Supplementary Table S2. List of peptides that bound MHC class II monomers and served as IgG epitopes in serum from patients with acute pulmonary *Mtb (n=35/35). These epitopes were not recognized in serum obtained from 34 healthy subjects (n=34).*

Protein ID	**Peptide /-HLA- DR1**	**HLA-DR2**	**HLA-DR4**
10 KDA CULTURE FILTRATE ANTIGEN ESXB CAA17966			AAGTAAQAAVVRFQE
10 KDA CULTURE FILTRATE ANTIGEN ESXB CAA17966			GSLQGQWRGAAGTAA
10 KDA CULTURE FILTRATE ANTIGEN ESXB CAA17966			QVESTAGSLQGQWRG
3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642			PEVDTNRLMVSIGTG
3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642			STNNDDPAGACRPFD
3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE 2 KASB CAA94642	VVAGEPRPGNYRYAI		VVAGEPRPGNYRYAI
60 kDa chaperonin 2 P0A521	IRGTFKSVAVKAPGF	IRGTFKSVAVKAPGF	IRGTFKSVAVKAPGF
60 kDa chaperonin 2 P0A521			LENADLSLLGKARKV
60 kDa chaperonin 2 P0A521			LNALADAVKVTLGPK
ALTERNATE RNA POLYMERASE SIGMA FACTOR SIGF CAB07069			RLLAKSLARLRDQLE
BIOTINYLATED PROTEIN TB7.3 CAB08316			VASVLEVVVNEGDQI
CELL SURFACE LIPOPROTEIN MPT83 CAA98350			HQTLQGADLTVIGAR
CELL SURFACE LIPOPROTEIN MPT83 CAA98350			LQGADLTVIGARDDL
CELL SURFACE LIPOPROTEIN MPT83 CAA98350	PTNAAFDKLPAATID		
CONSERVED HYPOTHETICAL PROTEIN CAB06237			EFPAIPGFPALPGLP
CONSERVED HYPOTHETICAL PROTEIN CAB06237			LPTVGQVTATMGQLQ
CONSERVED HYPOTHETICAL PROTEIN CAB08634			AADPEVVFVSGEVRS
CONSERVED HYPOTHETICAL PROTEIN CAB08634	DGVGALLRYAATNRL	DGVGALLRYAATNRL	DGVGALLRYAATNRL
CONSERVED HYPOTHETICAL PROTEIN CFP17 CAB01474	EVQIGKFRLVFLTGP	EVQIGKFRLVFLTGP	EVQIGKFRLVFLTGP
CONSERVED HYPOTHETICAL PROTEIN CFP17 CAB01474			KDQTSDEVTVETTSV
CONSERVED HYPOTHETICAL PROTEIN CFP17 CAB01474	NGDEVQIGKFRLVFL	NGDEVQIGKFRLVFL	NGDEVQIGKFRLVFL
CONSERVED HYPOTHETICAL PROTEIN CFP17 CAB01474			PNAGSRFLLDQAITS
CONSERVED HYPOTHETICAL PROTEIN TB16.3CAD97060			VTYELAVDLAVPMIG
CONSERVED HYPOTHETICAL PROTEIN TB18.5CAD93033	VKGAWVLARYDDGRP	VKGAWVLARYDDGRP	VKGAWVLARYDDGRP

ESAT-6 LIKE PROTEIN ESXQ CAA16102			DIASERTAPSRACQG
ESAT-6 LIKE PROTEIN ESXQ CAA16102	DSSDCGTIRVGSFRG		DSSDCGTIRVGSFRG
ESAT-6 LIKE PROTEIN ESXQ CAA16102			LERPVGDSSDCGTIR
ESAT-6 LIKE PROTEIN ESXQ CAA16102			LGADIASERTAPSRA
HEAT SHOCK PROTEIN HSP CAA17343		LTVRVAGAYKAPAET	LTVRVAGAYKAPAET
HEAT SHOCK PROTEIN HSP CAA17343			SEAIAASYDAGVLTV
HYPOTHETICAL PROTEIN RV2623 NP_217139			RKIPLTLVHAVSPEV
HYPOTHETICAL PROTEIN RV2623 NP_217139			VRDQPARQLVQRSEE
HYPOTHETICAL PROTEIN RV2626C NP_217142			PVISEHRLVGIVTEA
IMMUNOGENIC PROTEIN MPT63 CAB06500			SSTAVIPGYPVAGQV
IMMUNOGENIC PROTEIN MPT63 CAB06500			VNAIRGSVTPAVSQF
IMMUNOGENIC PROTEIN MPT64 CAA98382			INISLPSYYPDQKSL
IMMUNOGENIC PROTEIN MPT64 CAA98382			IQMSDPAYNINISLP
IMMUNOGENIC PROTEIN MPT64 CAA98382			TQVLVPRSAIDSMLA
IRON-REGULATED CONSERVED HYPOTHETICAL PROTEIN CAB08889			DRAAQIAGADAKLII
IRON-REGULATED CONSERVED HYPOTHETICAL PROTEIN CAB08889			MSAYKTVVVGTDGSD
IRON-REGULATED CONSERVED HYPOTHETICAL PROTEIN CAB08889			RPIVGAPVDALVNLA
IRON-REGULATED CONSERVED HYPOTHETICAL PROTEIN CAB08889			SSMRAVDRAAQIAGA
IRON-REGULATED CONSERVED HYPOTHETICAL PROTEIN CAB08889			VGLSTIAGRLLGSVP
LIPOPROTEIN LPQH PRECURSOR P0A5J0			AAGTTASPGAASGPK
LOW MOLECULAR WEIGHT T-CELL ANTIGEN TB8.4 NP_215690			AMAAQLQAVPGAAQY
LOW MOLECULAR WEIGHT T-CELL ANTIGEN TB8.4 NP_215690		AMSLTVGAGVASADP	
MAJOR SECRETED IMMUNOGENIC PROTEIN CAA98373		ALAVAVSPPAAAGDL	ALAVAVSPPAAAGDL
MAJOR SECRETED IMMUNOGENIC PROTEIN CAA98373	QTSPANVVGTRQTLQ		
MCE-FAMILY PROTEIN MCE1AYP_177701			DSALLAAAGFGNTTA
MCE-FAMILY PROTEIN MCE1AYP_177701			GPYLQRGVADLVPTA
MCE-FAMILY PROTEIN MCE1AYP_177701		LVAGLIAPPLAVAAN	
MCE-FAMILY PROTEIN MCE1AYP_177701	RGGPGGAPGCWQPIT	RGGPGGAPGCWQPIT	RGGPGGAPGCWQPIT
MCE-FAMILY PROTEIN MCE1AYP_177701	TKRRITPKDVIDVRS		TKRRITPKDVIDVRS

MTB48 AAK31576	GEVDEEAATALDNDG		
MTB48 AAK31576			LVLSADNMREYLAAG
MTB48 AAK31576			YQQRSEKVLTEYNNK
MTB81 (publication)	FLRVLNRDRNYTAPG	FLRVLNRDRNYTAPG	FLRVLNRDRNYTAPG
MTB81 (publication)	PILHRRRREFKARAA	PILHRRRREFKARAA	PILHRRRREFKARAA
MTB81 (publication)			SADVRASLERMAPLV
MTB81 (publication)			SGVDAEITTTAGPQL
MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE U75685			DAMARLGAIKREVTS
MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE U75685			QEITRGRCAAISVPG
MYCOBACTERIUM BOVIS ACYL-COA SYNTHASE GENE U75685	WDGVAITLTWSQLYR	WDGVAITLTWSQLYR	WDGVAITLTWSQLYR
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808			CLFSSGAALLGSPGQ
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808	EFEGELPRLFVVTRQ	EFEGELPRLFVVTRQ	EFEGELPRLFVVTRQ
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808	EIGKADVYGNTRLGL	EIGKADVYGNTRLGL	EIGKADVYGNTRLGL
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808			GLREVADGDALYDAA
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808	GYGVDIVLNSLTGAA		GYGVDIVLNSLTGAA
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808	IEYRSLARVYGAGTP	IEYRSLARVYGAGTP	IEYRSLARVYGAGTP
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808	KADVYGNTRLGLFPF	KADVYGNTRLGLFPF	KADVYGNTRLGLFPF
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808	SAGTVGLIKAILSLR	SAGTVGLIKAILSLR	SAGTVGLIKAILSLR
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808			VLSWLSDHQVHNVAA
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808			VRDLIARWEQRDVMA
MYCOBACTERIUM BOVIS MYCOCEROSIC ACID SYNTHASE GENE M95808	VTLGAAFGGLTTAHT		
PE FAMILY PROTEIN CAE55335			APTTGVLPPAANDVS
PE FAMILY PROTEIN CAE55335			AVCAPTTGVLPPAAN
PE FAMILY PROTEIN CAE55335	GTAVSARNTAVCAPT		GTAVSARNTAVCAPT
PE FAMILY PROTEIN CAE55335			LPPAANDVSVLTAAR
PE FAMILY PROTEIN CAE55335			TGVLPPAANDVSVLT

PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS1 YP_177770			GKSPGFGTTVDFPAV
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS1 YP_177770			GVNLPGTAVVPLHRS
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS1 YP_177770	IDGPAPDGYPIINYE		
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS1 YP_177770			LDQASQRGLGEAQLG
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS2 YP_177769	AAIGPGQEGLDQYGS		
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS2 YP_177769	MKFARSGAAVSLLAA		
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS2 YP_177769	PVAITTESVGKTIAG		
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS2 YP_177769		QEGLDQYGSIPLPKS	
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS2 YP_177769			SALLQTTDGSITYNE
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS3 YP_177768	FTLPGERIHVVFRSD	FTLPGERIHVVFRSD	FTLPGERIHVVFRSD
PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS3 YP_177768			GTAVKAFLQSTIGAG
POSSIBLE GLYCOSYL TRANSFERASE CAB05415	FGVRLVKLLYRLERP	FGVRLVKLLYRLERP	FGVRLVKLLYRLERP
POSSIBLE GLYCOSYL TRANSFERASE CAB05415	FRHHAIHTIPSERFF	FRHHAIHTIPSERFF	FRHHAIHTIPSERFF
POSSIBLE GLYCOSYL TRANSFERASE CAB05415	LLRTERLKSQRVAGA	LLRTERLKSQRVAGA	LLRTERLKSQRVAGA
POSSIBLE GLYCOSYL TRANSFERASE CAB05415			LRVLDEIAPDLVVGD
POSSIBLE GLYCOSYL TRANSFERASE CAB05415	PSERFFGNLTQGRFY	PSERFFGNLTQGRFY	PSERFFGNLTQGRFY
POSSIBLE GLYCOSYL TRANSFERASE CAB05415	RHGLSSLGWNLCRIF	RHGLSSLGWNLCRIF	
POSSIBLE GLYCOSYL TRANSFERASE CAB05415	RLVKLLYRLERPLLF	RLVKLLYRLERPLLF	RLVKLLYRLERPLLF
POSSIBLE GLYCOSYL TRANSFERASE CAB05418	ALAAGVPVIGLPSNM		ALAAGVPVIGLPSNM
POSSIBLE GLYCOSYL TRANSFERASE CAB05418	EVLLKIAQGRLFYNT	EVLLKIAQGRLFYNT	EVLLKIAQGRLFYNT
POSSIBLE GLYCOSYL TRANSFERASE CAB05418	RKYIAADRKILNEIA	RKYIAADRKILNEIA	RKYIAADRKILNEIA
POSSIBLE GLYCOSYL TRANSFERASE CAB05418	RRFPLPDVPWTRFFG		RRFPLPDVPWTRFFG
POSSIBLE GLYCOSYL TRANSFERASE CAB05418	TQQALAAGVPVIGLP		TQQALAAGVPVIGLP
POSSIBLE GLYCOSYL TRANSFERASE CAB05418			WSPQARRRFPLPDVP
POSSIBLE GLYCOSYL TRANSFERASE CAB05419			FSIIIPTLNVAAVLP
POSSIBLE HEMOLYSIN CAA16235		RVVRVTGRASARGLI	
POSSIBLE HEMOLYSIN-LIKE PROTEIN CAA17201	AAPRSVGVPLYLLLG	AAPRSVGVPLYLLLG	AAPRSVGVPLYLLLG

POSSIBLE HEMOLYSIN-LIKE PROTEIN CAA17201	VLAGASLVAVSWAVG		
PPE FAMILY PROTEIN CAE55334	AFAMTVPPSLVAANR		AFAMTVPPSLVAANR
PPE FAMILY PROTEIN CAE55334			ELTSAAVSYGSVVST
PPE FAMILY PROTEIN CAE55334		GGAAPVSAGVGHAAL	
PPE FAMILY PROTEIN CAE55334			GLLPPEVNSSRMYSG
PPE FAMILY PROTEIN CAE55334		HIGLYGNAGGLGPTQ	
PPE FAMILY PROTEIN CAE55334			VAAELTSAAVSYGSV
PPE FAMILY PROTEIN CAE55371	AENRAELMILIATNL		AENRAELMILIATNL
PPE FAMILY PROTEIN CAE55371			AVQTAAQNGVRAMSS
PPE FAMILY PROTEIN CAE55371			LIATNLLGQNTPAIA
PPE FAMILY PROTEIN CAE55371		MSSLGSSLGSSGLGG	
PPE FAMILY PROTEIN CAE55371			VGSWIGSSAGLMVAA
PPE FAMILY PROTEIN CAE55371			YVAWMSVTAGQAELT
PPE FAMILY PROTEIN CAE55489			PIAHSTVLVAPVSPS
PPE FAMILY PROTEIN CAE55489	WRSLDVEMTAVQRSF		WRSLDVEMTAVQRSF
PPE FAMILY PROTEIN CAE55504	ANRTRLASLVAANLL		
PPE FAMILY PROTEIN CAE55504		FEATLAATVSPAMVA	FEATLAATVSPAMVA
PPE FAMILY PROTEIN CAE55504			FGKPANPDVLVVGNG
PPE FAMILY PROTEIN CAE55504			FSIPQLGFTLSGATP
PPE FAMILY PROTEIN CAE55504	GFTLSGATPADAYPT		
PPE FAMILY PROTEIN CAE55504	GNPLADLIQPDLRVL		
PPE FAMILY PROTEIN CAE55504			IGNIGDRNLGIGNTG
PPE FAMILY PROTEIN CAE55504			LNSLTYDVSVAQGVT
PPE FAMILY PROTEIN YP_177963		AIPLTSATLGGLALP	
PPE FAMILY PROTEIN YP_177963	AMSNLLGQNAAAIAA		
PPE FAMILY PROTEIN YP_177963			GFTIPGGTLIPQLPL
PPE FAMILY PROTEIN YP_177963			GLAAGLAGMGNIGLG
PPE FAMILY PROTEIN YP_177963			IGPATIIPPIHIPSI
PPE FAMILY PROTEIN YP_177963	LALNISVPDSSVPII		
PPE FAMILY PROTEIN YP_177963	LNLGSGLSGIYNTST		
PPE FAMILY PROTEIN YP_177963			LSGIYNTSTLPLGTP
PPE FAMILY PROTEIN YP_177963	LTGDNQTGIGGLNSG		
PPE FAMILY PROTEIN YP_177963	NISVPDSSVPIIIVP		

PPE FAMILY PROTEIN YP_177963			NQSLIINLGLADVGS
PPE FAMILY PROTEIN YP_177963	PGIGNTTTVPSSGFF	PGIGNTTTVPSSGFF	
PPE FAMILY PROTEIN YP_177963			PPITIDRIPLNLGAS
PPE FAMILY PROTEIN YP_177963			SGIPTLSTTGPVHAV
PPE FAMILY PROTEIN YP_177963		SIIDIPALPGFGNST	
PPE FAMILY PROTEIN YP_177963			STGMSGGFVTAPTQG
PPE FAMILY PROTEIN YP_177963	TIFPNGISIPNNPLA		TIFPNGISIPNNPLA
PPE FAMILY PROTEIN YP_177963	VDISGMFNVSTLGSA		VDISGMFNVSTLGSA
PPE FAMILY PROTEIN YP_177963			VGEQLSGLSSAGTAL
PPE FAMILY PROTEIN YP_177963			VTIPTITTSPIPLKI
PROBABLE CUTINASE PRECURSOR CFP21 NP_216500			SQGATVIDLSTSAMP
PROBABLE CUTINASE PRECURSOR CFP21 NP_216500			YPASDDYRASASNGS
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	AEFPDYLTEEQRVPD		
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247			CERLVRGLDTIAATG
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247			GKLKDTKAVNPESTF
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	GLSDLYSKIESLPAS		GLSDLYSKIESLPAS
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	HPIVFGHAVRIFYKD	HPIVFGHAVRIFYKD	HPIVFGHAVRIFYKD
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247			KDTKAVNPESTFSRI
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247			NLAELGRLTQLPDTN
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247			PHENELIKKVKTYLK
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	QLPDTNIIKLPNISA	QLPDTNIIKLPNISA	QLPDTNIIKLPNISA
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247	SPSRKTGELDNRGSQ		SPSRKTGELDNRGSQ
PROBABLE ISOCITRATE DEHYDROGENASE CAA16247			VPDNLAELGRLTQLP
PROBABLE ISOCITRATE DEHYDROGENASE CAA17111		GTVTRHYRQYQAGKP	GTVTRHYRQYQAGKP
PROBABLE ISOCITRATE DEHYDROGENASE CAA17111		REPIVISNVPRLVPG	REPIVISNVPRLVPG
PROBABLE ISOCITRATE DEHYDROGENASE CAA17111			YQAGKPTSTNPIASI
PROBABLE LIPOPROTEIN LPRJ CAB10947			DGTRTWRTGRQATTL
PROBABLE LIPOPROTEIN LPRJ CAB10947			LALLAGVFGGAASCA
PROBABLE LIPOPROTEIN LPRJ CAB10947			MMGNAFLTALTNAGI
PROBABLE LIPOPROTEIN LPRJ CAB10947			QPATTVALGRSVCPM
PROBABLE LIPOPROTEIN LPRJ CAB10947	TTVALGRSVCPMVVA		TTVALGRSVCPMVVA
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN CAA16030			CAPVFVMAAPGQPLP

PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN CAA16030		DALRIVMADSRPLTN	DALRIVMADSRPLTN
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN CAA16030			GQRCAPVFVMAAPGQ
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN CAA16030	GVRLAFVCAVDMPYL		GVRLAFVCAVDMPYL
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN CAA16030			LVEHMVGILGQRCAP
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN CAA16030			TLPVPVLRDELPGLG
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN CAA16030			TTTLVEHMVGILGQR
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN CAA16030			YRTDLADRVDTLVGA
PROBABLE SERINE PROTEASE PEPA CAB09453			GVDVVGYDRTQDVAV
PROBABLE SERINE PROTEASE PEPA CAB09453	INAFSVGSGQTYGVD		INAFSVGSGQTYGVD
PROBABLE SERINE PROTEASE PEPA CAB09453			LQLRGAGGLPSAAIG
PROBABLE SERINE PROTEASE PEPA CAB09453			LTNNHVIAGATDINA
PROBABLE SERINE PROTEASE PEPA CAB09453	QTYGVDVVGYDRTQD		QTYGVDVVGYDRTQD
PROBABLE SERINE PROTEASE PEPD CAA17582			AAKVVPSVVMLETDL
PROBABLE SERINE PROTEASE PEPD CAA17582			AAPSIPAANMPPGSV
PROBABLE SERINE PROTEASE PEPD CAA17582			AASAAPSIPAANMPP
PROBABLE SERINE PROTEASE PEPD CAA17582			EQVAAKVVPSVVMLE
PROBABLE SERINE PROTEASE PEPD CAA17582			FQDPSGGSRTVQVTL
PROBABLE SERINE PROTEASE PEPD CAA17582			GAAASLVGFNRAPAG
PROBABLE SERINE PROTEASE PEPD CAA17582			IGSPLGLEGTVTTGI
PROBABLE SERINE PROTEASE PEPD CAA17582			LGSSSDLRVGQPVLA
PROBABLE SERINE PROTEASE PEPD CAA17582			PLGLEGTVTTGIVSA
PROBABLE SERINE PROTEASE PEPD CAA17582			RVQGVSGLTPISLGS
PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	EQQRLARQRVAAAGF	EQQRLARQRVAAAGF	EQQRLARQRVAAAGF
PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE UFAA1 NP_854118	FRSGYLDVYQWTLIR	FRSGYLDVYQWTLIR	FRSGYLDVYQWTLIR
PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE UFAA1 NP_854118			LVYSDGTATGAADPR
RNA POLYMERASE BETA-SUBUNIT AAA21416	GAPNRVSFAKLREPL		
RNA POLYMERASE BETA-SUBUNIT AAA21416			GLTHKRRLSALGPGG
RNA POLYMERASE BETA-SUBUNIT AAA21416			LQELLTIKSDDTVGR

RNA POLYMERASE BETA-SUBUNIT AAA21416			NMQRQAVPLVRSEAP
RNA POLYMERASE BETA-SUBUNIT AAA21416	NRVSFAKLREPLEVP		
RNA POLYMERASE BETA-SUBUNIT AAA21416	QGLLSCTLPNRDGDV		
RNA POLYMERASE BETA-SUBUNIT AAA21416	VEYVPSSEVDYMDVS	VEYVPSSEVDYMDVS	VEYVPSSEVDYMDVS
RNA POLYMERASE BETA-SUBUNIT AAA21416			YVAQKRKISDGDKLA
SECRETED ANTIGEN 85-B FBPB (85B) CAB10044	AVVLPGLVGLAGGAA		
SECRETED ANTIGEN 85-B FBPB (85B) CAB10044			LPVEYLQVPSPSMGR
SECRETED ANTIGEN 85-B FBPB (85B) CAB10044		QSGLSIVMPVGGQSS	
SECRETED ANTIGEN 85-B FBPB (85B) CAB10044	QSSFYSDWYSPACGK		QSSFYSDWYSPACGK
SECRETED ANTIGEN 85-B FBPB (85B) CAB10044			TAAAVVLPGLVGLAG
SECRETED L-ALANINE DEHYDROGENASE ALD CAA15575	PTTYDHPTFAVHDTL	PTTYDHPTFAVHDTL	PTTYDHPTFAVHDTL
SECRETED L-ALANINE DEHYDROGENASE ALD CAA15575			SAITDADFKAAGAQL
SECRETED L-ALANINE DEHYDROGENASE ALD CAA15575			VGTADQVWADADLLL
SECRETED L-ALANINE DEHYDROGENASE ALD CAA15575	VKRADLVIGAVLVPG		VKRADLVIGAVLVPG
TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446	ASDFAYLVDFGIARA		
TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446	LLKQYGPLTPARAVA	LLKQYGPLTPARAVA	LLKQYGPLTPARAVA
TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446			LVLRPSWSPTQASGQ
TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446			PALDQVIAKGMAKNP
TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446	TGDEVTYRADIYALA	TGDEVTYRADIYALA	TGDEVTYRADIYALA
TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446	TVLPFTGLNTPLAVA	TVLPFTGLNTPLAVA	TVLPFTGLNTPLAVA
TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446	VYVADRGNNRVVKLA	VYVADRGNNRVVKLA	VYVADRGNNRVVKLA
TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND NP_215446	YPEGLAVDTQGAVYV		
TWO COMPONENT TRANSCRIPTIONAL REGULATORY PROTEIN DEVR NP_217649		TSYTSDEAMLDAILA	