

Supplementary Table 5. Comparison of MTB peptides defined by IgG in patients from Armenia and from Sweden.

Peptides	Protein	Index value in 34 TB+ patients from Armenia	Peptides	Protein	Index value in 6 TB+ patients from Sweden
QSSFYSDWYSPACGK	CAB10044.1; SECRETED ANTIGEN 85-B FBPB (85B)	1,7776	MGCRLPGGINSPODKL	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	3,2663
MTAHTHDGTRTWRTG	CAB10947.1; PROBABLE LIPOPROTEIN LPRJ	1,4567	WLADLVRRSPWGEMF	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	2,0054
VRRRHGLSSLGWNL	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	1,3994	TGRSLDMSVAALAGM	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	1,9423
PILGAPWLADLVRRS	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	1,3324	PILGAPWLADLVRRS	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	1,8986
KAMLFDRSGEPFPY	RNA POLYMERASE BETA-SUBUNIT AAA21416	1,2314	KAMLFDRSGEPFPY	RNA POLYMERASE BETA-SUBUNIT AAA21416	1,8126
IRLAKCGPWHRGGWD	POSSIBLE HEMOLYSIN CAA16235	1,141	VKAPGFGDRRKAMLQ	60 kDa chaperonin 2 P0A521	1,7968
ALMSGNFSNGILWRG	YP_177963; PPE FAMILY PROTEIN	1,0973	PTIMGEVRRHFRDNS	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	1,7872
YRADSVRLIAAHL	TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446	1,0307	GMYNFKESIRDFARA	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	1,7756
GYIPILGAPWLADLV	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,956	GELDNRSQFYLYMY	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	1,7505
FRMELLSLPQDEWAG	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,9553	LTAANTKKVAMAAPM	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	1,7085
AFDLDRLLFKRNICH	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,9176	AFDLDRLLFKRNICH	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	1,6717
GELDNRSQFYLYMY	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,8795	MTAHTHDGTRTWRTG	CAB10947.1; PROBABLE LIPOPROTEIN LPRJ	1,6451
YRLERPLLALQCMF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,8753	QSSFYSDWYSPACGK	CAB10044.1; SECRETED ANTIGEN 85-B FBPB (85B)	1,6311
HWLRPITPTFRPSWP	PUTATIVE CYCLOPROPANE-FATTY-ACYL-	0,783	VIPTMTPPPGMVRQR	CAA17582.1; PROBABLE SERINE PROTEASE PEPPD	1,5876

	PHOSPHOLIPID SYNTHASE UFAA1 NP_854118				
PFNVNLKLQFLHDAF	YP_177963; PPE FAMILY PROTEIN	0,7652		LKMCWPAAPRSVGVP	POSSIBLE HEMOLYSIN-LIKE PROTEIN CAA17201 1,5409
AIANAYWSPQARRRF	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,7299		RSLHWLRPITPTFRP	PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE UFAA1 NP_854118 1,5054
WRSLDVEMTAVQRSF	PPE FAMILY PROTEIN CAE55489	0,7127		ALMSGNFNGLWRG	YP_177963; PPE FAMILY PROTEIN 1,4496
RRFPLDPVWTRFFG	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,6965		YRADSVRLIAAHL	TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446 1,432
GVYKVGKLEKIPLL	CAB06237.1; CONSERVED HYPOTHETICAL PROTEIN	0,6757		FCGRIHTRYSSAYEL	SECRETED L-ALANINE DEHYDROGENASE ALD CAA15575 1,4222
EMIEAVGYRSWPRYF	PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,6748		GLRGLLRVISSEHPM	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808 1,3622
QAQYVAQLHVWARRE	MTB48 AAK31576	0,6624		HWLRPITPTFRPSWP	PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE UFAA1 NP_854118 1,3283
FCGRIHTRYSSAYEL	SECRETED L-ALANINE DEHYDROGENASE ALD CAA15575	0,6143		GYIPILGAPWLADLV	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808 1,27
LRPASCRFVPTCSQY	POSSIBLE HEMOLYSIN CAA16235	0,6097		WGGAFDLDRLLFKRN	POSSIBLE GLYCOSYL TRANSFERASE CAB05419 1,2687
RHGLSSLGWNLCRIF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,5962		AMRTLRLKYVEADLRV	POSSIBLE GLYCOSYL TRANSFERASE CAB05415 1,2657
WGGAFDLDRLLFKRN	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,5502		LSPLRPASCRFVPTC	POSSIBLE HEMOLYSIN CAA16235 1,2146
RLVKLLYRLERPLLF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,5502		LRPASCRFVPTCSQY	POSSIBLE HEMOLYSIN CAA16235 1,2138
ARASFSYGLNAKWPV	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,5338		YCGKYKRVRFKGIIC	RNA POLYMERASE BETA'-SUBUNIT AAA21417 1,1718
DVPWTRFFGVRPVS	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,5333		PKVISRAMVMRTVIS	POSSIBLE GLYCOSYL TRANSFERASE CAB05419 1,1702
WLADLVRRSPWGEMF	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,5301		PEFQRHRDKIVQRCL	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069 1,1516
PWDGRNHLYAAVYRT	CAA16030.1;	0,5262		LRLMPENRPTWLAS	POSSIBLE 1,125

	PROBABLE MOLYBDOPTERIN- GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN				GLYCOSYL TRANSFERASE CAB05415	
LVVKRGNAGSRFL	CAB01474.1; CONSERVED HYPOTHETICAL PROTEIN CFP17	0,5166		PVTHIWYFKGVPSRL	RNA POLYMERASE BETA'-SUBUNIT AAA21417	1,0922
GVRLAFVCAVDMPYL	CAA16030.1; PROBABLE MOLYBDOPTERIN- GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN	0,5089		IRLAKCGPWHRGWD	POSSIBLE HEMOLYSIN CAA16235	1,0881
LSPLRPASCRFVPTC	POSSIBLE HEMOLYSIN CAA16235	0,4868		AVAVGCAQPACLRAY	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	1,0307
PVTHIWYFKGVPSRL	RNA POLYMERASE BETA'-SUBUNIT AAA21417	0,4781		YRLERPLLALQCMF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	1,0282
VKGAWVLARYDDGRP	CONSERVED HYPOTHETICAL PROTEIN TB18.5CAD93033	0,4771		DVPWTRFFGVRPVS	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	1,0253
AITNTARPWHIGLYG	PPE FAMILY PROTEIN CAE55334	0,4769		NMREYLAAGAKERQR	MTB48 AAK31576	1,001
FRHHAIHTIPSERFF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,465		GVRLAFVCAVDMPYL	CAA16030.1; PROBABLE MOLYBDOPTERIN- GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN	0,9976
FNIRCFSPALVTRY	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,4586		VRRRHGLSSLGWNLC	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,9946
PSERFFGNLTQGRFY	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,4571		PVAVIGMGCRPLGGI	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,9943
PTIMGEVRRHFRDNS	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	0,4569		WRSLDVEMTAVQRSF	PPE FAMILY PROTEIN CAE55489	0,9935
FTLPGRSLMFVRNVG	MTB81 (publication)	0,4539		AIANAYWSPQARRRF	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,9873
SQFGPYQLRLGRG	TRANSMEMBRANE SERINE/THREONINE- PROTEIN KINASE D PKND NP_215446	0,451		FRMELLSLPQDEWAG	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,9579
PDFKWPPTPGSPLFP	CAB06237.1; CONSERVED HYPOTHETICAL PROTEIN	0,4411		RMRKFARSNHGTCAN	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,9493
RTLRYIAADRKILN	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,4273		GVYKVCKGLEKIPLL	CAB06237.1; CONSERVED HYPOTHETICAL PROTEIN	0,9396

IQMSDPAYNINISLP	CAA98382.1; IMMUNOGENIC PROTEIN MPT64	0,4247		QAQYVAQLHVWARRE	MTB48 AAK31576	0,8876
NYRYAINNSFGFGGH	3-OXOACYL-[ACYL- CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642	0,4105		FACDPRFNKLLGLPL	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,8726
SFYRPKRPGSYPIVL	PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS3 YP_177768	0,407		LVVKRGNAGSRFLL	CAB01474.1; CONSERVED HYPOTHETICAL PROTEIN CFP17	0,869
AATIKRFADRFARN	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,4066		HPIVFGHAVRIFYKD	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,8627
LRISQLLANWLRHG	MTB81 (publication)	0,4058		KIHARSTGPYMITQ	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,855
YNQLLGPLPFRHHAI	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,4034		SRTGSIYIVKPKMHG	MTB81 (publication)	0,8511
FTLPGERIHVVFRSD	PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS3 YP_177768	0,392		RRFPLPDVPWTRFFG	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,8376
HPIVFGHAVRIFYKD	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,3856		PDFKWPPTPGSPLFP	CAB06237.1; CONSERVED HYPOTHETICAL PROTEIN	0,8202
RSLHWLRPITPTFRP	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,3799		RQRVAAAGFGHRVEI	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,7801
MLATRHTQTWIKYI	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,3777		ARASFSYGLNAKWPV	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,7763
SCVYATASRWGGPPV	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,3697		RCLPLADHIARRFEG	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	0,7725
VRPVSILYRLYRPLI	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,3589		AVLDPDHDGMRVQVR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,7721
FYRRGLFGTIGPYNL	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,3525		MLATRHTQTWIKYI	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,7599
TRYSSAYELEGAVKR	SECRETED L- ALANINE DEHYDROGENASE ALD CAA15575	0,3507		SCVYATASRWGGPPV	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,7582
AVAVGCAQPACLRAY	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,3436		FTLPGRSLMFVRNVG	MTB81 (publication)	0,747
RYARCLGSAVNPVLR	PROBABLE	0,3428		EMIEAVGYRSWPRYF	PUTATIVE	0,7395

	ISOCITRATE DEHYDROGENASE CAA16247				CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	
QAIFYRRGLFGTIGP	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,3288		PWDGRNHLYAAVYRT	CAA16030.1; PROBABLE MOLYBDOPTERIN- GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN	0,7307
EAVGYRSWPRYFAAL	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,3231		MIDGTSLRALLKQYG	TRANSMEMBRANE SERINE/THREONINE- PROTEIN KINASE D PKND NP_215446	0,7116
RSEYRQAAARLADAF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,3201		SPAMVAANRTRLASL	PPE FAMILY PROTEIN CAE55504	0,7048
RKYIAADRILNEIA	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,3156		EQAGLRGLLRVISSE	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,6865
LFIHRPDALARRIGR	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,3114		KYKRVRFKGIICERC	RNA POLYMERASE BETA'-SUBUNIT AAA21417	0,6861
NGDEVQIGKFRVLFL	CAB01474.1; CONSERVED HYPOTHETICAL PROTEIN CFP17	0,2974		MSVAALAGMRREQPL	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,6787
FGVRLVKLLYRLERP	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,2921		RTLRYIAADRILN	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,6733
RVNPFQFIETPYRKV	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,2893		RVNPFQFIETPYRKV	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,6619
GMYNFKESIRDFARA	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,2874		GDFYAGEKSMTLDRA	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,6608
FRSGYLDVYQWTLIR	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,2852		RGPGQMLGGLPVGQM	CAE55371.1; PPE FAMILY PROTEIN	0,6593
YRATNFKVDQPGTVT	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,2784		DLVRRSPWGEMFAST	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,6586
FGTIGPYNLRYRVLA	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,2738		RVGFQPHVENALRLM	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,6453
TGDEVTYRADIYALA	TRANSMEMBRANE SERINE/THREONINE- PROTEIN KINASE D PKND NP_215446	0,2714		KIRAWGRRLMIGTAA	CAB10044.1; SECRETED ANTIGEN 85-B FBPB (85B)	0,6345
PLNWLRRKHGLSSLG	POSSIBLE	0,2405		AITNTARPWHIGLYG	PPE FAMILY	0,6268

	GLYCOSYL TRANSFERASE CAB05418				PROTEIN CAE55334	
WSVKVPRRLKELHLR	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	0,2347		PPSLVAANRSRLMSL	PPE FAMILY PROTEIN CAE55334	0,6126
KAVKEYARKHPHSMG	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,2334		DPTQQIPKLVANNTR	CAB10044.1; SECRETED ANTIGEN 85-B FBPB (85B)	0,5906
AAIANRLLRRTATHL	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,2259		QRVAVRVSQLHAGPR	CONSERVED HYPOTHETICAL PROTEIN CAB08634	0,585
WPVYLSTKNTILKAY	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,2243		TRYSSAYELEGAVKR	SECRETED L- ALANINE DEHYDROGENASE ALD CAA15575	0,5797
EVQIGKFRLLVFLTGP	CAB01474.1; CONSERVED HYPOTHETICAL PROTEIN CFP17	0,2181		WSVKVPRRLKELHLR	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	0,5761
YGSFRRSFRLPAHVT	CAA17343.1; HEAT SHOCK PROTEIN HSP	0,2164		AATIKRFADRFARFN	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,5613
IEYRSLARVYGAGTP	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,208		DAARVICRRSKLMTR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,5602
RDFARASFSYGLNAK	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,2078		VYVTSEGMYGRVVKL	TRANSMEMBRANE SERINE/THREONINE- PROTEIN KINASE D PKND NP_215446	0,5358
IKRFADRFARFNLQE	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,2071		LLEQAAAVEEASDTA	CAE55371.1; PPE FAMILY PROTEIN	0,534
LKIAQGRLFYNTRL	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,1868		FYRRGLFGTIGPYNL	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,5246
DGRTLREIRYGSFRR	CAA17343.1; HEAT SHOCK PROTEIN HSP	0,1839		SQMHVSRLAKSLAR	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	0,5245
VGDPDEHSLLAGREQ	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1807		CIRAAARGAHIRSVT	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,5159
FTAHTKHYRVVSKPA	CAE55335.1; PE FAMILY PROTEIN	0,1789		ERCGVEVTRAKVRRE	RNA POLYMERASE BETA'-SUBUNIT AAA21417	0,5031
KADVYGNTLGLFPF	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1781		GGATSLISYMLPRSP	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,5025
LRLMPENRPRTWLAS	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,1776		AGAVMQVISRSEYRQ	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,4996
GPMVRKGTMKSQPWI	MTB81 (publication)	0,1774		VKGAWVLARYDDGRP	CONSERVED	0,499

					HYPOTHETICAL PROTEIN TB18.5CAD93033	
WDLTSAEFTRRRYAE	CONSERVED HYPOTHETICAL PROTEIN CAB08634	0,1748		LFIHRPDALARRIGR	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,4989
FFGVRPVSILYRLYR	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,1699		TELAQAQRKIDRL	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,495
ANRLLRRTATHPLR	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,1695		NYRYAINNSFGFGGH	3-OXOACYL-[ACYL- CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642	0,4885
FACDPRFNKLLGPLP	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,1662		RLARQRVAAAGFGHR	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,4731
EIGKADVYGNTLGL	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1651		RRERMGHIELAAPVT	RNA POLYMERASE BETA'-SUBUNIT AAA21417	0,473
VRPFVLARSLDPSRY	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,1648		RSEYRQAAARLADAF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,4708
RMRKFARSNHGTCAN	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,1633		DIILNTHGVPRRMNI	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,4596
MGCRLPGGINSPOKL	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1605		KAVKEYARKHPHSMG	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,4521
YCGKYKRVRFKGIIC	RNA POLYMERASE BETA'-SUBUNIT AAA21417	0,1555		RKYIAADRKILNEIA	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,4468
ASDFAYLVDFGIARA	TRANSMEMBRANE SERINE/THREONINE- PROTEIN KINASE D PKND NP_215446	0,1554		NRAAALMAKLRGAA	TWO COMPONENT TRANSCRIPTIONAL REGULATORY PROTEIN DEVR NP_217649	0,4113
TIRVGSFRGRWLDPR	CAA16102.1; ESAT-6 LIKE PROTEIN ESXQ	0,1474		RVGRYKVNKKLGLHV	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,4071
SRTGSIYIVKPKMHG	MTB81 (publication)	0,1458		RLVKLLYRLERPLL	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,404
VAITLWSQLYRRTL	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,1403		KGSQQEALYTEDR	MTB48 AAK31576	0,4011
GAAFGLTTAHTPRR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1389		WDLTSAEFTRRRYAE	CONSERVED HYPOTHETICAL PROTEIN CAB08634	0,3953

DLVRRSPWGEMFAST	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1389		RDFARASFSYGLNAK	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,3855
GRAGGGAALGGGGMG	MTB48 AAK31576	0,1355		SFYRPKRPGSYPIVL	PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS3 YP_177768	0,3787
YVAWMSVTAGQAELT	CAE55371.1; PPE FAMILY PROTEIN	0,1354		MTSAGGLLEQAAAVE	CAE55371.1; PPE FAMILY PROTEIN	0,3707
TILKAYDGMFKDEFE	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,1256		DSGFVTDGKMFIIGR	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,3603
AAAQFNASPVAQSYL	LOW MOLECULAR WEIGHT T-CELL ANTIGEN TB8.4 NP_215690	0,1232		GPMVRKGTMTKSQPWI	MTB81 (publication)	0,3553
PPSLVAAANRSRLMSL	PPE FAMILY PROTEIN CAE55334	0,1203		WPVYLSTKNTILKAY	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,3529
DPTQQIPKLVANNTR	CAB10044.1; SECRETED ANTIGEN 85-B FBPB (85B)	0,1202		FRHHAIHTIPSERFF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,3521
FGGLTTAHTPRREPR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1178		VGDPDEHSLLAGREQ	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,3507
RAPTESTRRCWTLVS	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1167		RFARFNLQERVIRPS	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,3472
AFAMTVPPSLVAANR	PPE FAMILY PROTEIN CAE55334	0,1164		TATLLPFEEAPEMTS	CAE55371.1; PPE FAMILY PROTEIN	0,3462
DARAADILKDESYKV	CAB08889.1; IRON-REGULATED CONSERVED HYPOTHETICAL PROTEIN	0,1123		PSERFFGNLTQGRFY	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,3446
SSGLLRHAHCPVVII	HYPOTHETICAL PROTEIN RV2623 NP_217139	0,1105		PSVMADVASGNLPAL	CONSERVED HYPOTHETICAL PROTEIN CAA15739	0,3374
MSVAALAGMRREQPL	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1071		RVTPVAVIGMGCRLP	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,3348
RLARQRVAAAGFGHR	PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,1052		IKRFADRFARFNLQE	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,3329
RRSGSSRAPTESTRR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1045		QAAAVEEASDTAAAN	CAE55371.1; PPE FAMILY PROTEIN	0,319
QRVAVRVSQLHAGPR	CONSERVED HYPOTHETICAL PROTEIN CAB08634	0,1039		IAAAAKPPLGSPPPK	CAA17582.1; PROBABLE SERINE PROTEASE PEPD	0,3094
TRHTQTWIKYIFPG	PUTATIVE CYCLOPROPANE-	0,1036		MMGNAFLTALTNAGI	CAB10947.1; PROBABLE	0,3017

	FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118				LIPOPROTEIN LPRJ	
AEDDCPPPGYDITAL	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1033		NGIELCRDLLSRMPD	TWO COMPONENT TRANSCRIPTIONAL REGULATORY PROTEIN DEVR NP_217649	0,3012
KDTKAVNPESTFSRI	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,1023		RRSGSSRAPTESTRR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,2936
AGAVMQVISRSEYRQ	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,0998		FGGLTTAHTPRREPR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,2863
AMSLTVGAGVASADP	LOW MOLECULAR WEIGHT T-CELL ANTIGEN TB8.4 NP_215690	0,0961		DGRTLREIRYGSFRR	CAA17343.1; HEAT SHOCK PROTEIN HSP	0,2843
TELAAQRRKIDRLL	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,0959		RHGLSSLGWNLCRIF	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,284
DLVYGDVIMRSTNFR	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,0952		ATATATLLPFEEAPE	CAE55371.1; PPE FAMILY PROTEIN	0,2801
MIDGTSLRALLKQYG	TRANSMEMBRANE SERINE/THREONINE- PROTEIN KINASE D PKND NP_215446	0,0949		ATVSPAMVAANRTRL	PPE FAMILY PROTEIN CAE55504	0,2754
SADNMREYLAAGAKE	MTB48 AAK31576	0,0933		PLNWLRRKHGLSSLG	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,2735
WSQLYRRTLNVAREL	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,0842		MAKTIAYDEEARRGL	60 kDa chaperonin 2 P0A521	0,2711
VKKPETINYRTLKPE	RNA POLYMERASE BETA'-SUBUNIT AAA21417	0,0832		YTEPILHRRRREFKA	MTB81 (publication)	0,27
RQRVAAAGFGHRVEI	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,0809		AGAATEVELKERKHR	60 kDa chaperonin 2 P0A521	0,2637
PVAVIGMGCRLPGGI	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,0773		FNIRCFSPALVTRY	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,2446
RVGRYKVNKKLGLHV	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,0751		FGTIGPYNLRYRVLA	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,239
RAPKAVKEYARKHPH	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,0748		AERVGISQMHVSRLL	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	0,2359
WSPQARRRFLPDVP	POSSIBLE GLYCOSYL	0,0744		AFAMTVPPSLVAANR	PPE FAMILY PROTEIN CAE55334	0,2342

	TRANSFERASE CAB05418					
PEFQRHRDKIVQRCL	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	0,0739		TTLALVSAPAGGRAA	PROBABLE CUTINASE PRECURSOR CFP21 NP_216500	0,2311
EKAIKERYARCLGSA	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,0737		DFTPAAEIVKDGDGA	CAA17343.1; HEAT SHOCK PROTEIN HSP	0,2213
FRGEFTPKTQLTMLS	MCE-FAMILY PROTEIN MCE1AYP_177701	0,0736		AASAAPSIPAANMPP	CAA17582.1; PROBABLE SERINE PROTEASE PEPD	0,2175
MDFGLLPPEVNSSRM	PPE FAMILY PROTEIN CAE55334	0,0725		STGMSGGFVTAPTQG	YP_177963; PPE FAMILY PROTEIN	0,2166
GEAQLGNSSGNFLLP	PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS1 YP_177770	0,0724		INAFSVGSGQTYGVD	CAB09453.1; PROBABLE SERINE PROTEASE PEPA	0,2139
VLASGLVAVSWAVG	POSSIBLE HEMOLYSIN-LIKE PROTEIN CAA17201	0,0714		WDATATELNNALQNL	CAE55648	0,2136
QNTMKIGIMDEERRT	MTB81 (publication)	0,0685		YGRLRHGQILFTFLH	SECRETED L- ALANINE DEHYDROGENASE ALD CAA15575	0,2054
KYKRVRFKGIICERC	RNA POLYMERASE BETA'-SUBUNIT AAA21417	0,0685		ENPSARDQILPVYAE	MTB48 AAK31576	0,1932
YGRLRHGQILFTFLH	SECRETED L- ALANINE DEHYDROGENASE ALD CAA15575	0,0667		AEAADAIRAMSNAEH	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1922
TGRSLDMSVAALAGM	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,0666		TATELNNALQNLART	CAE55648	0,1917
VEYVPSSEVDYMDVS	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,0662		YNQLLGPLPFRHHAI	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,1824
IDGPAPDGYPINIYE	PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS1 YP_177770	0,065		DANRALMGANMQRQA	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,1811
GDFYAGEKSMTLDRA	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,0626		MNPDIEKDQTSDEVT	CAB01474.1; CONSERVED HYPOTHETICAL PROTEIN CFP17	0,177
HSLLAGREQVRHLVR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,0603		TILKAYDGMFKDEFE	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,1768
YTEPILHRRRREFKA	MTB81 (publication)	0,0597		WSQLYRRTLNVAREL	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,1726
VRGDKVIAYARKFLD	MTB81 (publication)	0,0593		AAGFSGRAQVGKGMW	MTB81 (publication)	0,1691
VIPTMTPPPGMVRQR	CAA17582.1; PROBABLE SERINE PROTEASE PEPD	0,0591		GAAFGGLTTAHTPRR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1685
DIILNTHGVPRRMNI	RNA POLYMERASE	0,0587		ERNDPQTQIPKLVAN	CAB10044.1;	0,1631

	BETA-SUBUNIT AAA21416				SECRETED ANTIGEN 85-B FBPB (85B)	
DLATGTWLLFLGADD	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,0571		ANRLLRRTATHLPLR	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,1621
DVILESAITTIMDFE	MTB81 (publication)	0,0561		LDRLLFKRNICHQAI	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,1618
GRGGYAGMLVGSVGE	HYPOTHETICAL PROTEIN RV2623 NP_217139	0,0558		GVVLAGGESRRMGRD	CAA16030.1; PROBABLE MOLYBDOPTERIN- GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN	0,1615
MAKTIAYDEEARRGL	60 kDa chaperonin 2 P0A521	0,0544		RAPTESTRRCWTLVS	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,1573
GLRGLLRVISSEHPM	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,0526		NNKAALEPVNPPKPP	MTB48 AAK31576	0,1496
GLGLFFASKLAAAGC	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,0511		VAAMFGYHSAASAVA	PPE FAMILY PROTEIN CAE55504	0,1483
EAAAARSAVVLCNGG	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,0484		DVTVSRRHAEFRLEN	CAB01474.1; CONSERVED HYPOTHETICAL PROTEIN CFP17	0,1367
TESTRRCWTLVSSRS	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,047		VGNGYWQKPDESERT	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,1357
GGQFTLPGRSLMFVR	MTB81 (publication)	0,0468		TPGTGMPAAPMPVPT	MTB48 AAK31576	0,128
PTTYDHPTFAVHDTL	SECRETED L- ALANINE DEHYDROGENASE ALD CAA15575	0,0461		WSPQARRRFPLPDVP	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,1277
TIKAERTEQKDFDGR	CAA17245.1; HEAT SHOCK PROTEIN HSPX	0,0436		FRGEFTPKTQLTMLS	MCE-FAMILY PROTEIN MCE1AYP_177701	0,1248
ANRTRLASLVANLL	PPE FAMILY PROTEIN CAE55504	0,0417		AMAAQLQAVPGAAQY	LOW MOLECULAR WEIGHT T-CELL ANTIGEN TB8.4 NP_215690	0,1226
HDSDSVMHPQQAPV	HYPOTHETICAL PROTEIN RV2623 NP_217139	0,0413		VRPFVLARSLDPSRY	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	0,1202
IAKEIELEDPYEKIG	60 kDa chaperonin 2 P0A521	0,041		FKEMTLLELSDFVKK	CAB07109.1; PROBABLE 50S RIBOSOMAL PROTEIN L7/L12 RPLL	0,1107
GDGGVSGFGNFGAGS	YP_177963; PPE FAMILY PROTEIN	0,0408		AAPSIPAANMPGGSV	CAA17582.1; PROBABLE SERINE PROTEASE PEPD	0,1072
EFEGELPRLFVVTRQ	MYCOBACTERIUM BOVIS	0,0399		YPADPKTDQEKAIKE	PROBABLE ISOCITRATE	0,0996

	MYCOCEROSIC ACID SYNTHASE GENE; M95808				DEHYDROGENASE CAA16247	
GGATSLISYMLPRSP	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,0382		SQFGPYQLLRLLGRG	TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446	0,095
RCLPLADHIARRFEG	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	0,0376		DVVVLESMKMEIPV	CAB08316.1; BIOTINYLATED PROTEIN TB7.3	0,0858
VAAMFGYHSAASAVA	PPE FAMILY PROTEIN CAE55504	0,0371		YQAGKPTSTNPIASI	CAA17111.1; PROBABLE ISOCITRATE DEHYDROGENASE	0,0794
LTAANTKKVAMAAPM	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,0368		SYNTGSFNVGDTNTG	YP_177963; PPE FAMILY PROTEIN	0,0779
GNRGDANIGIGNIGD	PPE FAMILY PROTEIN CAE55504	0,0363		ADDEGYPKRARMMLMD	CONSERVED HYPOTHETICAL PROTEIN TB16.3CAD97060	0,0626
TLTWSQLYRRTLNV	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,0341		SSGLLRHAHCPVVII	HYPOTHETICAL PROTEIN RV2623 NP_217139	0,0544
SPAMVAANRTRLASL	PPE FAMILY PROTEIN CAE55504	0,0339		PDSDMTTAVMRPSKT	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,045
ERNPTQIQIPKLVAN	CAB10044.1; SECRETED ANTIGEN 85-B FBPB (85B)	0,0337		NELVRVYVAQKRKIS	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,0405
AEFPDYLTEEQRVPD	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,0334		VPPPVIAENRAELMI	CAE55371.1; PPE FAMILY PROTEIN	0,0383
PKVISRAMVMRTVIS	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,0334		LPDFLGGFAGLPSLG	CAB06237.1; CONSERVED HYPOTHETICAL PROTEIN	0,0381
EGYPKRARMMLMDAAI	CONSERVED HYPOTHETICAL PROTEIN TB16.3CAD97060	0,0327		EAVGYRSWPRYFAAL	PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,0362
LYLTIMTLMNATNLR	CAB06237.1; CONSERVED HYPOTHETICAL PROTEIN	0,0318		TIRVGSFRGRWLDPR	CAA16102.1; ESAT-6 LIKE PROTEIN ESXQ	0,0323
RVGFQHVNALRLM	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,0312		KADVYGNTLGLFPF	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,0238
EGVARVLTKPRFRGW	POSSIBLE HEMOLYSIN-LIKE PROTEIN CAA17201	0,0306		LDEHGTVLLAVRGLR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,0238
NELVRVYVAQKRKIS	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,03		YELEGAVKRADLVIG	SECRETED L-ALANINE DEHYDROGENASE ALD CAA15575	0,0127
TLAKIFNGSITQWNN	PERIPLASMIC PHOSPHATE-BINDING	0,0295		NSGVSMNTLSSMLK	CAE55371.1; PPE FAMILY PROTEIN	0,0126

	LIPOPROTEIN PSTS3 YP_177768					
VIGVAGNLDQHLNME	POSSIBLE GLYCOSYL TRANSFERASE CAB05415	0,0293		FRSGYLDVYQWTLIR	PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	0,0088
VYVTSEGMYGRVVKL	TRANSMEMBRANE SERINE/THREONINE- PROTEIN KINASE D PKND NP_215446	0,0282		VVAVGPGRWDEDGEK	CAB01005.1; 10 KDA CHAPERONIN GROES	0,0012
GLFNSGSFNTGIGNS	YP_177963; PPE FAMILY PROTEIN	0,0253		VEYVPSSEVDYMDVS	RNA POLYMERASE BETA-SUBUNIT AAA21416	-0,0021
LFNVGGFNTGVANVG	YP_177963; PPE FAMILY PROTEIN	0,0246		GKSPGFGTTVDFAV	PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS1 YP_177770	-0,0087
DGVGALLRYAATNRL	CONSERVED HYPOTHETICAL PROTEIN CAB08634	0,0241		TRIEAVPIAGFAQMR	3-OXOACYL-[ACYL- CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642	-0,0095
RFARFNLQERVIRPS	MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE; U75685	0,0232		VGISQMHVSRLAKS	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	-0,0119
GGLNSGTGNIGLFNS	YP_177963; PPE FAMILY PROTEIN	0,0221		SADNMREYLAAGAKE	MTB48 AAK31576	-0,0198
LDRLLFKRNICHQAI	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,0219		AEFPDYLTEEQRVPD	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	-0,0231
NANIGFGNRGDANIG	PPE FAMILY PROTEIN CAE55504	0,0201		VAASDLAYTLARGRR	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	-0,0241
PPQEQGLIPGFLMPP					PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS3 YP_177768	
	MTB48 AAK31576	0,0196		FTLPGERIHVVFRSD		-0,0268
MLVTAVVLLCCSGVA	CAA98382.1; IMMUNOGENIC PROTEIN MPT64	0,0196		SKLMTRIAGAGAMGS	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	-0,0279
SRPQSSSNNSVPGAP	RNA POLYMERASE BETA-SUBUNIT AAA21416	0,0171		DMEGTFARPMTLVT	3-OXOACYL-[ACYL- CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642	-0,0285
DMEGTFARPMTLVT	3-OXOACYL-[ACYL- CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642	0,0169		APEMTSAGGLLEQAA	CAE55371.1; PPE FAMILY PROTEIN	-0,0288
					PUTATIVE CYCLOPROPANE- FATTY-ACYL- PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	
TGNLGLFNSTGNIG	YP_177963; PPE FAMILY PROTEIN	0,0167		TMPHHRMLATRHTQT		-0,0291
MSGQADTATTAEART	POSSIBLE HEMOLYSIN-LIKE PROTEIN CAA17201	0,0157		ILTVSVAVSEGKPT	CAA17245.1; HEAT SHOCK PROTEIN HSPX	-0,03
VNIGASDAYLSEGDM	PERIPLASMIC PHOSPHATE- BINDING	0,0146		VRDLIARWEQRDVMA	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID	-0,031

	LIPOPROTEIN PSTS1 YP_177770				SYNTHASE GENE; M95808	
SAITDADFKAAAGL	SECRETED L- ALANINE DEHYDROGENASE ALD CAA15575	0,0142		YVAWMSVTAGQAEIT	CAE55371.1; PPE FAMILY PROTEIN	-0,0315
NNSFGFGGHNVAIAF	3-OXOACYL-[ACYL- CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642	0,0138		RMTSGSSSGFKVRPS	YP_177963; PPE FAMILY PROTEIN	-0,0345
GGNLGGQNLGLGNLG	YP_177963; PPE FAMILY PROTEIN	0,0129		QRHRDKIVQRCLPLA	ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069	-0,0419
VGASGNNGTSALLQT	PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS2 YP_177769	0,0127		DAQSIQAAAAGFASK	PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS1 YP_177770	-0,0453
QLATWVEEHQDCVAA	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	0,0122		ANRTRLASLVAANLL	PPE FAMILY PROTEIN CAE55504	-0,0461
FNSGDGGVSGFGNFG	YP_177963; PPE FAMILY PROTEIN	0,0115		RYARCLGSAVNPVLR	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	-0,0467
NNQTVLPFDGLNYPE	TRANSMEMBRANE SERINE/THREONINE- PROTEIN KINASE D PKND NP_215446	0,0113		ELAIPMSGIAMAVVG	CAB06237.1; CONSERVED HYPOTHETICAL PROTEIN	-0,0479
VEQAALQSAWQGDTG	CAA17363.1; LOW MOLECULAR WEIGHT PROTEIN ANTIGEN 7 ESXH	0,0106		TSYTSDEAMLDAILA	TWO COMPONENT TRANSCRIPTIONAL REGULATORY PROTEIN DEVR NP_217649	-0,0482
ATATATLLPFEEAPE	CAE55371.1; PPE FAMILY PROTEIN	0,0102		QNTMKIGIMDEERT	MTB81 (publication)	-0,0484
AMNRGVDLATGTWLL	POSSIBLE GLYCOSYL TRANSFERASE CAB05419	0,01		PLSGLTHKRRLSALG	RNA POLYMERASE BETA-SUBUNIT AAA21416	-0,0499
NALFAGPAKMLRLNA	YP_177963; PPE FAMILY PROTEIN	0,01		TESTRRCWTLVSSRS	MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE; M95808	-0,0518
AFLAAQELILSGAQQ	MTB81 (publication)	0,0096		AAAFNPNASPVASQYL	LOW MOLECULAR WEIGHT T-CELL ANTIGEN TB8.4 NP_215690	-0,0531
DSALLAAGFGNTTA	MCE-FAMILY PROTEIN MCE1AYP_177701	0,009		EGVARVLTKPRFRGW	POSSIBLE HEMOLYSIN-LIKE PROTEIN CAA17201	-0,0553
GSTAQANAMTRFVNV	PERIPLASMIC PHOSPHATE- BINDING LIPOPROTEIN PSTS3 YP_177768	0,0085		ILVQANEAEITTTASG	CAB01005.1; 10 KDA CHAPERONIN GROES	-0,0559
LKMCWPAAPRSVGVP	POSSIBLE HEMOLYSIN-LIKE PROTEIN CAA17201	0,0085		GAPNRVSFAKLREPL	RNA POLYMERASE BETA-SUBUNIT AAA21416	-0,0561
GKLKDTKAVNPESTF	PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	0,0076		VRPVSYLYRLYRPLI	POSSIBLE GLYCOSYL TRANSFERASE CAB05418	-0,0571
RVAGAYKAPAEITQAG		0,0075		TRHTQTWIKYIFPG		-0,0574
QGYGSLGLMTSVLMT		0,0074		DVDKDVNVELDPGQP		-0,0588

DAFPNEFPDPTISVQ	0,0064	GLGLFFASKLAAAGC	-0,0622
VKAPGFGDRRKAMLQ	0,0053	YPEGLAVDTQGAVYV	-0,0637
AARSAVVLNCNGGSPT	0,0048	PIPEGLTTGRSCQTD	-0,0647
DANRALMGANMQRQA	0,0047	RVSVGNLRIARVLYD	-0,0674
YTSGSTRTPAGVVMS	0,0042	TWKLLLDQRSGIRTL	-0,0678
VVAVGPGRWDEDGEK	0,0027	LERPVGDDSDCGTIR	-0,0698
AAGFSGRAQVGKGMW	0,0026	TGNLGLFNSTGNIG	-0,072
QKVQAAGNNMAQTDS	0,0018	TGMELRAAIDAATSS	-0,073
ARTISEAGQAMASTE	-0,0013	GRAGGGAAALGGGGMG	-0,0739
VGAGERKMSALVDAS	-0,0013	PLDDGDVIDSMFMSK	-0,0752
PGEPTTKESAQTLE	-0,0017	ARDADMLSELGEPVD	-0,0787
FVTDGKMFIIIGRIKD	-0,0018	RVQAAATIKRFADRFA	-0,0789
VGSWIGSSAGLMVAA	-0,0023	YQQRSEKVLTEYNNK	-0,0794
KIHARSTGPYSMITQ	-0,0029	PRRPREPRRCWPRSRCP	-0,0801
CAPVFVMAAPGQPLP	-0,0031	FTAHTKHRYVVSHPA	-0,0829
AERVGISQMHVSRLL	-0,0043	AGNLGLFNSTGNIG	-0,0878
QEITRGRCAAISVPG	-0,0044	RKIPLTLVHAVSPEV	-0,0882
YELEGAVKRADLVIG	-0,0049	TRGRCAAISVPGDRR	-0,0902
SRMYSGPGPESMLAA	-0,0052	FVTDGKMFIIIGRIKD	-0,0914
FAGYTGAESPTSVL	-0,0055	NRANEVEAPMADPPT	-0,0921
DSGFVTDGKMFIIIG	-0,0077	VGAENLGAANAGSGN	-0,0981
LEKDNTVGTDEALLD	-0,0084	LVDFGIARAASDPGL	-0,1036
PNGYTFKEDEYPSTA	-0,0089	AAERGPQMLGGLPV	-0,105
NYNLPGVSEHLKLNG	-0,0098	ASGLVIPDTAKEKPQ	-0,1059
GAGTVYVTDNFNRVV	-0,0102	PGAARWSPGDSATVA	-0,1066
SGMTSQAATFAANRL	-0,0118	LLKGAKVETKEQIA	-0,1082
WDGVAITLWSQLYR	-0,012	HSLLAGREQVRHLVR	-0,1083
AHMKPGAVLVDAID	-0,0124	PLAGVVLGGESRRM	-0,1106
DAARVICRRSKLMTR	-0,0127	NTMAMMARDTAEAAK	-0,1117
WDATATELNNALQNL	-0,0129	SSDLRVGQPVLAIGS	-0,1136
KIDPPPPPQEQGLIP	-0,0131	PELVPTYNLPANHRY	-0,1203
AMRTLRYVEADLRV	-0,0144	EIGKADVYGNTRLGL	-0,1232
VAPVSPSTASSRTDT	-0,0144	LLRYAATNRLGSHRS	-0,1234
VLSACGNDDNVTGGG	-0,015	MLEGCILADSRQSKT	-0,1262
QTYGVDVVGYDRTQD	-0,0151	MEAGPMVRKGTMSQ	-0,1268
TGQHTGLRIVDAASL	-0,0153	AGVLLRTERLKSQRV	-0,1296
VAASDLAYTLARGRR	-0,0153	VSEHLKLNKVLAAAM	-0,132
VDGAPINSATAMADA	-0,0154	TGDEVTYRADIYALA	-0,1361
LVVGNNGPGVTALVM	-0,0159	FFGVRPVSILYRLYR	-0,1365
GQRCAPVFVMAAPGQ	-0,016	NSTELPSSGFNTGG	-0,1409
SPSRKTGELDNRRSQ	-0,0163	SEAIAASYDAGVLT	-0,1433
DVTVSRRHAEFRLEN	-0,0164	AQAASLEAEHQAIVR	-0,1444
QAAAVEEASDTAAAN	-0,0168	VNIGASDAYLSEGDM	-0,1456
QNAASIAGLFLTTEA	-0,0169	QTYGVDVVGYDRTQD	-0,1478
ALGDNWIVGASNSTG	-0,0172	TTVALGRSVCPMVVA	-0,1489
ERCGVEVTRAKVRRE	-0,0172	VFRARMQREADTAGR	-0,1505
NNKAALEPVNPPKPP	-0,0174	DNQSGIGGLNSGTGN	-0,1507
EFRLNNEFNVDVVG	-0,0179	LSSMLKGFAPAAAAQ	-0,1519
EIELEDPYEKIGAEI	-0,0182	NALFAGPAKMLRLNA	-0,1523
FGKPANPDVLVVGNG	-0,0183	LRISSQLLANWLRHG	-0,1594
APAQANPVDDAFIAA	-0,0187	QLAEHFASLADVLTK	-0,1596
APSLFIHRPDALARR	-0,02	QPVVLAATGDLPTI	-0,1604
LNSLTYDVSVAQGV	-0,0205	DSVAADVDAADKVLGY	-0,1628
IAAAAKPPLGSPPPK	-0,0206	LIPGFLMPPSDGSGV	-0,1634
NGTPNELGGANIPAE	-0,0206	TLTWSQLYRRTLNV	-0,1657
MVDFGALPPEINSAR	-0,0221	GPYLQRGVADLVPTA	-0,1676
AAGTAAQAAVVRFQE	-0,0226	KDTKAVNPESTFSRI	-0,1685
HSTVLVAPVSPSTAS	-0,0228	EFRLNNEFNVDVVG	-0,1718
SGFFNSGDGGVSGFG	-0,0231	YVAQKRKISDGDKLA	-0,174
GADGKLKDTKAVNPE	-0,0231	TGMPAAPMVPPTGSP	-0,1747
DVDKDVNVLDPGQP	-0,0232	HDEDSVMPPHPQAPV	-0,1762
DKGDVVVLLESMMKE	-0,0237	EIVKDGDDAVVRLEL	-0,1775
AHVVRPFALAQSLDP	-0,0242	TAAQNGVRAMSSLGS	-0,1784
SMTNSGVSMNTLSS	-0,0242	PAVFAVQVALAATME	-0,179
GNIGLGNAGSGNVGF	-0,0243	EKAIKERYARCLGSA	-0,1812
CIRAAARGAHIRSVT	-0,0244	RNFLAAPPQRAAMA	-0,1822

TANGSGAGISEFNGN	-0,0246	LGGQNLGLGNLGDGN	-0,1837
PTQYROPYEALGGTR	-0,0252	HEGQTTMTVPGGVEV	-0,1873
NVTGGGATTGQASAK	-0,0255	DLARVGRYKVNKKLG	-0,1902
DAQSIQAAAAGFASK	-0,0265	GQARLAASAFEATLA	-0,1934
NGTSALLQTTDGSIT	-0,0271	LKIAQGRLFYNTRTL	-0,1937
KRADHSMIFVFIAGS	-0,0281	KGAGKSFQGGVGEGA	-0,1942
AHTPRREPRRCWPRS	-0,0282	GTAVSARNTAVCAPT	-0,1972
LVDAADPEVVVFSGE	-0,0283	PILDDLAAAALADIAP	-0,1978
GLPQNTMKIGIMDEE	-0,0287	AHTPRREPRRCWPRS	-0,1988
DYMDVSPRQMVSVAT	-0,0289	NPGELLPEAAGPTQV	-0,1989
AESNNQVVLPFTDIT	-0,0291	MVDFGALPPEINSAR	-0,2008
AVLDPDHDGMRVQVR	-0,0293	WDGVAITLTWSQLYR	-0,201
ELTRVLTVLAGSVDE	-0,0296	FGVRLVKLLYRLERP	-0,2049
LVAANRSRLMSLVAA	-0,03	IEYRSLARVYGAGTP	-0,2061
RSNPALAKGLSTHEG	-0,0304	RVVRVTGRASARGLI	-0,2062
RVVRVTGRASARGLI	-0,0307	VGADEDDIKATYDKG	-0,2072
DSVAAVDAADKVLGY	-0,0314	APSLFIHRPDALARR	-0,2087
NVVDVGS LN GTYVNR	-0,0316	GLFNSGSFNTGIGNS	-0,2096
MEAGPMVRKGTMKSQ	-0,0322	HEHRPELAMVDSARG	-0,2098
GQARLAASAFEATLA	-0,0322	YPITGKLGSSELTMTD	-0,2108
VGAGTGIVIDPNGVV	-0,0325	GLNYPEGLAVDTQGA	-0,2116
MMGNAFLTALTNAGI	-0,0329	AHLRPGLDLSFTLT	-0,2124
ADPGEVMKAIADIEA	-0,033	AGSWLLIDTSNAVDT	-0,2127
SDGTATGAADPRAPS	-0,0331	GVDVVGYDRTQDVAV	-0,2128
ARQTCGDFELVLVDG	-0,0334	EPVVAMGNSGGQGGT	-0,214
SYNTGSFNVGDTNTG	-0,0336	AENRAELMILIATNL	-0,2146
GLGDKFGESIVNANT	-0,0342	EFPAIPGFPAIPGLP	-0,2165
PDTISGATIPQGEQS	-0,0344	MDFGLLPPEVNSSRM	-0,2173
TILRRGDNATLLATP	-0,0348	PFNVNLKQLFLHDAF	-0,2216
RGGPGGAPGCWQPIT	-0,0348	ALGQTVQASDSLGA	-0,2222
TSSSQESGVIEEVSA	-0,0349	APTTGVLPPAANDVS	-0,2238
AQAASLEAEHQAIVR	-0,0353	TSSSQESGVIEEVSA	-0,2249
PDEHSLLAGREQVRH	-0,0355	ITTTAGPQLVVPVLN	-0,2272
GLGNAGSSNYGLANL	-0,0356	NRVSFAKLREPLEVP	-0,2275
WGGPPVASEVRGDAA	-0,036	EIELEDPYEKIGAEI	-0,2279
KLRPGEPPTKESAQT	-0,0365	ARWSPGDSATVAGPL	-0,2296
LGIGNIGLNAGSTN	-0,037	LPDIIDGLWPPKLPD	-0,2312
LLRYAATNRLGSHRS	-0,0371	LPQWLSANRAVKPTG	-0,232
VRDLIARWEQRDVMA	-0,0371	AVCAPTTGVLPPAAN	-0,2324
GITGNGQIGFGKPAN	-0,0377	PAATIDQLKTDKLL	-0,236
DFAGSDVPLNPSTGQ	-0,0378	DDLMMVNAGLVCGGV	-0,2369
LLEQAAAVEEASDTA	-0,0388	SLIGLAMGDAGGYKA	-0,2375
EDYLVLT TTAGGLAS	-0,0392	LVAANRSRLMSLVAA	-0,2414
QSGLSIVMPVGGQSS	-0,0402	EAVIGNRRRQDSKES	-0,2421
PRREPRRCWPRS RCP	-0,0402	PAVPGALGNGNGGM	-0,2496
GLGGLGLFFASKLAA	-0,041	IRGTFKSVAVKAPGF	-0,2509
DGPTLAKIFNGSITQ	-0,041	GLYNTGGLPPGTPAV	-0,2514
NNAVAGAGTGIVIDPN	-0,0415	YTSGSTRTPAGVMS	-0,2519
ATLAHVVRPFVLARS	-0,0416	LLKQYGPLTPARAVA	-0,2531
NAGSSNYGLANLGVG	-0,0417	QAIFYRRGLFGTIGP	-0,2543
ERLIHRD TDQGVYD	-0,0422	WLLIDTSNAVDT PDM	-0,2552
AATQAAGAGAVADAQ	-0,0423	LEGTYRLAPKSGSTE	-0,2553
FAGAGLGPM LAAASA	-0,0432	IKGMELARAVKDVGA	-0,2591
AANMPPGSVEQVAAK	-0,0434	HGMLTD RD DIVIKGLA	-0,2598
VFAPTNAAFDKLPAA	-0,0434	GIRLTPKVIATNKTA	-0,2609
GDVITAVDGAPINSA	-0,0435	GLGGLGLFFASKLAA	-0,2621
GSGAGISEFNGNQTD	-0,0437	RRLKELHLRLGTATA	-0,2621
VQAKPAAAASLAIA	-0,044	TILRRGDNATLLATP	-0,2621
TSVLMTADGKTVEAE	-0,0446	LIATNLLGQNTPAIA	-0,2657
ARMQREADTAGRLTE	-0,0459	TPADGSAPIVHEMVS	-0,2658
ADDEGYPKRARM LMD	-0,0459	AARSAVVL CNGGSPT	-0,2658
TAAQNGVRAMSS LGS	-0,0462	DESERTFGGKIVTPS	-0,2666
AMFGYAAATATATAT	-0,0465	ASDFAYLVDFGIARA	-0,2669
QAAGNNMAQTD SAVG	-0,0471	PLPTLPVPVLRDELP	-0,2679
GTGSTGLFNAGNFNT	-0,0476	FAWTRGLQHRGKLDG	-0,2701
DRAGVKDVILESAIT	-0,0477	QQVSIAPNAGLDPVN	-0,2706

HPDSDFLDDVTVSR	-0,0482	HIGLYGNAGGLGPTQ	-0,2709
AADILKDESYKVGT	-0,0487	PDEHSLLAGREQVRH	-0,2743
GSDVPLNPSTGQPDR	-0,0489	RAGAGVLLRTERLKS	-0,2746
VGGGNVGFNGIGDAN	-0,0489	MYCPSVMADVASGNL	-0,275
QVRRPGDLQTLFVA	-0,0491	AIPPRGTQAVVLKVY	-0,2751
GDVQSDTVAQGYGSL	-0,0492	PPQEQLIPGFLMPP	-0,2753
GVAVDSAGNVYVTSE	-0,05	PTTYDHPTFAVHDTL	-0,2754
TRFVNVFEQACPGQT	-0,05	LESSLLKSLEGTyr	-0,2782
DIGIKTGNERAKLLG	-0,0504	VGADPTSDIAVVRVQ	-0,2795
EVLLKIAQGRLFYNT	-0,0506	NAGSTNVGLANMGVG	-0,2821
TSAGREAAALSGDVA	-0,0507	VAITLTWSQLYRRTL	-0,2826
FGMSGTNVHAIVEEA	-0,051	PELDVVGEAGSVAEA	-0,2832
GQMGARAGGGLSGVL	-0,0513	YAGLTAANTKKVAMA	-0,2845
EDKILVQANEAEETT	-0,0514	RVAGAYKAPAETQAAQ	-0,286
AGAGEGSAITDADFK	-0,0516	GLREVADGDALYDAA	-0,2876
YAGLTAANTKKVAMA	-0,0519	VGGGNVGFNGIGDAN	-0,2884
LVLSADNMREYLAAG	-0,052	KHRIEDAVRNAKAAV	-0,2896
DRAAQIAGADAKLII	-0,0521	VPDNLAELGRLTQLP	-0,2901
PAAEIVKDGDDAVVR	-0,0525	HFRDNSWSVKVPRRL	-0,2918
PLPATGRGLRAAAEA	-0,0526	VDMANPMPSPVKSFE	-0,2918
PDSDMTTAVMRPSKT	-0,053	STNNDPAGACRPFDP	-0,2929
TVIGARDDLVMVNNAG	-0,0536	QEITRGRCAAISVPG	-0,2944
FGSGVSGLYNTGGLP	-0,0541	LDPSQGMGPSLIGLA	-0,2945
TQYLSKQDPEGWGKS	-0,0542	NSGSFNTGIGNGGTG	-0,295
PISVIFRSKSGTSD	-0,0545	AKERAHNAGAKNVEE	-0,2951
GASVTVGPIINGVN	-0,0547	AGVTCVGEHETLTAA	-0,2957
VTSALSSSHGLSVAD	-0,0548	VLASGLVAVSWAVG	-0,296
REPIVISNVPRLVPG	-0,0552	IQMSDPAYNINISLP	-0,2967
LVAGVPVIGVAGNLD	-0,0554	AESNNQVVLPTDIT	-0,2971
INTGWFTGNANTGI	-0,0562	NDDPAGACRPFDRDR	-0,2979
MKFARSGAAVSLLA	-0,0564	DAMARLGAIKREVTS	-0,2991
GALLRYAATNRLGSH	-0,0566	DGVGALLRYAATNRL	-0,3007
GLTVPPPVAENRAE	-0,0566	ILELGTSAKMLSVVP	-0,3017
TPANQAISMIDGPAP	-0,0569	ARGANILARIMGASI	-0,3019
SLIGLAMGDAGGYKA	-0,0569	LLPFEEAPEMTSAGG	-0,3026
VSVDIPAVTITGTRI	-0,0571	NGDEVQIGKFRLVFL	-0,3037
PGIGNTTVPSSGFF	-0,0574	VTLGPKGRNVVLEKK	-0,3043
GTAVKAFQSTIGAG	-0,0575	EIVCSKYPDATTGTA	-0,3047
KIRAWGRRLMIGTAA	-0,0578	DKRDTVGVRIIDRKR	-0,3069
TGPGSVAGMAQDPVA	-0,0587	LVVGNGGPGVTALVM	-0,3075
LEDPYEKIGAELVKE	-0,0592	IAGAKIMGQGNLVL	-0,3077
ELKGTDTGQACQIQM	-0,0594	GQPVLAIGSPLGLEG	-0,308
HAVFNAASQAFNTPA	-0,0594	TPDAAPGLAARRRRI	-0,309
GNVDTGALMSGNFSN	-0,0595	FGSGVSGLYNTGGLP	-0,3102
TAPFTTVVGADPTSDI	-0,0598	RVQGVSGLTPISLGS	-0,3104
HACVAASAQGMLSST	-0,0599	PANAFVADYLPGEAA	-0,3125
QQALVAGVPVIGVAG	-0,0604	IGKLLDNDKSPSRKT	-0,3138
DSGTTISAIYETVQTA	-0,061	RAVDRAAQIAGADAK	-0,3151
GLLPPEVNSSRMYSG	-0,0611	LAQIKAGDKVLIHSA	-0,3154
AGNLGLFNSGTGNIG	-0,0613	DEDDIKATYDKGILT	-0,3169
MRVQVRRPGDLQTL	-0,0615	GTGSTGLFNAGNFNT	-0,319
NNGNGARVQRVVGSA	-0,0618	RGGPGGAPGCWQPIT	-0,3194
LGSSSDLRVGPVLA	-0,0619	ADFPALPLDPSAMVA	-0,3205
VRAMSSLGSSLGSSG	-0,0622	PDTAKEKPQEGTVVA	-0,3206
VTVGPIINGVNIPA	-0,0623	AMFGYAAATATATAT	-0,3213
ATVSPAMVAANRTRL	-0,0625	RAPKAVKEYARKHPH	-0,3235
LSSMLKGFAPAAAAQ	-0,0626	DNQTGIGGLNSGAGN	-0,3239
GGLNSGTGNLGLFNS	-0,063	GKLKDTKAVNPESTF	-0,3249
ALVREGLRNVAAGAN	-0,0632	VFAPTNAAFDKLPAA	-0,3254
RVTVPVAVIGMGCRLP	-0,0634	GLERHAKAGVMTPTS	-0,3261
APPLAVAAANLAGALP	-0,0635	HACVAASAQGMLSST	-0,3263
TPDAAPGLAARRRRI	-0,0638	GTAVKAFQSTIGAG	-0,3267
IGNIGDRNLGIGNTG	-0,0639	DRARNVRMELLAKSG	-0,3275
FSIIPTLNVAVLP	-0,0642	EIVCSKYPDSQVGTA	-0,3291
GLNTPLAVAVDSRT	-0,0644	HGTVLLAVRGLRMGT	-0,3303
VFRARMQREADTAGR	-0,0645	YGSFRRSFRLPAHVT	-0,3321

TATLLPFEEAPEMTS	-0,0648	NMQRQAVPLVRSEAP	-0,333
TPADGSAPIVHEMVS	-0,0652	AFGRFPIIDDERPQL	-0,3332
TSGKVRRGACVEQYR	-0,0654	SGIPTLSTTGPVHAV	-0,3342
RPGRVPPALDQVIAK	-0,0658	MLSSTSSDALRQTAR	-0,3346
AVQTAAQNGVRAMSS	-0,0658	GAAEKQDPLSGLTDQ	-0,3346
MPVLSKTVETADAA	-0,0658	SDQDAMARLGAIKRE	-0,3356
EFPAIPGFPALPGLP	-0,066	RRCRRALRQIGVLER	-0,3356
QNQALLNARDELQAAQ	-0,0661	NISVPDSSVPIIIVP	-0,3363
VNINTKLGYNNAVGA	-0,0661	AGSNNQTVLPFDGLN	-0,3371
RVQAATIKRFADRFA	-0,0661	VKKPETINYRTLKPE	-0,3372
WYVARLTPSPLGHEE	-0,0676	VGAPVDALVNLADEE	-0,3402
GFTLSGATPADAYPT	-0,0676	AGSPEFQRHRDKIVQ	-0,3402
SSSAGADPTALNGMP	-0,0687	LTSAAERGPGQMLGG	-0,3406
LDQASQRGLGEAQLG	-0,0689	NNQTVLPFDGLNYPE	-0,3412
GKSPGFGTTVDFAV	-0,069	GLGDKFGESIVNANT	-0,3422
GAAASLVGFNRAPAG	-0,069	CAPVFVMAAPGQPLP	-0,343
RLAKSLARLRDQLE	-0,0691	LPNISASVPQLVAAI	-0,3431
AGSPEFQRHRDKIVQ	-0,0692	SMTNSGVSMNTLSS	-0,3433
KHLESRAKQELIDS	-0,0693	AAIDAATSSSQESGV	-0,3433
VIGAGKPLIIAEDV	-0,0694	GGPVLTALVMGGTDSL	-0,3438
PILHRRRREFKARAA	-0,0696	GGLNSGTGNLGLFNS	-0,345
MGATVTVLDINIDKL	-0,0698	GAYHLMRTQGGRGVL	-0,3453
QRHRDKIVQRCLPLA	-0,0701	QSESGIAGAGTGPPT	-0,3465
VGAQNLGAANAGSGN	-0,0703	TLPVPVLRDELPGLG	-0,3469
PLSGLTHKRRLSALG	-0,0706	ATLAHVVRPFVLARS	-0,3473
ELTSAAVSYGSSVST	-0,0708	GITGNGQIGFGKPAN	-0,3475
AGSNNQTVLPFDGLN	-0,0708	HVSRLAKSLARLRD	-0,3482
GVPVIGVAGNLDQHL	-0,0709	VPVLRDELPGLGPLP	-0,3485
EAYPPEVNSANIYAG	-0,0713	VARAQGMSQDMAQTF	-0,3487
GPKVVIDGKDQNVTG	-0,0715	SRPQSSNNSVPGAP	-0,351
IRGTFKSVAVKAPGF	-0,0716	AITRVVVRDQPARQL	-0,3512
GIMDEERRTTVNLKA	-0,072	MSAYKTVVVGTDGSD	-0,3516
QNPTGPGSVAGMAQD	-0,0721	MADVASGNLPALPDM	-0,3516
QVGPQVVNINTKLG	-0,0723	GEAQLGNSSGNFLLP	-0,3522
DGKDQNVTSVSVCTT	-0,0724	GQRCAPVFVMAAPGQ	-0,3529
DLARVGRYKVNKKLG	-0,0725	EGYPKRARMLMDAAI	-0,3534
AADPEVVVFVSGEVRS	-0,0728	GRGCAQYAAQNPTGP	-0,3536
PVTVIAATAGRSDLK	-0,0729	TKDGSYHYKITGTATG	-0,3546
VAAELTSAAVSYGSV	-0,0732	CAQYAAQNPTGPGSV	-0,3556
HFRDNSWSVKVPRRL	-0,0736	TFESITSRMAEINGM	-0,3557
IVGLERLYAENPSAR	-0,0738	DYMDVSPRQMVSVAT	-0,3584
GTTGGGGTRSGTSTD	-0,0738	SALLDPSQGMGPSLI	-0,3587
AYTLARGRRHRPVRT	-0,074	DKPEKEKASVPGGGD	-0,3599
QSESGIAGAGTGPPT	-0,074	LFNVGGFNTGVANVG	-0,361
TGIGGLNSGTGNLGL	-0,0741	TSVAGDGPDPAGTST	-0,3611
YPADPKTDQEKAIKE	-0,0742	VSGGLGLKEAKDLVDG	-0,3616
PNGYTEPILHRRRRE	-0,0745	AAIANRLLRRTATHL	-0,3627
KLNPDVNLVDTLNGG	-0,0748	DIMVRDQQLTIKAER	-0,363
AGVQYSRADEEQQQA	-0,0751	EKEKASVPGGGDMGG	-0,3632
TAPTQGILHTGPSS	-0,0751	HLMRTQGGRGVLMGG	-0,3637
TVTVDINIDKLRLQL	-0,0753	TIKAERTEQKDFDGR	-0,3668
PAVFAVQVALAATME	-0,0754	GLILTNNHVIAAAAK	-0,3683
FKEMTLLELSDFVKK	-0,0755	VASPOSTVIGGTSMT	-0,3692
NQNTVLDAIQTDAAI	-0,0758	AFELAARRTTDDDMA	-0,3695
AGLMRHTIGQAEQAA	-0,076	KTDDVAGDGTATV	-0,3696
NAGSYNTGSFNVGDT	-0,0762	WNQAQTEVAGAGSGF	-0,3697
GNAGTASTGLFNVGG	-0,0764	TQVLVPRSAIDSMIA	-0,3701
RAVDRAAQIAGADAK	-0,0765	YRTDLADRVDTLVGA	-0,3702
ELAIPMSGIAMAVVG	-0,0766	FSVSGGQTYGVVDVVG	-0,3703
LGSELTMTDTVGQVV	-0,0768	NSEEFLLDAIADNLEK	-0,3705
SNGAWGKGAGKSFQGG	-0,0768	TIFPNGISIPNNPLA	-0,371
GTDGTGQACQIQMSDP	-0,0769	VITSADVRASLERMA	-0,3711
YPITGKLGSELTMTD	-0,0771	CQGDLMGSHQDWQAQ	-0,3722
LKASDVNGPLINSRT	-0,0775	AATQAAGAGAVADAQ	-0,3742
ISFLDQASQRGLGEA	-0,0775	NQNTVLDAIQTDAAI	-0,3742
GAAHQGGGAKSKGS	-0,0786	GGQFTLPGRSLMFVR	-0,3753

DVVVLLESMKMEIPV	-0,0786	VRAMSSLGSSLGSSG	-0,3755
GNWPSQTGHSPAVPN	-0,0786	VKRADLVIGAVLVPG	-0,3756
EIVCSKYDPDATTGTA	-0,0792	LTSLTSAERGPGQM	-0,3758
QNLARTISEAGQAMA	-0,0795	ARLFIDDDGQEQRQAQ	-0,3761
MGVPPLAGASRTDME	-0,08	LVLSADNMREYLAAG	-0,3771
VSQLHAGPRKSALDE	-0,0801	SDGSGVTPGTGMPAA	-0,3773
SEAIAASYDAGVLTV	-0,0804	VGSWIGSSAGLMVAA	-0,3778
QVVKLLAGSTTSTVL	-0,0805	NVTGGGATTGQASAK	-0,3783
AAKAGLMRHTIGQAE	-0,0805	VLSWLSDHQVHNVA	-0,3791
PTFSSSAGADPTALN	-0,0806	LTVRVAGAYKAPAET	-0,3802
ALSGQLNPQVNLVDT	-0,0806	PAFSPPAQALGGGVG	-0,3814
GSVAEAMARVPAARP	-0,0811	AQDPVATAASNNPML	-0,3817
SLAAIAIAFLAGCSS	-0,0813	KERKHRIEDAVRNAK	-0,3834
AAPRSVGVPLYLLLG	-0,0821	FGGRFVEIGKADVYG	-0,3836
TIFPNGISIPNNPLA	-0,0825	GAHQGGGAKSKGS	-0,3839
GTVTRHYRQYQAGKP	-0,0826	RLAKSLARLRDQLE	-0,3839
FMQAAIGPGQEGLDQ	-0,0827	GQMGARAGGGLSGVL	-0,3848
RGAHIRSVTLSEVQQ	-0,0827	PGVDPDKDVIDIMVRD	-0,3849
DPDKDVIDIMVRDGQL	-0,0828	IVGLERLYAENPSAR	-0,3855
VTLGAAFGGLTTAHT	-0,0833	TLARVAFIGEHEPS	-0,3857
VARAQGMSQDMAQTF	-0,0835	MAEMKTDATLAQEA	-0,3866
TTIVEGAGDTDAIAG	-0,0836	VGAGERKMSALVDAS	-0,3869
TTGSGETTTAAGTTA	-0,0838	QNQALLNARDELQAQ	-0,3869
GEHEPSDLVYGDVIM	-0,084	DPDKDVIDIMVRDGQL	-0,3876
DDRPINSADALVA	-0,0845	GNAGTASTGLFNVGG	-0,3881
TAVVPLHRSDBGSGDT	-0,0855	QALNSGTDLPPTPIS	-0,3883
VDPVKLNLTLASAAE	-0,0858	QSGLSIVMPVGGQSS	-0,3888
HGLHIEILIDPESQV	-0,0859	SGMTSQAATFAANRL	-0,3899
YPEGLAVDTQGA	-0,0868	AYTLARGRRHRPVRT	-0,3911
YVAQKRKISDGDKLA	-0,0874	GNPNRPDGGILTRFG	-0,3928
VNAIRGSVTPAVSQF	-0,0876	QNAASIAGLFLTTEA	-0,3929
HLMRTQGGRGVLMGG	-0,0876	LAQPTQGTTPSSKLG	-0,3929
NGNQTDFFGSDVPLS	-0,0876	AALPAFSPPAQALGG	-0,3929
MTSAGGELLEQAAVE	-0,0877	QGELSKQTGQQV	-0,393
QRRKIDRLLDVAGVQ	-0,0883	ASLVGFNRAPAGPSG	-0,3932
GLRMGTGTSEDERD	-0,0883	PGEPTKESAQTLL	-0,3938
LLRTERLKSQRVAGA	-0,0883	ARLGAIKREVTSALS	-0,395
FAWTRGLQHRGKLDG	-0,089	AYAIAKHG	-0,3952
DPNGVVLTNHVIAG	-0,0895	AVQTAAQNGV	-0,3961
AFELAARRTTDDDMA	-0,0899	FMQAAIGPGQEGLDQ	-0,3961
PGVDPDKDVIDIMVRD	-0,09	KVNTLLDVAQANLGE	-0,3967
CLFSSGAALLGSPGQ	-0,0901	RRSPWGEMFASTGQR	-0,3983
TAALAKETATQARAA	-0,0902	RQRPRAGMLAIGAVT	-0,3991
YCEELKGTDTGQACQ	-0,0907	EFEGELPRLFVVTRQ	-0,3995
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VGNGYWQKPDESERT	-0,091	LTNNHVIAGATDINA	-0,4002
LTNNHVIAGATDINA	-0,0911	ASQRLGGEAQLGNSS	-0,4006
VYVADRGNNRVVKLA	-0,0914	ARGTHQASGLGDVGE	-0,4011
QPRAGASTAWVPSPT	-0,0917	FVVTRQAQIVKPHDS	-0,4015
PGGVEVPVETDDIDH	-0,0917	PKTQLTMLSARAGLV	-0,4016
GIRLTPKVIATNKTA	-0,0917	FEATLAATVSPAMVA	-0,4029
GGAAPVSAGVGHAA	-0,0923	GSDVPLNPSTGQPDR	-0,4033
AFVDSLTSQVGGRSI	-0,0925	LRHGQILFTFLHLAA	-0,4041
RLAGWQERYPNVAIT	-0,0928	SDLAYTLARGRRHRP	-0,4047
GIMDALFTGLIAIHG	-0,093	AMSNLLGQNAIAA	-0,4047
VTGKARTTVARDADM	-0,093	HWAITDGNKASFLDQ	-0,4053
PNAGSRFLDQAITS	-0,0932	RLAGWQERYPNVAIT	-0,4056
EAVIGNRRRQDSKES	-0,0934	TRFVNVFEQACPGQT	-0,4071
EAAEEQSEFDVILEA	-0,0935	AGMAQDPVATAASNN	-0,4075
LPDFLGGFAGLPSLG	-0,0948	HLVEGVARVLT	-0,408
NDDNVTGGGATTGQA	-0,0948	LMDAWAGPVVMQLME	-0,4089
TPGCVAYIGISFLDQ	-0,0954	DGTRTWRTGRQATTL	-0,4092
PTQGHPLSSATDEPE	-0,0955	TIDAIELPAISFSQS	-0,4096
AEAYLNQNIQQQLRA	-0,0956	HPMLRRTTLIDVDEHT	-0,4098
TMPHHRMLATRHTQT	-0,0959	SEEGSGIILSAEGLI	-0,4103
LIARWEQRDVMAREV	-0,0959	KDQTSDEVTVETTSV	-0,4105

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MGTVPNVGLMAQQAE	-0,0961	FGMSGTNVHAIVEEA	-0,4128
GLNYPEGLAVDTQGA	-0,0962	NALGGNRPAVYAPKS	-0,4131
VPLNPSTGQPDRSAE	-0,0964	GVAVDSAGNVYVTSE	-0,4132
NSEEFDAIADNLEK	-0,0965	SSSAGADPTALNGMP	-0,4136
AGDTDAIAGRVAQIR	-0,0966	LSTDELLDAFKEMTL	-0,4162
TRGRCAAISVPGDRR	-0,0967	AVDGAGTVYVTDFFNN	-0,4172
QPATTVALGRSVCPM	-0,0968	GGCAVLLEPHACVAA	-0,4173
LENNEFNVVDVGS LN	-0,0971	DQQEILNRANEVEAP	-0,4176
LVSGAGNVGQQLSGV	-0,0972	QGYGSLGLMTSVLMT	-0,4186
DRARNVRMELLAKSG	-0,0974	GSKPPSGSPETGAGA	-0,419
VVRGTATNQDGR TET	-0,0975	RSTLEKDNTVGTDEA	-0,4191
GQLNPQVNLVDTLNS	-0,0981	KAVEKVTETLLKGAK	-0,4193
ISGATIPQGEQSTGK	-0,0983	GNVDTGALMSGNFSN	-0,4194
ALAVAVSPAAAAGDL	-0,0993	VEERPVGAPVDALV	-0,4204
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MSNAPKIKVSGPVVE	-0,1002	IGVLERPVGDSSDCG	-0,4217
AQVGAYHLMRTQGGGR	-0,1004	AGADPTALNGMPAGL	-0,4218
SVAVKAPGFGDRRKA	-0,1005	AEAMARVPAARPDVA	-0,4224
KGSQGEDEALYTEDR	-0,1006	VGPGC AEYAAANPTG	-0,4226
QLAEHFASLADVLTK	-0,1006	SVAVKAPGFGDRRKA	-0,4245
TLDYNANGSGAGVTQ	-0,1011	ALPGIVGGAPNPYTY	-0,4255
GTTDRAGVKDVILES	-0,1011	NAGSYNTGSFNVGDT	-0,4277
KQKQELDEISTNIRQ	-0,1015	LGSELTMTDTVGQVV	-0,4284
PVAITTESVGKTIAG	-0,1015	PGALGENGNNGMVTG	-0,4285
TTGEAGNQNTVLDAI	-0,1016	TPANQAISMIDGPAP	-0,4286
SGIPTLSTTGPHAV	-0,1038	GNWPSQTGHSPAVPN	-0,4293
QVTNDKDTLGAKIVE	-0,104	PVTVIAATAGRSDLK	-0,4299
AMAAQLQAVPGAAQY	-0,1044	MTVPGGVEVPVETDD	-0,4302
KDEAAAAQRRCGSPA	-0,1046	AADILKDESYKVTGT	-0,4322
LEGTYRLAPKSGSTE	-0,1047	PALDQVIAKGMAKNP	-0,4329
IPALNPNTGVS VFGF	-0,1048	VVPSVVMLETDLGRQ	-0,4336
RKIPLTLVHAVSPEV	-0,105	KVPRRLKELHLRLGT	-0,4344
LYGNAGGLGPTQGHF	-0,1055	MGTVPNVGLMAQQAE	-0,4348
EQGLIPGFLMPPSDG	-0,106	QLVAAGGGPSQLASM	-0,4355
VGEQLSGLSSAGTAL	-0,1067	DAFPNEFPDPTISVQ	-0,4361
MSSLGSSLGSSGLGG	-0,1073	NANIGFGNRGDANIG	-0,4391
RRTTVNLKACIAAAA	-0,1075	EHTDVERVAQQLLSG	-0,4406
KVNTLLDVAQANLGE	-0,1077	GAGSGFANFGSLGSG	-0,4408
ITTTAGPQLVVPVLN	-0,1077	VPLNPSTGQPDRSAE	-0,4411
EPVDSAVLANGDEVQ	-0,1078	YRATNFKVDQPGTVT	-0,4422
AQTDDQQLAEHFASL	-0,1079	QNIAQQLRAQVMGDL	-0,4424
LVAGLIAPLAVAN	-0,1086	DVVSVVASPQSTVI	-0,4427
LSVEQQLRARQRVAA	-0,1086	PVDALVNLADEEKAD	-0,4427
SFRLPAHVTSEAIAA	-0,1088	GWRAACRSNPALAKG	-0,4427
ATVDPAAVAVNRMAM	-0,109	VAPVSPSTASSRTDT	-0,4435
PVISEHRLVGIVTEA	-0,1092	DLVYGDVIMRSTNFR	-0,4442
DDLMMVNNAGLVC GG	-0,1096	DLQTLFVASDRVPP	-0,4446
TKRRITPKDVIDVRS	-0,1097	AVGEPVVAMGNSGGQ	-0,4475
EAETTTASGLVIPDT	-0,1105	DDRPINSADALVAAV	-0,4479
GVNLPGTAVVPLHRS	-0,1105	TSVLMTADGKTVEAE	-0,4482
INAFSVGSGQTYGVD	-0,1106	DGSAPIVHEMVSIP	-0,4494
RVQGVSGLTPISLGS	-0,111	ARIFAGAGLGPM LAA	-0,4495
NTGNWNIGIGITGNG	-0,1115	EVLLKIAQGRLFYNT	-0,4504
VVAGEPRPGNYRYAI	-0,1117	AVVLPGLVGLAGGAA	-0,4519
NSGLEPGVVAEKVRN	-0,1123	PMLSTLTSALSGKLN	-0,4531
ILTVSAVSEGKPYTE	-0,1125	QNPTGPGSVAGMAQD	-0,4534
RFNLQERVIRPSYGL	-0,1129	NTAASDNFQLSQGGQ	-0,4534
VSGIGNVGEQLSGLS	-0,1132	APKIKVSGPVVELDG	-0,4564
VGADEDDIKATYDKG	-0,1138	RTVSLPVGAEDEDDIK	-0,4573
IPETDGAEEKGPTYNK	-0,1138	LKRGIEKAVEKVTET	-0,4576
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DGQIDGFSTPPITID	-0,1156	GDTNTGGFNPGSTNT	-0,4583
DGALPLLAPMSEVAG	-0,1158	RPVVGAPVDALVNLA	-0,4597
QPVVLAATGDLPTI	-0,1159	TGVANSNGNVDTGALM	-0,4597

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GPYLQRGVADLVPTA	-0,116	GALLRYAATNRLGSH	-0,4609
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PDKSTGLANPGQFAG	-0,1161	VTIPTITTSPIPLKI	-0,4619
FEAALAATVDPAAVA	-0,1161	PAIKIDPPPPPEQG	-0,4627
DVVVSVVASPQSTVI	-0,1165	DKLPAATIDQLKTD	-0,4637
GLAAGLDPNTATAGE	-0,1166	SRQSKTAASPSRSP	-0,465
VVVNEGQIDKGDVV	-0,1167	TGIGGLNSGTGNLGL	-0,4684
LSGAQQPNGYTEPIL	-0,1169	AGDTDAIAGRVAQIR	-0,4698
TVLPFTGLNTPLA	-0,117	VTYELAVDLAVPMIG	-0,4699
QATPTFSSSAGADPT	-0,117	AATALDNDGEGTVQA	-0,4701
AVDVASHSPQVDPIL	-0,1171	WTHARLFIDDDGQEQ	-0,4713
QLMNNVPQALQQLAQ	-0,1176	DALRIVMADSRPLTN	-0,4722
AAPSIPAANMPPGSV	-0,1176	LRALLKQYGPLTPAR	-0,4731
LVYSDGTATGAADPR	-0,1176	ASNNPELTTLTAALS	-0,4744
DLQTFVASDRVPP	-0,1178	DAKQELIDSLEEAVR	-0,4751
AGVNYGDPVDAKALG	-0,1179	EQRVPDNLAEELGRLT	-0,4767
LNRPVSTTGEAGNQ	-0,1181	IAFNSSGLEPGVVAEK	-0,4808
IAFNSSGLEPGVVAEK	-0,1182	DLAAAVDKDGTAFRL	-0,4819
GTRTGNVTLAEGPPA	-0,1186	PQNAIPLTIDASGVL	-0,4835
VKRADLVIGAVLVPG	-0,1188	RSNHGTCANQCPIVD	-0,4842
AIAIAFLAGCSSTKP	-0,1189	GLSDLYSKIESLPAS	-0,4859
VHEMVSIPEDGGVVL	-0,1189	ATVDPAAVAVNRMAM	-0,4862
QTGQQVSIAPNAGLD	-0,1191	RLNTEGVAAAVKQVL	-0,4882
TSYTSDEAMLDAILA	-0,1192	QATPTFSSSAGADPT	-0,4928
CERLVRGLDTIAATG	-0,1193	TGVLPPAANDVSVLT	-0,4945
PELVPTYNLPANHRY	-0,1193	LLSFASLPTVGQVTA	-0,4965
AGSLASGVNLNSGVDI	-0,1195	GEVDEEAATALDNDG	-0,4976
QMLLLDEQTPIDAVA	-0,1204	IDTSNAVDTPDMLAS	-0,4978
LQSLGAIEAVEQAAL	-0,1214	MLSARAGLVMDPGSK	-0,4989
YRTDLADRVDTLVGA	-0,1214	GNPLADLIQPDRLVL	-0,5
DIDHVNHAHGTQVG	-0,1215	GIPDPGDIFNTGSSL	-0,5011
GFNDTTAPSSGFFN	-0,1216	VLAIGSPGLGEGTVT	-0,503
TTTAAGTTASPGAAS	-0,122	DLADRVDTLVGAGER	-0,5044
RNFLAAPPQRAAMA	-0,1221	GKSFQGGVGEARGN	-0,5121
VPGEVADVVVIGAG	-0,1221	PIAHSTVLVAPVSPS	-0,5184
HEGQTTMTVPGGVEV	-0,1227	NATNLRGILGRLEIM	-0,5236
AYAIAKHGVGVKCAT	-0,1238	ILSGSERVQAATIKR	-0,5412
VSEHLKLNGKVLAAM	-0,1238	VVIDRIPVELHASTT	-0,5428
IEEHEIDARDTKLGA	-0,1238	GFTIPGGTLIPQLPL	-0,5441
DFTPAAEIVKDGDDA	-0,1239	NKGDLAADVCKDGT	-0,5484
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TGVLPPAANDVSVLT	-0,1259	QSIGDLIAEAMDKVG	-0,5737
GRSLLDNRAAAALMA	-0,1259	AEINGMSRDMASTFT	-0,5843
MTVETSQTPSAIDS	-0,1274	VGEQLSGLSSAGTAL	-0,5899
PILDDLAAALADIAP	-0,1276	VEIDLCDYRDVDGQY	-0,5976
EEAPAEASAPESP	-0,1276	QLVVALPDKSTGLAN	-0,6021
NDDPAGACRPFDRDR	-0,1277	ADHLTRLVDAADPEV	-0,6202
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IAQTRDKFLSAATSS	-0,1288	RAELMILIATNLLGQ	-0,6511
GHGNVGFNGSGLGAA	-0,129	LDELKLEGDEATGAN	-0,6551
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CQGD LGMSHQDWQAQ	-0,1303	LAVAANLAGALPGIV	-0,7506
AGSWLLIDTSNAVD	-0,1305	LPSLPDIIDGLWPPK	-0,7516
ENSDDSYDREKLQER	-0,1313	VASHSPQVDPILDDL	-0,8035
LLPFEEAPEMTSAGG	-0,1314	LIDGALKDLKKRVEG	-0,8127
EEITRDIPNISDEVL	-0,1319	TVELIEDLARRAVQT	-0,8261
QYSRADEEQQALSS	-0,1319	VPFMFRELVLPGS	-0,8474
SNVGQNPIVNI	-0,1324	LENADLSLLGKARKV	-0,8481
QLTMLSARAGLVMDP	-0,1333	GYGVDIVLNSLTGAA	-0,8482
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DAKALGQSVCPILAE	-0,1348	LQQTIDAIELPAISF	-0,8819
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SGVDAEITTTAGPQL	-0,1382	LPPAANDVSVLTAAR	-1,1472
SAPAGGRAAHADPCS	-0,1383	MLKRKAERRLIDGAL	-0,1864
PDTAKEKPQEGTVVA	-0,1386	LGGANIPAEFLENFV	-0,4329
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IVDSBTCIECPDGT	-0,1396		
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APKIKVSGPVVELDG	-0,1569		
LLKGAKVETKEQIA	-0,1573		
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MLEGCILADSRQSKT	-0,1581		
DGTRTWRTGRQATTL	-0,1587		
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AVIGNRRRRQDSKESK		-0,181			
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CTDDGEMALGKNLLV		-0,1815			
STSSDALRQTARQLA		-0,1818			
VTYELAVDLAVPMIG		-0,1828			
INISLPSYYPDQKSL		-0,1837			
LLKQYGPLTPARAVA		-0,1852			
ESRDAKQELIDSLEE		-0,1855			
LRALLKQYGPLTPAR		-0,1868			
GGYSQGATVIDLSTS		-0,1896			
GMDFVGVTAVGEGV		-0,1897			
SYYPDQKSLNENYIAQ		-0,1914			
NVGQQLSGLLFAGTG		-0,1919			
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FEATLAATVSPAMVA		-0,1938			
DERSDSVLSDSSPVA		-0,1943			
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VPDNLAEGLTLQLP		-0,1963			
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VKLNLTLSAAAEALT		-0,2001			
ARIANGMGATVTVLD		-0,202			
HLVEGVARVLTTPRF		-0,2024			
VEFAEQIRRTDGYG		-0,2025			

DPRHAGPATAADAGD	-0,2032			
NKGDLA AA VDKDGT A	-0,2032			
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LAOPTQGTT PSSKLG	-0,2052			
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VKDVGAGRSLLDNRA	-0,2095			
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LAASRACTDALLD SG	-0,2126			
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NSTELPSSGFFNTGG	-0,2138			
SSTAVIPGYPVAGQV	-0,2142			
AAVYRTDLADRVDTL	-0,2149			
CSKYPDSQVGTAVKA	-0,2155			
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RRSPWGEMFASTGQR	-0,2166			
TLVVNKIRGTFKSVA	-0,217			
SDQDAMARLGAIKRE	-0,2174			
LVEHMGILGQRCAP	-0,2183			
TAAAVVLPGLVGLAG	-0,2192			
NP GELLPEAAGPTQV	-0,2194			
AANPTGPASVQGMSQ	-0,2203			
STNNDDPAGACRPF D	-0,2233			
HVSRLLAKSLARLRD	-0,2237			
AMDKVGNEG VITVEE	-0,2253			
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PHENELIKVKTYLK	-0,2258			
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RTVSLPVGADEDDIK	-0,2393			
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IVKGENIPEGP IES	-0,2432			
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PQNAIPLTIDASGVL	-0,256			
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STGKASHASLG VQVT	-0,267			

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DIASERTAPSRACQG	-0,3412			
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TIDQLKTDAKLLSSI	-0,3452			
AGVLLRTERLKSQRV	-0,3502			
ASLVGFNRAPAGPSG	-0,3504			
VDMPYLTVELIEDLA	-0,3518			
QTS PANVVGTRQT LQ	-0,361			
LKTQIDQVESTAGSL	-0,362			
ARGANILARIMGASI	-0,3622			
NATNLRGILGR LIEM	-0,3629			

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NRANEVEAPMADPPT	-0,3754		
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NALGGNRPAVYAPKS	-0,3814		
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LAGCSSTKPVSQDTS	-0,3926		
LTDLFPIELGTSK	-0,3946		
AMSNLLGQNAAAIAA	-0,395		
VGISQMHVSRLAKS	-0,395		
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VPVLRDELPGLGPLP	-0,3996		
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EVLADLDERGIVRIG	-0,4029		
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VTQPDRVRELLATVF	-0,4067		
DEDDIKATYDKGILT	-0,4076		
FDAAIQPGDSGGPVV	-0,4109		
LLRGDDLVTIIPPDR	-0,4111		
ARPDVAVLDVRLPDG	-0,4136		
KQLNMAQIITSAGPD	-0,4148		
TRGLQHRGKLDGTPE	-0,4168		
IGPATIIPPIHPSI	-0,4169		
AIPLTSATLGGLALP	-0,4189		
EVRAELPGVDPDKDV	-0,4217		
LERPVGDSSDCGTIR	-0,4233		
PEVDTNRLMVSIGTG	-0,4241		
VGLSTIAGRLLGSVP	-0,425		
LALNISVPDSSVPII	-0,4327		
TTLLALLAGVFGGAA	-0,4384		
NVARELSRCGSTGDR	-0,4395		
KFLSAATSSTPREAP	-0,4434		
STSAMPVADHVAA	-0,4585		
VDISGMFNVSTLGSA	-0,4619		
LDEHGTVLLAVRGLR	-0,4627		
NMAQIITSAGPDVPA	-0,4628		
VASHSPQVDPILDDL	-0,4652		
PDRVRELLATVFKLT	-0,4679		
PTNAAFDKLPAATID	-0,4691		
QGAVQGVNDALSGLG	-0,4719		
NMQRQAVPLVRSEAP	-0,4719		
LPSLPDIIDGLWPPK	-0,4763		
GFTIPGGTLIPQLPL	-0,4797		
AAKVVPVVMLETDL	-0,4838		
LELPGIDVDKDVNVE	-0,4846		
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LGADIASERTAPSRA	-0,4921		
DRQNAGDVAYRPMAP	-0,4924		
LPPAANDVSVLTAAR	-0,5001		
GYGVDIVLNSLTGAA	-0,5022		
VITSADVRSASLERMA	-0,5023		
LTSAAERGPQMLGG	-0,5073		
DGPCTDDGEMALGKN	-0,5112		
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EQVAAKVVPVVMLE	-0,5221		
SADVRSASLERMAPLV	-0,5231		
RAELMILIATNLLGQ	-0,5259		
PPITIDRIPLNLGAS	-0,5291		
VDMANPMSPVNKSFE	-0,5417		
PIDAGTAASQRQEG	-0,5469		
SALLDPSQGMGPSLI	-0,5515		
IGKLLDNDKSPSRKT	-0,5561		

QQVSIAPNAGLDPVN	-0,5571			
QGLLSCTLPNRDGDV	-0,561			
DKPEKEKASVPGGGD	-0,5642			
TQQALAAGVPVIGLP	-0,5709			
YQAGKPTSTNPIASI	-0,5761			
AGADPTALNGMPAGL	-0,5782			
DAKQELIDSLEEAVR	-0,5811			
ILSDILSALAANADP	-0,5885			
LRVLDEIAPDLVVGD	-0,5894			
GPDGMPGGEVSILQP	-0,5913			
EIVKDGDDAVVRLEL	-0,5921			
PITLTIPGLSLDAAV	-0,6155			
LNALADAVKVTLGPK	-0,6202			
AANADPLTSGLLGIA	-0,6346			
ALACVLGECLTGAPP	-0,6376			
PPGILSDILSALAAN	-0,6464			
LIATNLLGQNTPAIA	-0,6471			
LENADLSLLGKARKV	-0,6647			
VKMLLNNVLEHLAEN	-0,6658			
VSGLGKKEAKDLVDG	-0,6661			
SVPQLVAAIKELQDK	-0,6786			
NLRGILGRLEMLTT	-0,6892			
ATVALTFQDPSGGSR	-0,728			
DILSALAANADPLTS	-0,7457			
SVVMLETDLGRQSEE	-0,7471			
SVQDTPPNQAGLEK	-0,7487			
IKGMELARAVKDVGA	-0,7558			
EKLQERLAKLAGGVA	-0,7585			
AGKPLIIAEDVEGE	-0,7703			
STIAGRLLGSVPANV	-0,782			
DAAIGKLLDNDKSPS	-0,8085			
LIDGALKDLKKRVEG	-0,8086			
PVDALVNLADEEKAD	-0,8292			
MSGVLNAISDPLLGS	-0,8474			
GILGRLEMLTTLPK	-0,9109			
TVELIEDLARRAVQT	-0,9572			
AEIVASVLEVVENEG	-0,9657			
STVKDLLPLEKVIG	-1,0346			
PLLEKVAKEAADEAK	-1,0988			
PELDVVGEAGSVAEA	0,1002			
NMREYLAAGAKERQR	0,0362			
AQDPVATAASNNPML	-0,0356			
LGGANIPAEFLENFV	-0,1184			
RPIVGAPVDALVNLA	-0,1383			
FVPQAVTPWPNNGNDH	-0,1695			
IDTSNAVDTPDMLAS	-0,1783			
AAGVADPVKVTRSAL	-0,2049			
PLPTLPVPVLRDELP	-0,2552			
DTKLGAEIITRDIPN	-0,2644			
PLDDGDVIDSMFMSK	-0,2686			
VEERPIVGAPVDALV	-0,2848			
DGSAPIVHEMVSIP	-0,3052			
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MAEMKTAATLAQEA	-0,3455			
AVCAPTTGVLPPAAN	-0,3682			
KKELHSSGSTAQENA	-0,4079			
TQVLVPRSAIDSMILA	-0,4171			
DKLPAATIDQLKTD	-0,4355			
SQGATVIDLSTAMP	-0,4514			
VTIPTITTSPIPLKI	-0,455			
LSTDELLDAFKEMTL	-0,4623			
NGIELCRDLLSRMPD	-0,4827			
NLAELGRLTQLPDTN	-0,5231			
FVVTRQAQIVKPHDS	-0,5445			
NRVSFAKLREPLEVP	-0,5502			
AKNVEERPIVGAPVD	-0,2301			

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TLPVPVLRDELPGLG		-0,5232			
MNPDIEKDQTSDEVT		-0,5293			
AQQLRAQVMGDLDKL		-0,5766			
VLAAATGDLPTIGTA		-0,6067			
AAERGPQMLGGLPV		-0,462			
DVQVTMPVPEPMVKM		-0,501			
GLREVADGDALYDAA		-0,2997			
ALAAGVPVIGLPSNM		-0,6886			

The top 100 recognized epitopes, defined by the index values, are listed with the respective MTB protein and accession number.