKV	0,75	RVKN	orf4
WP_011799175.1	fatty acid desaturase [Mycobacterium]	RVFN	0,75	RVKN	orf4
WP_011799190.1	RND transporter MmpL12 [Mycobacterium]	RVKG	0,75	RVKN	orf4
WP_011799239.1	DEAD/DEAH box helicase [Mycobacterium]	RVDN	0,75	RVKN	orf4
WP_011799254.1	tRNA-dependent cyclodipeptide synthase [Mycobacterium]	AVKN	0,75	RVKN	orf4
WP_011799261.1	non-ribosomal peptide synthetase [Mycobacterium]	RVKI	0,75	RVKN	orf4
WP_011799262.1	Rv2407 family type 3 sulfatase [Mycobacterium]	RVKD	0,75	RVKN	orf4
WP_011799328.1	hypothetical protein [Mycobacterium]	RVKP	0,75	RVKN	orf4
WP_011799364.1	type I DNA topoisomerase [Mycobacterium]	KVKN	0,75	RVKN	orf4
WP_011799375.1	polyketide synthase Pks13 [Mycobacterium]	RIKN	0,75	RVKN	orf4
WP_011799379.1	type I polyketide synthase [Mycobacterium]	RVLN	0,75	RVKN	orf4
WP_015385278.1	CoA transferase [Mycobacterium]	RPKN	0,75	RVKN	orf4
WP_015385278.1	CoA transferase [Mycobacterium]	RVAN	0,75	RVKN	orf4
WP_031652105.1	DNA topoisomerase (ATP-hydrolyzing) subunit B [Mycobacterium]	RTKN	0,75	RVKN	orf4
WP_003402308.1	helix-turn-helix domain-containing protein [Mycobacterium]	FTSAESRT	0,625	ITVATSRT	orf5
WP_003404801.1	MBL fold metallo-hydrolase [Mycobacterium]	QTVRTSGT	0,625	ITVATSRT	orf5
WP_003406283.1	DUF1003 domain-containing protein [Mycobacterium]	YTPRTSRT	0,625	ITVATSRT	orf5
WP_003408781.1	DUF4407 domain-containing protein [Mycobacterium]	ETEAASRT	0,625	ITVATSRT	orf5
WP_003408797.1	type VII secretion system ESX-5 subunit EccB5 [Mycobacterium]	DTVATSSS	0,625	ITVATSRT	orf5
WP_003410152.1	two-component system sensor histidine kinase DosT [Mycobacterium]	MTVAVSGT	0,625	ITVATSRT	orf5
WP_003413196.1	endolytic transglycosylase MltG [Mycobacterium]	REVATSDT	0,625	ITVATSRT	orf5
WP_003414040.1	DNA translocase FtsK [Mycobacterium]	KTVARSGT	0,625	ITVATSRT	orf5
WP_003414750.1	DEAD/DEAH box helicase [Mycobacterium]	FTAATSRF	0,625	ITVATSRT	orf5
WP_003419740.1	ArsA family ATPase [Mycobacterium]	QTVATSLA	0,625	ITVATSRT	orf5
WP_003898768.1	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase [Mycobacterium]	GTSATSRL	0,625	ITVATSRT	orf5
WP_003899824.1	maltokinase [Mycobacterium]	IGVADDRT	0,625	ITVATSRT	orf5
WP_003904723.1	hypothetical protein [Mycobacterium]	DTVPTSRY	0,625	ITVATSRT	orf5
WP_010950416.1	hypothetical protein [Mycobacterium]	ITVARSVP	0,625	ITVATSRT	orf5
WP_010950499.1	nitrate reductase subunit alpha [Mycobacterium]	RTVDTPRT	0,625	ITVATSRT	orf5
WP_011799243.1	DUF5631 domain-containing protein [Mycobacterium tuberculosis]	PTVATATT	0,625	ITVATSRT	orf5
WP_011799253.1	cytochrome P450 [Mycobacterium]	IPVATSMW	0,625	ITVATSRT	orf5

WP_003420539.1	phosphotransferase family protein [Mycobacterium]	LLPAAD	1	LLPAAD	orf9
WP_003399828.1	type VII secretion system ESX-1 associated protein EspE [Mycobacterium]	LTTLPK	0,833333333	GTTLPK	orf9
WP_003400391.1	helix-turn-helix transcriptional regulator [Mycobacterium]	LLVAAD	0,833333333	LLPAAD	orf9
WP_003401347.1	PPE family protein [Mycobacterium]	LLPAAL	0,833333333	LLPAAD	orf9
WP_003402129.1	DUF2752 domain-containing protein [Terrabacteria group]	LLAAAD	0,833333333	LLPAAD	orf9
WP_003410786.1	PE family protein [Mycobacterium]	LAPAAD	0,833333333	LLPAAD	orf9
WP_003414086.1	PE domain-containing protein [Mycobacterium tuberculosis complex]	LLPAAE	0,833333333	LLPAAD	orf9
WP_003416804.1	zinc-dependent metalloprotease [Mycobacterium]	LLPATD	0,833333333	LLPAAD	orf9
WP_003417095.1	class I SAM-dependent methyltransferase [Mycobacterium]	LLDAAD	0,833333333	LLPAAD	orf9
WP_003911263.1	antitoxin VapB7 [Mycobacterium tuberculosis complex]	LLDAAD	0,833333333	LLPAAD	orf9
WP_010950351.1	PE-PPE domain-containing protein [Mycobacterium]	LLPTAD	0,833333333	LLPAAD	orf9
WP_003400134.1	murein biosynthesis integral membrane protein MurJ [Mycobacterium]	GTTDGK	0,666666667	GTTLPK	orf9
WP_003400364.1	FtsW/RodA/SpoVE family cell cycle protein [Mycobacterium]	GMTLPR	0,666666667	GTTLPK	orf9
WP_003401003.1	PE-PPE domain-containing protein [Mycobacterium]	VTTLPL	0,666666667	GTTLPK	orf9
WP_003401084.1	virulence factor Mce family protein [Mycobacterium]	ASTLPK	0,666666667	GTTLPK	orf9
WP_003401560.1	toxin-antitoxin system toxin [Mycobacterium]	GTLLPE	0,666666667	GTTLPK	orf9
WP_003401751.1	hypothetical protein [Mycobacterium]	GTTAPT	0,666666667	GTTLPK	orf9
WP_003402339.1	heparin-binding hemagglutinin HbhA [Mycobacterium]	GIELPK	0,666666667	GTTLPK	orf9
WP_003402688.1	hypothetical protein [Mycobacterium]	ETTLPA	0,666666667	GTTLPK	orf9
WP_003403363.1	ABC transporter ATP-binding protein [Mycobacterium]	LHTLPK	0,666666667	GTTLPK	orf9
WP_003403453.1	30S ribosomal protein S12 [Mycobacterium]	YTTTPK	0,666666667	GTTLPK	orf9
WP_003403870.1	HAMP domain-containing histidine kinase [Mycobacterium tuberculosis complex]	PTTLPS	0,666666667	GTTLPK	orf9
WP_003404278.1	DUF1416 domain-containing protein [Mycobacterium]	GLTLPA	0,666666667	GTTLPK	orf9
WP_003404316.1	LCP family protein [Mycobacterium]	TTTSPK	0,666666667	GTTLPK	orf9
WP_003404689.1	HAMP domain-containing histidine kinase [Mycobacterium]	DITLPK	0,666666667	GTTLPK	orf9
WP_003404761.1	transposase [Mycobacterium]	GTTAPS	0,666666667	GTTLPK	orf9
WP_003405123.1	two-component system sensor histidine kinase MprB [Mycobacterium]	GQTLPV	0,666666667	GTTLPK	orf9
WP_003405138.1	hypothetical protein [Mycobacterium]	ATTLPD	0,666666667	GTTLPK	orf9
WP_003405724.1	acetyl-CoA C-acetyltransferase [Mycobacterium]	GTTYEK	0,666666667	GTTLPK	orf9
WP_003405897.1	HNH endonuclease [Mycobacterium]	GLTLGK	0,666666667	GTTLPK	orf9
WP_003406243.1	DivIVA domain-containing protein [Mycobacterium]	ATTLPA	0,666666667	GTTLPK	orf9
WP_003408063.1	DNA polymerase I [Mycobacterium]	GTHLPH	0,666666667	GTTLPK	orf9

WP_003408080.1	mannosyltransferase [Mycobacterium]	GTYGPK	0,666666667	GTTLPK	orf9
WP_003408859.1	type VII secretion system ESX-5 subunit EccE5 [Mycobacterium]	GTTLGA	0,666666667	GTTLPK	orf9
WP_003408859.1	type VII secretion system ESX-5 subunit EccE5 [Mycobacterium]	DTRLPK	0,666666667	GTTLPK	orf9
WP_003409685.1	YqjF family protein [Mycobacterium]	GTALPI	0,666666667	GTTLPK	orf9
WP_003410677.1	class A beta-lactamase BlaA [Mycobacterium]	STTLPA	0,666666667	GTTLPK	orf9
WP_003410763.1	RNA helicase [Mycobacterium]	SMTLPK	0,666666667	GTTLPK	orf9
WP_003411425.1	DUF3043 domain-containing protein [Mycobacterium]	QTTGPK	0,666666667	GTTLPK	orf9
WP_003411486.1	alpha/beta hydrolase [Mycobacterium]	FQTLPK	0,666666667	GTTLPK	orf9
WP_003412309.1	gamma-glutamyltransferase family protein [Mycobacterium]	GTPAPK	0,666666667	GTTLPK	orf9
WP_003412373.1	ComEA family DNA-binding protein [Mycobacterium]	ATTGPK	0,666666667	GTTLPK	orf9
WP_003412516.1	glutamate-5-semialdehyde dehydrogenase [Mycobacterium]	GYTLPN	0,666666667	GTTLPK	orf9
WP_003412557.1	HAMP domain-containing protein [Mycobacterium]	GTTLLQ	0,666666667	GTTLPK	orf9
WP_003412771.1	acyl-CoA dehydrogenase [Mycobacterium]	GGILPK	0,666666667	GTTLPK	orf9
WP_003412938.1	L,D-transpeptidase LdtMt2 [Mycobacterium]	GGTLPG	0,666666667	GTTLPK	orf9
WP_003413395.1	4-aminobutyrate--2-oxoglutarate transaminase [Mycobacterium]	GTTEPD	0,666666667	GTTLPK	orf9
WP_003413917.1	APC family permease [Mycobacterium]	HTLLPK	0,666666667	GTTLPK	orf9
WP_003414061.1	type II toxin-antitoxin system VapB family antitoxin [Mycobacterium]	GTTTKK	0,666666667	GTTLPK	orf9
WP_003414409.1	hypothetical protein [Mycobacterium]	GTSLRK	0,666666667	GTTLPK	orf9
WP_003414748.1	signal recognition particle protein [Mycobacterium]	GPTPPK	0,666666667	GTTLPK	orf9
WP_003416079.1	wax ester/triacylglycerol synthase family O-acyltransferase [Mycobacterium]	GTTSPT	0,666666667	GTTLPK	orf9
WP_003416111.1	maleylpyruvate isomerase family mycothiol-dependent enzyme [Mycobacterium]	LTTLDK	0,666666667	GTTLPK	orf9
WP_003416124.1	hypothetical protein [Mycobacterium]	GTTTPT	0,666666667	GTTLPK	orf9
WP_003416381.1	PPE family protein [Mycobacterium tuberculosis complex]	LTTLPG	0,666666667	GTTLPK	orf9
WP_003417051.1	hypothetical protein [Mycobacterium]	GHTLRK	0,666666667	GTTLPK	orf9
WP_003417413.1	sigma-70 family RNA polymerase sigma factor [Mycobacterium]	GTWLPE	0,666666667	GTTLPK	orf9
WP_003418324.1	type VII secretion-associated protein [Mycobacterium]	GETLPG	0,666666667	GTTLPK	orf9
WP_003419226.1	PPE family protein [Mycobacterium]	MTTLPG	0,666666667	GTTLPK	orf9
WP_003419487.1	DNA repair protein RadA [Mycobacterium]	GTTLAT	0,666666667	GTTLPK	orf9
WP_003420801.1	exported repetitive protein [Mycobacterium]	GTTLAP	0,666666667	GTTLPK	orf9
WP_003420837.1	MBL fold metallo-hydrolase [Mycobacterium]	GTTLNS	0,666666667	GTTLPK	orf9
WP_003898475.1	DUF2993 domain-containing protein [Mycobacterium]	GFSLPK	0,666666667	GTTLPK	orf9

WP_003899099.1	hypothetical protein [Mycobacterium]	PTTTPK	0,666666667	GTTLPK	orf9
WP_003899212.1	cytochrome bc complex cytochrome b subunit [Mycobacterium]	GAPLPK	0,666666667	GTTLPK	orf9
WP_003899377.1	DUF2189 domain-containing protein [Mycobacterium]	GTYLPP	0,666666667	GTTLPK	orf9
WP_003899402.1	alpha/beta hydrolase [Mycobacterium]	GQGLPK	0,666666667	GTTLPK	orf9
WP_003899738.1	type VII secretion system ESX-1 FtsK/SpoIIIE family ATPase EccCa1 [Mycobacterium]	GTILDK	0,666666667	GTTLPK	orf9
WP_003900145.1	glutamate--cysteine ligase [Mycobacterium]	GETLPT	0,666666667	GTTLPK	orf9
WP_003900163.1	bifunctional uroporphyrinogen-III C-methyltransferase/uroporphyrinogen-III synthase [Mycobacterium]	GTDLPP	0,666666667	GTTLPK	orf9
WP_003900242.1	hypothetical protein [Mycobacterium]	GTALPP	0,666666667	GTTLPK	orf9
WP_003900533.1	phosphatidylinositol mannoside acyltransferase [Mycobacterium]	GLKLPK	0,666666667	GTTLPK	orf9
WP_003900650.1	phosphotransferase family protein [Mycobacterium]	VTTLPA	0,666666667	GTTLPK	orf9
WP_003900963.1	GDP-mannose-dependent alpha-mannosyltransferase [Mycobacterium]	VTTLPL	0,666666667	GTTLPK	orf9
WP_003901231.1	cytochrome P450 [Mycobacterium]	GTTLSD	0,666666667	GTTLPK	orf9
WP_003901422.1	type II toxin-antitoxin system VapB family antitoxin [Mycobacterium]	GTTGLK	0,666666667	GTTLPK	orf9
WP_003904400.1	cation-translocating P-type ATPase [Mycobacterium]	QTTKPK	0,666666667	GTTLPK	orf9
WP_003908489.1	molybdopterin oxidoreductase family protein [Mycobacterium]	GPTLPD	0,666666667	GTTLPK	orf9
WP_003909568.1	cobalt-precorrin-6A reductase [Mycobacterium]	GTALPR	0,666666667	GTTLPK	orf9
WP_003910308.1	PE family protein [Mycobacterium tuberculosis complex]	GTTGPD	0,666666667	GTTLPK	orf9
WP_003910705.1	hypothetical protein [Mycobacterium]	GTTGHK	0,666666667	GTTLPK	orf9
WP_010950379.1	DUF3060 domain-containing protein [Mycobacterium]	ATTLPP	0,666666667	GTTLPK	orf9
WP_010950382.1	maleylpyruvate isomerase family mycothiol-dependent enzyme [Mycobacterium]	GTPLPL	0,666666667	GTTLPK	orf9
WP_010950571.1	type I polyketide synthase [Mycobacterium tuberculosis]	GLTLPS	0,666666667	GTTLPK	orf9
WP_010950788.1	multidrug efflux MFS transporter EfpA [Mycobacterium]	GTTGPV	0,666666667	GTTLPK	orf9
WP_010950801.1	phthiocerol type I polyketide synthase PpsD [Mycobacterium]	GTTFPT	0,666666667	GTTLPK	orf9
WP_010950946.1	NAD(P)/FAD-dependent oxidoreductase [Mycobacterium]	AGTLPK	0,666666667	GTTLPK	orf9
WP_010950954.1	type VII secretion system ESX-1 serine protease mycosin MycP1 [Mycobacterium]	PTTLPG	0,666666667	GTTLPK	orf9
WP_011799079.1	RDD family protein [Mycobacterium]	PTTLPQ	0,666666667	GTTLPK	orf9
WP_011799098.1	peptidase [Mycobacterium]	PTELPK	0,666666667	GTTLPK	orf9
WP_011799126.1	PE family protein [Mycobacterium tuberculosis]	GATLGK	0,666666667	GTTLPK	orf9

WP_011799136.1	DNA-binding protein [Mycobacterium]	GTALPW	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GLTLPS	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GLTLPS	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GLTLPS	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GFTLPQ	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GFTLPQ	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GFTLPQ	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GFTLPQ	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GFTLPQ	0,666666667	GTTLPK	orf9
WP_011799214.1	PPE family protein [Mycobacterium tuberculosis]	GFTLPQ	0,666666667	GTTLPK	orf9
WP_011799240.1	type I polyketide synthase [Mycobacterium tuberculosis]	GGTLPP	0,666666667	GTTLPK	orf9
WP_011799327.1	UPF0182 family protein [Mycobacterium]	GTVKPK	0,666666667	GTTLPK	orf9
WP_011799362.1	type VII secretion system ESX-1 target EspA [Mycobacterium tuberculosis]	GTTTKK	0,666666667	GTTLPK	orf9
WP_087902221.1	IS3-like element IS987 family transposase [Bacteria]	GTTRGK	0,666666667	GTTLPK	orf9
WP_137054066.1	PPE family protein [Mycobacterium tuberculosis]	GYTLPL	0,666666667	GTTLPK	orf9
WP_137054066.1	PPE family protein [Mycobacterium tuberculosis]	STTLPS	0,666666667	GTTLPK	orf9
WP_162014417.1	hypothetical protein [Mycobacterium tuberculosis]	GTTGPV	0,666666667	GTTLPK	orf9
WP_162014417.1	hypothetical protein [Mycobacterium tuberculosis]	GTTGGK	0,666666667	GTTLPK	orf9
WP_003399839.1	type VII secretion system ESX-1 adaptor EspG1 [Mycobacterium]	LLPAGA	0,666666667	LLPAAD	orf9
WP_003400028.1	type VII secretion system ESX-2 associated protein EspG2 [Mycobacterium]	LLPRLD	0,666666667	LLPAAD	orf9
WP_003400028.1	type VII secretion system ESX-2 associated protein EspG2 [Mycobacterium]	RLPAGD	0,666666667	LLPAAD	orf9
WP_003400120.1	CCA tRNA nucleotidyltransferase [Mycobacterium]	LLTAAA	0,666666667	LLPAAD	orf9
WP_003400126.1	hypothetical protein [Mycobacterium tuberculosis complex]	YQPAAD	0,666666667	LLPAAD	orf9
WP_003400126.1	hypothetical protein [Mycobacterium tuberculosis complex]	LLSAAE	0,666666667	LLPAAD	orf9
WP_003400126.1	hypothetical protein [Mycobacterium tuberculosis complex]	LLPATA	0,666666667	LLPAAD	orf9
WP_003400364.1	FtsW/RodA/SpoVE family cell cycle protein [Mycobacterium]	LDPFAD	0,666666667	LLPAAD	orf9
WP_003400514.1	DUF2029 domain-containing protein [Mycobacterium]	LPLAAD	0,666666667	LLPAAD	orf9
WP_003400629.1	hypothetical protein [Mycobacterium]	GAPAAD	0,666666667	LLPAAD	orf9
WP_003400658.1	NADH-quinone oxidoreductase subunit B family protein [Mycobacterium]	PLPAAI	0,666666667	LLPAAD	orf9
WP_003400665.1	class I SAM-dependent methyltransferase [Mycobacterium]	LLPGAC	0,666666667	LLPAAD	orf9
WP_003400858.1	oxalyl-CoA decarboxylase [Mycobacterium]	LLPAPE	0,666666667	LLPAAD	orf9
WP_003400858.1	oxalyl-CoA decarboxylase [Mycobacterium]	LLEAAA	0,666666667	LLPAAD	orf9

WP_003400949.1	DUF427 domain-containing protein [Mycobacterium]	LEPSAD	0,666666667	LLPAAD	orf9
WP_003401003.1	PE-PPE domain-containing protein [Mycobacterium]	LLPTVD	0,666666667	LLPAAD	orf9
WP_003401153.1	hypothetical protein [Mycobacterium]	QLPAAW	0,666666667	LLPAAD	orf9
WP_003401224.1	acyl dehydratase [Mycobacterium]	PAPAAD	0,666666667	LLPAAD	orf9
WP_003401485.1	type VII secretion system ESX-3 target PE5 [Mycobacterium]	VPPAAD	0,666666667	LLPAAD	orf9
WP_003401488.1	type VII secretion system ESX-3 target PPE4 [Mycobacterium]	LLPAGL	0,666666667	LLPAAD	orf9
WP_003401528.1	type VII secretion system ESX-3 serine protease mycosin MycP3 [Mycobacterium]	NLPAAW	0,666666667	LLPAAD	orf9
WP_003401533.1	type VII secretion system ESX-3 subunit EccE3 [Mycobacterium]	ALVAAD	0,666666667	LLPAAD	orf9
WP_003401607.1	Hsp70 family protein [Mycobacterium]	ELPAGD	0,666666667	LLPAAD	orf9
WP_003401636.1	hypothetical protein [Mycobacterium]	LAPAAV	0,666666667	LLPAAD	orf9
WP_003401666.1	nuclear transport factor 2 family protein [Mycobacterium]	ALNAAD	0,666666667	LLPAAD	orf9
WP_003401827.1	PaaI family thioesterase [Mycobacterium]	LAVAAD	0,666666667	LLPAAD	orf9
WP_003401861.1	VWA domain-containing protein [Mycobacterium]	LLPGVD	0,666666667	LLPAAD	orf9
WP_003401863.1	MoxR family ATPase [Mycobacterium]	DLTAAD	0,666666667	LLPAAD	orf9
WP_003402284.1	PPE family protein [Mycobacterium]	LLVAAL	0,666666667	LLPAAD	orf9
WP_003402284.1	PPE family protein [Mycobacterium]	AQPAAD	0,666666667	LLPAAD	orf9
WP_003402344.1	DUF2599 domain-containing protein [Mycobacterium]	LSPEAD	0,666666667	LLPAAD	orf9
WP_003402870.1	hypothetical protein [Mycobacterium]	LEPAAG	0,666666667	LLPAAD	orf9
WP_003402886.1	DUF2064 domain-containing protein [Mycobacterium]	LDSAAD	0,666666667	LLPAAD	orf9
WP_003402917.1	AMP-binding protein [Mycobacterium]	PLVAAD	0,666666667	LLPAAD	orf9
WP_003403125.1	type II toxin-antitoxin system Phd/YefM family antitoxin [Mycobacterium]	WLPAAE	0,666666667	LLPAAD	orf9
WP_003403326.1	malonyl CoA-ACP transacylase [Mycobacterium tuberculosis complex]	LLPDAT	0,666666667	LLPAAD	orf9
WP_003403405.1	PIN domain-containing protein [Mycobacterium]	LLNAGD	0,666666667	LLPAAD	orf9
WP_003403490.1	mycofactocin radical SAM maturase [Mycobacterium]	LHPTAD	0,666666667	LLPAAD	orf9
WP_003403501.1	mycofactocin system glycosyltransferase [Mycobacterium]	LAPAAR	0,666666667	LLPAAD	orf9
WP_003403569.1	hypothetical protein [Mycobacterium]	LLAAKD	0,666666667	LLPAAD	orf9
WP_003403610.1	formylglycine-generating enzyme family protein [Mycobacterium]	LATAAD	0,666666667	LLPAAD	orf9
WP_003404002.1	transglutaminase domain-containing protein [Mycobacterium]	ALVAAD	0,666666667	LLPAAD	orf9
WP_003404007.1	GntR family transcriptional regulator [Mycobacterium]	DLDAAD	0,666666667	LLPAAD	orf9
WP_003404127.1	hypothetical protein [Mycobacterium]	TLPAPD	0,666666667	LLPAAD	orf9
WP_003404373.1	class I SAM-dependent methyltransferase [Mycobacterium]	KLPALD	0,666666667	LLPAAD	orf9

WP_003404404.1	transposase [Mycobacterium]	LIPDAD	0,666666667	LLPAAD	orf9
WP_003404596.1	DUF3027 domain-containing protein [Mycobacterium]	LAPAKD	0,666666667	LLPAAD	orf9
WP_003404684.1	peptidoglycan-binding protein ArfA [Mycobacterium]	LLIAAI	0,666666667	LLPAAD	orf9
WP_003404903.1	PIN domain-containing protein [Mycobacterium]	RLGAAD	0,666666667	LLPAAD	orf9
WP_003405171.1	dolichyl-phosphate-mannose--protein mannosyltransferase [Mycobacterium]	LVPVAD	0,666666667	LLPAAD	orf9
WP_003405293.1	septum formation initiator family protein [Mycobacterium]	LPPAAP	0,666666667	LLPAAD	orf9
WP_003405370.1	PE domain-containing protein [Bacteria]	LLPAEE	0,666666667	LLPAAD	orf9
WP_003405585.1	hypothetical protein [Mycobacterium]	LLTRAD	0,666666667	LLPAAD	orf9
WP_003405728.1	alpha/beta hydrolase [Mycobacterium]	LLPAST	0,666666667	LLPAAD	orf9
WP_003405746.1	mycothiol conjugate amidase Mca [Mycobacterium]	LNPAMD	0,666666667	LLPAAD	orf9
WP_003405749.1	hypothetical protein [Mycobacterium]	LDQAAD	0,666666667	LLPAAD	orf9
WP_003405884.1	alpha/beta hydrolase [Mycobacterium]	LEEAAD	0,666666667	LLPAAD	orf9
WP_003405919.1	PPE family protein [Mycobacterium tuberculosis complex]	QLWAAD	0,666666667	LLPAAD	orf9
WP_003405932.1	NAD(P)/FAD-dependent oxidoreductase [Mycobacterium]	LLPTAF	0,666666667	LLPAAD	orf9
WP_003406064.1	hypothetical protein [Mycobacterium]	QEPAAD	0,666666667	LLPAAD	orf9
WP_003406075.1	hypothetical protein [Mycobacterium]	LTPAAP	0,666666667	LLPAAD	orf9
WP_003406090.1	nitrate reductase subunit beta [Mycobacterium]	ELPAAA	0,666666667	LLPAAD	orf9
WP_003406105.1	PPE family protein [Mycobacterium tuberculosis complex]	LLPNAV	0,666666667	LLPAAD	orf9
WP_003406154.1	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy-alpha-D-glucopyranoside deacetylase [Mycobacterium]	VLPRAD	0,666666667	LLPAAD	orf9
WP_003406165.1	PE family protein [Mycobacterium]	LLPRAG	0,666666667	LLPAAD	orf9
WP_003406219.1	PucR family transcriptional regulator [Mycobacterium]	LDRAAD	0,666666667	LLPAAD	orf9
WP_003406304.1	type II toxin-antitoxin system VapC family toxin [Mycobacterium]	PLPTAD	0,666666667	LLPAAD	orf9
WP_003406359.1	MFS transporter [Mycobacterium]	LAPQAD	0,666666667	LLPAAD	orf9
WP_003406602.1	ABC transporter ATP-binding protein [Mycobacterium]	LLGLAD	0,666666667	LLPAAD	orf9
WP_003407211.1	carbamoyl-phosphate synthase large subunit [Mycobacterium]	LDPAAE	0,666666667	LLPAAD	orf9
WP_003407264.1	AraC family transcriptional regulator [Mycobacterium]	PLPQAD	0,666666667	LLPAAD	orf9
WP_003407315.1	lipoarabinomannan carrier protein LprG [Mycobacterium]	FGPAAD	0,666666667	LLPAAD	orf9
WP_003407347.1	excinuclease ABC subunit UvrC [Mycobacterium]	LDDAAD	0,666666667	LLPAAD	orf9
WP_003407371.1	alpha/beta hydrolase [Mycobacterium]	LLNAAN	0,666666667	LLPAAD	orf9
WP_003407376.1	PucR family transcriptional regulator [Mycobacterium]	LLEPAD	0,666666667	LLPAAD	orf9
WP_003407798.1	NlpC/P60 family peptidoglycan-binding protein RipD [Mycobacterium]	GLAAAD	0,666666667	LLPAAD	orf9
WP_003407926.1	lipase [Mycobacterium]	LLPSDD	0,666666667	LLPAAD	orf9
WP_003408257.1	ABC-F family ATP-binding cassette domain-containing	LAPFAD	0,666666667	LLPAAD	orf9

	protein [Mycobacterium]				
WP_003408390.1	copper transporter MctB [Mycobacterium]	KLSAAD	0,666666667	LLPAAD	orf9
WP_003408436.1	SMC-Scp complex subunit ScpB [Mycobacterium]	LLPDVD	0,666666667	LLPAAD	orf9
WP_003408448.1	cyclase family protein [Mycobacterium]	LLPWAV	0,666666667	LLPAAD	orf9
WP_003409271.1	malate synthase G [Mycobacterium]	LLPEPD	0,666666667	LLPAAD	orf9
WP_003409919.1	TetR family transcriptional regulator Mce3R [Mycobacterium]	PLPAGD	0,666666667	LLPAAD	orf9
WP_003410218.1	sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC [Mycobacterium]	LLPRAV	0,666666667	LLPAAD	orf9
WP_003410309.1	sugar epimerase family protein [Mycobacterium]	DLPAVD	0,666666667	LLPAAD	orf9
WP_003410735.1	protein kinase [Mycobacterium tuberculosis complex]	LLPPLD	0,666666667	LLPAAD	orf9
WP_003410793.1	hypothetical protein [Mycobacterium tuberculosis complex]	AAPAAD	0,666666667	LLPAAD	orf9
WP_003410814.1	antitoxin [Mycobacterium]	LQLAAD	0,666666667	LLPAAD	orf9
WP_003411023.1	proteasome subunit beta [Mycobacterium]	LLPASI	0,666666667	LLPAAD	orf9
WP_003411056.1	methionine synthase [Mycobacterium]	LNPAAR	0,666666667	LLPAAD	orf9
WP_003411110.1	hypothetical protein [Mycobacterium]	LRPGAD	0,666666667	LLPAAD	orf9
WP_003411137.1	YggS family pyridoxal phosphate-dependent enzyme [Mycobacterium]	LLAAAE	0,666666667	LLPAAD	orf9
WP_003411415.1	membrane protein [Mycobacterium]	LPPAAY	0,666666667	LLPAAD	orf9
WP_003411442.1	adenylate/guanylate cyclase domain-containing protein [Mycobacterium]	LATAAD	0,666666667	LLPAAD	orf9
WP_003411514.1	SURF1 family protein [Bacteria]	LLPQQD	0,666666667	LLPAAD	orf9
WP_003411559.1	malonyl CoA-acyl carrier protein transacylase [Mycobacterium]	LPGAAD	0,666666667	LLPAAD	orf9
WP_003411571.1	beta-ketoacyl-ACP synthase [Mycobacterium]	VAPAAD	0,666666667	LLPAAD	orf9
WP_003411668.1	hypothetical protein [Mycobacterium]	DLPPAD	0,666666667	LLPAAD	orf9
WP_003411905.1	hypothetical protein [Mycobacterium]	NLPADD	0,666666667	LLPAAD	orf9
WP_003412212.1	decaprenyl diphosphate synthase [Mycobacterium]	LPPAPD	0,666666667	LLPAAD	orf9
WP_003412212.1	decaprenyl diphosphate synthase [Mycobacterium]	ELPAAP	0,666666667	LLPAAD	orf9
WP_003412277.1	mycobactin polyketide synthase MbtD [Mycobacterium]	LVFAAD	0,666666667	LLPAAD	orf9
WP_003412384.1	SGNH/GDSL hydrolase family protein [Mycobacterium]	GLPADD	0,666666667	LLPAAD	orf9
WP_003412613.1	resuscitation-promoting factor protein RpfE [Mycobacterium]	LPPAPD	0,666666667	LLPAAD	orf9
WP_003412713.1	HAD-IB family hydrolase [Mycobacterium]	GLPAVD	0,666666667	LLPAAD	orf9
WP_003413027.1	chorismate synthase [Mycobacterium]	DLPAID	0,666666667	LLPAAD	orf9
WP_003413332.1	hypothetical protein [Mycobacterium]	LLVIAD	0,666666667	LLPAAD	orf9
WP_003413373.1	lipoprotein [Mycobacterium]	LSPATD	0,666666667	LLPAAD	orf9
WP_003413854.1	pyrimidine reductase family protein [Mycobacterium]	QLGAAD	0,666666667	LLPAAD	orf9

WP_003413866.1	class I SAM-dependent methyltransferase [Mycobacterium]	GLPAAT	0,666666667	LLPAAD	orf9
WP_003413927.1	alpha/beta fold hydrolase [Mycobacterium]	LAPAAQ	0,666666667	LLPAAD	orf9
WP_003413944.1	RNA polymerase sigma factor [Mycobacterium]	DLDAAD	0,666666667	LLPAAD	orf9
WP_003413944.1	RNA polymerase sigma factor [Mycobacterium]	KLPAAQ	0,666666667	LLPAAD	orf9
WP_003413958.1	sigma-70 family RNA polymerase sigma factor [Mycobacterium]	QSPAAD	0,666666667	LLPAAD	orf9
WP_003413958.1	sigma-70 family RNA polymerase sigma factor [Mycobacterium]	LLNAAG	0,666666667	LLPAAD	orf9
WP_003414055.1	type I restriction endonuclease subunit S [Mycobacterium]	DLPAAS	0,666666667	LLPAAD	orf9
WP_003414085.1	PPE family protein [Mycobacterium]	LTSAAD	0,666666667	LLPAAD	orf9
WP_003414198.1	DDE-type integrase/transposase/recombinase [Mycobacterium]	LTGAAD	0,666666667	LLPAAD	orf9
WP_003414579.1	glutamine synthetase [Mycobacterium]	LTPASD	0,666666667	LLPAAD	orf9
WP_003414630.1	cell surface glycolipoprotein Mpt83 [Mycobacterium]	ADPAAD	0,666666667	LLPAAD	orf9
WP_003414635.1	cytochrome c biogenesis protein DipZ [Mycobacterium]	DLPAAL	0,666666667	LLPAAD	orf9
WP_003414666.1	response regulator transcription factor [Mycobacterium]	LLNAAG	0,666666667	LLPAAD	orf9
WP_003414678.1	M23 family metallopeptidase [Mycobacterium]	LLGAAP	0,666666667	LLPAAD	orf9
WP_003414820.1	ribonuclease III [Mycobacterium]	LLDAAP	0,666666667	LLPAAD	orf9
WP_003414837.1	phthiocerol type I polyketide synthase PpsC [Mycobacterium tuberculosis complex]	LLWLAD	0,666666667	LLPAAD	orf9
WP_003414837.1	phthiocerol type I polyketide synthase PpsC [Mycobacterium tuberculosis complex]	LASAAD	0,666666667	LLPAAD	orf9
WP_003414837.1	phthiocerol type I polyketide synthase PpsC [Mycobacterium tuberculosis complex]	LHDAAD	0,666666667	LLPAAD	orf9
WP_003415973.1	class 1b ribonucleoside-diphosphate reductase subunit beta [Mycobacterium]	LSPNAD	0,666666667	LLPAAD	orf9
WP_003415991.1	ATP-dependent DNA ligase [Mycobacterium]	GLPAAT	0,666666667	LLPAAD	orf9
WP_003416051.1	HNH endonuclease [Mycobacterium]	LLGAAN	0,666666667	LLPAAD	orf9
WP_003416363.1	two-component system sensor histidine kinase DevS [Mycobacterium]	DMPAAD	0,666666667	LLPAAD	orf9
WP_003416815.1	AarF/ABC1/UbiB kinase family protein [Mycobacterium]	LSPGAD	0,666666667	LLPAAD	orf9
WP_003416829.1	NAD(+) diphosphatase [Mycobacterium]	LQPIAD	0,666666667	LLPAAD	orf9
WP_003416833.1	ATP-dependent helicase [Mycobacterium]	LPGAAD	0,666666667	LLPAAD	orf9
WP_003416879.1	isochorismate synthase [Mycobacterium]	LPPPAD	0,666666667	LLPAAD	orf9
WP_003416933.1	cation:proton antiporter [Mycobacterium]	GLPAAA	0,666666667	LLPAAD	orf9
WP_003417056.1	hypothetical protein [Mycobacterium]	GLIAAD	0,666666667	LLPAAD	orf9
WP_003417238.1	phospho-sugar mutase [Mycobacterium]	DLPAAR	0,666666667	LLPAAD	orf9
WP_003417251.1	hypothetical protein [Mycobacterium]	LNPAED	0,666666667	LLPAAD	orf9
WP_003417254.1	alpha/beta hydrolase [Mycobacterium]	SLNAAD	0,666666667	LLPAAD	orf9

WP_003417259.1	adenosine deaminase [Mycobacterium]	DLPATD	0,666666667	LLPAAD	orf9
WP_003417738.1	hypothetical protein [Mycobacterium]	LLPALG	0,666666667	LLPAAD	orf9
WP_003417741.1	hypothetical protein [Mycobacterium]	LLPANG	0,666666667	LLPAAD	orf9
WP_003417961.1	beta-phosphoglucomutase family hydrolase [Mycobacterium]	FDPAAD	0,666666667	LLPAAD	orf9
WP_003418005.1	GuaB3 family IMP dehydrogenase-related protein [Mycobacterium]	LLEAAA	0,666666667	LLPAAD	orf9
WP_003418326.1	type VII secretion system ESX-4 FtsK/SpoIIIE family ATPase EccC4 [Mycobacterium]	LLPARV	0,666666667	LLPAAD	orf9
WP_003419226.1	PPE family protein [Mycobacterium]	LLPIAP	0,666666667	LLPAAD	orf9
WP_003419534.1	membrane protein [Mycobacterium]	RAPAAD	0,666666667	LLPAAD	orf9
WP_003419574.1	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase [Mycobacterium]	LDPAAV	0,666666667	LLPAAD	orf9
WP_003419671.1	hypothetical protein [Mycobacterium]	LLPTLD	0,666666667	LLPAAD	orf9
WP_003419738.1	ArsA family ATPase [Mycobacterium]	KLPDAD	0,666666667	LLPAAD	orf9
WP_003419746.1	transglycosylase/D,D-transpeptidase PonA2 [Mycobacterium tuberculosis complex]	RLPAAI	0,666666667	LLPAAD	orf9
WP_003419770.1	DUF4129 domain-containing protein [Mycobacterium]	LNPAAG	0,666666667	LLPAAD	orf9
WP_003420511.1	tRNA adenosine deaminase-associated protein [Mycobacterium]	QRPAAD	0,666666667	LLPAAD	orf9
WP_003420615.1	hypothetical protein [Mycobacterium]	LLPSED	0,666666667	LLPAAD	orf9
WP_003420620.1	class I SAM-dependent methyltransferase [Mycobacterium]	ELDAAD	0,666666667	LLPAAD	orf9
WP_003420620.1	class I SAM-dependent methyltransferase [Mycobacterium]	LLAAHD	0,666666667	LLPAAD	orf9
WP_003420620.1	class I SAM-dependent methyltransferase [Mycobacterium]	DLPAAP	0,666666667	LLPAAD	orf9
WP_003420798.1	UDP-galactopyranose mutase [Mycobacterium]	ELPAAN	0,666666667	LLPAAD	orf9
WP_003420801.1	exported repetitive protein [Mycobacterium]	LDPGAD	0,666666667	LLPAAD	orf9
WP_003898417.1	SRPBCC family protein [Mycobacterium]	LLQLAD	0,666666667	LLPAAD	orf9
WP_003898437.1	MBL fold metallo-hydrolase [Mycobacterium]	LLPAVF	0,666666667	LLPAAD	orf9
WP_003898528.1	hypothetical protein [Mycobacterium]	SLPAND	0,666666667	LLPAAD	orf9
WP_003898655.1	ATP-dependent DNA ligase [Mycobacterium]	PLPARD	0,666666667	LLPAAD	orf9
WP_003898703.1	nucleotidyl transferase AbiEii/AbiGii toxin family protein [Bacteria]	LLLDAD	0,666666667	LLPAAD	orf9
WP_003898761.1	RND transporter MmpL10 [Mycobacterium]	GLGAAD	0,666666667	LLPAAD	orf9
WP_003898763.1	alpha/beta hydrolase [Mycobacterium]	MLPAGD	0,666666667	LLPAAD	orf9
WP_003898806.1	AAA family ATPase [Mycobacterium]	LAEAAD	0,666666667	LLPAAD	orf9
WP_003899131.1	IS110 family transposase [Mycobacterium]	NLWAAD	0,666666667	LLPAAD	orf9
WP_003899145.1	carboxylesterase/lipase family protein [Mycobacterium]	LLTAAA	0,666666667	LLPAAD	orf9
WP_003899145.1	carboxylesterase/lipase family protein [Mycobacterium]	LTAAAD	0,666666667	LLPAAD	orf9
WP_003899282.1	TPM domain-containing protein [Mycobacterium]	LLDAVD	0,666666667	LLPAAD	orf9

WP_003899437.1	DUF4193 domain-containing protein [Mycobacterium]	ELPGAD	0,666666667	LLPAAD	orf9
WP_003899500.1	DUF1802 family protein [Mycobacterium tuberculosis complex]	LGPAAA	0,666666667	LLPAAD	orf9
WP_003899670.1	PE domain-containing protein [Mycobacterium]	LLPAGA	0,666666667	LLPAAD	orf9
WP_003899883.1	5-oxoprolinase [Mycobacterium]	LGPAAP	0,666666667	LLPAAD	orf9
WP_003899932.1	wax ester/triacylglycerol synthase family O-acyltransferase [Mycobacterium]	LSPAAS	0,666666667	LLPAAD	orf9
WP_003899969.1	TIGR02569 family protein [Mycobacterium]	APPAAD	0,666666667	LLPAAD	orf9
WP_003900009.1	M20 family metallopeptidase [Mycobacterium]	LLPALE	0,666666667	LLPAAD	orf9
WP_003900066.1	NAD(P)-dependent oxidoreductase [Mycobacterium]	LTPPAD	0,666666667	LLPAAD	orf9
WP_003900072.1	PPE family protein [Mycobacterium tuberculosis]	LLPFED	0,666666667	LLPAAD	orf9
WP_003900072.1	PPE family protein [Mycobacterium tuberculosis]	LAPAAA	0,666666667	LLPAAD	orf9
WP_003900188.1	hypothetical protein [Mycobacterium]	LLEATD	0,666666667	LLPAAD	orf9
WP_003900310.1	oligopeptide ABC transporter substrate-binding protein OppA [Mycobacterium]	LAPTAD	0,666666667	LLPAAD	orf9
WP_003900492.1	hypothetical protein [Mycobacterium]	LLPPAR	0,666666667	LLPAAD	orf9
WP_003900516.1	elongation factor 4 [Mycobacterium]	QLPDAD	0,666666667	LLPAAD	orf9
WP_003900520.1	hypothetical protein [Mycobacterium]	QLPAAG	0,666666667	LLPAAD	orf9
WP_003900529.1	single-stranded DNA-binding protein [Mycobacterium]	DLPAAT	0,666666667	LLPAAD	orf9
WP_003900586.1	gamma-glutamyl-gamma-aminobutyrate hydrolase [Mycobacterium tuberculosis complex]	LDPAAY	0,666666667	LLPAAD	orf9
WP_003900617.1	GNAT family N-acetyltransferase [Mycobacterium]	ALPAAA	0,666666667	LLPAAD	orf9
WP_003900617.1	GNAT family N-acetyltransferase [Mycobacterium]	LPAAAD	0,666666667	LLPAAD	orf9
WP_003900628.1	patatin-like phospholipase family protein [Mycobacterium]	NLPYAD	0,666666667	LLPAAD	orf9
WP_003900761.1	galactofuranosyl transferase GlfT2 [Mycobacterium]	VLPAAS	0,666666667	LLPAAD	orf9
WP_003900801.1	alpha/beta hydrolase [Mycobacterium]	LRPGAD	0,666666667	LLPAAD	orf9
WP_003900845.1	hypothetical protein [Mycobacterium]	LHPSAD	0,666666667	LLPAAD	orf9
WP_003900866.1	LCP family protein [Mycobacterium]	SLPAPD	0,666666667	LLPAAD	orf9
WP_003901285.1	catalase/peroxidase HPI [Mycobacterium]	LEPKAD	0,666666667	LLPAAD	orf9
WP_003901413.1	glycerol-3-phosphate 1-O-acyltransferase [Mycobacterium]	LLPGRD	0,666666667	LLPAAD	orf9
WP_003901413.1	glycerol-3-phosphate 1-O-acyltransferase [Mycobacterium]	IAPAAD	0,666666667	LLPAAD	orf9
WP_003901420.1	type I polyketide synthase [Mycobacterium]	ALPAAP	0,666666667	LLPAAD	orf9
WP_003901458.1	hypothetical protein [Mycobacterium]	PLRAAD	0,666666667	LLPAAD	orf9
WP_003901461.1	glycosyltransferase [Mycobacterium]	GLPARD	0,666666667	LLPAAD	orf9
WP_003902383.1	DAK2 domain-containing protein [Mycobacterium]	VTPAAD	0,666666667	LLPAAD	orf9
WP_003903189.1	response regulator transcription factor [Mycobacterium]	RPPAAD	0,666666667	LLPAAD	orf9
WP_003903329.1	pyruvate, phosphate dikinase [Mycobacterium]	ALDAAD	0,666666667	LLPAAD	orf9
WP_003904400.1	cation-translocating P-type ATPase [Mycobacterium]	ALSAAD	0,666666667	LLPAAD	orf9

WP_003904931.1	DUF1802 family protein [Mycobacterium tuberculosis complex]	LGPAAA	0,666666667	LLPAAD	orf9
WP_003905015.1	ATP-dependent helicase [Mycobacterium]	LTPAAR	0,666666667	LLPAAD	orf9
WP_003908351.1	sulfolipid-1 RND transporter MmpL8 [Mycobacterium]	GLGAAD	0,666666667	LLPAAD	orf9
WP_003909410.1	Rv1355c family protein [Mycobacterium]	LLPQPD	0,666666667	LLPAAD	orf9
WP_003910253.1	hypothetical protein [Mycobacterium tuberculosis complex]	LLPGAQ	0,666666667	LLPAAD	orf9
WP_003910563.1	NAD-glutamate dehydrogenase [Mycobacterium]	GDPAAD	0,666666667	LLPAAD	orf9
WP_003910563.1	NAD-glutamate dehydrogenase [Mycobacterium]	LVVAAD	0,666666667	LLPAAD	orf9
WP_003911234.1	TlpA family protein disulfide reductase [Mycobacterium tuberculosis complex]	ELLAAD	0,666666667	LLPAAD	orf9
WP_003913037.1	GTP 3',8-cyclase MoaA [Mycobacterium]	WLPRAD	0,666666667	LLPAAD	orf9
WP_010950340.1	PPE family protein [Mycobacterium]	LLPIAA	0,666666667	LLPAAD	orf9
WP_010950341.1	cyclic nucleotide-binding domain-containing protein [Mycobacterium]	LLAAAV	0,666666667	LLPAAD	orf9
WP_010950351.1	PE-PPE domain-containing protein [Mycobacterium]	ELPAAL	0,666666667	LLPAAD	orf9
WP_010950413.1	adenosylcobalamin-dependent ribonucleoside-diphosphate reductase [Mycobacterium]	LRPAGD	0,666666667	LLPAAD	orf9
WP_010950423.1	exodeoxyribonuclease V subunit alpha [Mycobacterium]	LLGASD	0,666666667	LLPAAD	orf9
WP_010950484.1	resuscitation-promoting factor [Mycobacterium]	LYPAAG	0,666666667	LLPAAD	orf9
WP_010950506.1	membrane protein [Mycobacterium]	FLPAAP	0,666666667	LLPAAD	orf9
WP_010950539.1	PPE family protein [Mycobacterium]	LLSAAL	0,666666667	LLPAAD	orf9
WP_010950555.1	isoleucine--tRNA ligase [Mycobacterium]	RLVAAD	0,666666667	LLPAAD	orf9
WP_010950580.1	biotin carboxylase [Mycobacterium]	LTPAAP	0,666666667	LLPAAD	orf9
WP_010950583.1	respiratory nitrate reductase subunit gamma [Mycobacterium]	DGPAAD	0,666666667	LLPAAD	orf9
WP_010950613.1	aminomethyl-transferring glycine dehydrogenase [Mycobacterium]	LPPAAS	0,666666667	LLPAAD	orf9
WP_010950634.1	lipase LipD [Mycobacterium]	LLPQAK	0,666666667	LLPAAD	orf9
WP_010950704.1	non-ribosomal peptide synthetase [Mycobacterium]	LRPAAQ	0,666666667	LLPAAD	orf9
WP_010950740.1	aspartate--tRNA ligase [Mycobacterium]	LLGAAR	0,666666667	LLPAAD	orf9
WP_010950800.1	phthiocerol type I polyketide synthase PpsA [Mycobacterium tuberculosis]	LLPARN	0,666666667	LLPAAD	orf9
WP_010950845.1	alpha/beta hydrolase [Mycobacterium]	LAVAAD	0,666666667	LLPAAD	orf9
WP_010950867.1	arylsulfatase AtsB [Mycobacterium]	LFPAWD	0,666666667	LLPAAD	orf9
WP_010950941.1	terminal beta-(1-_2)-arabinofuranosyltransferase [Mycobacterium]	PLTAAD	0,666666667	LLPAAD	orf9
WP_011799082.1	L,D-transpeptidase family protein [Mycobacterium]	LPPALD	0,666666667	LLPAAD	orf9
WP_011799102.1	PPE family protein [Mycobacterium tuberculosis complex]	LLWRAD	0,666666667	LLPAAD	orf9
WP_011799123.1	arylsulfatase AtsA [Mycobacterium]	GLPLAD	0,666666667	LLPAAD	orf9

WP_011799125.1	PE family protein [Mycobacterium tuberculosis]	LLLGAD	0,666666667	LLPAAD	orf9
WP_011799126.1	PE family protein [Mycobacterium tuberculosis]	LLGAAG	0,666666667	LLPAAD	orf9
WP_011799137.1	transglycosylase family protein [Mycobacterium tuberculosis]	PLPAAP	0,666666667	LLPAAD	orf9
WP_011799137.1	transglycosylase family protein [Mycobacterium tuberculosis]	PLPAAP	0,666666667	LLPAAD	orf9
WP_011799137.1	transglycosylase family protein [Mycobacterium tuberculosis]	PLPAAP	0,666666667	LLPAAD	orf9
WP_011799137.1	transglycosylase family protein [Mycobacterium tuberculosis]	LAPPAD	0,666666667	LLPAAD	orf9
WP_011799138.1	diiron oxygenase [Mycobacterium]	ILPATD	0,666666667	LLPAAD	orf9
WP_011799146.1	hypothetical protein [Mycobacterium]	TLPAAV	0,666666667	LLPAAD	orf9
WP_011799163.1	RNA polymerase sigma factor SigI [Mycobacterium]	LSPRAD	0,666666667	LLPAAD	orf9
WP_011799172.1	LuxR family transcriptional regulator [Mycobacterium]	LLSAAT	0,666666667	LLPAAD	orf9
WP_011799173.1	PPE family protein [Mycobacterium tuberculosis]	LLPFED	0,666666667	LLPAAD	orf9
WP_011799190.1	RND transporter MmpL12 [Mycobacterium]	LNEAAD	0,666666667	LLPAAD	orf9
WP_011799195.1	fumarate reductase subunit C [Mycobacterium tuberculosis]	VLAAAD	0,666666667	LLPAAD	orf9
WP_011799198.1	ATP-dependent dethiobiotin synthetase BioD [Mycobacterium]	ALPARD	0,666666667	LLPAAD	orf9
WP_011799206.1	acyltransferase domain-containing protein [Mycobacterium tuberculosis]	VAPAAD	0,666666667	LLPAAD	orf9
WP_011799206.1	acyltransferase domain-containing protein [Mycobacterium tuberculosis]	LLSAAV	0,666666667	LLPAAD	orf9
WP_011799213.1	FAD-dependent oxidoreductase [Mycobacterium]	LLPEAT	0,666666667	LLPAAD	orf9
WP_011799220.1	PPE family protein [Mycobacterium]	VLPTAD	0,666666667	LLPAAD	orf9
WP_011799239.1	DEAD/DEAH box helicase [Mycobacterium]	LITAAD	0,666666667	LLPAAD	orf9
WP_011799239.1	DEAD/DEAH box helicase [Mycobacterium]	LKPGAD	0,666666667	LLPAAD	orf9
WP_011799240.1	type I polyketide synthase [Mycobacterium tuberculosis]	LLPATL	0,666666667	LLPAAD	orf9
WP_011799240.1	type I polyketide synthase [Mycobacterium tuberculosis]	GLDAAD	0,666666667	LLPAAD	orf9
WP_011799240.1	type I polyketide synthase [Mycobacterium tuberculosis]	LIPDAD	0,666666667	LLPAAD	orf9
WP_011799244.1	5'-3' exonuclease [Mycobacterium tuberculosis complex]	PLVAAD	0,666666667	LLPAAD	orf9
WP_011799261.1	non-ribosomal peptide synthetase [Mycobacterium]	SHPAAD	0,666666667	LLPAAD	orf9
WP_011799261.1	non-ribosomal peptide synthetase [Mycobacterium]	PLPTAD	0,666666667	LLPAAD	orf9
WP_011799265.1	ATP-dependent Clp protease ATP-binding subunit ClpX [Mycobacterium]	LIQAAD	0,666666667	LLPAAD	orf9
WP_011799284.1	membrane protein [Mycobacterium]	LGGAAD	0,666666667	LLPAAD	orf9
WP_011799284.1	membrane protein [Mycobacterium]	GLPAAA	0,666666667	LLPAAD	orf9
WP_011799301.1	[protein-PII]	LSLAAD	0,666666667	LLPAAD	orf9

WP_011799302.1	phthiocerol type I polyketide synthase PpsB [Mycobacterium tuberculosis]	LQPMAD	0,666666667	LLPAAD	orf9
WP_011799302.1	phthiocerol type I polyketide synthase PpsB [Mycobacterium tuberculosis]	LLAAAY	0,666666667	LLPAAD	orf9
WP_011799302.1	phthiocerol type I polyketide synthase PpsB [Mycobacterium tuberculosis]	LLPAPE	0,666666667	LLPAAD	orf9
WP_011799325.1	PPE family protein [Mycobacterium tuberculosis]	ALPAAP	0,666666667	LLPAAD	orf9
WP_011799326.1	DUF4129 domain-containing protein [Mycobacterium]	HLPADD	0,666666667	LLPAAD	orf9
WP_011799343.1	PPE family protein [Mycobacterium tuberculosis]	LMWAAD	0,666666667	LLPAAD	orf9
WP_011799362.1	type VII secretion system ESX-1 target EspA [Mycobacterium tuberculosis]	LGSAAD	0,666666667	LLPAAD	orf9
WP_011799362.1	type VII secretion system ESX-1 target EspA [Mycobacterium tuberculosis]	LRPRAD	0,666666667	LLPAAD	orf9
WP_011799364.1	type I DNA topoisomerase [Mycobacterium]	PEPAAD	0,666666667	LLPAAD	orf9
WP_011799379.1	type I polyketide synthase [Mycobacterium]	QLAAAD	0,666666667	LLPAAD	orf9
WP_015385225.1	transglycosylase/D,D-transpeptidase PonA1 [Mycobacterium]	LDPAVD	0,666666667	LLPAAD	orf9
WP_071854213.1	thiol reductant ABC exporter subunit CydD [Mycobacterium]	LAPAAW	0,666666667	LLPAAD	orf9
WP_162014417.1	hypothetical protein [Mycobacterium tuberculosis]	LLAAQD	0,666666667	LLPAAD	orf9
WP_003401003.1	PE-PPE domain-containing protein [Mycobacterium]	LPQIQLPQ	0,625	LPQRQKKQ	orf9
WP_003406369.1	amidase [Mycobacterium]	LPVRCGKQ	0,625	LPQRQKKQ	orf9
WP_003410003.1	DUF2384 domain-containing protein [Mycobacterium]	VPQRLNKQ	0,625	LPQRQKKQ	orf9
WP_010950678.1	hypothetical protein [Mycobacterium]	LPQRAAYQ	0,625	LPQRQKKQ	orf9
WP_003418002.1	cholesterol oxidase [Mycobacterium]	QGTDVPRW	0,625	QGTDYKHW	orf9
WP_011799069.1	endo-1,4-beta-glucanase [Mycobacterium]	TGTDYRGW	0,625	QGTDYKHW	orf9
WP_003400356.1	Stk1 family PASTA domain-containing Ser/Thr kinase [Mycobacterium]	SQASVDSP	0,625	SQASSRSS	orf9
WP_003402870.1	hypothetical protein [Mycobacterium]	FQASSGGS	0,625	SQASSRSS	orf9
WP_003405142.1	FmdB family transcriptional regulator [Mycobacterium]	STKSSGSS	0,625	SQASSRSS	orf9
WP_003405142.1	FmdB family transcriptional regulator [Mycobacterium]	SSGSSGSS	0,625	SQASSRSS	orf9
WP_003405142.1	FmdB family transcriptional regulator [Mycobacterium]	SSGSSGSS	0,625	SQASSRSS	orf9
WP_003405267.1	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU [Mycobacterium]	AQASKRAS	0,625	SQASSRSS	orf9
WP_003408092.1	excinuclease ABC subunit UvrA [Mycobacterium]	SAATSRSN	0,625	SQASSRSS	orf9
WP_003409877.1	hypothetical protein [Mycobacterium]	SQWSGRST	0,625	SQASSRSS	orf9
WP_003414001.1	tRNA (N6-isopentenyl adenosine(37)-C2)-methylthiotransferase MiaB [Mycobacterium]	SLPSSRES	0,625	SQASSRSS	orf9

WP_003418324.1	type VII secretion-associated protein [Mycobacterium]	RQASSGVS	0,625	SQASSRSS	orf9
WP_003898705.1	hypothetical protein [Bacteria]	SLPSSRPS	0,625	SQASSRSS	orf9
WP_003898731.1	hypothetical protein [Mycobacterium]	VQASHRSI	0,625	SQASSRSS	orf9
WP_003899255.1	pyridoxal phosphate-dependent aminotransferase [Mycobacterium]	ARASSGSS	0,625	SQASSRSS	orf9
WP_003900580.1	type III-A CRISPR-associated protein Cas10/Csm1 [Mycobacterium]	SQASNRAL	0,625	SQASSRSS	orf9
WP_003901356.1	DUF2236 domain-containing protein [Mycobacterium]	STASSPVS	0,625	SQASSRSS	orf9
WP_010950509.1	multifunctional oxoglutarate decarboxylase/oxoglutarate dehydrogenase thiamine pyrophosphate-binding subunit/dihydrolipoyllysine-residue succinyltransferase subunit [Mycobacterium]	SAPSSGSS	0,625	SQASSRSS	orf9
WP_010950554.1	type I polyketide synthase [Mycobacterium]	SQASERAR	0,625	SQASSRSS	orf9
WP_010950568.1	30S ribosomal protein S1 [Mycobacterium]	SSASSAPS	0,625	SQASSRSS	orf9
WP_010950615.1	solute-binding protein [Mycobacterium]	SQAISDSR	0,625	SQASSRSS	orf9
WP_010950660.1	PPE family protein [Mycobacterium]	SAASSAAS	0,625	SQASSRSS	orf9
WP_010950745.1	protein translocase subunit SecF [Mycobacterium]	TQASSQSA	0,625	SQASSRSS	orf9
WP_010950790.1	magnesium chelatase subunit D family protein [Mycobacterium]	SQPNSRSK	0,625	SQASSRSS	orf9
WP_011799143.1	PE domain-containing protein [Mycobacterium tuberculosis]	SQASSTYA	0,625	SQASSRSS	orf9
WP_011799362.1	type VII secretion system ESX-1 target EspA [Mycobacterium tuberculosis]	SLASSASL	0,625	SQASSRSS	orf9
WP_011799363.1	hypoxanthine phosphoribosyltransferase [Mycobacterium]	SYGSSASS	0,625	SQASSRSS	orf9
WP_003402100.1	protein kinase [Mycobacterium]	ALPPTEPR	0,625	TFPPTEPK	orf9
WP_003404395.1	S-sulfocysteine synthase CysK2 [Mycobacterium]	GQPPTEPD	0,625	TFPPTEPK	orf9
WP_003412373.1	ComEA family DNA-binding protein [Mycobacterium]	TGPKTAPK	0,625	TFPPTEPK	orf9
WP_003414748.1	signal recognition particle protein [Mycobacterium]	TRGPTPPK	0,625	TFPPTEPK	orf9
WP_003898724.1	hypothetical protein [Mycobacterium]	TPPPTTPP	0,625	TFPPTEPK	orf9
WP_003900169.1	hypothetical protein [Mycobacterium tuberculosis complex]	TAPPTTPV	0,625	TFPPTEPK	orf9
WP_003900169.1	hypothetical protein [Mycobacterium tuberculosis complex]	TTPPTTPP	0,625	TFPPTEPK	orf9
WP_003900169.1	hypothetical protein [Mycobacterium tuberculosis complex]	TTPPTTPV	0,625	TFPPTEPK	orf9
WP_003900169.1	hypothetical protein [Mycobacterium tuberculosis complex]	TTPPTTPP	0,625	TFPPTEPK	orf9
WP_003900169.1	hypothetical protein [Mycobacterium tuberculosis complex]	TTPPTTPV	0,625	TFPPTEPK	orf9
WP_003900169.1	hypothetical protein [Mycobacterium tuberculosis complex]	TTPPTTPP	0,625	TFPPTEPK	orf9
WP_003900169.1	hypothetical protein [Mycobacterium tuberculosis complex]	TTPPTTPV	0,625	TFPPTEPK	orf9
WP_010950435.1	DUF4226 domain-containing protein [Mycobacterium]	PFPPYQPK	0,625	TFPPTEPK	orf9
WP_010950506.1	membrane protein [Mycobacterium]	PFPPTAPP	0,625	TFPPTEPK	orf9
WP_011799356.1	PE family protein [Mycobacterium tuberculosis]	VFMPTEPQ	0,625	TFPPTEPK	orf9

WP_003899841.1	virulence factor Mce family protein [Mycobacterium]	QSFGRD	0,833333333	QQFGRD	sg
WP_011799314.1	acyl-CoA dehydrogenase [Mycobacterium]	QQFGRT	0,833333333	QQFGRD	sg
WP_003400000.1	type VII secretion system ESX-1 subunit EccE1 [Mycobacterium]	LYQQVI	0,666666667	LYQDVN	sg
WP_003400893.1	maltose alpha-D-glucosyltransferase [Mycobacterium]	GYQAVN	0,666666667	LYQDVN	sg
WP_003401309.1	acetyl-CoA C-acetyltransferase [Mycobacterium]	LYRDDN	0,666666667	LYQDVN	sg
WP_003402089.1	phosphate acetyltransferase [Mycobacterium]	LTQAVN	0,666666667	LYQDVN	sg
WP_003402097.1	acetate kinase [Mycobacterium]	LDQDRN	0,666666667	LYQDVN	sg
WP_003402143.1	hypothetical protein [Mycobacterium]	LYADGN	0,666666667	LYQDVN	sg
WP_003406167.1	bifunctional FO biosynthesis protein CofGH [Mycobacterium]	LARDVN	0,666666667	LYQDVN	sg
WP_003406887.1	co-chaperone YbbN [Mycobacterium tuberculosis complex]	LNQDVS	0,666666667	LYQDVN	sg
WP_003408180.1	argininosuccinate lyase [Mycobacterium]	LAQDVA	0,666666667	LYQDVN	sg
WP_003409339.1	GlsB/YeaQ/YmgE family stress response membrane protein [Mycobacterium]	LGVDVN	0,666666667	LYQDVN	sg
WP_003411972.1	PE family protein [Mycobacterium]	LAQVVN	0,666666667	LYQDVN	sg
WP_003413230.1	ABC transporter permease [Mycobacterium]	GYQTVN	0,666666667	LYQDVN	sg
WP_003414630.1	cell surface glycolipoprotein Mpt83 [Mycobacterium]	LNPDVN	0,666666667	LYQDVN	sg
WP_003414814.1	DNA-formamidopyrimidine glycosylase [Mycobacterium]	LYVNVN	0,666666667	LYQDVN	sg
WP_003416086.1	SPFH domain-containing protein [Mycobacterium]	LRQDVG	0,666666667	LYQDVN	sg
WP_003416605.1	hypothetical protein [Mycobacterium]	LHQHVN	0,666666667	LYQDVN	sg
WP_003419733.1	RidA family protein [Mycobacterium]	LGADVN	0,666666667	LYQDVN	sg
WP_003899294.1	molecular chaperone DnaJ [Mycobacterium]	LHPDVN	0,666666667	LYQDVN	sg
WP_003900467.1	PPE family protein [Mycobacterium]	LVPDVN	0,666666667	LYQDVN	sg
WP_003900866.1	LCP family protein [Mycobacterium]	DGQDVN	0,666666667	LYQDVN	sg
WP_003901231.1	cytochrome P450 [Mycobacterium]	LQQRVN	0,666666667	LYQDVN	sg
WP_003911668.1	accessory Sec system translocase SecA2 [Mycobacterium tuberculosis]	LVTDVN	0,666666667	LYQDVN	sg
WP_010950653.1	hypothetical protein [Mycobacterium]	LSQYVN	0,666666667	LYQDVN	sg
WP_010950668.1	hypothetical protein [Mycobacterium]	LDQDVR	0,666666667	LYQDVN	sg
WP_011799106.1	zinc metallopeptidase [Mycobacterium]	TYQLVN	0,666666667	LYQDVN	sg
WP_011799126.1	PE family protein [Mycobacterium tuberculosis]	LQQDVI	0,666666667	LYQDVN	sg
WP_011799357.1	PE family protein [Mycobacterium tuberculosis]	LSQDGN	0,666666667	LYQDVN	sg
WP_011799357.1	PE family protein [Mycobacterium tuberculosis]	LSQDGN	0,666666667	LYQDVN	sg
WP_011799357.1	PE family protein [Mycobacterium tuberculosis]	LSQDGN	0,666666667	LYQDVN	sg
WP_011799357.1	PE family protein [Mycobacterium tuberculosis]	LSQDGN	0,666666667	LYQDVN	sg
WP_071854216.1	ArsA family ATPase [Mycobacterium]	LVQDEN	0,666666667	LYQDVN	sg
WP_003400425.1	fatty acyl-AMP ligase [Mycobacterium]	EQFGRA	0,666666667	QQFGRD	sg

WP_003401234.1	hypothetical protein [Mycobacterium]	QEFGVD	0,666666667	QQFGRD	sg
WP_003401392.1	acyl-CoA dehydrogenase [Mycobacterium]	EQFGRP	0,666666667	QQFGRD	sg
WP_003401972.1	acyl-CoA dehydrogenase [Mycobacterium]	TQFGRP	0,666666667	QQFGRD	sg
WP_003402400.1	hypothetical protein [Mycobacterium]	AQNGRD	0,666666667	QQFGRD	sg
WP_003403114.1	virulence factor Mce family protein [Mycobacterium]	QAWGRD	0,666666667	QQFGRD	sg
WP_003403610.1	formylglycine-generating enzyme family protein [Mycobacterium]	HPFGRD	0,666666667	QQFGRD	sg
WP_003404651.1	NAD(P)/FAD-dependent oxidoreductase [Mycobacterium]	QLTGRD	0,666666667	QQFGRD	sg
WP_003404890.1	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Mycobacterium]	QWFGRS	0,666666667	QQFGRD	sg
WP_003404895.1	VWA domain-containing protein [Mycobacterium]	QQFSGD	0,666666667	QQFGRD	sg
WP_003406259.1	serine protease HtrA [Mycobacterium]	QAFGRP	0,666666667	QQFGRD	sg
WP_003407374.1	acyltransferase family protein [Mycobacterium]	KQFGED	0,666666667	QQFGRD	sg
WP_003408069.1	dephospho-CoA kinase [Mycobacterium]	DAFGRD	0,666666667	QQFGRD	sg
WP_003408165.1	ornithine carbamoyltransferase [Mycobacterium]	TQLGRD	0,666666667	QQFGRD	sg
WP_003408499.1	serine hydrolase [Mycobacterium]	QDFGRG	0,666666667	QQFGRD	sg
WP_003408854.1	type VII secretion system ESX-5 serine protease mycosin MycP5 [Mycobacterium]	WQFGRG	0,666666667	QQFGRD	sg
WP_003408859.1	type VII secretion system ESX-5 subunit EccE5 [Mycobacterium]	RRFGRD	0,666666667	QQFGRD	sg
WP_003409179.1	PPE family protein [Mycobacterium]	QGFGRA	0,666666667	QQFGRD	sg
WP_003409870.1	hypothetical protein [Mycobacterium]	GQLGRD	0,666666667	QQFGRD	sg
WP_003410221.1	carbohydrate ABC transporter permease [Mycobacterium]	QFRGRD	0,666666667	QQFGRD	sg
WP_003410775.1	YafY family transcriptional regulator [Mycobacterium]	QLGGRD	0,666666667	QQFGRD	sg
WP_003411056.1	methionine synthase [Mycobacterium]	QQRGRF	0,666666667	QQFGRD	sg
WP_003411130.1	hypothetical protein [Mycobacterium]	QQGGAD	0,666666667	QQFGRD	sg
WP_003411214.1	D,D-transpeptidase PbpB [Mycobacterium tuberculosis complex]	QQRLRD	0,666666667	QQFGRD	sg
WP_003411946.1	carbohydrate ABC transporter permease [Mycobacterium]	QFRGRD	0,666666667	QQFGRD	sg
WP_003411969.1	ATP-binding cassette domain-containing protein [Mycobacterium]	DQQGRD	0,666666667	QQFGRD	sg
WP_003413373.1	lipoprotein [Mycobacterium]	RQFGRV	0,666666667	QQFGRD	sg
WP_003414151.1	metallophosphoesterase [Mycobacterium]	QIFGRA	0,666666667	QQFGRD	sg
WP_003414201.1	AAA family ATPase [Mycobacterium]	MPFGRD	0,666666667	QQFGRD	sg
WP_003417889.1	wax ester/triacylglycerol synthase family O-acyltransferase [Mycobacterium]	QQSGRR	0,666666667	QQFGRD	sg
WP_003418289.1	glutamine--fructose-6-phosphate transaminase (isomerizing) [Mycobacterium]	LQAGRD	0,666666667	QQFGRD	sg
WP_003419352.1	acyl-CoA/acyl-ACP dehydrogenase [Mycobacterium]	VQFGRP	0,666666667	QQFGRD	sg

WP_003420783.1	esterase family protein [Mycobacterium]	QQFGGV	0,666666667	QQFGRD	sg
WP_003898783.1	trehalose ABC transporter substrate-binding protein LpqY [Mycobacterium]	QQFGGR	0,666666667	QQFGRD	sg
WP_003899696.1	arabinosyltransferase EmbA [Mycobacterium]	QAFGPD	0,666666667	QQFGRD	sg
WP_003899759.1	outer membrane channel protein/necrotizing toxin glycohydrolase CpnT [Mycobacterium]	APFGRD	0,666666667	QQFGRD	sg
WP_003899976.1	hypothetical protein [Mycobacterium tuberculosis complex]	QQFGLG	0,666666667	QQFGRD	sg
WP_003900650.1	phosphotransferase family protein [Mycobacterium]	QQDGRS	0,666666667	QQFGRD	sg
WP_003905015.1	ATP-dependent helicase [Mycobacterium]	QQLGRR	0,666666667	QQFGRD	sg
WP_003910308.1	PE family protein [Mycobacterium tuberculosis complex]	QQFVRA	0,666666667	QQFGRD	sg
WP_003911788.1	pyruvate dehydrogenase (acetyl-transferring), homodimeric type [Mycobacterium]	HFFGRD	0,666666667	QQFGRD	sg
WP_003915348.1	transposase [Mycobacterium tuberculosis]	LEFGRD	0,666666667	QQFGRD	sg
WP_010950361.1	trehalose monomycolate RND transporter MmpL3 [Mycobacterium]	QVYGRD	0,666666667	QQFGRD	sg
WP_010950488.1	PE family protein [Mycobacterium tuberculosis]	GQFGGD	0,666666667	QQFGRD	sg
WP_010950647.1	FMN-binding protein Acg [Mycobacterium]	VTFGRD	0,666666667	QQFGRD	sg
WP_010950910.1	acyl-CoA/acyl-ACP dehydrogenase [Mycobacterium]	TQFGRA	0,666666667	QQFGRD	sg
WP_011799096.1	PE family protein [Mycobacterium tuberculosis]	QLLGRD	0,666666667	QQFGRD	sg
WP_011799162.1	type I polyketide synthase [Mycobacterium]	TQCGRD	0,666666667	QQFGRD	sg
WP_011799185.1	transcriptional regulator [Mycobacterium]	QQVGRG	0,666666667	QQFGRD	sg
WP_011799190.1	RND transporter MmpL12 [Mycobacterium]	QIFSRD	0,666666667	QQFGRD	sg
WP_011799208.1	amino acid permease [Mycobacterium]	QQLGRG	0,666666667	QQFGRD	sg
WP_011799328.1	hypothetical protein [Mycobacterium]	QVDGRD	0,666666667	QQFGRD	sg
WP_003901535.1	sulfatase-like hydrolase/transferase [Mycobacterium]	AAQVAYRE	0,625	AMQMAYRF	sg
WP_003406299.1	sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC [Mycobacterium]	FGEVTLAP	0,625	FGEVFNAT	sg
WP_003899426.1	cell division protein ZapE [Mycobacterium]	FAEVSFAT	0,625	FGEVFNAT	sg
WP_010950583.1	respiratory nitrate reductase subunit gamma [Mycobacterium]	RGPVFMAT	0,625	FGEVFNAT	sg
WP_011799162.1	type I polyketide synthase [Mycobacterium]	FAEAFHAT	0,625	FGEVFNAT	sg
WP_011799173.1	PPE family protein [Mycobacterium tuberculosis]	FGGVSNAL	0,625	FGEVFNAT	sg
WP_003400075.1	hypothetical protein [Mycobacterium]	GAGDLASP	0,625	GAGICASY	sg
WP_003402855.1	PE family protein [Mycobacterium tuberculosis complex]	GAGGAASI	0,625	GAGICASY	sg
WP_003404004.1	LLM class flavin-dependent oxidoreductase [Mycobacterium]	GAGQCAPS	0,625	GAGICASY	sg
WP_003405370.1	PE domain-containing protein [Bacteria]	GAGNWASA	0,625	GAGICASY	sg
WP_003413891.1	1-deoxy-D-xylulose-5-phosphate synthase [Mycobacterium]	GTGVCASD	0,625	GAGICASY	sg

WP_003414032.1	transcriptional regulator ClgR [Mycobacterium]	GATIDAST	0,625	GAGICASY	sg
WP_003414086.1	PE domain-containing protein [Mycobacterium tuberculosis complex]	GAGNWASA	0,625	GAGICASY	sg
WP_003416381.1	PPE family protein [Mycobacterium tuberculosis complex]	GAGGAASV	0,625	GAGICASY	sg
WP_003418300.1	hypothetical protein [Mycobacterium]	TAGVAASY	0,625	GAGICASY	sg
WP_010886090.1	PE family protein [Mycobacterium tuberculosis]	GAGGAASG	0,625	GAGICASY	sg
WP_010950488.1	PE family protein [Mycobacterium tuberculosis]	GAGAGASG	0,625	GAGICASY	sg
WP_010950488.1	PE family protein [Mycobacterium tuberculosis]	GAGGQASP	0,625	GAGICASY	sg
WP_010950524.1	PE family protein [Mycobacterium tuberculosis complex]	GAGAYASA	0,625	GAGICASY	sg
WP_010950570.1	PE family protein [Mycobacterium tuberculosis]	GAGGNASL	0,625	GAGICASY	sg
WP_010950666.1	PE family protein [Mycobacterium tuberculosis]	GAGGSASG	0,625	GAGICASY	sg
WP_011799095.1	PE family protein [Mycobacterium tuberculosis]	GAGGVASS	0,625	GAGICASY	sg
WP_011799096.1	PE family protein [Mycobacterium tuberculosis]	GAGGRAST	0,625	GAGICASY	sg
WP_011799125.1	PE family protein [Mycobacterium tuberculosis]	GAGAYASA	0,625	GAGICASY	sg
WP_011799136.1	DNA-binding protein [Mycobacterium]	GAGVDASR	0,625	GAGICASY	sg
WP_011799231.1	PPE family protein [Mycobacterium tuberculosis]	GALISGSY	0,625	GAGICASY	sg
WP_011799340.1	PPE family protein [Mycobacterium tuberculosis]	GAGNVGSY	0,625	GAGICASY	sg
WP_011799357.1	PE family protein [Mycobacterium tuberculosis]	GAGAYASA	0,625	GAGICASY	sg
WP_011799359.1	PE family protein [Mycobacterium tuberculosis]	GAGAYASA	0,625	GAGICASY	sg
WP_011799359.1	PE family protein [Mycobacterium tuberculosis]	GAGISFSN	0,625	GAGICASY	sg
WP_011799380.1	septum formation family protein [Mycobacterium]	LAGYIASY	0,625	GAGICASY	sg
WP_011799380.1	septum formation family protein [Mycobacterium]	GAKINASF	0,625	GAGICASY	sg
WP_058901161.1	PE family protein [Mycobacterium tuberculosis]	GAGGFAST	0,625	GAGICASY	sg
WP_058901161.1	PE family protein [Mycobacterium tuberculosis]	GAGDFASG	0,625	GAGICASY	sg
WP_137054066.1	PPE family protein [Mycobacterium tuberculosis]	GAGISGVY	0,625	GAGICASY	sg
WP_003402100.1	protein kinase [Mycobacterium]	YSFLPQLN	0,625	GSFCTQLN	sg
WP_003403834.1	ribbon-helix-helix protein, CopG family [Mycobacterium]	RGIDLTSN	0,625	KGIYQTSN	sg
WP_003420436.1	DUF2330 domain-containing protein [Mycobacterium]	VDIYQTSR	0,625	KGIYQTSN	sg
WP_011799093.1	CopG family transcriptional regulator [Mycobacterium]	PGIDLTSN	0,625	KGIYQTSN	sg
WP_137054066.1	PPE family protein [Mycobacterium tuberculosis]	SGIYNTSV	0,625	KGIYQTSN	sg
WP_137054066.1	PPE family protein [Mycobacterium tuberculosis]	SGIYNTST	0,625	KGIYQTSN	sg
WP_003400000.1	type VII secretion system ESX-1 subunit EccE1 [Mycobacterium]	LYQQVIGT	0,625	LYQDVNCT	sg