SUPPLEMENTAL MATERIALS

Figure S1. Sequence alignment of gB sequences of 35 alphaherpesviruses. The alignment was generated using Clustal Omega (2-4), and represented in ESPript 3.x program (5), with the residues colored according to their conservation. Identical residues are shown in white letters on red background, while the residues conserved more than 75% are shown as red letters on white background. PrV gB sequence is shown on the top, with the corresponding numbering and secondary structure elements plotted above the alignment. FL1 and FL2 regions are indicated. Predicted N-glycosylation sites in PrV gB are marked with blue star symbols on the top, and the cysteine residues involved in formation of five disulfide bridges are shown in green numbers at the bottom of the alignment. Purple, vertical arrows indicate the boundaries of the expression construct, and dotted line shows regions not resolved in the structure. The FL residues investigate in this study are underlined in green.

35 sequences of gB of alphaherpesviruses used for the alignment (GenBank accession codes are given in brackets) correspond to gB of: **Suid alphaherpesvirus 1** (AEM64049), Human alphaherpesvirus 1 (AAF04615.1), Human alphaherpesvirus 2 (ADG45133.1), Human alphaherpesvirus 3 (AAP32845.1), Saimiriine alphaherpesvirus 1 (YP_003933812.1), Macropodid alphaherpesvirus 1 (AAD11960.1), Macropodid herpesvirus 4 (AGC54689.1), Macropodid alphaherpesvirus 2 (AAD11961.1), Leporid alphaherpesvirus 4 (YP_009230158.1), Macacine alphaherpesvirus 1 (BAC58067.1), Papiine alphaherpesvirus 2 (AAA85648.1), Cercopithecine alphaherpesvirus 2 (AAA88010.1), Chimpanzee alpha-1 herpesvirus (BAE47051.1), Spheniscid herpesvirus 2 (YP_009342376.1), Anatid herpesvirus 1 (YP_003084394.1), Falconid herpesvirus 1 (YP_009046525.1), Meleagrid alphaherpesvirus 1
(NP_073321.1), Gallid alphaherpesvirus 2 (YP_001033956.1), Cercopithecine alphaherpesvirus 9
(NP_077446.1), Lagenorhynchus alphaherpesvirus 1 (BAM99305.1), Caprine alphaherpesvirus 1
(AAD46114.2), Rangiferine herpesvirus 1 (AAD46113.2), Cervid alphaherpesvirus 1
(AAD46115.2), Bovine alphaherpesvirus 1 (AFB76670.1), Bovine alphaherpesvirus 5
(AAD46112.2), Bubaline alphaherpesvirus 1 (AFB76670.1), Felid alphaherpesvirus 1
(AAD46112.2), Bubaline alphaherpesvirus 1 (AF015888.1), Felid alphaherpesvirus 1
(AAD46112.2), Canid alphaherpesvirus 1 (AEK27122.1), Phocid alphaherpesvirus 1
(CAA92272.1), Equid alphaherpesvirus 3 (YP_009054936.1), Equid alphaherpesvirus 4
(AMB16237.1), Equid alphaherpesvirus 8 (YP_006273012.1), Equid alphaherpesvirus 9
(YP_002333514.1), Equid alphaherpesvirus 1 (AII81366.1), and Testudinid herpesvirus 3

		i	10	20	30	40
AEM64049.1		. MPAGGG .	LWRGPRGHRP	GHHGGAGLGRI	LWPAPHHAA	AARGA
AF04615.1					MRQGAPARGCR.	
DG45133.1						
AP32845.1						
P_003933812.1					MA PPAAKSR.	
AD11960.1					MAVHPPLRPRL.	
GC54689.1						
AD11961.1					MTTHSPPKROR.	
P 009230158.1					.	
AC58067.1					MRPR	
AA85648.1					MRPR GAR.	
AA88010.1					MRPR GTP.	
AE47051.1					MRDGAPAHGRG	
P 009342376.1						
P 003084394 1	MYRRTICYLRI	RMPAYECNS	SGPEWRNNP	RDVGCDROGRI	LIYALYGASTTGSR	NGGA
P 009046525 1	MOGRDLHHLRI	RLPSDGRPG	SGSGREDRS	GHDSYLRLGR	FSLVRGAPAAGAGH	RRKSOGGG
P 073321 1	ngonbunnun	JALL OD GAL		onbornhubok	r o i r nom minom on	nnnogooo.
P 001033956 1						
P 077446 1		MSPDCST	OOVCRYNYK	PHOCNLERER	TETVYSNSAACSCR	TKTV
AM99305 1		MSLGSG	LKOHLBANBR	OVSCHIRPGR	TEVA TVNETTT	GPRTO
AD46114 2		MPPPCSAR	PRACECOROR	CORCHIPPORT	FPALPCLAAPCAC	CPPAA
AD46113 2		MAADCDAE	PAACACDCPP	CODCULDDCD	TALLCAAABCACP.	DCCCCPP
AD40115.2		MAARGRAD	BAACBCDCBB	CORRUPCICION	TAALRGAAAF GAGA	C ADAA
EP76670 1		MAARGGAN	PAACACDCRR	CODDUIDDCD	ITAALKGFAAFGAA.	C ADAA
AD46112 2		MATRCCAL	DAACACVCDD	CORDUIDECEN	I ANI BORANDONCO	C ADAA
AD40112.2		MATRGGAN	PAAGAGIGRR	CODDUIDDCD	LAALRGPAAPGAGG	G. ARAA
PO15666.1		MCEDCOL	PAAGAGDGRR	GURCHERODO	EAALKGPAAPGAGG	G. ARAA
NG05542.1		MSTRGDLU	. KRERGSRWQ	GHSGIFRQRCI	FPSLLGIAATGSRH	GNG55
EKZ/122.1						
AA922/2.1		NAADAG	ACROCKCR			NORICATOR
P_009054936.1		MSSRGGV	AGPGGIGPG	GDRCHLRRRR	LSPLKGPAADGSGV	WGELGAIGD
MB160/9.1		MSTCCRAI	CGPQRCYWR	RDCGNLRQRR	LASIHRTPAAGSWL	WSQLGNVNL
P_006273012.1						
P_002333514.1						
II81366.1		MSSGCRSV	GGSKWGHWR	GDGGYLRQRR	VLAPVCSAPAAGSWI	GSQLGNVGN

		· · · · ·
AEM64049.1		
	50	60
AEM64049.1	ALALLLLALA.AAP.J	PCGAAAVTRAASA.
AAF04615.1		PSSPGTPGV
ADG45133.1		PAAPRASGG
AAP32845.1		FAVVSVSPSS.
YP_003933812.1	ASRVAPLTSLVSMLAAAAAAVALCAAFAEA	ARGVTPVYSDDAD.
AAD11960.1		VDTGGN
AGC54689.1		GGTTGH
AAD11961.1	QITRLWY	GGPTGH
YP_009230158.1		TRAAAPRRARPEGR
BAC58067.1	AGPLPLPSPLVPLLALAL	LA.ATRPLG
AAA85648.1	ALPIPIPIPIPIPIPIPIPPPALLALALL	AA . AGRAGP
AAA88010.1		AA. AGRAAP
BAE47051.1		
YP 009342376.1	SVNTNVVIVLTFLLVS	LVRSEDPGDNS.
YP_003084394.1	TTAVR.RKEFDRMNRARRVSALHLTAPRRSRFVL.SLIMVSV	LFRPIQPQPIV.
YP_009046525.1	ERGARKRERLSSRAFVPMSPDVYVPTTSPCVQLVAFVVMHLLLGSLP	MVSSQTAAPAA.
NP_073321.1		ILS
YP 001033956.1		ILY
NP_077446.1	LNVCYITSFA	ILFACVHPSL.
BAM99305.1	PASLMWLEYS.LLCVCLLIY	PGGAAREYP.PSS.
AAD46114.2	AAALLWAAWA.LLLAA	PAAALPTAP.PSA.
AAD46113.2	ALALLWPLLL.LLPLLAP	PAAAAPVTP.APP.
AAD46115.2		PAAGLPATP.APP.
AFB76670.1	AAALLWATWA.LLLAA	PAAGRPATT.PPA.
AAD46112.2		PAAGRPTTP.PVP.
AP015888.1		PAAGRPTTP.QVP.
ANG65542.1	GGBTRLARYVSFIWIVLF	LVGPRPVEGQSGS.
AEK27122.1		ICDPTTPES
CAA92272.1	MYLITLVFFINILVI	OCVPTTOPT
YP 009054936.1	SPGAVAGARPPPHF	RCGAT PTSPPA.
AMB16079.1	ASPMS.KDSTSLGVRTIV.IACLVLLG(CCIVEAVPTTPSS.
YP 006273012.1		
YP 002333514.1		
AII81366.1	AAPHPLGKQASSRVGTIV.LACLLLFG	SCVVRAVPTTPSP.
YP 009176910.1	MIMWLSFMMTLWSLSLVY	GOTIVPPT
AMB16079.1 YP_006273012.1 YP_002333514.1 AII81366.1 YP_009176910.1	ASPMS.KDSTSLG.V.N.RTI.V.IACLVLLG.G AAPHPLGKQASSRV.V.GTI.V.LACLLLFG.S MIMWLSFMMTLWSLSLVY.	CIVEAVPTTPSS SCVVRAVPTTPSP GQTIVPPT.

AEM64049.1						
		70	80	90	100	110
AEM64049.1		SPTPVPGSPGI	TPN. DVSAEAS	SLEEIEAFTP	GPS.EAPDG	EYGDLDARTA
AAF04615.1	AAATQAANGGI	PATPAPPALGA	APTGDPKPKK	NKKPKNPTPP	RPAGDNATV.	AAGHATL <mark>R</mark> EHLF
ADG45133.1	VAATVAANGGI	PASRPPPVPSP	ATTRARKRKT	KKPPERPEAT	PPPDANATV.	AAGHATLRAHLF
AAP32845.1	1	LYESLQVEP		TQ	SEDITRSAH.	LGDGDEI <mark>R</mark> EAIF
YP_003933812.1	ESSESIITG. (GAELPGEDAGE	PGPEPGLPDRI	TKPRKPRPG	RRQRANKTR	EDARAQLRESVE
AAD11960.1	AKPTOPLNKOTRSI	PERGSDPSPPE		PDE	VEPRENQTV	ESGHAQLREHIF
AGC54689.1	TKPAVSPRRQDATI	PKYPP PPNE	SSS	SDE	YEPQFNETV	ELGHAQLREHLF
AAD11961.1	AKPAVSLSRQAATI	HKHPPPPPPP	PSS	SDE	YEPOFNETV	ELGHAQLREHLF
YP 009230158.1	ARGEGRE RGKO	GRRPPPPLPSE	PAPTPLLOY.	S	TGAPTNASA	PANSAELREEIF
BAC58067.1	PAAATPVVSPI	RASPAPPVPA	TPTFPDDDN.	DGEAGAAP	GAPGTNASV	EAGHATLRENLE
AAA85648.1	AAAN. PV ASLI	PATPAPPAPGA	TPTFPE	DGDEEGVAP	PAPAANASV	EAGRATLREDLE
AAA88010.1	AAAAAPTAD.		TPALPEDEEVI	DEDGEGVAT	PAPAANASV	EAGRATLREDLE
BAE47051.1	VAVTPAA NVSI	PASRPPPIOSE	ATTKARKOKT	KOPKRPEPT	PPPDVNATV	AAGHATLRAHL
YP 009342376.1		S. EKRSA			DN. GNAAAA	NKGTVPFR. TI
YP 003084394.1		ATDRPHO	I.M.	NDO	DTHLDGERL	ORGKLSARELI
VP 009046525 1		AAAAAAAA	AAA	AVA	ANGSOANPO	AGPKVTTTELMI
NP 073321 1					TATSET	KLPNVTARETVS
YP 001033956 1					GTNSSP	STONVTSREVVS
NP 077446 1		STSOPPVNND	K		POYDTSPIT	TEECODIPKAL
BAM99305 1		DN DEVECCE	TEV DIKT	OPTER	OPGTNDT	TREOTOTRETI
AD46114 2		DATCOAL	DEA D	CA CA	TAAACN	FTAADDUPAULI
AD46113 2		DCADADT	FD.	ррстр	C DEDIDAA	ACNESDIPANTI
AD40115.2		TDADAACA CE	TDA DACD	CRCCD	ABDDDBDDC	ASNCEDURARLI
AFD76670 1		DDDFFAADA.GE	DAC DCDD	GF GGD	CPDCDDAAS	PONSTOVPAAL
APD/6112 2		CACCACEDAE	DAC DADC	ACTOD	ADCBDDCDD	PDNSTDVRAAL
AAD40112.2		CAGGAGSPAR	PAS.PAPS	ACDDD	ADGPDDGDD	PDNSTDVRAAL
APOIDEELO 1		GA. GAGSPAR	PAS.PAPP	ASPRP	ADSPDDGDD.	PDNGTDVRAAL
ANG05542.1		rs. EQP		TVATPEVGG	TPPKPTTD.	PTDMSDMREAL
AEK2/122.1				TINP.LN	HHNLSTP	KPTSDDI K EILI
CAA92272.1				ESTPPITPS	PPPKNSSSN	TELNDDMREILO
YP_009054936.1		PP.APPTTPSE	PSS.ESSE	PAEPSPLPS	G.GEEDGDG	PETSEDLRGAV
AMB16079.1		QPSTPAS	S. T.QSAK	. TVDQTLLP.		TETPDPLRLAVI
YP_006273012.1			MST.HSQG	. TVNPTLLP.		TETPDPLRQAVI
YP_002333514.1			MST.HSRG	. TVDPSMLP.		TETPDPLRLAVI
AII81366.1		PTSTPTS	SMLT.HSHG	. TVDPTLLP.		TETPDPLRLAVI
YP_009176910.1						DDVGISMSELMI

		β2	β3		β4	β5
AEM64049.1	► T.T 120	→ 130	TT	150	160	170 180
AEM64049.1	RAAATE . RDI	REYVCPPI	SGSTVVRLEPE	ACPEYSOGR	NFTEGIAVLFK	NIAPHKFKAHIYKNV
AAF04615.1	IKAEST . DA	NFYVCPPI	TGATVVQFEQP	RRCPTRPEGQ	NYTEGIAVVFK	NIAPYKFKATMYYK DV
ADG45133.1	IKVENA.DA	OFYVCPPI	TGATVVQFEQP	RRCPTRPEGQ	NYTEGIAVVFK	NIAPYKFKATMYYKDV
AAP32845.1	SQDAET . KP	TFYVCPPI	TGSTIVRLEPT	RTCPDYHLGK	NFTEGIAVVYK	NIAAYKFKATVYYK DV
YP_003933812.1	IRAENA. TSI	MFYVCPPI	TGATVVQFEEP	RPCPDVAAGK	NFTEGIAVIFK	NIAPYKFTATMYYKEI
AAD11960.1	VKAGDG . DSI	EFYVCPAI	TGATVLQFEKP	HPCPSAPTGD	NYTEGIAIIFKI	NIAPYKFKAMMYYK DV
AGC54689.1	IKVKDG.DS	EFYVCPPI	TGATVIQFEKP	YPCPSAPTGD	NYTEGIAIIFKI	NIAPYKFKAMMYYK DV
AAD11961.1	IKVKDG.DSI	EFYVCPPI	TGATVIQFEKP	YPCPSAPTGD	NYTEGIAIIFKI	NIAPYKFKATMYYK DV
YP_009230158.1	LRGSSE.DPI	RFYVCPPI	TGATVIRLEEP	RACPDAPKGL	NFTEGIAVIFK	NLAPYKFKATMYYK AV
BAC58067.1	IKALDG.DA	TFYVCPPI	TGATVVQFEQP	RPCPRAPDGQ	NYTEGIAVIFK	NIAPYKFKATMYYK DV
AAA85648.1	IKARDG.DA	TFYVCPPI	TGATVVQFEQP	RPCPRAPHGQ	NYTEGIAVVFK	NIAPYKFRATMYYK DV
AAA88010.1	IKARDG.DA	TFYVCPPI	TGATVVQFEQP	RPCPRAPDGQ	NYTEGIAVVFKI	NIAPYKFKATMYYK DV
BAE47051.1	IKVENA.DA	OFYVCPPI	TGATVVQFEQP	RRCPTRPEGQ	NYTEGIAVVFK.	NIAPYKFKATMYYK DV
YP_009342376.1	SAQSED . DG	VFYVCPPI	TGATVLRLEPP	RQCPDYKTGK	NFTEGIAVIFK	NISPYKFKATLYYK NV
YP_003084394.1	VQSTRE.ED	KFYVCPPI	TGTTVLRFEPS	RKCPEAYKGR	NWTEGVAVIFK.	NINPLKFKAMIYYK NV
YP_009046525.1	IQVTGD.EA	TFYVCPPI	TGATVMRLEPP	RPCPEAHKGK	RWTEGIAVIFK	NISPYKFKAKLYYK NV
NP_073321.1	IQLSED.ET	TFYVCPPI	VGSTIVRLEPP	RKCPEPLKST	EWGEGIAILFK	NISPYKFKVTLYYK NV
YP_001033956.1	VQLSEE.ES	TFYLCPPI	VGSTVIRLEPP	RKCPEPRKAT	EWGEGIAILFK	NISPYKFKVTLYYK NI
NP_077446.1	SRDIYN.EA:	SFYVCPPI	TGSTVVTLESP	RVCPDYHLGK	NFTEGIAVIYK	NIAAYKFKATVYYK DV
BAM99305.1	SQRAGE . DD	TFYMCPPI	TGATVVRMAPP	RACPQYSQGR	NFTEGIGVIFK	NIAPYKFKAHIYYK NV
AAD46114.2	AQAAGE . HS	QFFVCPPI	SGATVVRLAPG	RPCPEYELGR	NYTEGIGIIYK	NIAPYKFKAHIYYK NV
AAD46113.2	AQAADE . SSI	RFFVCPPI	SGATVVRLAPA	RPCPDYELGR	NYTEGIGVIYK	NIAPYTFKAYIYYKNV
AAD46115.2	AQAAGE . SSI	RFFVCPPI	SGATVVRLAPA	RPCPEYELGR	NYTEGIGVIYK	NIAPYTFKAYIYYKNV
AFB76670.1	AQAAGE . NSI	RFFVCPPI	SGATVVRLAPA	RPCPEYGLGR	NYTEGIGVIYK	SNIAPHTLKAYI<mark>Y</mark>YK NV
AAD46112.2	AQAAGE . NSI	RFYVCPPI	SGATVVRLAPA	RPCPEYELGR	NYTEGIGAIYK	NIAPYTFKAYIYYK NV
AP015888.1	AQAAGE . NSI	RFYVCPPI	SGATVVRLAPA	RPCPEYELGR	NYTEGIGAIYK	NIAPYTFKAYIYYK NV
ANG65542.1	SQIEANGPS	TFYMCPPI	PSGSTVVRLEPP	RACPDYKLGK	NFTEGIAVIFK	NIAPYKFKANIYYKNI
AEK27122.1	SQIESDDTS	TFYMCPPI	PSGSTLVRLEPP	RACPNYKLGK	NFTEGIAVIFKI	NISPYKFKANIYYK NI
CAA92272.1	SQIESDDTA	TFFMCPPI	SGSTLVRLEPP	RACPNYKLGK	NFTEGIAVIFK	NISPYKFKANIYYK NI
YP_009054936.1	AQVLAA. SA	DFFTCPPI	TGSTVVRLEPP	RACPKFNLGR	NFTEGIAVIFK	NIAPYKFRGTVYYK DV
AMB16079.1	SGILAE . DG	DFYTCPPI	TGSTVVRIEPP	RSCPKFDLGR	NFTEGIAVIFK	NIAPYKFRANVYYKDI
YP_006273012.1	SGILAE . DG	DFYTCPPI	TGSTVVRIEPP	RTCPKFDLGR	NFTEGIAVIFK	NIAPYKFRANVYYK DI
YP_002333514.1	SGILAE . DG	DFYTCPPI	PTGSTVVRIEPP	RTCPKFDLGR	NFTEGIAVIFK	ENIAPYKFRANVYYK DI
AII81366.1	SGILAE.DG	DFYTCPPI	PTGSTVVRIEPP	RTCPKFDLGR	NFTEGIAVIFK	NIAPYKFRANVYYK DI
YP_009176910.1	ITNTEGLNT	NFTICGLS	STGTDIVRLSPP	SPCHKYTEDN	NYDEGIAVIFK	DIVPYVFPLTFYTKEV
		1		2		

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	LO MATHING NEW OF AND											
	05					0.7	0.0		0.0		0	
	po po		α1		α2	β7	188		β9 -	η1	β10	
AEM64049.1	190 200		210	le	lee	220		230		200	· —	
			219								·	
AEM64049.1	IVTTVWSGSTYAAITNRFTDRVI	PVPV	VQDI	TDV	IDR	RGKC	VSKAEY	VRNNHI	KVT AI	FDRD	ENPVEV	. D
AAF04615.1	TVSQVWFGHRYSQFMGIFEDRA	PVPJ	FEEV	IDK	INA	KGVC	RSTAKY	VRNNLI	ETTAI	FHRD	DHETDM	. E
ADG45133.1	TVSQVWFGHRYSQFMGIFEDRA	PVPI	FEDV	IDK	INA	KGVC	RSTAKY	VRNNMI	ETTAI	FHRD	DHETDM	. E
AAP32845.1	IVSTAWAGSSYTQITNRYADRVI	PIPV	VSDI	TDT	IDK	FGKC	SSKATY	VRNNHI	KVE AI	FNED	KNPQDM	. P
YP_003933812.1	TVTQTWQGSRYLQLTGLYNDRAI	PVPF	FEEI	TDV	INA	KGLC	RSDVTY	VRSQRI	RVTA	YDRD	EWGREV	. K
AAD11960.1	TVSHVWYGSSYAQLTGLFEDRAI	PIPF	FAEI	MDF	IND	KGVC	KSTVKY	TRHNLI	ETTAI	FHED	SGEKEM	. P
AGC54689.1	SVAHVWYGSSYAQITDLYEDRAI	PVPJ	FAEI	MDL	IND	KGVC	KSSVKY	SRHNTI	ETTAI	FHKD	SSETEM	. P
AAD11961.1	SVAHVWYGSSYAQITDLHEDRAI	PVPJ	FADI	MDL	IND	KGVC	KSSVTY	SRHNII	ETTAI	FHKD	SGETEM	. P
YP_009230158.1	TVSKVWSGYSYSQLTNIFEDRAL	PIPF	FE <mark>D</mark> I	VDR	IHG	RGV	LSTAKY	IRNNLI	ETTAI	FHND	ENEHEM	. K
BAC58067.1	TVSQVWFGHRYSQFMGIFEDRA	PVPJ	FEEV	IDK	INA	RGVC	RSTAKY	VRNNMI	ESTAI	FHRD	DDESDM	. K
AAA85648.1	TVSQVWFGHRYSQFMGIFEDRA	PVPJ	FEEV	IDK	INA	KGVC	RSTAKY	VRNNMI	ESTAI	FHRD	DHESDM	. A
AAA88010.1	TVSQVWFGHRYSQFMGIFEDRAI	P V P J	FEEV	MDK	INA	KGVC	RSTAKY	VRNNMI	ESTAI	FHRD	DHESDM	. A
BAE47051.1	TVSQVWFGHRYSQFMRIFEDRA	5 A b 1	FEDV	IDK	INA	KGVC	RSTAKY	VRNNLI	ETTAI	FHRD	DHETDM	. E
YP_009342376.1	VTTTTWSGTTYRQITNRYADRVI	PVQ:	T D 🖸 I	TDL	VDK	KGKC	LSKARY	RRNNA	VES	YDKD	EAVREV	. D
YP_003084394.1	IQTTTWSGTWYKQITNRYTDRVI	PVA?	LDDI	TDR	IDR	FGKC	LSAAKY	LRNNV	YVDAI	FDRD	ESAKEV	. P
YP_009046525.1	IQTTTWAGTTYRTITNRYTERVI	PVL:	IE <mark>D</mark> I	TDL	IDR	KGKC	SSGAKY	LKNNVI	VVEAD	FDMD	TYAREV	. D
NP_073321.1	IQTTTWTGTTYRQITNRYTDRT	PVS	IDEI	TDL	IDG	KGKC	SSKARY	LRNNV	YVDA	YDRD	ENEKQV	. L
YP_001033956.1	IQTTTWTGTTYRQITNRYTDRT	PVS:	IE 🖸 I	TDL	IDG	KGRC	SSKARY	LRNNV	YVE AI	FDRD	AGEKQV	. L
NP_077446.1	IVSTSWAGSSYTQLTNRYADRVI	PIP	VSEI	TAT	IDK	FGKC	STKATY	VRNNHO	2LE <mark>A</mark> I	FNED	KNPHDA	. P
BAM99305.1	IVTTTWSGSTYAAITNQYTDRVI	PVK	VSDI	TEL	IDG	QGK	LSKADY	IRSNRI	EVTAI	FDRD	EDPTAV	. R
AAD46114.2	IVTTTWSGSTYAAITNQHTDRVI	PVG	VSDI	TDV	VDK	KWRC	LSKAEY	LRSGRI	KVV <mark>A</mark> I	FDRD	ADPWEA	. P
AAD46113.2	IVTTTWAGSTYAAITNQYTDRVI	P V GI	MADI	TDV	VDK	KWRC	LSKAEY	LRSGRI	RVEA	FDRD	ADAWEA	. P
AAD46115.2	IVTTTWAGSTYAAITNQYTDRVI	I U V	MG <mark>D</mark> I	TDV	VDK	KWRC	LSKAEY	LRSGRI	RVAA	FDRD	EDAWEA	. P
AFB76670.1	IVTTTWAGSTYAAITNQYTDRVI	P V GI	MG <mark>B</mark> I	TDL	ANK	KWRC	LSKAEY	LRSGRI	KVVA	FDRD	DDPWEA	. P
AAD46112.2	IVTTTWAGSTYAAITNQYTDRVI	P V GI	LG <mark>E</mark> I	TDL	VDK	KWRC	LSKAEY	LRSGRI	KVVA.	FDRD	EDPWEA	. P
AP015888.1	IVTTTWAGSTYAAITNQYTDRVI	P V GI	LG <mark>E</mark> I	TDL	VDK	KWRC	LSKAEY	LRSGRI	KVAAI	FDRD	EDPWEA	. P
ANG65542.1	IMTTVWSGSSYAVTTNRYTDRVI	PVK	VQEI	TDL	IDR	RGMC	LSKADY	VRNNY	QFTA	FDRD	EDPREL	. P
AEK27122.1	IITTVWSGSTYAVITNRYTDRVI	PIG	VPDI	TEL	IDR	RGM	LSKADY	IRNNYI	EFTAI	FDKD	EDPREV	. H
CAA92272.1	IITTVWSGSSYAVVTNMHTDRVI	PIK	VQEI	TEL	IDR	RGMC	LSKADY	IRNNYI	EFTAI	FDKD	EDPREM	. H
YP_009054936.1	VVSKLWKGWSHTSITNRYTDRVI	PVS	VEDI	MNT	IDA	KGNC	SSKAEY	LRDNI	ГННА	YНKD	ADEEEM	. I
AMB16079.1	VVTKVWKGYSHTSLSDRYNDRVI	PVS	VEEI	FTL	IDSI	KGKC	SSKAEY	LRDNI	MHHA:	YHDD	EDEVEL	. D
YP_006273012.1	VVTRVWKGYSHTSLSDRYNDRVI	PVS	VEEI	FSL	IDSI	KGKC	SSKAEY	LRDNI	MHHA:	YHDD	EDEVEL	. D
YP 002333514.1	VVTRVWKGYSHTSLSDRYNDRVI	PVST	VEEI	FGL	IDSI	KGKC	SSKAEY	LRDNI	HHA	YHDD	EDEVEL	. D
AII81366.1	VVTRVWKGYSHTSLSDRYNDRVI	PVST	VEDI	FGL	IDSI	KGKC	SSKAEY	LRDNI	AHHA	YHDD	EDEVEL	. D
YP_009176910.1	TTLTTYKDLWEKSIGHRTTIRY	ALQI	RDEI	ID.	VDT	книс	STESKV	YQANT	ILTL	RHKD	AGEKTM	LP
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				F	L2	- distri						
	R11	B12	-	114-104 (A	ນດໍ່າກ <mark>ດ</mark> ີ		B13			B14	ß	15
AFM64049 1	- TT	тт —	-		-		p15		-	, p14	-mm =	15
ALMO4049.1	250	260	-	270	1111	280		290		300		310
AEM64049 1	BPSRT.N	ALCTRONH		TKIG	AAGE	YHT CO	SWNC	TVEEVE	RSVVP	VDSEAT	STONT	VYMS
AAF04615 1	KPANAA	TRTSROWH	TDLK	NPSR	VEAF	HRYCT	TVNC	TVEEVD	RSVYP	VDEEVI	ATCDF	VYMS
ADG45133_1	KPAKVA	TRTSRGWH	TDLK	NPSR	VEAF	HRYCT	TVNC	IVEEVD	RSVYP	YDEEVI	ATCDF	VYMS
AAP32845 1	TASKYN	SVGSKAWH	TNDT	MVAG	TPGT	YRTGT	SVNC	TTEEVE	RSTEP	YDSEGL	STGDT	TYMS
VP 003933812 1	VPSKTS	TPNSPGWY	TTDRM	ADNA	HAGE	VKACT	TVNC	TVEEVE	RSAVE	VSNEVI	ATCDE	vvvvs
AAD11960 1	TPAKMT	LNTARGWN	TVGLK	LPSW	TTGEL	HRACT	TVDC	VVEEVE	RSVYP	YKEEVI	ATCDE	VYMS
AGC54689 1	MPAKMT	LTTAKGWN	VGLK	LPSW	TSGEL	HRTGT	TVDC	VVEEVE	RSVYP	YKEEVI	ATCDF	VYMS
AAD11961 1	MPAKMT	LTTAKGWN	VGLK	LPSW	TTGEL	HRTCT	TVDC	VVEEVE	RSVYP	YKEEVI	ATCDF	VYMS
YP 009230158 1	VPAEPA	PGSHRGWH	TKLK	NPTG	SAWV	YRHGT	TVNC	TVDEVE	KSAYP	VNEEVI	ATCDF	VYAS
BAC58067.1	KPAKAA	TRTSRGWH	TDLK	NPSR	TEAF	HRYGT	TVNC	IVEEVE	RSVYP	YDEEVI	ATGDE	VYMS
AAA85648.1	KPAKAA	TRASEGNE	TDLK	NPSR	VEAF	HRYGT	TVNC	TVEEVE	RSVYP	YDEEVI	ATCDF	VYMS
AAA88010 1	KPAKAA	TRTSROWH	TDLK	NPAR	VEAF	HRYCI	TVNC	TVEEVE	RSVYP	VDEEVI	ATCDF	VYMS
BAE47051 1	KPAKVA	TRTSRGWH	TDLK	NPSR	VEAF	HRYGT	TVNC	TVEEVD	RSVYP	YDEEVI	ATCDF	VYMS
YP 009342376.1	KASREN	TPDSBAWH	TNDT	TVFG	SPWV	YRTGT	SVNC	IVEEVE	RSVYP	YDHEGL	STGDT	VEMS
YP 003084394.1	LASREN	TPDSRAWH	TNDT	TVFG	SPWI	YRTST	SVNC	IVEEVM	RSAFP	YDYFAL	ANGDV	VNMS
YP 009046525 1	RPSRFS	TAESKAWH	TNDT	TVFG	SVWT	YRTST	SVNC	TVEETD	RSLYP	YDSFAL	SNGDV	VT.MS
NP 073321 1	RPSKES	TAESBAWH	TNET	TVWG	SPWV	YRTGT	SVNC	TVEEMD	RSAFP	YTYFAM	ANGDT	ANMS
YP 001033956.1	KPSKEN	TPESBAWH	TNET	TVWG	SPWT	YRTGT	SVNC	IVEEMD	RSVEP	YSYFAM	ANGDI	ANTS
NP 077446.1	TASKYN	NVGSKAWH	TINDT	MIAG	TPGT	YRTGT	SVNC	IVEEVD	RSYIP	YDSEGI	STGDV	IYMS
BAM99305.1	KPSKFN	TOGARGWH	TTOETH	VVVG	SPGE	YRTGT	SVNC	IVEEVD	RSVYP	YDSFAL	STGDI	IYMS
AAD46114.2	LKPSRLN	APGARGWH	TTDEVE	TVVG	SVGL	YRTGT	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	TYMS
AAD46113.2	KPARLN	APGARGWH	TTDEV	TAVG	TAGL	YRTGT	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	IYMS
AAD46115.2	KPARLN	APGARGWH	TDEV	TALG	SAGL	YRTGT	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	TYMS
AFB76670.1	KPARLS	APGVRGWH	TTDDV	TALG	SAGL	YRTGT	SVNC	IVEEVE	RSVYP	YDSFAF	STGDI	IYMS
AAD46112.2	LKPARLS	APGVRGWH	TTDEV	TALG	SAGL	YRTGT	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	IYMS
AP015888.1	LKPARLS	APGVRGWH	TTDEV	TALG	SAGL	YRTGT	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	IYMS
ANG65542.1	LKPSKFN	TPESRGWH	TTNET	TKIG	AAGE	HHSGT	SVNC	IVEEVD	RSVYP	YDSFAI	STGDV	IHMS
AEK27122.1	LKPSKFN	TPGSRGWH	TVNDT	TKIG	GSGE	YHSGT	SVNC	IVEEVD	RSVYP	YDSFAI	STGDI	THMS
CAA92272.1	LKPSKFN	TPGSRGWH	TINDT	TKIG	SPGE	YRTGT	SVNC	IVEEVD	RSVYP	YDSEGI	STGDI	THMS
YP 009054936.1	RASKET	TPGSRAWH	TTNRT	AYLG	VRMI	HYTST	SVNC	IVEEVD	RSVYP	YDSFAL	STGDV	VYIS
AMB16079.1	LVPSKFA	TPGARAWC	TINDT	SYVG	MPWR	HYTST	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	VYTS
YP 006273012.1	LVPSKFA	TPGARAWO	TINDT	SYVG	MPWR	HYTST	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	VYAS
YP 002333514.1	LVPSKFA	TPGARAWO	TINDT	SYVG	MPWR	HYTST	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	VYAS
AII81366.1	LVPSKFA	TPGARAWC	TINDT	SYVG	MPWR	HYTST	SVNC	IVEEVE	RSVYP	YDSFAL	STGDI	VYAS
YP 009176910.1	YPSRFG	TDTTSSYS	TVNET	VEFT	VIAG	YKTCT	TVNC	RVIDTI	KSPYP	YNYFSI	ATGDV	VEMS
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		η2	η3 β16			β17	β18	α3
AEM64049.1	тт	eee	222			>	\rightarrow	2222
		320	330	340	350	360	370	
AEM64049.1	PFYGLR	EG.AHGEHIG	YAPGREQOV	EHYYPIDLD	SRLRASESV	RNFLRTPHE	TVANDWAP	KTRRV
AAF04615.1	PFYGYR	EG.SHT <mark>E</mark> HTS	YAADRFKQV	DGFYARDLT	TKARATAP T	FRNLLTTPKF	TVAWDWVF	KRPSV
ADG45133.1	PFYGYR	EG.SHTEHTS	YAADRFKQV	DGFYARDLT	TKARATSPT	FRNLLTT PKF	TVAWDWVP	KRPAV
AAP32845.1	PFFGLR	DG.AYREHSN	YAMDRFHQF	EGYRQRDLD	TRALL . EPA	ARNFLVTPHI	TVGWNWKF	KRTEV
YP_003933812.1	PFYGLG	ED.AHREYNA	YSADRFKQV	DGFFPRDLD	SGETAPEPV	VRNLLTTPKF	'TIGWDWKF	KDPSV
AAD11960.1	PFYGYR	EG.AHKEHIA	YSTDRFKQV	ENFYLR <mark>DL</mark> T	DGSRATNPT	FRNMLTTPKF	TVGWDWVF	KKPSV
AGC54689.1	PFYGYR	DG.AHKEHIA	YSTDRFKQV	ENFYLRDLT	TKARATNPS	FRNMLTTPKF	'TVGWDWVF	KKPSV
AAD11961.1	PFYGYR	DG.AHKEHIA	YSTDRFKQV	ENFYLRDLT	TKSRATNPS	FRNMLTTPKF	'TVGWDWVF	KKPSV
YP_009230158.1	PFYGYR	DG.SHAEHTA	YTADRFRQV	DGFFPRNLD	TGRRAQTPS	TYNLLTTPSF	TVGWNWAP	KRPSV
BAC58067.1	PFYGYR	DG.AHAEHTA	YAADRFROV	DGYYERDLS	TGRRASTPAT	FRNLLTTPKF	TVGWDWAF	KRPSV
AAA85648.1	PFYGYR	DG.SHA <mark>E</mark> HTA	YAADRFRQV	DGYYERDLS	TGRRAEAPV	FRNLLTT PKF	TVGWDWAP	KRPSV
AAA88010.1	PFYGYR	DG.SHG <mark>E</mark> HTA	YAADRFRQV	DGYYERDLS	TGRRAAAPV	FRNLLTT PKF	TVGWDWAP	KRPSV
BAE47051.1	PFYGYR	EG.SHT <mark>E</mark> HTS	YAADRFKQV	DGFYARDLT	TKARATSPT	FRNLLTTPKF	TVAWDWVP	KRPAV
YP_009342376.1	AFYGYT	GD.SPK <mark>E</mark> HTS	YSNERFRQF	EGYRRIDLD	THK. TSEST	FRNFLTTEKY	TVAWDWVP	KKSRV
YP_003084394.1	PFYGYG	PTESR. EHNS	Y SSN R YK Q L	DGYKVMDLD	THR.LASPII	KRNFLTTEHY	TVGWDWMP	KRERV
YP_009046525.1	PFFGYA	PPEAAKENMG	YAADRFRQL	DNYFQFDLD	TKQKNKLPSI	KRNFLTTQF	TVGWDWEA	KERV
NP_073321.1	PFYGTT	PTDAAAEPMS	YPQDRFRQF	DSYFPMDLD	TRRKLVTPVI	KRNFLVT QHF	'TVGWTWAP	KISRV
YP_001033956.1	PFYGLS	PPEAAAEPMG	YPQDNFKQL	DSYFSMDLD	KRRKASLPVI	KRNFLITSHF	'TVGWDWAP	KTTRV
NP_077446.1	PFYGLR	EG.AYK <mark>E</mark> QSN	YAMDRFHQF	EGYRQRDID	TRGYM.EPT	FRNFLVT PHI	. TVG <mark>W</mark> NWKP	KRTEV
BAM99305.1	PFYGHR	EE.GKH <mark>E</mark> HSS	YAPERFKQL	EEYQARDLD	TNTHI.KPT	FRNFLTT PHV	TVAWNWVF	KLTNV
AAD46114.2	PFYGLR	EG.AHREHTS	YSPDRFQQI	EGYYSRDLT	SGRRAGDPVS	SRNFLRTQHV	TVAWDWVF	KRKNV
AAD46113.2	PFYGLR	EG.AHR <mark>E</mark> HTS	YSPERFQQV	EGYYRRDMA	TGRRVKEPVS	SRNFLRTQHV	TVAWDWVP	KRRNV
AAD46115.2	PFYGLR	EG.AHR <mark>E</mark> HTS	YSPERFRQI	EGYYKRDMA	TGRRLKEPVS	SRNFLRTQHV	TVAWDWVP	KRKNV
AFB76670.1	PFYGLR	EG.AHR <mark>E</mark> HTS	YSPERFQQI	EGYYKRDMA	TGRRLKEPVS	SRNFLRTQHV	TVAWDWVP	KRKNV
AAD46112.2	PFYGLR	DG.AHREHTS	YSPERFQQI	EGYYKRDMA	TGRRLKEPVS	SRNFLRTQHV	TVAWDWVF	KRKNV
AP015888.1	PFYGLR	DG.AHR <mark>E</mark> HTS	YSPERFQQI	EGYYKRDMA	TGRRLKEPVS	SRNFLRTQHV	TVAWDWVP	KRKNV
ANG65542.1	PFFGLR	DG.AHVEHTS	YSSDRFQQI	EGYYPIDLD	TRLQLGAPVS	SRNFLETPHV	TVAWNWTP	KSGRV
AEK27122.1	PFFGLR	DG.AHTEYIS	YSTDRFQQI	EGYYPIDLD	TRLQLGAPVS	SRNFLTTQHV	TVAWNWVP	KIREV
CAA92272.1	PFFGLR	DG.AHT <mark>E</mark> HTS	YSNDRFQQI	EGYYPIDLD	TRLQVGGPVS	SRNFLTTQHV	TVAWNWVP	KIREV
YP_009054936.1	PFYGLR	DG.AHLEHTS	YAPERFROV	EGYRARDLD	TGKIADTPV	TRNFVKTPHV	TVGWDWHF	KKPHA
AMB16079.1	PFYGLR	SA.AQL <mark>E</mark> HNS	YAQERFRQV	EGYQPRDLD	SKLQAGEPV	IKNFITTPHV	TVSWNWTE	KKIEA
YP_006273012.1	PFYGLR	AA.ARI <mark>E</mark> HNS	YAQERFRQV	EGYRPRDLD	SKLQAEEPV	IKNFITTPHV	TVSWNWTE	KKVEA
YP_002333514.1	PFYGLR	AA.ARI <mark>E</mark> HNS	YAQERFROV	EGYRPRDLD	SKLQAEEPV	FKNFITTPHV	TVSWNWTE	KVEA
AII81366.1	PFYGLR	AA.ARI <mark>E</mark> HNS	YAQERFROV	EGYRPRDLD	SKLQAEEPV	TKNFITTPHV	TVSWNWTE	KKVEA
YP_009176910.1	PFYDRT	DE. TKTETMN	EDPEYFWIF	ENYSSVDRK	TKEEI.PARI	RRAFLQKPEF	LVSMDVKK	KQEQV

YP_009176910.1	PFYDRTDE.	TKTETMNED	PEYFWI	FENYSSVDRKT	FKEEI.P	ARRRAFLO	KPEFLVS	WDVKKKQEQV
	β19	β20	β21	β22		n4		α4
AEM64049.1		тт →	TT	→	+	200 1	0000000	0000000000
	380	390	400	410		420	430	440
AEM64049 1	SLAKOREA		DGSER	SRALGASEVS	SDVTOLDI	OBVHIGI	VIREAS	EATDATYBER
AAF04615.1	TMTKWOEV	DEMLRSEYG	GSERES	SSDAISTTFTT	TNLTEYPI	SRVDLGI	GIGKDAR	DAMDRIFARR
ADG45133.1	CTMTKWOEV	DEMLRAEYG	GSFRE	SSDAISTTFTT	INLTOYS	LSRVDLGI	GIGRDAR	EAIDRMFARK
AAP32845.1	CSLVKWREV	EDVVRDEYA	HNFRE	TMKTLSTTFIS	SETNEFN	LNOIHLSO	CVKEEAR	AIINRIYTTR
YP 003933812.1	CSVTKWOEV	EEMMRAEYG	STER	TSSSLSATFT	INVTOYPI	PORIELSI	VAGEAO	AAVDAIYARR
AAD11960.1	CTMTKWOEV	DEMLRSEHG	RSLRES	SSKSLSTTFTT	INTTEYP	LANVDLGI	CVRKDAR	AAIDSIFRKK
AGC54689.1	CTMAKWQEV	DEMLRSEHG	. PSFREZ	ASKTLSTTFTT	INLTEYS	LSKVDLGI	CVGQEAR	AAIESIYRKK
AAD11961.1	CTMAKWQEV	DEMLRSEHG	. PSFRF7	ASKTLSTTFTT	INLTEYS	LSKVDLGI	CVGQEAR	AAIESIYRKK
YP_009230158.1	CTMTKWREV.	AEMLRAEYG	. SSFRES	SSSEL <mark>S</mark> ATFTT	INLTEYAL	LARVDLGE	CISKDAR	EAIDRIYTQR
BAC58067.1	CTLTKWQEV	DEMLRAEYG	. PSFRES	SSSALSTTFTT	INRTEYAL	LSRVDLGI	V GREAR	EAVDRIFLRR
AAA85648.1	CTLTKWREV	DEMMRAEYG	. PSFRES	SSAAL <mark>STTF</mark> TA	ANRTEYAL	LSRVDLAI	OCVGREAR	EAVDRIFLRR
AAA88010.1	CTLTKWREV	DEMLRAEYG	. PSFRES	SSAAL <mark>STTF</mark> TA	ANRTEYAL	LSRVDLAI	OCVGREAR	EAVDRIFLRR
BAE47051.1	CTMTKWQEV	DEMLRSEYG	GSFRES	SSDAI <mark>STTF</mark> T7	INLTEYS	LSRVDLGI	CIGRDAR	EAIDRIFARK
YP_009342376.1	CSMSKWQEV	DEMMRAEFN	DGKFRE	EARSLSATFIS	SKTTQFDI	MSQVYLGQ	QCVSTDSS	AAIDNIYKTK
YP_003084394.1	CSMAKWQEV	NEMMRAEY.	GTRYRE	ASKTL <mark>S</mark> ASFIS	SNMTQFN	LDRLY <mark>L</mark> GI	CVKRDSE	EAIKRIFEEQ
YP_009046525.1	CSMSKWQTV	DEMLRANYD	GGRMREN	MSKSLSATFIA	ANSTQFN	PDRIILGÇ	CVRKEAE	EEIKKIFATK
NP_073321.1	CSMAKWKEV	TEMLRARV.	GKKFREN	MARELSATFIS	SNTTEFN	PDRIILGÇ	2CVKRDAE	AEIDKIFKRK
YP_001033956.1	CSMTKWKEV	TEMLRATV.	NGRYRF	MARELSATFIS	SNTTEFD	PNRIILGÇ	CIKREAE	AAIEQIFRTK
NP_077446.1	CSLVKWREV	EDVVRDEYA	. NSFRE	TMKTLSTTFIS	SETSEFN	LNEIHLSE	ICVKDEAR	KVINRIYNTK
BAM99305.1	SLTKWREV.	DALIRDTTN	. TSYRET	TSKTMSATFVC	GEPMPFN	LSKVHLSE	EVERDAR	VSINRIYTEK
AAD46114.2	CSLARWRAA.	EEMLRDESR	GOTT	PARALSATEVS	SDTHAFS	LOHVPLSI	OVLEDAE	AEVERVYRER
AAD46115.2	CTLAKWREV.	DEMLRDESK	CNED D		SDGHAFE		OUTEEAE	AAVERVIKER
AAD46115.2	CTLANKEA.	DEMLEDERE	CNERE		SDGHAFA		UTEEAE	AAVERLIKER
APB/00/0.1	COLTRED DA		CNEPE	TARSLSAIL VS	DCUTEA	ONVPLSI	UTEEAE	AAVERVIRER
ARD40112.2	CSLTKWPFA		CNEPE	PADSISATEVS	SDGHTFA	ONVPLSI	UTEEAG	AAVEDUVDED
ANG65542 1	CTLAKERET	DEMIBDEYO	GSYRE	TAKTISATETS	SNTSOFE	INBIRIGI	ATKEAA	EATDRTYKSK
AEK27122.1	TLAKWRET	DETTRDEYK	GSYRE	TAKSTSATETS	SDTTOFD	DRVKLSI	CAKREAT	EATDKTYKKK
CAA92272.1	CTLAKWREI	DEIIRDEYK	GSYRE	TAKSISATEIS	SDATOFD	INRVKLSI	CAKREAT	EAIDKIYKNK
YP 009054936.1	CTLTKWREA	DEILRDEVG	GSYRE	TIRALSTTELS	SNKTOFD	LKKVPLSC	CVTDEAE	KAINDIYKRR
AMB16079.1	CTLTKWKEV	DELVRDEFR	. GSYRE	TIRSISSTFIS	SNTTOFK	LEDAPLTI	CVSKEAK	DAIDSIYRKO
YP_006273012.1	CTLTKWKEV	DELVRDEFR	GSYRE	TIRSISSTFIS	SNTTQFK	LESAPLTI	CVSKEAK	DAIDSIYRKO
YP_002333514.1	CTLTKWKEV	DELVRDEFR	. GSYRE	TIRSISSTFIS	SNTTQFK	LDSAPLTE	CVSKEAK	EAIDSIYRKQ
AII81366.1	CTLTKWKEV	DELVRDEFR	. GSYRE	FIRSI <mark>S</mark> STFIS	SNTTQFK	LESAPLTE	CVSKEAK	EAIDSIYKKQ
YP_009176910.1	CSMKLWQSV	ENVIRVEQN	. PSYHE	FAKELTATFT?	APMDQFD	IKRLVNSM	VPTEGK	KEIDRIYSSR
	4				505 2010 2010 0 17 8 296 000		4	

	β23	β24	β25	α.5			
AEM64049.1	$ \rightarrow $	\rightarrow -		- eeee			
	450	460	470		480	490	
AEM64049.1	YNNTHVLAGE	RPEVYLARGGE	VVAFRPL	ISNELA	QLYARE	LE <mark>R</mark> LGLAGVV	GPASPA
AAF04615.1	YNATHIKVGQ	. PQYYLANGGE	LIAYQPL	LSNTLA	ELYVRE	HLREQSRKPPNP	TPPPP
ADG45133.1	YNATHIKVGQ	. PQYYLATGGE	LIAYQPL	LSNTLA	ELYVRE	YM <mark>R</mark> EQDRKPRNA	TPAPLR
AAP32845.1	YNSSHVRTGD	. IQTYLARGGE	VVVFQPL	LSNSLA	RLYLQE	LVRENTNHSPQK	HP
YP_003933812.1	YNASHVKVGG	. LQYY <mark>L</mark> ATGGI	LVVYQPL	ISNSLA	EMYLRE	AEARALEPA	PL
AAD11960.1	YNSTHLRVGD	. IQYY <mark>L</mark> ANGGI	VIAYQPL	LSNNLA	DLYLQE	IVKEQARRAPEP	KQSP.PN
AGC54689.1	YNSTHLRVGD	. IQYY <mark>L</mark> GNGG]	LIAYQPL	LSTSLA	DLYLQE	VIKEQSRKPADP	KTPASPN
AAD11961.1	YNSTHLRVGD	. IQYY <mark>L</mark> ANGGE	LIAYQPL	LSTSLA	DLYLQE	VIKEQSRKPTDH	KTPVSPN
YP_009230158.1	YNSTHLRVGS	. VQYYLATGGE	LVAYQPL	LSNSLAI	DLYVKE	LL <mark>R</mark> EQGRAKNDS	SPR
BAC58067.1	YNGTHVKVGQ	. VQYYLATGGE	LIAYQPL	LSNALVI	ELYVRE	LLREQERRPGD.	AAAT
AAA85648.1	YNGTHVKVG Q	. VQYY <mark>L</mark> AAGGI	LIAYQPL	LSNALVI	ELYVRE	LVREQERRPAG.	.PGEAAT
AAA88010.1	YNGTHVKVG Q	. VQYY <mark>L</mark> ATGGE	LIAYQPL	LSNALVI	ELYVRE	LV <mark>R</mark> EQTRRPAGG	DPGEAAT
BAE47051.1	YNATHIKVGQ	. PQYYLATGGE	LIAYQPL	LSNTLA	ELYVRE	YV <mark>R</mark> EQNRKPRDA	TPPPLR
YP_009342376.1	YADTHIRVGQ	. PQTYLAIGGE	IIVYQPL	ISNNLA	DMYIKE	IV <mark>R</mark> DGRTDIQNL	FARGGNGRPFA.RS
YP_003084394.1	YASTHVKAGA	IEYY <mark>I</mark> TS <mark>GG</mark> E	ILAYOPV	VSNTLV	KMYVQE	LTRDNRTELALD	LLGAMRG.DKT.RE
YP_009046525.1	YNETHVLSGI	. VEY <mark>YL</mark> TV <mark>GG</mark> E	VVAYQPI	MSRTLAS	SMYIKE	LIRDNRTDVALD	LLSRQSN.PSG.SS
NP_073321.1	YND THVKMGH	. VQYFLTLGG	VVAYQPI	LSKSLA	HMYLRE	LLRDNRTDEMLD	LVNNKHA.IIS.NN
YP_001033956.1	YNDSHVKVGH	VQYF <mark>l</mark> Algge	IVAYQPV	LSKSLA	HMYLRE	LMRDNRTDEMLD	LVNNKHA.IYK.KN
NP_077446.1	YNSSHVRTGD	. IQTYLTRGGE	VIVFQPM	LSNSLA	RLYLQE	LVKQTEGTPPKR	H V
BAM99305.1	YNRTHIKVGP	. IQTYLVRGGE	IVAFQAM	VSNTLA	KLYLRE	QAMANQTATHVR	PKR
AAD46114.2	YNGTHVLAGK	. TDTYLARGGE	VVAFRPL	LSNELA	KLYLQE	LARSNRTLDGVL	GPRLPAGAAPAG
AAD46113.2	YNATHVLAGA	. LETYLARGGE	VVAFRPL	LSNALA	KLYLQE	LARSNATLGGLF	DAARGAP
AAD46115.2	YNGTHVLAGG	. LETYLARGGE	VVAFRPM.	LSNALA	KLYLQE.	LARSNGTLDGLF	PAGPPGPR
AFB76670.1	YNGTHVLSGS	. LETYLARGGE	VVAFRPM.	LSNELA	KLYLQE.	LARSNGTLEGLF	AA
AAD46112.2	FNATHVLSGG	. LETYLARGGE	VVAFRPM.	LSNALA	KLYLQE.	LARSNGTLEGLF	AAGGSGAAAAAAPK
AP015888.1	FNATHVLSGG	. LETYLARGGE	VVAFRPM:	LSNALA	KLYLQE.	LARSNGTLEGLF	AAGGSGAA . AAAPK
ANG65542.1	YSKTHIQTGI	. LETYLARGGE	LIAFRPM	ISNELA	KLYINE.	LARSNRTVDLSA	LLNPSGETVQ.
AEK27122.1	YNKTHIQTGE	. LETYLARGGE	TIIAFRPM	ISNELA	KLYINE.	LVRSNRTVDLKS	LLNPSVRGGA.
CAA92272.1	YNKTHIQTGE	. LETYLARGGE	TILAFRPM	ISNELA	KLYINE.	LARSERIVDLNA	LLNPSHSVGG.
YP_009054936.1	YESTHVFSGP	. METYLARGGE	VIAFRPM.	LSNELA	RLYLNE.	LVRSNRTYDPKS	ILQHSGNDVAS
AMB16079.1	YESTHVFSGD	. VEFYLARGGE	LIAFRPM	ISNELA	RLYLNE.	LVRSNRTYDLKN	LLNPNANHNT.
YP_006273012.1	YESTHVFSGD	. VEFYLARGGE	LIAFRPM	LSNELA	RLYLNE.	LVRSNRTYDLKN	LLNPNANHNN.
12_002333514.1	TESTHVFSGD	. VEYYLARGGE	LIAF RPM.	LSNELA	RLILNE.	LVKSNRTYDLKN	LLHPNANHNN.
AII81366.1	YESTHVFSGD	. VEYYLARGGE	LIAFRPM	LSNELA	KLYLNE.	LVRSNRTYDLKN	LLNPSANNNN.
YP_009176910.1	XKDTHLRVNE	. TQYYLATGG	LIMXOBT	IAKSIA	DLAANQ	<mark>.</mark> K	

	+
AEM64049.1	200
	500 510 520 530
AEM64049.1	. AARRARRSPGP
AAF04615.1	
ADG45133.1	
AAP32845.1	TRNTRSRRSVPVELRANRTITTSSVEFA
YP_003933812.1	
AAD11960.1	
AGC54689.1	
AAD11961.1	
YP_009230158.1	K. NATEVISTIS VEFA
BAC58067.1	
AAA85648.1	
AAA88010.1	
BAE47051.1	
YP_009342376.1	DNSTVNGRNNGRGRSSTSRSRGKRDIDTTSTGNNTIIKTTTVHFA
YP_003084394.1	DGRSRHARSVDGGPDGLIRGARNIDFYKNYTVRSARVARNADFYKNTTVVKSVMSAQFA
YP_009046525.1	GGGAAGKRKKRAAAAVDANKIDENTMIRTTSSAQYA
NP_073321.1	ATSVSRLRRDLHRASSGKAILNDSVIIRSTASVQFA
YP_001033956.1	ATSLSRLRRDIRNAPNRKITLDDTTAIKSTSSVQFA
NP_077446.1	SNG.RORRSLIVNKTITTSSVEFA
BAM99305.1	
AAD46114.2	ALRRARRAAP
AAD46113.2	QGPRRARRSAPAARG
AAD46115.2	PGPRRARRAAPDEPA
AFB76670.1	PGPRRARRAAPSAPGGPGAANGPAGDGDAGGRVTTVSSAEFA
AAD46112.2	PVPRRARRSASPTPPAP.AASGDGGDGDANKRVTTVSSAEFA
AP015888.1	PVPRRARRSASPTPPAP.AASGGGGD.DANKRVTTVSSAEFA
ANG65542.1	RTRRSVPS
AEK27122.1	RKRRSVEENKRSK.RNIEGGIENVNNSTIIKTTSSVHFA
CAA92272.1	RKKRSIETETLGRSK.RDVDGGVQNVNNATLIKTTSSIHFA
YP 009054936.1	SEGKRTRRSLLSVAEAVPAAOPS.GGHELHRLRRRAADAATOA.GKDGKDAOLELIKTTSSVEFA
AMB16079.1	NRTRRSLLSIPEPTPTQESLHREQILHRLHKRAVEAANSTNSSNVTAKQLELIKTTSSIEFA
YP_006273012.1	TTRRRRSLLSIPEPOPTODSGHREQILHRLHKRAVEATEGTDSSNITAKOLELIKTTSSIEFA
YP 002333514.1	. NTTRRRRSLLSVPEPOPTODGGHREQILHRLHKRAVEATAGTDSSNVTAKOLELIKTTSSIEFA
AII81366.1	. NTTRRRRSLLSVPEPOPTODGVHREOILHRLHKRAVEATAGTDSSNVTAKOLELIKTTSSIEFA
YP_009176910.1	.PPSRVRREAEEPSTGLIESVRTAAFI

		α6			α7	β26	β27
AEM64049.1	540	550 STO	0000000 560	<u>570</u>	<u>202020000</u> 580	590	600
AEM64049.1	LOFTYDHIOAH	NDMLGRIATA	CELONK	DRTLWSEMSRLN	PSAVATAALG	RVSARMLGI	VMAIS
AAF04615.1	LOFTYNHIORH	VNDMLGRVAIA	CELQNH	ELTLWNEARKLN	PNAIASATVG	RRVSARMLGD	VMAVS
ADG45133.1	LOFTYNHIORH	VNDMLGRIAVA	CELONH	ELTLWNEARKLN	PNAIASATVG	RRVSARMLGD	VMAVS
AAP32845.1	LOFTYDHIOEH	VNEMLARISSS	COLONR	ERALWSGLFPIN	PSALASTILD	ORVKARILGE	VISVS
YP 003933812.1	LOFTYDHIOKH	VNEMLGRIAAA	COLONO	ELVLWNEARKLN	PNAIASATVG	RRVGARMLGI	VMAVS
AAD11960.1	LOFTYDHIOOH	VNEMLGRIAIA	CELONR	ELTLWNEARKLN	PSAIASATMG	YRVGARMLG	VMAVS
AGC54689.1	LOFTYDHIOOH	VNEMLGRIAIS	CELONR	ELTLWNEARKLN	PTAIASATMG	YRVGARMLGI	VMAVS
AAD11961.1	LOFTYDHIOOH	VNEMLGRIAIA	CELONR	ELTLWNEARKLN	PAAIASATMG	YRVGARMLGI	VMAVS
YP 009230158.1	LOFTYDHIORH	VNEMLGRLAVS	CELONO	ELTLWNEAOKLN	PSAIASATVR	RRVSARMLGI	VLAVS
BAC58067.1	LOFTYDHIORH	VNDMLGRIAIA	CELONH	ELTLWNEARKLN	PNAIASATVG	RRVSARMLG	VMAVS
AAA85648.1	LOFTYDHIORH	VNDMLGRIAIA	CELONR	ELTLWNEARRLN	PGAIASATVG	RRVSARMLGE	VMAVS
AAA88010.1	LOFTYDHIORH	VNDMLGRIAIA	CELONR	ELTLWNEARRLN	PGAIASATVG	RRVSARMLGE	VMAVS
BAE47051.1	LOFTYNHIORH	VNDMLGRIAVA	CELONH	ELTLWNEARKLN	PNAIASATVG	RRVSARMLGI	VMAVS
YP 009342376.1	LOFTYDHIORH	VNEMLGRIAKA	CELONR	ESVLWREMRKMN	PNAIASTMLG	RRVGARMLGI	VMAV:
YP 003084394.1	LOYTYDHIOAH	VNDMLSRIAVS	CELONK	ESVLWAEMRKVN	PSLIASTTVG	RRVGARMLGD	VLAV
YP 009046525.1	LOFTYDHIOGH	VNDMFSRIAVA	CELONK	ERVLWSEALKIS	PSSISSAHVG	TRVSARLLGI	VLSVS
NP 073321.1	LOFLYDHIOAH	INEMFSRIATA	CELONK	ELVLWREAIKIN	PSATASATLG	KRVGAKMLGI	VAAVS
YP 001033956.1	LOFLYDHIOTH	INDMFSRIATA	CELONR	ELVLWHEGIKIN	PSATASATLG	RRVAAKMLGI	VAAVS
NP 077446.1	LOFTYDHIOEH	VNEMLARISTS	COLONK	ERALWSSLFPVD	PSALASSILD	ORVKARVLGI	VIAVS
BAM99305.1	LOFTYDHIOAH	VNEMFARIATA	CMLONO	EOALWRETAKLN	PSVIASTMLA	KKVSARMLGE	VMAVS
AAD46114.2	LOFTYDHIODH	VNAMFSRLATS	CLLONK	ERALWAEAAKLN	PSAAASAALN	RRAAARMLGI	AMAV
AAD46113.2	LOFTYDHIODH	VNAMFSRLATS	COLONK	ERTLWAEAAKLN	PSAAASAALN	RRAAARMLGE	AMAV
AAD46115.2	LOFTYDHIODH	VNTMFSRLATS	CLLONK	ERALWAEAAKLN	PSAAASAALN	RRAAARMLGI	AMAV
AFB76670.1	LOFTYDHIODH	VNTMFSRLATS	CLLONK	ERALWAEAAKLN	PSAAASAALD	RRAAARMLGE	AMAV
AAD46112.2	LOFTYDHIODH	VNTMFTRLATS	CLLONK	ERALWAEAAKLN	PSAAASAALD	RRAAARMLGE	AMAV
AP015888.1	LOFTYDHIODH	VNTMFSRLATS	CLLONK	ERALWAEAAKLN	PSAAASAALD	RRAAARMLGE	AMAV
ANG65542.1	LOFAYDYIOAH	VNEMLSRIATA	CTLONR	EHVLWTETLKLN	PGGVVSMALE	RRVSARLLGI	AVAV
AEK27122.1	LOFAYDHIOSH	VNEMLSRIATA	CNLONK	ERTLWNEVMKLN	TSVASVAMD	ORVSARMLGE	VLAV
CAA92272.1	LOFAYDHIOSH	VNEMLSRIATA	CNLONK	ERTLWNEVMKLN	PTSITSTIMD	KVSARLLGE	VIAV
YP 009054936.1	LOFAYDHIOAH	VNEMLSRIATA	CTLONK	ERVLWNEMVKIN	PSAIASSSLN	RVAARVLGD	VIAI
AMB16079.1	LOFAYDHIOSH	VNEMLSRIATA	CTLONK	ERTLWNEMVKVN	PSAIVSATLD	ERVAARVLGI	VIAI
YP 006273012.1	LOFAYDHIOSH	VNEMLSRIATA	CTLONK	ERTLWNEMVKIN	PSAIVSATLD	ERVAARVLGE	VIAI
YP 002333514.1	LOFAYDHIOSH	VNEMLSRIATA	CTLONK	ERTLWNEMVKIN	PSAIVSATLD	ERVAARVLG	VIAI
AII81366.1	LOFAYDHIOSH	VNEMLSRIATA	CTLONK	ERTLWNEMVKIN	PSAIVSATLD	ERVAARVLGI	VIAI
YP 009176910.1	IOYTYDKLOAH	NAMFSRIVYA	CELONR	DITMWEOLNKIN	PSAVMSAIMK	RRVSAKKLGI	VVAV
			2				

AEM64049.1 TT 610 620 630 TT 640 650 AEM64049.1 CVEVRGGVYVQNSMRVPGERGTCYSRELVTFEH.NGTGVIEGOLGDDNELLI AAF04615.1 CVPVAA.DNVIVQNSMRISSRPGACYSRELVSFRYEDQGPLVEGOLGENNELRL ADG45133.1 CVPVAP.DNVIVQNSMRVSSRPGTCYSRELVSFRYEDQGPLIEGOLGENNELRL AAP32845.1 NCPELGSDTRIILQNSMRVSGSTTRCYSRELISIVSINGSGTVEGOLGENNELRL AAP10960.1 TCRAIKA.DNVINQNSMRVFGKPGTCYSRELISFKQDDNGPLIEGOLGEDNEIRL AGC54689.1 TCRPIKA.DNVINQNSMRVFGKPGTCYSRELISFKQDDNGPLIEGOLGEDNEIRL AAD11960.1 TCRPIKA.DNVINQNSMRVFGKPGTCYSRELISFKQDDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVINQNSMRVFGKPGTCYSRELVSFKQEDNGPLIEGOLGEDNEIRL AAAD1961.1 TCVVVPA.ENVINQNSMRVPGKPGTCYSRELISFKQEDNGPLIEGOLGEDNEIRL AAA35648.1 TCVAVPA.ENVINQNSMRVPARPGTCYSRELSFKQEDNGPLIEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRELSFKYADGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRELSFKYEGGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRELVSFRYEGGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRELVSFRYEGAGPLVEGOLGEDNEIRL	
610 620 630 640 650 AEM64049.1 RCVEVRGGVYVQNSMRVPGERGTCYSRPLVTFEH.NGTGVIEGOLGDDNELLI AAF04615.1 TCVPVAA.DNVIVQNSMRVSSRPGTCYSRPLVSFRYEDQGPLVEGOLGENNELRL ADG45133.1 TCVPVAP.DNVIVQNSMRVSSRPGTCYSRPLVSFRYEDQGPLVEGOLGENNELRL AAP32845.1 NCPELGSDTRIILQNSMRVSGSTTRCYSRPLIVSFRYEDQGPLVEGOLGENNELRL AAD1960.1 TCRAIKA.DNVIIQNSMRVPGRPKTCYARPLVSFRYEDQGPLVEGOLGEDNEIRL AAC54689.1 TCRPIKA.DNVINQNSMRVPGKPGTCYSRPLISKQDDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVINQNSMRVPGKPGTCYSRPLVSFRQEDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVINQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVINQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL AAD11961.1 CVVPVP.DNVINQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL AAD11961.1 CVPVP.DNVINQNSMRVPARPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL BAC58067.1 TCVPVP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEGGGPLVEGOLGEDNEIRL AAA85648.1 CVPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEAGGPLVEGOLGEDNEIRL AAA85010.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL	
AEM64049.1RCVEVRGGVYVQNSMRVPGERGTCYSRELVTFEH.NGTGVIEGOLGDDNELLIAAF04615.1TCVPVAA.DNVIVQNSMRVSSRPGACYSRELVSFRYEDQGPLVEGOLGENNELRLADG45133.1TCVPVAP.DNVIVQNSMRVSSRPGTCYSRELVSFRYEDQGPLVEGOLGENNELRLAAP32845.1NCPELGSDTRIILQNSMRVSGSTTRCYSRELVSFRYEDQGPLIEGOLGENNELRLAAD11960.1TCRAIKA.DNVINQNSMRVPGRPGTCYSRELVSFRYEDQGPLIEGOLGEDNEIRLAAD11960.1TCRPIKA.DNVINQNSMRVPGKPGTCYSRELISIVSKQDDNGPLIEGOLGEDNEIRLAAD11961.1TCRPIKA.DNVINQNSMRVPGKPGTCYSRELVSFKQDDNGPLIEGOLGEDNEIRLYP_009230158.1TCVAVPA.ENVINQNSMRMPAKPGTCYSRELVSFKQEDNGPLIEGOLGEDNEIRLYP_009230158.1TCVPVP.DNVIMQNSMRMPARPGTCYSRELVSFKYADGGDLVEGOLGEDNEIRLAAA85648.1TCVPVP.DNVIMQNSMRVPARPGTCYSRELVSFKYEGGGPLVEGOLGEDNEIRLAA888010.1TCVPVP.DNVIMQNSMRVPARPGTCYSRELVSFKYEGG.GPLVEGOLGEDNEIRLAA888010.1TCVPVAP.DNVIMQNSMRVPARPGTCYSRELVSFRYEAGGPLVEGOLGEDNEIRLAA888010.1TCVPVAP.DNVIMQNSMRVPARPGTCYSRELVSFRYEAGGPLVEGOLGEDNEIRLAA888010.1TCVPVAP.DNVIMQNSMRVPARPGTCYSRELVSFRYEADGPLVEGOLGEDNEIRL	
AAF04615.1 TC VPVAA.DNVIVQNSMRISSRPGACYSRPLVSFRYEDQGPLVEGQLGENNELRL ADG45133.1 TC VPVAP.DNVIVQNSMRVSSRPGTCYSRPLVSFRYEDQGPLVEGQLGENNELRL AAP32845.1 NCPELGSDTRIILQNSMRVSGSTTRCYSRPLVSFRYEDQGPLVEGQLGENNELRL AAP32845.1 NCPELGSDTRIILQNSMRVSGSTTRCYSRPLVSFRYEDQGPLVEGQLGENNELRL AAP328312.1 TC IAVAP.HNVIMQNSMRLPARPKTCYARPLVSFRYEDGGELIEGQLGEDNEIRL AAD11960.1 TC RAIKA.DNVIIQNSMRVPGKPGTCYSRPLVSFRYEDDNGPLIEGQLGEDNEIRL AAD11961.1 TC RPIKA.DNVIMQNSMRVPGKPGTCYSRPLVSFRYEQDNGPLIEGQLGEDNEIRL AAD11961.1 TC RPIKA.DNVIMQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGQLGEDNEIRL AAD11961.1 TC RPIKA.DNVIMQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGQLGEDNEIRL BACS8067.1 TC VPVTP.DNVIMQNSMRVPARPGTCYSRPLVSFKQEDGPLVEGQLGEDNEIRL BAA85648.1 TC VPVTP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEEGGPLVEGQLGEDNEIRL AAA88010.1 TC VPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEEGGPLVEGQLGEDNEIRL	SRDL
ADG45133.1 TCVPVAP.DNVIVQNSMRVSSRPGTCYSRPLVSFRYEDQGPLIECOLGENNELRL AAP32845.1 NCPELGSDTRIILQNSMRVSGSTTRCYSRPLISIVSLNGSGTVEGOLGEDNELRL YP_003933812.1 TCIAVAP.HNVINQNSMRVFGRPKTCYSRPLISIVSLNGSGTVEGOLGEDNEIRL AAD11960.1 TCRAIKA.DNVINQNSMRVFGRPKTCYSRPLISFKQDDNGPLIEGOLGEDNEIRL AGC54689.1 TCRPIKA.DNVINQNSMRVFGRPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVINQNSMRVFGRPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVINQNSMRVFGRPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL BAC58067.1 TCVAVPA.ENVINQNSMRVPARPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL BAC58067.1 TCVPVP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEEGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEGG.GPLVEGOLGEDNEIRL AAA88010.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL	RDA
AAP32845.1 NCPELGSDTRIILQNSMRVSGSTTRCYSRPLISIVSLNGSGTVEGQLGTDNELIM YP_003933812.1 TCIAVAP.HNVIMQNSMRJPARPKTCYARPLVSFRYADEGELIEGQLGEDNEIRL AAD11960.1 TCRAIKA.DNVIIQNSMRVPGKPGTCYSRPLVSFRYADEGPLIEGQLGEDNEIRL AGC54689.1 TCRPIKA.DNVIMQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGQLGEDNEIRL YP_009230158.1 TCRPIKA.DNVIMQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGQLGEDNEIRL YP_009230158.1 TCVAVPA.ENVIMQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGQLGEDNEIRL BACS8067.1 TCVPVPD.DNVIMQNSMRVPARPGTCYSRPLVSFKYEGGGPLVEGQLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEEGGPLVEGQLGEDNEIRL AAA88010.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEADGPLVEGQLGEDNEIRL	FRDA
YP_003933812.1 TC IAVAP.HNVIMQNSMRLPARPKTCYARPLVSFRYADEGELIEGOLGEDNEIRL AAD11960.1 TCRAIKA.DNVIIQNSMRVPGKPGTCYSRPLISFKQDDNGPLIEGOLGEDNEIRL AGC54689.1 TCRPIKA.DNVIMQNSMRVPGKPGTCYSRPLISFKQDDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVIMQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL YP_009230158.1 TCVAVPA.ENVIMQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL BAC58067.1 TCVPVTP.DNVIMQNSMRVPARPGTCYSRPLVSFKQEGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFKYEEGGPLVEGOLGEDNEIRL AAA88010.1 TCVPVAP.DNVIMQNSMRVPARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL	SRDL
AAD11960.1 TCRAIKA.DNVIIQNSMRVPGKPGTCYSRPLISFKQDDNGPLIEGOLGEDNEIRL AGC54689.1 TCRPIKA.DNVINQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVINQNSMRVPGKPGTCYSRPLVSFKQEDNGPLIEGOLGEDNEIRL P009230158.1 TCVAVPA.ENVINQNSMRVPGKPGTCYSRPLLVSFKQEDNGPLIEGOLGEDNEIRL BAC58067.1 TCVAVPA.ENVINQNSMRVPAKPGTCYSRPLLVSFKYADGGPLVEGOLGEDNEIRL BAA85648.1 TCVPVPP.DNVINQNSMRVPARPGTCYSRPLVSFRYEEGGPLVEGOLGEDNEIRL AA888010.1 TCVPVAP.DNVINQNSMRVPARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL	ZONN
AGC54689.1 TCRPIKA.DNVIMONSMRVPGKPGTCYSRPLVSFKOEDNGPLIEGOLGEDNEIRL AAD11961.1 TCRPIKA.DNVIMONSMRVPGKPGTCYSRPLVSFKOEDNGPLIEGOLGEDNEIRL YP_009230158.1 TCVAVPA.ENVIMONSMRVPAKPGTCYSRPLUSFKVADGGPLVEGOLGEDNEIRL BAC58067.1 TCVPVP.DNVIMONSMRVPARPGTCYSRPLVSFRVEGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMONSMRVPARPGTCYSRPLVSFRVEGGPLVEGOLGEDNEIRL AAA85010.1 TCVPVAP.DNVIMONSMRVAARPGTCYSRPLVSFRVEADGPLVEGOLGEDNEIRL	RDG
AAD11961.1 TCRPIKA.DNVIMONSMRVPGKPGTCYSRPLVSFKOEDNGPLIEGOLGEDNEIRL YP_009230158.1 TCVAVPA.ENVIMONSMRMPAKPGTCYSRPLLSFKYADGGDLVEGOLGEDNEIRL BAC58067.1 TCVPVTP.DNVIMONSMRVPARPGTCYSRPLVSFRYEEGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMONSMRVPARPGTCYSRPLVSFRYEEGGPLVEGOLGEDNEIRL AAA85010.1 TCVPVAP.DNVIMONSMRVPARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL	FRDS
YP_009230158.1 TCVAVPA.ENVIMONSMRMPAKPGTCYSRPLLSFKVADGGDLVEGOLGENNEIRL BACS8067.1 TCVPVTP.DNVIMONSMRVPARPGTCYSRPLVSFRYEEGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMONSMRVPARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL AAA88010.1 TCVPVAP.DNVIMONSMRVAARPGTCYSRPLVSFRYEADGPLVECOLGEDNEIRL	ARDS
BAC58067.1 TCVPVTP.DNVIMONSMRVPARPGTCYSRPLVSFRYEEGGPLVEGOLGEDNEIRL AAA85648.1 TCVPVAP.DNVIMONSMRVPARPGTCYSRPLVSFRYEAGGPLVEGOLGEDNEIRL AAA88010.1 TCVPVAP.DNVIMONSMRVAARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL	ERDA
AAA85648.1 TCVPVAP.DNVIMONSMRVPARPGTCYSRPLVSFRYEDGGPLVEGOLGEDNEIRL AAA88010.1 TCVPVAP.DNVIMONSMRVAARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL	ERDA
AAA88010.1 TCVPVAP.DNVIMONSMRVAARPGTCYSRPLVSFRYEADGPLVEGOLGEDNEIRL	ERDA
	ERDA
BAE47051.1 TOVPVAP.DNVIVQNSMRVSSRPGTCYSRPLVSFRYEDQGPLIECOLGENNELRL	FRDA
YP_009342376.1 SCVEIDS.TQVNLQNSMNVPGKPSTCYSRPIVTFTIGNDTEGIIEGQLGENNELLP	FRDH
YP_003084394.1 SCIEVPS.SQISLSNSMRIPGGSSCYSRPPVTFSYEKDGGTIDGMLGENNELLL	FREY
YP_009046525.1 SCIKVRP.EDVVLENSMKVPTSTSSCYSRPLVLFSYEAKQEKVTCOLGEDNELIP	FRDA
NP_073321.1 SCIEIDS.DSVTLQNSMRVVTSTNTCYSRPLVLFSYGDRQDKIQGQLGENNELIP	FLEA
YP_001033956.1 SCTAIDA.ESVTLQNSMRVITSTNTCYSRPLVLFSYGENQGNIQGQLGENNELLP	FLEA
NP_077446.1 YCPKLGTDTRVVLQNSMRVSGDSKRCYSRPLISILNTNTSGIVEGOLGTENELLM	FRNL
BAM99305.1 SCARLNG.SNVYIQNSMRIIGDPHTCYSRPLVSFAYGNRTEYIDGOLGDDNELLT	DRSL
AAD46114.2 YCRELGA.GRVFIENSMRMPGG.AACYSRPLVSFAYGNESEPLEGOLGEDNELLL	SRDL
AAD46113.2 YCHELGA.GRVFIENSMRAPGGTOYSRPLVSFAVGNASEPVEGOLGEDNELLP	GREL
AAD46115.2 YCRELGE.GRVFIENSMRAPGGVCYSRPPVSFALGNESEPVEGOLGEDNELLP	SREL
AFB76670.1 YCHELGE.GRVFIENSMRAPGGVCYSRPPVSFAFGNESEPVEGOLGEDNELLP	GREL
AAD46112.2 YCHELGE. GRVFIENSMRAPGG. VCYSRPPVSFAFGNESEPVEGOLGEDNELLP	GREL
APO15888.1 ICHELGE. GRVFIENSMAAPGG. VCTSRPPVSFAFGNESEPVEGOLGEDNBLLP	SKEL
ARG65542.1 QCVNISS.GHVIIQNSMAVIGSSTTCISKPLVSFRAINDSETIEGOLGENNELV	SKKL
ARZ/122.1 QCVNISG.SSVFIQNSMAVIGSTTTCISRPILSFRALENSTNIEGOLGENNELLV	SKKL
CAR922/2.1 QCVNISG.SNVFIQNSMAVIGSTTTCISRPLISFRALENS.TDILEGOLGENNELV	DKKL
AWD16079 1 UCWIEG. EVELONSWITGDGRSCHSRPVTFTTVKNAT.GGTIEGOLGEDNELLI	PPVT
VD 006273012 1 HOWKIEG. NVILQNSMOSM DSNTOVEDDUTTETTENANNGGILGONGLENDVIL	
VD 00233514 1 HCANTEC NVI DONDAM DSNTCVSDDWTTTTNANNGSIEGELGENTT	PKT
ATTRIACE HOLKEE NULLONSMEST DENTER TEKDANDEST DOLLENDER	RKL
VP 0.09176910 1 DCLTTEP NNVPITNOVITNCNLVGSCVCVGDDLVVVVTPCNS TPSTVCULTATINTTE	VCL
	. Og L
-	

	β34	β35	β36	β37		-		α8
AEM64049.1	660	670 TT	680	r	· ·	700	710	720
AEM64049.1	IPPCTO	NHRRYEKLGS	VYYED	SYVRMVEVE	?ETI	TRVTLNLT	LLEDREFLPLE	YTREELA
AAF04615.1	IEPCTV	GHRRYFTFGG	YVYFDE	AYSHQLSRA	ADITTVS	TFIDLNIT	MLEDHEFVPLEV	YTRHEIK
ADG45133.1	LEPCTV	SHRRYFIFGG	YVYFDE	AYSHOLSRA	ADVTTVS	TFIDLNIT	MLEDHEFVPLEV	YTRHEIK
AAP32845.1	VEPCVI	NHKRYFLFGHI	TYVYYDD	RYVREIAVE	DVGMI	TYVDLNLT	LLKDREFMPLO	YYTRDELR
YP_003933812.1	LEPCTV	GHKRYFVFGD	YVYFEE	AYSHQVSRA	ADVPVVS	TFVDLNLT	MLEDHEFLPLE	YYTROEIK
AAD11960.1	IEQCTV	GHRRYETFGS	YVYFEE	TYSHHLSR	ADITTVS	TFIPLNIT	MMEDHEFVPLEV	YYTRHEIK
AGC54689.1	LEQCTV	GHRRYFTFGS	YVYFEE	TYSHHLGR	ADITTVS	TFVPLNIT	MMEDHEFIPLEV	YYTRQEIK
AAD11961.1	LEQCT	GHRRYFTFGS	GYVYFEE	TYSHHLSR	ADITTVS	TFVPLNIT	MMEDHEFVPLEV	YYTRQEIK
YP_009230158.1	IEPCSV	GHKRYFSFGA	GYVYFEN	AYSHQLPRS	SDVMSVS	TFIDLNLT	MLSDHEFVPLEV	YYTRREIK
BAC58067.1	LEPCTV	GHRRYFTFGA	GYVYFED	AYSHQLGR	ADVTTVS	TFINLNT	MLEDHEFVPLEV	YYTRQEIK
AAA85648.1	LEPCTV	GHRRYFTFGA	GYVYFEE	AYSHQLGR	ADVTTVS	TFINLNT	MLEDHEFVPLEV	YYTRQEIK
AAA88010.1	LEPCTV	GHRRYFTFGA	GYVYFEE	AYSHQLGR	ADVTTVS	TFINLNT	MLEDHEFVPLEV	YYTRQEIK
BAE47051.1	LEPCTV	GHRRYFIFGG	GYVYFBE	AYSHQLSR	ADITTVS	TFIDLNIT	MLEDHEFVPLEV	YYTRHEIK
YP_009342376.1	LEPCSI	ANHRRYEMYGSI	TVYFEN	QFVKQVDS	ADIQMV	TFVDLNLT	MLEDREILPLT	YYTREELR
YP_003084394.1	KEPCAI	NHKRYEMFGPI	VVLYDE	QFVRQVEA	ADIQMV	TFVELNLT	MLEDREILPLOV	YYTREEIR
YP_009046525.1	IEQCVI	ANHRRYFLFGDI	KYAYFED	VFIKMVDLS	SEVQML	TYVELNLT	MLEDREILPLE	YYTKEEIR
NP_073321.1	IEPCSI	ANHRRYFLFGD	GYAFYEN	NFVKMVDA	ADIQLAS	TFVELNLT	LLEDREILPLS	YYTKEELR
YP_001033956.1	VEPCSI	ANHRRYFLFGS	GYALFEN	NFVKMVDA	ADIQIA	TFVELNLT	LLEDREILPLS	YYTKEELR
NP_077446.1	IEQCV	ANHKRYFRFGHI	VYFED	I I VREVPA	HEVGLIS	TYVDLNLT	LLKDREFMPLQ	YYTRDELR
BAM99305.1	IEPCVV	/NHKRYFRFGAI	YVYYED	LYVHTIPV	AEIETIS	AHVDLNLV	MLEDREFLPLE	YYTRAELA
AAD46114.2	VEPCAR	ANHRRYFRFGAI	YVYYEN	AYVRRVPL	FEIETI	TFVDLNLT	VLEDREFLPLEV	YYTRAELA
AAD46113.2	VEPCAI	HHKRYFRFGEI	YVYYEN	AYVRRVPPS	SELELIS	TFVDLNLT	LLEDREFLPLE	YYTRAELA
AAD46115.2	VEPCAI	ANHKRYFRFGAI	YVYYEN	AYVRRVPL	AELETIS	TFVDLNLT	VLEDREFLPLEV	YYTRAELA
AFB76670.1	VEPCT	ANHKRYERFGAI	YVYYEN	AYVRRVPL	AELEVIS	TFVDLNLT	VLEDREFLPLEV	YYTRAELA
AAD46112.2	VEPCAI	NHKRYFRFGAI	YVYYEN	AYVRRVPL	AELEVIS	TFVDLNLT	VLEDREFLPLEV	YYTRAELA
AP015888.1	VEPCAI	NHKRYFRFGAI	DYVYYEN.	AYVRRVPL	AELEVIS	T F V D L N L T	VLEDREFLPLEV	YYTRAE LA
ANG65542.1	IEPCTV	NNKRYFKFGAI	DYVYFED	AYVRKVPLS	SEIELI	AYVDLNLT	LLEDREFLPLE	YYTRAELE
AEK27122.1	IEPCT	ANHKRYFKFGVI	YVYFEN	AYVRKVPL	NEIEMI	AYVDLNIT	LLEDREFLPLE	YYTRAELE
CAA92272.1	IEPCT	ANNKRYFKFGVI	YVYF EN	VYIRKVPL	NEIEMI	TYVDLNIT	LEDREFLPLE	YYTRAELE
YP_009054936.1	VEPCAI	LNHKRYFKFGSI	DYVY YEN	TYVRNVPL	FEIEMI	TYVDLNLT	LEDREFLPLEV	YYTRAELE
AMB16079.1	IEPCSI	INQKRYFKFGKI	EYVYYEN	TYVRKVPP	reievi	TYVELNLT	LEDREFLPLEV	YYTRAE LE
YP_006273012.1	IEPCAI	NQKRYFKFGKI	EYVYYEN	TYVRKVPP	reievi <mark>s</mark>	TYVELNLT	LLEDREFLPLE	YTRAELE
YP_002333514.1	IEPCAI	NQKRYFKFGKI	EYVYYDN	TYVRKVPP	reievi	TYVELNLT	LEDREFLPLE	YTRAELE
AII81366.1	IEPCAI	NQKRYFKFGKI	EYVYYDN	TFVRKVPP	reievi <mark>s</mark>	TYVELNLT	LEDREFLPLEV	YYTRAE LE
YP_009176910.1	TENCER	KSRKLELYEN	AMLYDN	NFVRMVPL	DIPEV	TYINLDLT	MLENVDFVALD	YSAGELK
	5							

	α9	α10	1		
AEM64049.1	00000000	20000	750 760	770	780
AEM64049.1	DTGLLDYSEIQRRNG	LHALKFYDI	DRVVKVDHNVVLLRGIAN	FEQGLGDVGAA	VGKVVLGATGAVI
AAF04615.1	DSGLLDYTEVQRRNG	LHDLRFADI	DTVIHADANAAMFAGLGA	FFEGMGDLGRA	VGKVVMGIVGGVV
ADG45133.1	DSGLLDYTEVQRRN	LHDLRFADI	DTVIRADANAAMFAGLCA	FFEGMGDLGRA	VGKVVMGVVGGVV
AAP32845.1	DTGLLDYSEIQRRNG	OMHSLRFYDI	DKVVQYDSGTAIMQGMAQ	FFQGLGTAGQA	VGHVVLGATGALL
YP_003933812.1	DSGLLDYAEVQRRN	MHALRFSDI	DHIINDTTNAALMDGLFR	FFDGLGAAGQA	IGKAVLGVTEAVI
AAD11960.1	DSGLLDYTEVQRRNG	LHALRFHDI	DTIIRPDHYSAIFSGLYS	FFDGLGEIGRA	VGRVVTGIVGGVV
AGC54689.1	DSGLLDYTEVQRRNG	LHALRFHDI	DTIIHPDPYSAIFSGLYS	FFDGLGEIGRA	VGRVVTGIVGGVV
AAD11961.1	DSGLLDYTEVQRRS	LHALRFHDI	DTIIHPDPYSAIFSGLYS	FFDGLGEIGRA	VGRVVTGIVGGVV
YP_009230158.1	DSGLLDYAEVQRRNG	LHALRFADI	DTVIKADASAAMFAGLHA	FFDGLGDAGRA	LGSVVLGIASGVV
BAC58067.1	DSGLLDYTEVQRRNG	LHALRFADI	DTVIKADAHAPLFAGLYS	FFEGLGDVGRA	VGKVVMGIVGGVV
AAA85648.1	DSGLLDYTEVQRRNG	LHALRFADI	DTVIKADAHAALFAGLYS	FFEGLGDVGRA	VGKVVMGLVGGVV
AAA88010.1	DSGLLDYTEVQRRNG	LHALRFADI	DTVIKADAHAALFAGLYS	FFEGLGDVGRA	VGKVVMGIVGGVV
BAE47051.1	DSGLLDYTEVQRRNG	LHDLRFADI	DTVIRADANAAMFAGLCA	FFEGMGDVGRA	VGKVVMGIVGGVV
YP_009342376.1	DTGVLDYDEVQRRNG	OMHSLRFYDI	DKVVNTDNNMIFMEGLAN	FFQGLGEAGQA	IGKVVVGAAGAIV
YP_003084394.1	DSGVLDYAEVQRRNG	LHSLRFYDI	DKVIDIDSNYAFMADLTN	FFKGLGEAGQA	IGKVVVGVAGAVV
YP_009046525.1	DAGVLDYAEVAKRNA	ALHELKFYDI	DKVIEVDTQYAFMQGLTE	FFNGLGQAGQA	IGKVVVGAAGAVV
NP_073321.1	DVGVLDYAEVARRNO	<i>LHELKFYDI</i>	NRVIEVDTNYAFMNGLAE	LFNGMGQVGQA	IGKVVVGAAGAIV
YP_001033956.1	DVGVLDYAEVARRNO	LHELKFYDI	NKVIEVDTNYAFMNGLAE	LFNGMGQVGQA	IGKVVVGAAGAIV
NP_077446.1	DTGLLDYSEIQRRNG	OMHSLRFYDI	DRVVQYDSGTAIMQGMAQ	FFQGLGTAGQA	VGQVVLGATGALL
BAM99305.1	DTGLLDYSEIQRRNG	LHSLKFYDI	DSVVKLDNNLVIMRGMAN	FFQGLGDVGKA	VGSVVLGAAGLAL
AAD46114.2	DTGLLDYSEIQRRNG	2LHELKFYDI	DRVVKLDSNMVIMRGLAS	FFQGMGAVGQA	VGTVVLGAAGAAL
AAD46113.2	DTGLLDYSEIQRRNG	LHELRFYDI	DRVVKVDNNMAIMRGLAG	FFQGLGAVGQA	VGTVVLGAAGAAL
AAD46115.2	DTGLLDYSEIQRRNG	LHELRFYDI	DRVVKTDTNMAIMRGLAN	FFQGLGAVGQA	VGTVVLGAAGAAL
AFB76670.1	DTGLLDYSEIQRRNG	<u>2LHELRFYDI</u>	DRVVKTDGNMAIMRGLAN	FFQGLGAVGQA	VGTVVLGAAGAAL
AAD46112.2	DTGLLDYSEIQRRNG	<u>2LHELRFYDI</u>	DRVVKTDGNMAIMRGLAN	FFQGLGAVGQA	VGTVVLGAAGAAL
AP015888.1	DTGLLDYSEIQRRNG	LHELRFYDI	DRVVKTDGNMAIMRGLAN	FFQGLGAVGQA	VGTVVLGAAGAAL
ANG65542.1	DTGLLDYSEIQRRNG	2LHALKFYDI	DSIVRVDNNLVIMRGMAN	FFQGLGDVGAG	FGKVVLGAASAVI
AEK27122.1	DTGLLDYSEIQRRNG	<u>2LHALKFYDI</u>	DSVVKVDNNVVIMRGIAN	FFQGLGDVGAG	FGKVVLGAANAVI
CAA92272.1	DTGLLDYSEIQRRNG	<u>LHALKFYDI</u>	DSVVKVDNNLIIMRGMLT	FFQGLGDVGAG	FGKVVLGAANAVI
YP_009054936.1	DTGLMDYSEIQRRNG	LHALKFYDI	DSVITVDTDTVIMQGLAN	FFQGLGKAGQA	IGKLVIGAAGAVV
AMB16079.1	DTGLLDYSEIQRRNG	LHALRFYDI	DSVVNVDNTAVIMQGIAT	FFKGLGKVGEA	VGTLVLGAAGAVV
YP_006273012.1	DTGLLDYSEIQRRN	LHALRFYDI	DSVVNVDNTAVIMQGIAS	FFKGLGKVGEA	VGTLVLGAAGAVV
YP_002333514.1	DTGLLDYSEIQRRNG	LHALRFYDI	DSVVNVDNTAVIMQGIAS	FFKGLGKVGEA	VGTLVLGAAGAVV
AII81366.1	DTGLLDYSEIQRRN	LHALRFYDI	DSVVNVDNTAVIMQGIAS	FFKGLGKVGEA	VGTLVLGAAGAVV
YP_009176910.1	EANVNNLDELLRFQA	ADRHAISTL	ANAVYSTAGVEFLKGIEK	IFAGFGVVGEA	ICKAIGTIGGALA

	790	800	810	820	830	840	
AEM64049.1	SAVGGMVS	FLSNPFGALA	IGLLVLAG	LVAAFLAYR	HISRLRRNPM	ALYPVTTKTLKE	DGVD
AAF04615.1	SAVSGVSS	FMSNPFGALA	AVGLLVLAG	LAAAFFAFR	YVMRLQSNPM	ALYPLTTKELKN	PTN PD.
ADG45133.1	SAVSGVSS	FMSNPFGAL	AVGLLVLAG	LVAAFFAFR	YVLQLQRNPM	ALYPLTTKELKT	SDPGG
AAP32845.1	STVHGFTI	FLSNPFGAL	AVGLLVLAG	LVAAFFAYR	YVLKLKTSPM	ALYPLTTKGLKQ	LPEGMDP
YP_003933812.1	SVVSGVSS	FLSNPFGAL	AVGLLVLAG	LTAAFFALR	Y I M R L R A N P M F	ALYPITTHGIKA	EAKASLA
AAD11960.1	AAVEGVES	FMSNPFGALA	AIGLLVIAG	LVAAFFAFR	YVLRLQSNPMF	ALYPLTTKELKH	AGKLQVS
AGC54689.1	ATVEGVGS	FMSNPFGALA	AIGLLVVAG	LVAAFFAFR	YVLRLQSNPM	ALYPLTKELKH	EGKLQLS
AAD11961.1	ATVEGVGS	FMSNPFGALA	AIGLLVVAG	LVAAFFAFR	YVLRLQSNPM	ALYPLTTKELKH	EGKLQLS
YP_009230158.1	ATVTGVTS	FLSNPFGALA	AVGLLVLAG	LVAAFFALR	YVMRIQRNPM	ALYPLTTKDLKN	ADA
BAC58067.1	SAVSGVSS	FLSNPFGAL	AVGLLVLAG	LAAAFFAFR	YVMRLQRNPM	ALYPLTTKELKS	DGPSPAG
AAA85648.1	SAVSGVSS	FLSNPFGAL	AVGLLVLAG	LAAAFFAFR	YVMRLQRNPMF	ALYPLTTKELKS	DGAPLSG
AAA88010.1	SAVSGVSS	FLSNPFGAL	AVGLLVLAG	LAAAFFAFR	YVMRLQRNPM	ALYPLTTKELKS	DGAPLAG
BAE47051.1	SAVSGVSS	FMSNPFGAL	AVGLLVLAG	LAAAFFAFR	YVLRLQSNPM	ALYPLTTKELKN	PDP QG
YP_009342376.1	STVSGVAS	FLSNPFGAL	AIGLLVLAG	LVAAFLAFR	Y V N K I R S N P M F	ALYPLTTKSLKQ	SGSGKGS
YP_003084394.1	STVSGISS	LLSNPFGAL	AIGLIVVAG	LVVAFLAYR	Y I SKLRND <mark>P M</mark> H	TLYPMTMKTLKN	EAKLTPR
YP_009046525.1	STVNGLAS	FMSNPFGALA	VGLIVVAA	VVAAFLAYR	Y M H K L R S N P M H	ALYPMTTQELKK	KAKGEDG
NP_073321.1	STVSGISA	FMSNPFGAL	AIGLIVIAG	IIAAFLAYR	Y V N K L K S N P M F	ALYPMTTEELKD	QATRKPR
YP_001033956.1	STISGVSA	FMSNPFGALA	AIGLIIIAG	LVAAFLAYR	Y V N K L K S N P M F	ALYPMTTEVLKA	QATRELH
NP_077446.1	STVHGFTI	FMSNPFGAL	AVGLLVLAG	LVAAFFAYR	YVLKLKAS <mark>PM</mark> H	ALYPLTTKGLKT	LADGVDP
BAM99305.1	STVKGVAS	FLSNPFGAL	ALGLIVLAG	LVAAFLAYR	YVMRLRNNPM	ALYPVTTQTLKE	EARDG
AAD46114.2	STVAGITS	FLSNPFGALA	AVGLLVVAG	LVAAFLAYR	YVSKIRSN <mark>PM</mark> H	ALYPITTRALKD	DARGG
AAD46113.2	STVSGIAS	FLSNPFGALA	ATGLLVVAG	LVAAFLAYR	Y V S R L R R N P M F	ALYPITTRALKD	DAQNG
AAD46115.2	STVSGIAS	FLANPFGAL	ATGLLVVAG	LVAAFLAYR	YVSRLRSNPM	ALYPITTRALKD	DARGA
AFB76670.1	STVSGIAS	FIANPFGALA	ATGLLVLAG	LVAAFLAYR	Y I S R L R S N P M F	ALYPITTRALKD	DARGA
AAD46112.2	STVSGIAS	FVANPFGAL	ATGLLVLAG	LVAAFLAYR	Y I S R L R S N P M F	ALYPITTRALKD	DAKGA
AP015888.1	STVSGIAS	FVANPFGALA	ATGLLVLAG	LVAAFLAYR	Y I S R L R S N <mark>P M</mark> F	ALYPITTRALKD	DAKGA
ANG65542.1	STVSGVSS	F LNNPF GAL	AVGLLILAG	IVAAFLAYR	Y I S R L R A N P M F	ALYPVTTRNLKQ	TAKSPAS
AEK27122.1	ATVSGVSS	FLNNPFGALA	AVGLLILAG	LFAAFLAYR	Y V S K L K S N P M F	ALYPVTTRNLKE	SVKNGNS
CAA92272.1	STVSGISS	FLNNPFGAL	AVGLLILAG	LFAAFLAYR	Y V S K L K S N P M F	ALYPVTTRNLKE	SSKEK
YP_009054936.1	STVSSIIS	FVKNPFGAL	AVGLLVLAG	LVAAFFAYR	YVMQLRAN <mark>PM</mark> H	ALYPITTQGLKN	SAKAAM.
AMB16079.1	STVSGIAS	FINNPFGGL	AIGLLVIAG	LVAAFFAYR	YVMQLRSNPM	ALYPITTRSLKN	KAKASY.
YP_006273012.1	STVSGIVS	FLNNPFGGL	AIGLLVIAG	LVAAFFAYR	YVMQIRSNPM	ALYPITTKALKN	KAKASY.
YP_002333514.1	STVSGIAS	FLNNPFGGL	IGLLVIAG	LVAAFFAYR	YVMQIRSNPM	ALYPITTKALKN	KAKTSS.
AII81366.1	STVSGIAS	FLNNPFGGL	AIGLLVIAG	LVAAFFAYR	YVMQIRSNPM	ALYPITTKALKN	KAKTSY.
YP 009176910.1	GVVSGVVG	FFSNPFGGFT	TILLVAGO	LVAAFLAFK	FIOLYKKDPM	TLEPMTAKSLAO	RDPS

AEM64049.1		050	0.00	070		
		850	860	870	880	890
AEM64049.1		EGDV	EAKLDQARDMIF	YMSIVSALE	QQEHKARKK.	NSGPAL
AAF04615.1	SGEGE	EGGDFL	EAKLAEAREMIF	YMALVSAME	HTEHKAKKK.	GTSAL
ADG45133.1	GGEGE	EGAEGGGF	EAKLAEAREMIF	YMALVSAME	RTEHKARKK.	GTSAL
AAP32845.1	AEKPNATDTPIEEIGDSQNT	EPSVNSGF	PDKFREAQEMIE	YMTLVSAAE	RQESKARKK.	NKTSAL
YP_003933812.1	GEP	GPGGIEDF	EAKLEEARTMIN	YMTLVSAME	RTAHKAKKR.	. GTSAR
AAD11960.1	GGEVSHG.	GGEEF	ETKLDAAREMIF	YMAMVSALE	RTKHKASKR	G.SSSL
AGC54689.1	GGKISGDA	GGEDGNDF	EKKLQAAQEMIF	YMAMVSALE	RTKHKALKK.	NTNSSL
AAD11961.1	GGKISSEA	GGEDGSDF	EKKLQAAQEMIF	YMAMVSALE	RTKHKALRK.	NKDSSL
YP_009230158.1	GD	KEGPAEDFL	ERKLEAARDMIF	YMALVSAME	RTKHKAKKR.	GGTSAI
BAC58067.1	GGDGA	SGGGEEDF	EAKLAQAREMIF	YMALVSAME	RTEHKARKK.	GTSAL
AAA85648.1	GGD	PGDGAEDF	EAKLAQAREMIF	YMALVSAME	RTEHKARKK.	GTSAL
AAA88010.1	GE	DGAEDFL	EAKLAQAREMIF	YMALVSAME	RTEHKARKK.	GTSAL
BAE47051.1	GGEGE	EGGGF	EAKLAEAQEMIF	YMALVSAME	RTEHKAKKK.	GTSAL
YP_009342376.1	G	DDFDDEEF	EKKLEQAREMVE	YLSLL <mark>SA</mark> SE	RVEHKAKRK.	GKTSAL
YP_003084394.1	EA	DGEDEDEF	ESKLEQAREMVF	YMALLSASE	RTEKKARKK.	NSRTAL
YP_009046525.1	GAGEE	GGEEEEE	ENKLQMARDMIF	YMALISAEE	RQQKKLRKKF	KHGTSAF
NP_073321.1	DG.	SDSELMSI	ERKLEAAREMIK	YMALVSAEE	RHQKKLRKKF	RGTTAI
YP_001033956.1	EES	DDLERTSI	ERKLEEAREMIN	YMALVSAEE	RHEKKLRRKF	RRGTTAV
NP_077446.1	ENEDNDNSNPVETLNE	NSKKGF	ATKFKEAQEMIK	YMTLVSAAE	RQESKARKK.	NKTSAL
BAM99305.1	. I	NSPEDFD	ETKLEQARDMIF	YMSMVSAME	REEHKAKKK.	NKGTAL
AAD46114.2	.AGG	DAAGDEEFD	EAKLEQAREMIN	YMSFVSAAE	RQEHKAKKR.	NKGGPL
AAD46113.2	.GGE	SEGGEDDF	PDKLEQAREMI	YMSFV <mark>SA</mark> AE	RQEHKARKK.	NKGAPL
AAD46115.2	.GVA	GEGEEEEF	AAKLEQAREMI	YMSLV <mark>SA</mark> VE	RQEHKAKKS.	NKGGPL
AFB76670.1	.TAP	GEE.EEEFD	AAKLEQAREMI	YMSLV <mark>SA</mark> VE	RQEHKAKKS.	NKGGPL
AAD46112.2	.GAP	GEEGEEEF	AAKLEQAREMI	YMSLVSAVE	RQEHKAKKS.	NKGGPL
AP015888.1	.GAP	GEEGEEEF	AAKLEQAREMI	YMSLVSAVE	RQEHKAKKS.	NKGGPL
ANG65542.1	AGGD	SDPGVDDF	EEKLMQAREMI	YMSLV <mark>SA</mark> ME	QQEHKAMKK.	NKGPAI
AEK27122.1	NNSD	GEENDDNI	EEKLQQAKEMIK	YMSLVSAME	QQEHKAIKK.	NSGPAL
CAA92272.1	.IGD	GDEDGDEF	EDKLSQAKEMIK	YMTLISAME	KQEHKAMKK.	NSGPAI
YP_009054936.1	M	GGGDGPEFD	EDKLEQAREMIF	YMSMV <mark>SA</mark> ME	KQEKKALKK.	NSGPAL
AMB16079.1	.GQN	DDDDTSDF	EAKLEEAREMIN	YMSMVSALE	KQEKKAMKK.	NKGVGL
YP_006273012.1	.GQI	DEDDESDFD	EAKLEEAREMIN	YMSMV <mark>SA</mark> le	KQEKKAIKK.	NSGVGL
YP_002333514.1	.GQI	DEDDGSDFD	EAKLEEAREMIN	YMSMVSALE	KQEKKAIKK.	NSGVGL
AII81366.1	.GQI	DEDDGSDFD	EAKLEEAREMIN	YMSMVSALE	KQEKKAIKK.	NSGVGL
YP_009176910.1		DPDNVEEM	DEARRETMLIAF	RLHLLSAEQ	RLAAR	D L

AEM64049.1	222	010
	900	910
AEM64049.1	LASRVGAMATRRHYQ	RLESEDPDAL
AAF04615.1	LSAKVTDMVMRKRR.NTNYT	QVPNKDGDADEDDL
ADG45133.1	LSSKVTNMVLRKRN.KARYS	PLHNEDEAGDEDEL
AAP32845.1	LTSRLTGLALRNRRGYS	RVRTENVTGV
YP_003933812.1	ISAHLTDMVLRKRNTARPPSSEYQ	PILEDEDDAAV
AAD11960.1	INANVTDMILRKRRAPAKYS	PINETDET
AGC54689.1	INAGLTSMLLRKPSTPKYS	P
AAD11961.1	INAGLTNMLLRKPSTPKYS	PVNETDET
YP_009230158.1	LTARATDMILRRRAGAARYE	PLNDEDM
BAC58067.1	LSAKVTNMVMRKRA.KPRYS	PLGDTDEEEL
AAA85648.1	LSAKVTNMVMRKRA.RPRYS	PLPDTDEEEL
AAA88010.1	LSAKVTDAVMRKRA.RPRYS	PLRDTDEEEL
BAE47051.1	LSSKVTNMVLRKRN.KTRYS	PLHNEDEAGDEDEL
YP_009342376.1	LTAKLANMALRSRKQPKYS	KLENSDTDSDEGDF.V
YP_003084394.1	LSNHLSNLRSRS.NGKKYS	KVEDEYEDGDSADE. TEILVTDRV
YP 009046525.1	LADHLTGLRLRN.KSPKYE	RLRTDGSEDDPDDN.YKDVIV
NP_073321.1	LSDHLSNMRLMN.GHRKYD	KLNDTDSETDDEIV
YP_001033956.1	LSDHLAKMRIKN.SNPKYD	KLPTTYSDSEDDAV
NP_077446.1	LSSRLTQLALKNRGKSRYS	RVSTEDT.GV
BAM99305.1	INSRIIDMAMRRRGPKYQ	RLPDTETDVGKQPL.YP
AAD46114.2	LANRLTQ LALRORAR PAYO	QLPMSDVGGA
AAD46113.2	LANRLTQ LALRRRPP PAYO	QLPMSDVGGA
AAD46115.2	LATRLTO LALRRRAP PAYO	OLPMADVGGA
AFB76670.1	LATRLTO LALRRAP PEYO	OLPMADVGGA
AAD46112.2	LATRLTQLALRRAPPEYQ	QLPMADVGGA
AP015888.1	LANRLTQLALRRRAPPAYQ	QLPMSDVGEP
ANG65542.1	LTSHLTNMALRRGPKYO	RLNNLDSGDDTETN.LV
AEK27122.1	LASHITNLSLKHRGPKYK	RLKNVNENESKV
CAA92272.1	LANRVANLALKHRGPKYK	RLKNMDDENDEV
YP 009054936.1	IANHVSNLALRKRGPKYT	AVPSEDEAESYTVV
AMB16079.1	IASNVSKLALRRRGPKYT	RLREDDPMESEKMV
YP_006273012.1	IASNVSKLALRRRGPKYT	RLQQNDTMEDEKMV
YP_002333514.1	IASNVSKLALRRRGPKYT	RLQQNDDMEDEKMV
AII81366.1	IASNVSKLALRRRGPKYT	RLQQNDSMEDEKMV
YP_009176910.1	KRRNL PKFLGRFRHR NGYS	KLIDEDTELHEIDDS.SQ