

-----MKXXLLVVXLLLTL-----SLSWAKTEI--LSDE-----

10 20 30 40 50 60 70 80

TmB27 -----MKIGLLVVAISTL-----PYCWSKTEI--LSDK----- 28

TmB26 -MQKMKITILVVAISTL-----SYCWAKTEI--LSNK----- 32

TmB25 -----MKITILVVAISTL-----SYCWAKTEI--LSNK----- 28

TmB24 -----ILVVAVSTL-----SYCWAKTEI--LSDE----- 24

TcB\_XP\_966750 -----MRSYL VVVFVLTFS-----SALSAQNPI--LSDE----- 28

TcB\_XP\_966663 -----MKSLVLLLALFL-----PKSSPKTPI--LSQQ----- 26

\*TmB32 -MALTNWTRGLVAITIIAVGSA LMDDYFDLPGPYCQRGCGCPGRQDDCSVPILGTL CYCDDFCNRTRNEDCCPDFWSHCR 79

\*TcB\_XP\_008195382 -MASFSWLCPVALTLLTLTTA QFSDYSDLRGPYCQRGCGCPGRQDDCSEPI LGTL CYCDDFCNRTRNEDCCPDFWTHCK 79

Papain MAMIPSISKLLFVAICLFVYM-----GLSFGDFSIVGYSQN----- 37

TmB28 -----MRHAFLLYALTIF-----SLCEVK-KCQYLTKT----- 28

TcB\_XP\_008196465 -----MRKIIILFALT-----PFSWSKPSTPSLQPQ----- 28

TcB\_XP\_008196467 -----MHKITFLCALTL-----PLSWSKPNTSSLQ----- 26

\*TcB\_XP\_968689 -----MQKLLLLCALL-----PLSWTKPNAS----- 22

TcB\_XP\_968767 -----MQKIIILCALL-----PLSWSNPNVTL----- 23

TmB23 -----MICPLLVSVLSLV-----SPCLQE-EIQMTRHE----- 29

TmB22 -----MNYSLVSTLILXV-----LFTTXVTLISPRRS----- 28

TmB19 -----MNYIIVSTLLCLTL-----LDTPATLASSRRS----- 28

TmB20 -----MKIFLSFVVLVAVL-----SASLAEIDV--LSSE----- 28

TcB\_XP\_974244 -----MYFLIFLLLASI-----SVSRAEIDI--QSQD----- 26

TmB33 -----MKCVLLCIVVLASV-----ALSYGGVKLHPLSDE----- 30

TcB\_XP\_974298 -----MKCVLLCAVVLATI-----ALSYGGLNPHPLSDE----- 30

TmB18 -----MKCVLLFVAVLGTV-----ALTHGGVRVHPLSDE----- 30

TcB\_NP\_001164205 -----MKYFLHFVAVLATV-----ALVYGGVHLHPLSDD----- 30

TmB17 -----MKNLAYIAVLCTAI-----STILAVNPLSKE----- 27

TcB\_XP\_974220 -----MRTLPIILTICTAA-----SLSVAVHPLSKE----- 27

HsCathB -----MWQLWASLCCLLVL-----ANARSRPSFHPVSDE----- 30

-----FINSINSKQST--WXAGR--N-----

90 100 110 120 130 140 150 160

TmB27 -----FIESINQKRTT--WVARR--N 44

TmB26 -----FIESINQKRST--WVARR--N 48

TmB25 -----FIESINQKRST--WVARR--N 44

TmB24 -----FIESINQKRST--WVARR--N 40

TcB\_XP\_966750 -----FINSINAQQST--WTAGR--N 44

TcB\_XP\_966663 -----FINAINQKHPS--WLAGP--N 42

TmB32 GVTPPP-IAAPIIGCTYEGTVYPIGKQLKKNKNVCKCERVGMS-GDMLCEQHRCIIEPTITDAINSDPSN-GWTASNYSE 156

TcB\_XP\_008195382 GLPPPPEPPSPILGCTYEGRVYPLNKQIKKNKNVCKCEKMGQNQADMLCEQHQLIEPSITEAINSNYANYGWSASNYSK 159

Papain -----DLTSTERLIQLFESWMLKHNKIYKNIDEKIYRFEIFKDNLYIDETNKKNNYSY-WLGLN--V 95

TmB28 -----FIDFINKNQSS--WRAGK--F 44

TcB\_XP\_008196465 -----LIQEINSRQTS--WKAG--- 43

TcB\_XP\_008196467 -----VIQEINSEQIS--WKAE--- 41

TcB\_XP\_968689 -----LINQINSQSSA--WTAGI--- 38

TcB\_XP\_968767 -----LINQINSQSS--WTARI--- 39

TmB23 -----LINFINTNQSN--WTAGD--N 45

TmB22 -----LINRVNIIQST--WVAGE--N 44

TmB19 -----FINRINNVSS--WVAGE--N 44

TmB20 -----FIDSINRIQSS--WVAGR--N 44

TcB\_XP\_974244 -----FIDSINQKQSH--WVARR--N 42

TmB33 -----FINEINSKQTT--WKAGR--N 46

TcB\_XP\_974298 -----FINAINSCKTT--WKAGR--N 46


TmB18 -----FIASINNQKTT--WKAGR--N 46

TcB\_NP\_001164205 -----FINRINSRKST--WKAGR--N 46

TmB17 -----FIQSINDAQST--WKAGP--N 43


TcB\_XP\_974220 -----FIQQINEKQST--WKAGP--N 43

HsCathB -----LVNYVKNRNTT--WQAGH--N 46



	170	180	190	200	210	220	230	240
	FPEN-TPIEXLKRLNGFLG-DPDPXYKLP-LKVHKXDX-NAIPESFDAREKWPQC-DSIGNIRDQSGSCSWAFGAVEVM							
TmB27	FPED-TPIEQLKRLNGALD-DLRHKYQVK-LKVHRVNV-SAIPDTFDGRTYWSQC-ESLKDIRNQGNGCGSWVFGGVEAI	119						
TmB26	FPED-TPIEQLRRLNGAIE-DPHYKSQIK-LKVHKVDV-SAIPDTFDGRTHWPQC-ESLKNIRNQGQCGSCWAFGSTTEAM	123						
TmB25	FPED-TPIEQLRRLNGAIE-DPHYKSQVK-LKVHKVDV-SAIPDTFDGRTHWPQC-ESLKNIRNQGQCGSCWAFGSTTEAM	119						
TmB24	FPED-TPIEELRRLNGAIE-DPHYKSQLK-LKVHKVNA-SEIPDTFDGRTYWPQC-ESLKTIRNQGCGSCWAFSTVEPM	115						
TcB_XP_966750	FPED-TPIEHLKRLNGALI-TPDLVGKNQ-THVINVIP-EAIPETFDGRTHWSQC-PSLKNIRNQGNGCGSCWAFGSVEVM	119						
TcB_XP_966663	FPPN-TPHSHLRSLNGARD-DPAFFTDTE-TKNVTI-P-EQIPQNFARIVWPQC-ESIRKIRNQGSCGSCWAFGAVETM	116						
TmB32	FWGR-TLEEGIKLRLGTLQ-PQRFVMKMT-PVRHTYDP-QSFPREFESEMKWP---RWISGIQDQGWCGSWAISTAAVA	229						
TcB_XP_008195382	FWGH-KLEEGIKLRLGTLQ-PQRFVMHMN-PVRRYIDP-NSLPREFDSEFKWP---GWMSEIQDQGWCGSWAITTAAVA	232						
Papain	FADM-SNDEFKEKYTGSAI-GNYTTTELS-YEEVLNDGDVNIPEYVD---WRQK-GAVTPVKNQSGCGSCWAFSAVVTI	167						
TmB28	FLENVTSRNFVHRYHRPVL---NVGNEVR-VKDCYLED-LHIPDSFDAREKWPACDVIIGNIRDQSGSCSWAFSSTGVM	119						
TcB_XP_008196465	-----TNSLDIKSRLGFLGLHPDPDYKIQ-TKHHKIA--KSIPESFDAREKWPCKDVIKIRNQGTCGSCWAFASTEVM	114						
TcB_XP_008196467	-----TNCLDIKSRLGFLGLHPDPNYKIQ-TKQHKISRIISIPEESFDAREKWPCKDVIKIRNQGNGCGSCWAFASTEVM	114						
TcB_XP_968689	-----NPFDDIESRLGFLGIHPDPNFKPE-IKEPQATQ-NVIPETFDAREYWPCCADIIIGNIRNQGKCSWAFAAAEM	110						
TcB_XP_968767	-----NPFDDIESRLGFLGIHPDPNFQLE-VLEWEPR-TVIPATFDAREYWPQCKDVIIGNIRNQGKCSWAFAAAEM	111						
TmB23	FPEI-TSTEVLKRLNGVLGIDDPPEYQVT-LRRHKIGK-TKMPFEFFDARDAWAECGVIQYVVDQGGCGSWAFAAAEM	122						
TmB22	FPDS-TTTEDLKHLNGFLGVDPDPDFTIQ-KKTHVIPR-NEIPARFDAREKWPCCRGIENIMDQGXCGSWAFSSAEM	121						
TmB19	FPDS-IPTEHLHYLNGFLGIDPPDNFIIA-ENTHVIPR-NQIPAEFDAREAWPECRDIIENIMAQGACGSCWAFASTEVM	121						
TmB20	FPEN-TTNEYLYKLNGLFGLHPDPNYKPP-VLVHTFNA-RDVPEESFDARTKWPNCDLSLNRIRDQGACGSCWAFASIESM	120						
TcB_XP_974244	FPEN-TTNEYLYKLNGLFGLHPDPNYMPE-KIKHNFNP-QDIPKTFDARKKWPKC-DSLNRIRDQSGCGSCWAFAAVETM	118						
TmB33	FDVN-TPISHVRRLLGVLP-KKANAPKLP-VKTHAVNL-DAIPESFDAREAWPECTSIIIGEIRDQASCGSCWAFGAVEAM	122						
TcB_XP_974298	FDIH-TPLANIKKLLGVLP-KKANARQLE-LKVHSDVD-NAIPESFDAREAWPECASIIIGDIRDQASCGSCWAFGAAEAM	122						
TmB18	FDVN-TPLPQIKKLLGVLP-KTENTPKLP-LKIHPGV-LDIPESFDAREAWPDCASIIIGEIRDQASCGSCWAFGAVEAM	122						
TcB_NP_001164205	FDID-TPISHIKQLLGVLP-ETENTPKLP-KKIHSINA-QEIPDSFDAREAWPDCAPIIGNIRDQSTCGSCWAFGAVEAM	122						
TmB17	FAEN-VDMYSIRRLMGV---HPHSKYHKPSIKTHQLDA-TAIPASFDARQEWPNCP-TIREIRDQSGCGSCWAFGAVEAM	117						
TcB_XP_974220	FAEN-VPMSYIRRLMGV---PPNSKYHMPVSRHLLDA-MEIPDDFDARKQWPNCP-TIREIRDQSGCGSCWAFGAVEAM	117						
HsCathB	FY-N-VDMGYLKRLCGTFLGGPKPPQVRM-FTED-----LKLPAESFDAREQWPQC-PTIKEIRDQSGCGSCWAFGAVEAI	117						

Occluding Loop



	250	260	270	280	290	300	310	320
	SDRLCIASNGTVKFEFSAEDLLSCCTD-CGD---GCN-GGYPARAWDYWINSQIVSGGDY---NSNEGQPYSCSA XV							
TmB27	TDRICIATGGKVKFQFSAEDVLSCTD-CGD---GCD-GGYPYSTWTYWINSQIVSGGDY---QSQQGCQPYT---KSAFV	189						
TmB26	TDRLCIATDGKVKFQFSPEDLLSCCKE-CGD---GCD-GGSSATAWAYWMNSQIVSGGDYQSQSQEGCQPYL---ESTFV	195						
TmB25	TDRLCIATNGKV-----ACCTA-CGD---GCD-GGWPSSKSFQYWMSSQIVSGGDY---QSQQGCQPYA---KSAFD	179						
TmB24	TDRLCIATNGTVKFEFSAEDLLSCCTD-CGK---GCQ-GGAPSKAWAYWKSSGIASGGDY---QSQQGCQPYA---KSAFI	185						
TcB_XP_966750	TDRLCIASKGKTKFEFSADDLLACCTA-CGK---GCD-GGAPYRAFEYVWAKGIVSGGDY---NSNEGQPYE---GSAFL	189						
TcB_XP_966663	SDRLCIASNATKKFEFSAQDLLACCKE-CGH---GCG-GGYSRAWQYVWTDGIVSGGDF---NTSQQCHPYS---VQAFR	186						
TmB32	SDRFAILSKGREQIMLSAQHLVSCDIR-GQQ---SCN-GGYLDRAWSYIRKFLV-----DEQCFPYTASNEKCKV	295						
TcB_XP_008195382	SDRFAILSKGREKVTLSAQHLLSCDRR-GQQ---SCN-GGYLDRAWSYIRKIGLV-----DEQCFPYATNEKCRI	298						
Papain	EGIIKIRTGNLN--EYSEQELLDCRR--SY---GCN-GGYPNSALQLVAQYGIHYRNTY---PYEGVQRY---CRSRE	232						
TmB28	TDRLCIQSEGEVKFQFSPQDILSCCEN-CSNSTYGCAGGSSDRAWRYWTESGIVSGGDY---DSYQGCVFYQ---ESEFY	193						
TcB_XP_008196465	TDRLCIGTKGETKVFVSPENLLTCCED-CRL---ECV-GGYTAKAWDYINEGIVSGGDY---NSSEGCQPYSC---KASFQ	184						
TcB_XP_008196467	TDRLCISSK-----D-CGC---GCK-GGYIKNAWDYINEGIVSGGDY---NSSEGCQPYSC---ESSFQ	167						
TcB_XP_968689	SDRLCIATNGKVKIQLSPEDLIDCCHY-CGN---QCK-GGYTYAWNYFMTGLVSGGDY---NTSTGCQPYSC---ELNYY	180						
TcB_XP_968767	SDRLCVATNGSVKFEFSPEDLINCCTE-CGK---KCK-GGYSYAWKYTSTGLVSGGDY---NTSRGCQPYSC---KSNFN	181						
TmB23	SDRLCIATGGQDKVMSPEDLLQCCTD-CGL---GCD-GGYVNAKAWYWLTYGVVSGGDY---NSNTGCKPYSC---ALAYL	192						
TmB22	SDRLCIASNGTEKVFVSPEDLLECCVN-CRN---QCL-GGYMNAFQYWIKNVSGGDY---NSNLGCKPYSC---GSAYI	191						
TmB19	SDRLCISSKATKKVFVSPEDLLECCTS-CRD---QCE-GGYINSAFKYWINNGVSGGDY---NSLGLCKPYSC---KEAHI	191						
TmB20	SDRICHSSGSAQFMFSPEDLLSCCTS-CGD---CG-GGYMSALDFYINEGIVSGGDV---NSNEGCRPYT---ADAHD	189						
TcB_XP_974244	SDRICHSSGAKKFFFSADLLSCCTA-CGS---CS-GGYMAAFDFYIKQGVVSGGDL---NSNEGCRPYT---ADAHD	187						
TmB33	SDRICHSDASVKVRI SAEDLNDCCYD-CGD---GCN-GGWPDLAWSYWSSTGIVTGGY---GVDEGCKAYSIKPCDHHV	195						
TcB_XP_974298	SDRICHSNATVKVSI STEDLNTCCYE-CGD---GCN-GGWPAAEWAWAETGIVTGGY---ETKDGCKAYTVPPCEHHV	195						
TmB18	SDRICHSNATVKVISAEDLTSCCVL-CGL---GCN-GGWPMAWLWYSDSGIVTGGY---GSHEGCRTYSIPECEHHV	195						
TcB_NP_001164205	SDRICHSNATVKVNISAEDPLDCCTI-CGM---GCN-GGMPAMAWLHWTVNGIVTGGY---EDTNGCKAYSFAPCEHHV	195						
TmB17	SDRVCIHSGKGINVHVSADDLVSCCVT-CGM---GCN-GGFPGAAWHYVWKTGIVSGGTY---GSHQGRPYEIPAPCEHHV	190						
TcB_XP_974220	SDRVCIHSGKAVNVRLSADDLVSCCYSCGM---GCN-GGFPGAAWHYVWVNGIVSGGSF---GSNQGCRPYEIPAPCEHHV	190						
HsCathB	SDRICHHTNAHVSVEVSAEDLLTCCGSMCGD---GCN-GGYPAAEAWNFWRKGLVSGGLY---ESHVGRPYSIPPCEHHV	191						

Occluding Loop

	DGT	TPXCXKTC	NTGYKTPYXQDKH	FGSS	XYXIS	XNVXQIQTE	IMTNG	PVEASFXVY	EDFYSYK	
	330	340	350	360	370	380	390	400		
TmB27	DNT	TPECANTC	NTNYTISYQQDKH	FGVD	HYSIA	EDVEIQTEIL	TNG	PVEASYSVY	GDFYSYD 253	
TmB26	NGV	TPECATTC	RNXDYKTPXQDKH	SATE	HYQIA	QNVEIQTEIL	NNG	PVSASYTVY	DDFYNYG 259	
TmB25	DYI	TPKCATTC	NTGYKTSYQQDKH	FGTQ	HYRIA	QNVQIQTEI	INNG	PVSASYTVY	EDFYNYD 243	
TmB24	DGK	TPACANTC	NTDYKTPYQDKH	FGID	HYAIAK	KDVLQIQTEIL	TNG	PVSAMFGVY	DDFYNY 250	
TcB_XP_966750	NSV	TPKCSTKC	NSKYTTPYAKDKH	YGTDF	IYMTS	KNVAEQTEI	MNG	PVVTHTMDVY	EDFYSYK 254	
TcB_XP_966663	DST	TPNCSSFCT	NPKYQKNYSEDKR	YGAR	SYRIA	KNIEIQIAE	IMTSG	PVQASYVVY	DDFYSYQ 250	
TmB32	LRK	GGLAEAKC	KLPELVDRRSKYK	VAPAYRIG	NETDIMH	DIMTSG	PVQATMKVY	HDFFTYK	356	
TcB_XP_008195382	PRR	GDLVTANC	QLPTNVDRRSKYK	VAPAYRVG	NETDIMY	EILHSG	PVQATMKVY	HDFFTYK	359	
Papain	KGP	YAAKT	DGVRQVQPYNE	GAL	LYSIA	NQ	PVSVVLEA	AGKDFQLYR	278	
TmB28	LKT	KSPCMKSC	NNPHYKISYAEDKH	FGSD	YYQVK	PAEKCIQAE	IMSNG	PVEAIFALY	EDFYFYK 257	
TcB_XP_008196465	YAV	ASKCVKAC	QNDKYDVKYDDDKH	YGDS	FYTLE	TNVTQIQTEIL	TNG	PVMATFNVF	EDIIYYK 248	
TcB_XP_008196467	YAE	ASECVKAC	QNDKYDVNYDDDKH	YGDS	XYTLE	TNVAQIQMEIL	TNG	PVMAYYNVF	EDFACHK 231	
TcB_XP_968689	R-I	TPPCNTTC	QNDKYPIPVSDKH	FGDS	IYYIP	QNETAIQNEIL	SGGGPVVA	AFDVY	GDFKIYR 244	
TcB_XP_968767	DGV	SPECSKTC	QNTKYPTSYLNDRH	FGDG	TYYIL	KNVTTIQQEIL	LRGGPVMA	GFDVY	EDFKLYR 246	
TmB23	YKT	TPPCQKRC	QLNYNTPYEVDKS	FALS	IYKVS	SEEEIQIME	IMTNG	PVMTTYTVF	EDFYSYQ 255	
TmB22	NGR	VSTCTKNC	QVGYTTIYNDKK	FGGS	VYGV	SAVDQIQMEI	MLNG	PVVAGYQVY	EDFYLYK 254	
TmB19	NSR	IPTCVKNC	QTGYKTSYKDDK	FGVS	VYGV	AIVEIQIMEI	MLNG	PVIAGYEVY	EDFYLYK 254	
TmB20	QGQ	TPACTKSC	RNGYSTSYSADKH	YGSN	DYVVS	SAIDQIQYEV	MTNG	PIIVNFVVF	QDFYNYV 252	
TcB_XP_974244	KGV	TPSCTKSC	RKGYPTSYSDDKH	YGSK	DYIVD	AGVSNIQYEV	MTNG	PIIVSFKVY	QDFYNYG 250	
TmB33	DGNL	GPC-GDIQRT	PACKKSC-DSTSDLE	EYKSDLR	RGSA	YSIP	KSESQIQTE	IMTNG	PVEADYDVY	SDFLTYK 266
TcB_XP_974298	EGDL	PAC-GDIVPT	PQCKKEC-DAGVDIE	EYKSDLR	KGSA	YQTS	SDESQIQTE	IMTNG	PVEADFVY	EDFLNYK 266
TmB18	DGDL	PAC-GDIQPT	PACQRVC-DADSDLE	YEPDLR	TGSS	YTVG	GSVIQIQTEIL	TNG	PVEASYEVY	EDFLSYK 266
TcB_NP_001164205	DGDL	PPC-GPTKPT	PDCKKEC-DSGSSL	TYQNDLT	HGSN	YGID	PYPKQIQTE	IMTNG	PVEASFVY	EDFLSYK 266
TmB17	NGTR	PPCTGDGNK	TPSCKKVC-EKGYN	VPYNKDRN	FGKE	AYSIS	SDVQQIQKE	IMTNG	PVECAFIVY	ADLLSYK 263
TcB_XP_974220	NGTR	PPCTGDDNK	TPSCKQCC-EKGYN	VPYKDKN	FGKE	AYSIS	SEVQQIQKE	IMTNG	PVECAFVY	EDLLSYK 263
HsCathB	NGSR	PPCTGEGD	TPKCSKIC-EPGYS	PITYKQDKH	YGYN	SYSVS	NSEKDIMAEI	YKNG	PVECAFVY	SDFLLYK 263

	SGVYQH	VSGXYVGGH	AVKILGWGT	ENGTP	YWL	VANSWGS	WDGDLGGFFKIL	RGXNE	CGIESNIXAGX					
	410	420	430	440	450	460	470	480						
TmB27	SGVYQH	VDGKYAGNH	AVKILGWGT	EDGTP	YWL	VANSWGGN	WGDLGGFFKIL	RGADH	LGIESNILGGT 321					
TmB26	SGVYQH	VSGDVAGAH	AIKILGWGT	ENGTP	YWL	VANSWGDW	SSLDGGFFKIL	RGXNE	CGIESN 321					
TmB25	SGVYQH	LSGDESGSH	AIKILGWGT	ENGTP	YWL	VANSWGDW	SSLDGGFFKIL	RGXNE	CGIESNIQAGT 311					
TmB24	SGVYQH	LSGNRSGNH	GKILGWGT	EDGTP	YWL	VANSWGTN	WAGLGGFFKIL	RGKNS	AGIELNVMGGT 318					
TcB_XP_966750	SGVYQH	VSGNSMGCH	AVKIIGWTE	GKVP	YWL	IAN\$W	GAKWADLDG	FYKILRGKNH	CKIETYIYGGT 322					
TcB_XP_966663	NGVYQH	VLGNVSGRH	SVKILGW	RENGTD	YWL	VANSWGRD	WGLGGFFKFL	RGXNE	CDIESNILGGD 318					
TmB32	TGIYKHS	PLSSADRT	GYSVRIVG	WGEEYS	QGVK	KYKVAN	SWGRLWGD	NGYFKI	ARGTNE	CEIESFVLGTW 430				
TcB_XP_008195382	RGIYRHS	PISTNDRT	GYSVRIVG	WGEEYS	PEGL	KKYK	VAN\$W	PEWGE	NGYFRIL	RGXNE	CEIESFVLGTW 433			
Papain	GGIFV	G---PCGNKV	DHAVA	AVGYGPN	YIL	IKN\$W	GTGWGE	NGYIRIK	RGTGNSY	GVCGLY	SSFYVPV 344			
TmB28	DGVYTY	TIGGLV	SAHVKI	IIGW	VENGNP	YWL	AAAN\$W	NCN	WGLKGGFFK	IRRGVDE	CGIEQHVL	LAGTAR 326		
TcB_XP_008196465	SGVYYH	VSGDCT	XHVVK	IIGW	TGEGVP	YWL	IAN\$W	GTW	WGLGGFFK	IKIRGTNE	CAIEQEMA	AGNVH 316		
TcB_XP_008196467	SGVYYY	KSGKFV	GRH\$V	KVIG	WTGEGIP	YWL	IAN\$W	GSEW	GELGGFFK	MRRGTNE	CWIEQEM	TAGKVH 300		
TcB_XP_968689	DGVYIY	TSGALF	GRTAVK	IIGW	TENGWA	YWL	AAAN\$W	GKDW	GALGGFFK	IRRGTNE	CGFEE	SI	IAGQVR 313	
TcB_XP_968767	EGVYVH	TSGALL	GSHAVK	IIGW	TENGWA	YWL	VANSW	GKDW	GALGGV	FKIRRGTNE	CKIEQ	SI	ITGHVR 315	
TmB23	RGVYHH	VAGKYM	GCHAVK	IIGW	VENKIP	YWIV	VANSW	GRW	GALGGFFK	ILRGVNH	CGIEE	Y	IVSD 323	
TmB22	KGVYKH	VTGQKM	GNHAVK	IIGW	TENGTP	YWL	VANSW	GRN	WGLGGFFK	ILRGKNH	CGIES	N	IVTAK 322	
TmB19	KGVYQY	VTGPKV	GNHVK	IIGW	TENDTP	YWL	VANSW	GRD	WGLGGFFK	ILRGKNH	CDIEN	Y	ITAGK 322	
TmB20	SGVYRH	VSGESV	GRHVK	IIGW	VENGMP	YWL	IAN\$W	GSS	WGDHG	FFKML	RGONE	CGIEN	Y	PYAAM 319
TcB_XP_974244	SGVYHH	VSGNYT	GNHIVK	IIGW	TEKEQD	YWL	IAN\$W	GSS	WGEHG	FFKIL	RGKNE	CGIEN	N	PYAVL 317
TmB33	SGVYQH	VSGEAG	GCHAVK	IIGW	VEDGTP	YWL	VANSW	NES	WGD	KGYFK	ILRGQDE	CGIES	D	IIGGI 333
TcB_XP_974298	SGVYQQ	TTGNYA	GCHAIK	IIGW	VEDGTP	YWL	AAAN\$W	NED	WGD	KGYFK	ILRGQNE	CGIES	D	IIGGI 333
TmB18	SGVYQH	VSGEEG	GCHAVK	IIGW	VEDGTP	YWL	VANSW	NED	WGD	KGYFK	ILRGQDE	CGIEE	D	ITAGL 333
TcB_NP_001164205	SGVYQH	LEGEYA	GCHAIK	IIGW	VENDTP	YWL	VANSW	NED	WGD	KGYFK	ILRGXNE	CGIEG	S	IVAGI 333
TmB17	SGVYQH	VTGAEL	GCHAIR	ILGW	VEKNTP	YWL	IAN\$W	N	SDWGD	NGIFK	ILRGKD	CGIE	S	IVAGL 330
TcB_XP_974220	KGVYQH	VKGEAL	GCHAIR	ILGW	TEKGTGTP	YWL	IAN\$W	N	SDWGD	NGTFK	ILRGED	CGIE	S	IVAGI 330
HsCathB	SGVYQH	VTGEM	GCHAIR	ILGW	VENGTP	YWL	VANSW	N	TDWGD	NGFFK	ILRGQD	CGIE	S	IVAGI 330

	-----PKX-----	
	490      500      510      520      530      540	
TmB27	-----PKV	323
TmB26		321
TmB25	-----PKV	313
TmB24	-----PKV	320
TcB_XP_966750	-----PQV	324
TcB_XP_966663	-----PKI	320
TmB32	-----PEIENKLLLNEIRRIRYPK	449
TcB_XP_008195382	-----AEVENKLLLRNEI	445
Papain	-----KN	345
TmB28	LKTKTSSSS-----PWLLVALVSAGIVIAVMAIALFVKKKSMESVINYFRLKS	374
TcB_XP_008196465	IGGRETTHKA-----PSSGGRIKGAIEFGVLIATILFRHIAIKPW	356
TcB_XP_008196467	IEGNERTEEMTTNATSKA-----PSSGFRTKGPEFRGVLIAIILLCQISIKCCLF	350
TcB_XP_968689	--EGGSTSPTPVTFATVTPPTPGSGVRVAGCGIGLVL-SMMLFYLLK-----F	360
TcB_XP_968767	KDEKSSTSTTPV-----PGSGVRVVGSGVGAVL-AMVLFYLLK-----F	353
TmB23	-----KSHSSQMLPLPLLIV--TLPLVCKVVIFFAKF	352
TmB22	-----SSSSSSYISSLLFILTAAAVNSTSFLSK	349
TmB19	-----SSASSVYICYFLMLLATVINSTFFLSR	348
TmB20	-----PRL	321
TcB_XP_974244	-----PKL	319
TmB33	-----PEL	335
TcB_XP_974298	-----PVV	335
TmB18	-----PNL	335
TcB_NP_001164205	-----PEL	335
TmB17	-----PPAQS	334
TcB_XP_974220	-----PKDSS	334
HsCathB	-----PRTDQYWEKI	339