

## 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 (APO15888.1), Felid alphaherpesvirus 1 (ANG65542.1), 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 (YP\_009176910.1).

AEM64049.1

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      1           10           20           30           40
AEM64049.1  . . . . . MPAGGG . LWRGPRGHRPGHHGGAGLGRWPAPHHAA . . . . . AARGA . . . .
AAF04615.1  . . . . . MRQGAPARGCR . . . . .
ADG45133.1  . . . . . MRG . . . . .
AAP32845.1  . . . . .
YP_003933812.1  . . . . . MA . PPAKSR . . . . .
AAD11960.1  . . . . . MAVHPPLRPRL . . . . .
AGC54689.1  . . . . . HQL . . . . .
AAD11961.1  . . . . . MTHSPPKQR . . . . .
YP_009230158.1  . . . . .
BAC58067.1  . . . . . MRPR . . . . .
AAA85648.1  . . . . . MRPR . . . GAR . . . . .
AAA88010.1  . . . . . MRPR . . . GTP . . . . .
BAE47051.1  . . . . . MRDGAPAHGRG . . . . .
YP_009342376.1  . . . . .
YP_003084394.1  MYRRITCYLRDRMPAYFCNS . SGPEWRNNPRDVGCDRQGRLLYALYGASTTGSR . . . . . NGGA . C
YP_009046525.1  MQGRDLHHLRDLRPSDGRPG . SGSGREDRSGHDSYLRLGRVFSLVRGAPAAGAGHRKKSQGGG . G
NP_073321.1  . . . . .
YP_001033956.1  . . . . .
NP_077446.1  . . . . . MSPDCSIT . QQYCRYNYKRHDCNLRRRRFLFIVYSNSAACSGRTKTY . . . . .
BAM99305.1  . . . . . MSLGSG . LKQHLRANRRQYSCHIRPGRIFYAIYNFTT . . . . . GPRIQ . . . . .
AAD46114.2  . . . . . MPPRGSERRAGPDRQRGQRCHLRPGRVFPALRGLAAPGAG . . . . . GPRAA . . . . .
AAD46113.2  . . . . . MAARGRAERAAGAGDGRRGQRGHLRPGRVLAALRGAAAPGAGRDGGGGPR . . . . .
AAD46115.2  . . . . . MAARGGAERAAGPGDGRRGQRHHPGPGRVLAALRGPAPGAA . G . . . . . ARAA . . . . .
AFB76670.1  . . . . . MAARGGAERAAGAGDGRRGQRHRLRPGRVLAALRGPAPGAG . G . . . . . ARAA . . . . .
AAD46112.2  . . . . . MATRGAEPAAGAGYGRRGQRHRLRPGRVLAALRGPAPGAGG . . . . . ARAA . . . . .
APO15888.1  . . . . . MAARGGAEPAAGAGDGRRGQRHRLRPGRVLAALRGPAPGAGG . . . . . ARAA . . . . .
ANG65542.1  . . . . . MSTRGDLG . KRRGRSRWQGHSGYFRQRCFFPSLLGIAATGSRHNGNSS . . . . .
AEK27122.1  . . . . .
CAA92272.1  . . . . .
YP_009054936.1  . . . . . MSSRGGVV . AGPGGYGPGGDRCHLRRRVLSPLRGPADGSGVWVWELGAIIGDRC
AMB16079.1  . . . . . MSTCCRAI . CGPQRCYWRDCGNLRQRRVLASIHRTPAAGSWLWSQLGNVNLP
YP_006273012.1  . . . . .
YP_002333514.1  . . . . .
AII81366.1  . . . . . MSSGCRSV . GGSKWGHWRGDGGYLRQRRVLAPVCSAPAAGSWIGSQLGNVGNLL
YP_009176910.1  . . . . .

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AEM64049.1

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      50           60
AEM64049.1  . . . . . V . . . . . ALALLLALA . AA . . . . . P . . PCGAAAVTRAASA .
AAF04615.1  . . . . . WVVVAL . . . . . LGLTLGLVASAA . . . . . PSSPGTPGV
ADG45133.1  . . . . . GGLICAL . . . . . VVGALVAVASAA . . . . . PAAPRASGG
AAP32845.1  . . . . . . . . . . MFV . TAVV . . . . . SVSPSS .
YP_003933812.1  . . . . . ASRVAP . . . . . LTVSLVSMIAAAAAVALCAAFEAARGVTPVYSDDD .
AAD11960.1  . . . . . WLTRFWY . . . . . MFIVGGIL . . . . . VDTGGN
AGC54689.1  . . . . . RLTRLWY . . . . . IFLACGVF . . . . . GGTTGH
AAD11961.1  . . . . . QITRLWY . . . . . IFLAWGVF . . . . . GGPTGH
YP_009230158.1  . . . . . M . . . . . RLTMRGILVILVAVPLLAAA . . . . . STRAAAPRRARPEGR
BAC58067.1  . . . . . . . . . . AGPLPLPSPVPLLALAL . . . . . LA . ATRPLG
AAA85648.1  . . . . . ALPIPIPIPI . . . . . PIPPIPIPIPLPPALLALALL . . . . . AA . AGRAGP
AAA88010.1  . . . . . PSF . . . . . LPLPVLLALAV . I . . . . . AA . AGRAP
BAE47051.1  . . . . . GGLICAL . . . . . VVGTLMAAVVLA . . . . . PSPSGA
YP_009342376.1  . . . . . MIG . . . . . SVNTNVVIVLTFLLVS . . . . . LVRSEDPGDN .
YP_003084394.1  TTA VR . RK . . . . . EFDRMNRARRVSALHLTAPRRS . . . . . REVL . SLIMVSV . . . . . LRFPIQPPIV .
YP_009046525.1  ERGARKRERLSSRAFVPMSPDVYV . . . . . PTTSPCVQLVAFVVMHLLGSLP . . . . . MVSSQTAAPAA .
NP_073321.1  . . . . . MLMTPT . . . . . MKYFN . . . . . RSLFIFLTP . . . . . ILS . . . . .
YP_001033956.1  . . . . . . . . . . MHYFR . . . . . RNCIFFLIV . . . . . ILY . . . . .
NP_077446.1  . . . . . . . . . . L . . . . . NVCYITFA . . . . . ILFA . . . . . CVHPSL .
BAM99305.1  . . . . . Y . . . . . PASLMWLEYS . LLCVCLLIY . . . . . PGGAAREYP . PSS .
AAD46114.2  . . . . . L . . . . . AAALLWAAWA . L . . . . . LLA . A . PAAALPTAP . PSA .
AAD46113.2  . . . . . A . . . . . ALALLWPLL . LLPLLA . P . PAAAAPVTP . APP .
AAD46115.2  . . . . . L . . . . . AAALLWAAWA . L . . . . . LLA . A . PAAGLPATP . APP .
AFB76670.1  . . . . . L . . . . . AAALLWATWA . L . . . . . LLA . A . PAAGRPATT . PPA .
AAD46112.2  . . . . . L . . . . . AAALLWAAWA . L . . . . . LLA . A . PAAGRPTTP . PVP .
APO15888.1  . . . . . L . . . . . AAALLWAAWA . L . . . . . LLA . A . PAAGRPTTP . QVP .
ANG65542.1  . . . . . G . L . . . . . TRLARYVSEFI . . . . . WIVLF . . . . . LVGPRFVEGQSGS .
AEK27122.1  . . . . . M . . . . . FSlylyiffi . . . . . IYTL . . . . . ICDPTTPES . . . . .
CAA92272.1  . . . . . . . . . . MYLITLVFFI . . . . . NILVI . . . . . QCVPTTQPT . . . . .
YP_009054936.1  SPGAVAGARPPPH . . . . . F . . . . . KPWTLLVLVL . LSGLLAAG . . . . . RCGAT . PTSPPA .
AMB16079.1  ASPMS . KDSTSLG . . . . . V . . . . . RTI . . . . . V . IACLVLG . . . . . CCIVEAVPTTPSS .
YP_006273012.1  . . . . .
YP_002333514.1  . . . . .
AII81366.1  AAPHPLGKQASSR . . . . . V . . . . . GTI . . . . . V . LACLLLF . . . . . SCVVRVPTTPSP .
YP_009176910.1  . . . . . . . . . . MIMWLSFMMTLWLSLVLVY . . . . . GQITVPP . T .

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AEM64049.1 ..... 70 80 90 100 110 .....

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AAF04615.1 AAATQAA...NGGPATPAPPALGAAPTGDPKPKKKKKNFPPRRPAGDNATVAAGHATLREHLRD
ADG45133.1 VAATVAA...NGGPASRPPVPVSPATTRARKRRTKKKKPERPEATPPPDRANATVAAGHATLREHLRE
AAP32845.1 .....LYESLQVEP.....TQSEDI1TRSAHLGDGDEIREA1IKH
YP_003933812.1 ..ESSESIITG.GAELPAGEDAGPPEPGLPDRPTKPKRFRPGRRRQRANKTRESARAQ1LRESVQ1
AAD11960.1 AKPTQPLNKQTRSPERGS1DPSP...PDEVEPRFNQTVESGHAQLREH1IRG
AGC54689.1 TKPAVSPRRQDATPKYPP.PPNPSSS.....SDEYEPQFN1ETVELGHAQLREHLRG
AAD11961.1 AKPAVSLSRQAATHKHP1PPPPPPSS.....SDEYEPQFN1ETVELGHAQLREHLRG
YP_009230158.1 ARGEGRE...RGKGRPPPPPLPSEAPTPLLQY.....STGAPTNASAPANS1AE1LREIRA
BAC58067.1 PAAATPV...VSPRASAPPVPAAT1TFPDDDN...DGEAGAAPGAPGNASVEAGHATLREN1LRD
AAA85648.1 AAAN.PV...ASLPATPAPPAPGAT1PFPE...DGDEEGVAPPAPAPANASVEAGRATLRE1DLRG
AAA88010.1 AAAAAPT...AD.....PAATPALPEDEEVPDEDGEGVATPAPANASVEAGRATLRE1DLRE
BAE47051.1 VAVTPAA...NVSPASRPPPIQSPATTKARKQKTKKQPKRPEPTPPP1VDVNATVAAGHATLREHLRD
YP_009342376.1 .....S.EKRSA.....DN.GNAAAANKGTVPFR.TIAN
YP_003084394.1 .....N..ATDRPHGLM.....NDQDTHLDGERLQRGKLSRELIRG
YP_009046525.1 .....A.AAAAA1PA1AAAAA.....AVAANGSQANPQAGPKVTTTEL1MKN
NP_073321.1 .....IATSEIKLNPVTAREIVSG
YP_001033956.1 .....GTNSSPSTQNVTSREIVSS
NP_077446.1 .....STSQPPVNDQK.....VTVTPQYDTSPITIEGGDIDIKALHE
BAM99305.1 .....PN.RKVSGGPTFV.DLKI.....QPTKR.QRGTNDTIPGQIDIRE1TLRQ
AAD46114.2 .....PATSPAPPSA.D.....TAAAGNETAADDVRAVLRE
AAD46113.2 .....APSAPAPT.....EP...PPGTPS.PEDLDAAGNGSDLR1AAALS
AAD46115.2 .....GPAPAASA.GPTPA.PASP.....GPGGDAPDDDDGGAANGTDVRAELRR
AFB76670.1 .....PPPEEAASAPPAS.PSPP.....GPDGDDAASPDNSTD1VRAALRL
AAD46112.2 .....GGAGGAGSPAPPAS.PAPS.....ASLRPADGPD1DDPNSTD1VRAALRL
APO15888.1 .....GGA.GAGSPAPPAS.PAPP.....ASPRPADSPDDGDDPNSTD1VRAALRL
ANG65542.1 .....TS.EQP.....RR...TVATPEVGGTTPKPTD.PTMSDMREALRA
AEK27122.1 .....TINP.LN...HNLSTPKPTSDDI1REILRE
CAA92272.1 .....ESTPPI1TSPPPPKNSSSNT1ELNDMDI1GEILGE
YP_009054936.1 .....TP.APPTTSPSPSS.ESSE...PAEPSPLPSG.GEEDGDPETSD1DLRGAVD
AMB16079.1 .....QPSTPAS.T.QSAK...TVDQTL1LP.....TETPD1PLRLAVRE
YP_006273012.1 .....MST.HSQG...TVNPTLLP.....TETPD1PLRQAVRE
YP_002333514.1 .....MST.HSRG...TVDP1SMLP.....TETPD1PLRLAVRE
AII81366.1 .....PTSTPT1SM1LT.HSHG...TVDP1TLLP.....TETPD1PLRLAVRE
YP_009176910.1 .....DDVGIMSSELMEN
    
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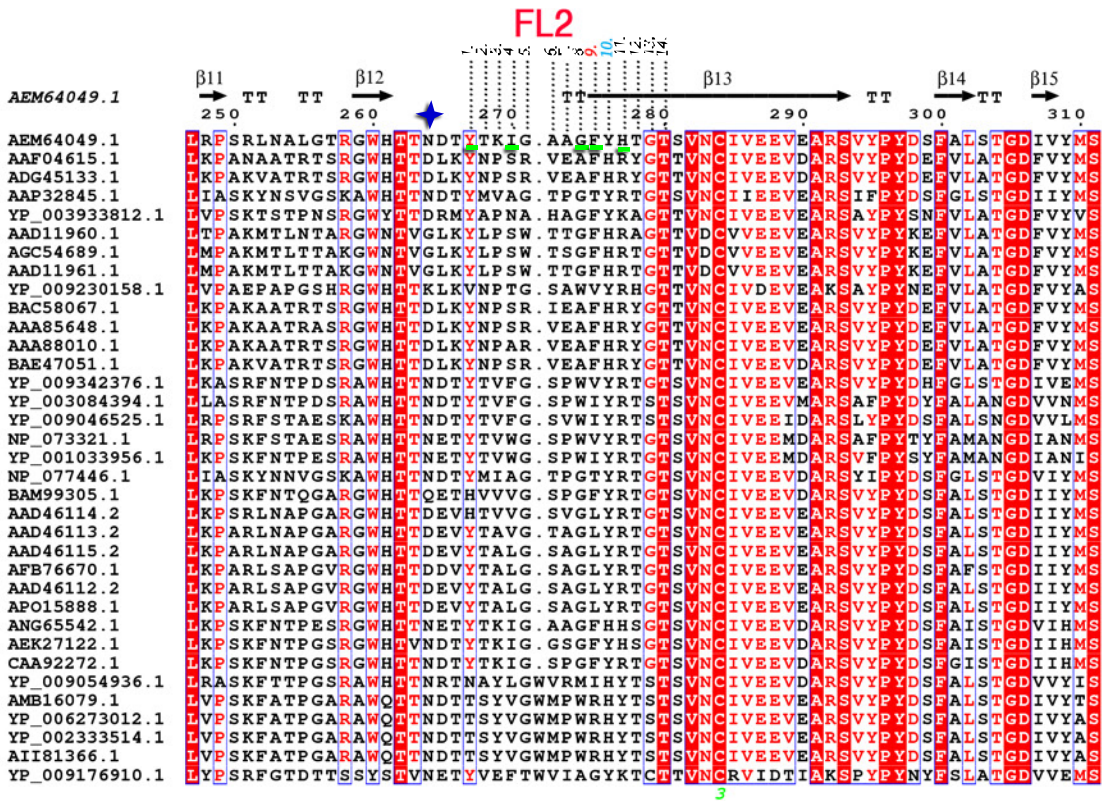
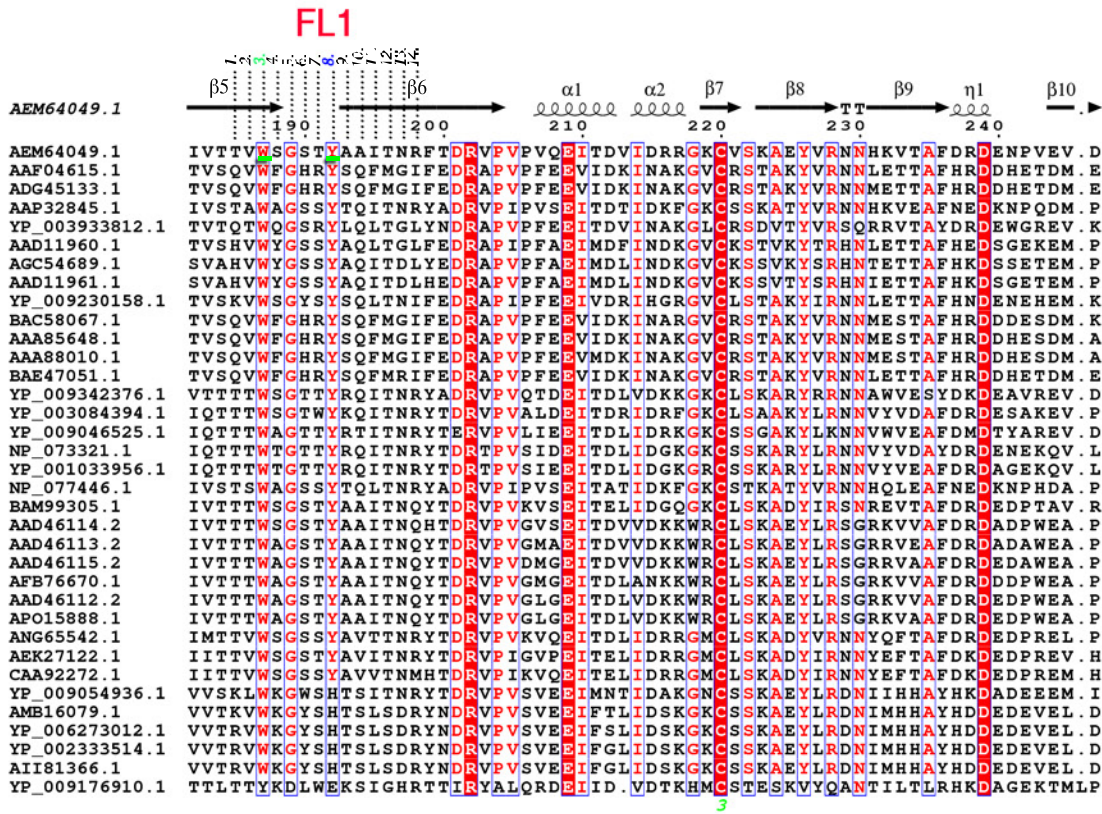
AEM64049.1     ▶     β2     β3     β4     β5

120 T.T     130 TT     140     150     160     170     180

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AEM64049.1 RAAATE.RDRFYVCPPTSGSTVVRLEPF1EQACPEYSQGRNFT1EGIAVLFKENIAPHKFKAH1IY1KNV
AAF04615.1 IKAEST.DANFYVCPPTTGATVVQFEPQRRCPTRPEGQNYTEGIAVVF1KENIAPYKFKATMY1KDV
ADG45133.1 IKVENA.DAQFYVCPPTTGATVVQFEPQRRCPTRPEGQNYTEGIAVVF1KENIAPYKFKATMY1KDV
AAP32845.1 SQDAET.KPTFYVCPPTTGATVVQFEPQRRCPTRPEGQNYTEGIAVVF1KENIAPYKFKATMY1KDV
YP_003933812.1 IRANA.TSMFYVCPPTTGATVVQFEPQRRCPDVAAGKNFT1EGIAVIFKENIAPYKFKATMY1REI
AAD11960.1 VKAGDG.DSEFYVCPPTTGATVVQFEPKHPHCP1SAPTGDNYTEGIAIIFKENIAPYKFKAMMY1KDV
AGC54689.1 IKVKDG.DSEFYVCPPTTGATVVQFEPKHPHCP1SAPTGDNYTEGIAIIFKENIAPYKFKAMMY1KDV
AAD11961.1 IKVKDG.DSEFYVCPPTTGATVVQFEPKHPHCP1SAPTGDNYTEGIAIIFKENIAPYKFKATMY1KDV
YP_009230158.1 LRSGS.DPRFYVCPPTTGATVIRLEPFRACPDAPKGLNFT1EGIAVIFKENLAPYKFKATMY1KAV
BAC58067.1 IKALDG.DATFYVCPPTTGATVVQFEPQRRCPRAPDQNYTEGIAVIF1KENIAPYKFKATMY1KDV
AAA85648.1 IKARDG.DATFYVCPPTTGATVVQFEPQRRCPRAPHGQNYTEGIAVVF1KENIAPYKFKATMY1KDV
AAA88010.1 IKARDG.DATFYVCPPTTGATVVQFEPQRRCPRAPDQNYTEGIAVVF1KENIAPYKFKATMY1KDV
BAE47051.1 IKVENA.DAQFYVCPPTTGATVVQFEPQRRCPTRPEGQNYTEGIAVVF1KENIAPYKFKATMY1KDV
YP_009342376.1 SAQSED.DGVFYVCPPTTGATVLRLEPFRQCPDYKTGKNFT1EGIAVIFKENISPYKFKATLY1KNV
YP_003084394.1 VQSTRE.EDK1FYVCPPTTGTVLRLEPFRQCP1EAYKGRNWT1EGVAVIFKENINPLKFKAMIY1KNV
YP_009046525.1 IQVTGD.EATFYVCPPTTGATVVRLEPFRQCP1EAHKGKRWTEGIAVIFKENISPYKFKAKLY1KNV
NP_073321.1 IQLSED.ETTFYVCPPTVSTVIRLEPFRQCP1EPLKSTEWEGE1IAILFKENISPYKFKVTLTY1KNV
NP_077446.1 VQLSEE.ESTFYLCPPPVGSTVIRLEPFRQCP1EPRKATEWEGE1IAILFKENISPYKFKVTLTY1KNI
SRDIYN.EASFYVCPPTTGSTVVTLSPRVCPDYHLGKNFT1EGIAVIFKENIAPYKFKATMY1KDV
BAM99305.1 SQRAGE.DDTFYMCPPTTGATVVRMAPFRACQ1YSQGRNFT1EGIGVIFKENIAPYKFKAHY1KNV
AAD46114.2 AQAAGE.HSOFVCPPTSGATVVRLAPGRPC1EYELGRNYTEGIGIY1KENIAPYKFKAHY1KNV
AAD46113.2 AQAAGE.SSRFFVCPPTSGATVVRLAPARP1CPDYELGRNYTEGIGVIF1KENIAPYKFKAHY1KNV
AAD46115.2 AQAAGE.SSRFFVCPPTSGATVVRLAPARP1CPDYELGRNYTEGIGVIF1KENIAPYKFKAHY1KNV
AFB76670.1 AQAAGE.NSRFFVCPPTSGATVVRLAPARP1CPDYELGRNYTEGIGVIF1KENIAPYKFKAHY1KNV
AAD46112.2 AQAAGE.NSRFFVCPPTSGATVVRLAPARP1CPDYELGRNYTEGIGVIF1KENIAPYKFKAHY1KNV
APO15888.1 AQAAGE.NSRFFVCPPTSGATVVRLAPARP1CPDYELGRNYTEGIGVIF1KENIAPYKFKAHY1KNV
ANG65542.1 SQIEANGPSTFYMCPPTSGSTVVRLEPFRAC1PDYKLGKNFT1EGIAVIFKENIAPYKFKAHY1KNI
AEK27122.1 SQIESDDTSTFYMCPPTSGSTLVRLEPFRAC1PNYKLGKNFT1EGIAVIFKENISPYKFKAHY1KNI
NP_009054936.1 AQVLAA.SADFFTCPPPTTGSTVVRLEPFRAC1PKFNLGRNFT1EGIAVIFKENIAPYKFKRGTV1KDV
AMB16079.1 SGILAE.DGDFYTCPPPTTGSTVVRLEPFRS1CPKFDLGRNFT1EGIAVIFKENIAPYKFKRANVY1KDI
YP_006273012.1 SGILAE.DGDFYTCPPPTTGSTVVRLEPFRS1CPKFDLGRNFT1EGIAVIFKENIAPYKFKRANVY1KDI
YP_002333514.1 SGILAE.DGDFYTCPPPTTGSTVVRLEPFRS1CPKFDLGRNFT1EGIAVIFKENIAPYKFKRANVY1KDI
AII81366.1 SGILAE.DGDFYTCPPPTTGSTVVRLEPFRS1CPKFDLGRNFT1EGIAVIFKENIAPYKFKRANVY1KDI
YP_009176910.1 ITNTEGLNTNFITIGLSTGTDIVRLEPFRS1CPKRYTEDNNYDEGIAVIFKE1DIVPVYVFLTFY1REV
    
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1                      2



AEM64049.1      TT      η2      η3      β16      β17      β18      α3  
                          320      330      340      350      360      370

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AEM64049.1  PFYGLREG.AHGHEHIGYAPGRFQVEHYYPIDLDSRLRASESVTRNFLLTPHFVVAWVWPKTRRV
AAF04615.1  PFYGYREG.SHTEHTSYAADRFKQVDGFFYARDLTTKARATPTTRNLLTTPKFTVAWVWPKRPSV
ADG45133.1  PFYGYREG.SHTEHTSYAADRFKQVDGFFYARDLTTKARATPTTRNLLTTPKFTVAWVWPKRPAV
AAP32845.1  PFYGLRDG.AYREHNSYAMD RFHQVDFGFRDLDTDRALL.EPAARNFLTPHLLTVGNWPKRTEV
YP_003933812.1 PFYGLGED.AHREYNASADRFKQVDFGFRDLDSGETAPEVVRNLLTTPKFTIGDWKPKDPSV
AAD11960.1  PFYGYREG.AHKEHIAYSTDRFKQVENFYLRDLTTKARATNPTTRNMLTTPKFTVGNWVWPKPSV
AGC54689.1  PFYGYRDG.AHKEHIAYSTDRFKQVENFYLRDLTTKARATNPTTRNMLTTPKFTVGNWVWPKPSV
AAD11961.1  PFYGYRDG.AHKEHIAYSTDRFKQVENFYLRDLTTKSRATNPTTRNMLTTPKFTVGNWVWPKPSV
YP_009230158.1 PFYGYRDG.SHAHTAYTADRFQVDGFFPRNLDTGRRAQPTSTYNLLTTPSFTVGNWVWPKRPSV
BAC58067.1  PFYGYRDG.AHAHTAYTADRFQVDGFFYERDLSTGRRASPTATRNLLTTPKFTVGNWVWPKRPSV
AAA85648.1  PFYGYRDG.SHAHTAYTADRFQVDGFFYERDLSTGRRAEAVTRNLLTTPKFTVGNWVWPKRPSV
AAA88010.1  PFYGYRDG.SHGHTAYTADRFQVDGFFYERDLSTGRRAAVTRNLLTTPKFTVGNWVWPKRPSV
BAE47051.1  PFYGYREG.SHTEHTSYAADRFKQVDGFFYARDLTTKARATPTTRNLLTTPKFTVAWVWPKRPAV
YP_009342376.1 AFYGYTGD.SPKEHTSYSNRFRQVEGYRRIIDLTHK.TSESSTTRNFLTTEKYVVAWVWPKKSRV
YP_003084394.1 PFYGYGPTESR.EHNSYSSNRKQLDGYKVMDLDTHR.LASPIKRNFLTTEHYTVGNWVWPKRERV
YP_009046525.1 PFYGYAPPEAAKENMGYAADRFQLDNYFQFLLDTKQKNKLPVSKRNFLTTPQFTVGNWVWPKRERV
NP_073321.1  PFYGTTPDAAAEPMSPYQD RFRQFDSYFPMDLDTRRKLVTVKRNFLTTPHFVVAWVWPKISRIV
YP_001033956.1 PFYGLSPPEAAAEPMGYQDNFKQLDSYFSDLDKRRKASLVKRNFLTTPHFVVAWVWPKTRMIV
NP_077446.1  PFYGLREG.AYKEQSNYAMD RFHQVDFGFRDLDTDRGYM.EPTTRNFLTTPHFVVAWVWPKRTEV
BAM99305.1  PFYGHREE.GKHHEHSSYAPERFKQLEEYQARLDLDTNTHI.KPTTRNFLTTPHFVVAWVWPKLTVN
AAD46114.2  PFYGLREG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
AAD46113.2  PFYGLREG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
AAD46115.2  PFYGLREG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
AFB76670.1  PFYGLREG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
AAD46112.2  PFYGLRDG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
APO15888.1  PFYGLRDG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
ANG65542.1  PFYGLRDG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
AEK27122.1  PFYGLRDG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
CAA92272.1  PFYGLRDG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
YP_009054936.1 PFYGLRDG.AHREHTSYSPDRFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
AMB16079.1  PFYGLRSA.AQLEHNSYAQERFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
YP_006273012.1 PFYGLRAA.ARIEHNSSYAQERFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
YP_002333514.1 PFYGLRAA.ARIEHNSSYAQERFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
AIT81366.1  PFYGLRAA.ARIEHNSSYAQERFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
YP_009176910.1 PFYDRTDE.TKTEHNSYAEERFQVEGYRRIIDLDTKQKNKLPVSKRNFLTTPHFVVAWVWPKRKNV
  
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AEM64049.1      β19      β20      β21      β22      η4      α4  
                          380      390      400      410      420      430      440

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AEM64049.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAF04615.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
ADG45133.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAP32845.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
YP_003933812.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAD11960.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AGC54689.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAD11961.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
YP_009230158.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
BAC58067.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAA85648.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAA88010.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
BAE47051.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
YP_009342376.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
YP_003084394.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
YP_009046525.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
NP_073321.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
YP_001033956.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
NP_077446.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
BAM99305.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAD46114.2  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAD46115.2  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AAD46112.2  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
APO15888.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
ANG65542.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AEK27122.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
CAA92272.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
YP_009054936.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AMB16079.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
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YP_002333514.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
AIT81366.1  CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
YP_009176910.1 CSLAKKREVAEEMLRDESR.GGFRRTARSLSATFVSDGHAFELGRVPLSDCVREEAEAVERVYRER
  
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AEM64049.1

β23      β24      β25      α5

450      460      470      480      490

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AAF04615.1 YNAHIKVGQ.PQYLANGGFLIAYQPLLNTLAEYVREHLREQSRKFPNPTPPP.....

ADG45133.1 YNAHIKVGQ.PQYLANGGFLIAYQPLLNTLAEYVREYMRREQDRKPRNATPAPLR.....

AAP32845.1 YNSSHVRTG.IQTYLARGGFVVFVQPLLSSNLARLYLQELVRENTNHSFPKH.....P

YP\_003933812.1 YNASHVKVG.LQYLANGGFLVVFVQPLLSSNLAEMLYREAEARALEPA.....PL.....

AAD11960.1 YNSTHLRVG.IQYLANGGFVVIAYQPLLSSNLADLYLQELVKEQARRAPEPKQSP.PN.....

AGC54689.1 YNSTHLRVG.IQYLANGGFLIAYQPLLSTSLADLYLQELVIKEQSRKPADPKTPASFN.....

AAD11961.1 YNSTHLRVG.IQYLANGGFLIAYQPLLSTSLADLYLQELVIKEQSRKPTDHKTPVSPN.....

YP\_009230158.1 YNSTHLRVGS.VQYLANGGFLVAYQPLLSSNLADLYVKEELREQGRAKNDSSPR.....

BAC58067.1 YNGTHVKVGQ.VQYLANGGFLIAYQPLLSSNLVLYVRELLREQERRPGD.....AAAT.....

AAA85648.1 YNGTHVKVGQ.VQYLANGGFLIAYQPLLSSNLVLYVRELVREQERRPAG.PGEAAT.....

AAA88010.1 YNGTHVKVGQ.VQYLANGGFLIAYQPLLSSNLVLYVRELVREQTRRPAGGDPGEAAT.....

BAE47051.1 YNAHIKVGQ.PQYLANGGFLIAYQPLLNTLAEYVREYVREQNRKRPDTPPPLR.....

YP\_009342376.1 YADTHIRVGQ.PQTYLANGGFIIIVYQPLLSSNLADMYIKELIVR DGRTDIQNLFARGGNRPFA.RS

YP\_003084394.1 YASTHVKAGA.IEYLANGGFIIAYQPLVVSNTLVKMYVQELTRDNRTDELADLLGAMRG.DKT.RE

YP\_009046525.1 YNETHVLSGT.VEYLANGGFVVFVAYQPLMSRSLASMYIKELIRDNRTDVALDLLSRQSN.PSG.SS

NP\_073321.1 YNDTHVKMGH.VQYFLLGGFVVFVAYQPLVLSKSLAHMYLRELLRDNRTDEMLDLVNNKHA.IIS.NN

YP\_001033956.1 YNDSHVKVGH.VQYFLLGGFVVFVAYQPLVLSKSLAHMYLRELMRDNRTDEMLDLVNNKHA.IYK.KN

NP\_077446.1 YNSSHVRTG.IQTYLARGGFVIVFQPLMSSNLARLYLQELVQTEGTFPKRH.....V

BAM99305.1 YNRTHIKVGP.IQTYLVRGGFVVFVAYQPLVSNLAKLYLREQAMANQTATHVRPKR.....

AAD46114.2 YNGTHVLAGK.TDTYLARGGFVVFVAYQPLLSSNLAKLYLQELARSNRTL DGVLGPRLPAGAAPAG..

AAD46113.2 YNAHVLGA.LETYLARGGFVVFVAYQPLLSSNLAKLYLQELARSNATLGGLFDAAR.....GAP

AAD46115.2 YNGTHVLAGG.LETYLARGGFVVFVAYQPLLSSNLAKLYLQELARSNRTL DGLFFPAGPP.....GPR

AFB76670.1 YNGTHVLSGS.LETYLARGGFVVFVAYQPLLSSNLAKLYLQELARSNGTLEGLFAA.....AAPK

AAD46112.2 AAD46112.2 FNAHVLSSG.LETYLARGGFVVFVAYQPLLSSNLAKLYLQELARSNGTLEGLFAAGGSGAAAAAPK

AP015888.1 FNAHVLSSG.LETYLARGGFVVFVAYQPLLSSNLAKLYLQELARSNGTLEGLFAAGGSGAA.AAAPK

ANG65542.1 YSKTHIQGT.LETYLARGGFIIAYQPLMISNELAKLYINELARSNRTVDLSALLNPSVGTG...Q.

AEK27122.1 YNKTHIQGT.LETYLARGGFIIAYQPLMISNELAKLYINELVRSNRTVDLKSLLNPSVRRG...A.

CAA92272.1 YNKTHIQGT.LETYLARGGFIIAYQPLMISNELAKLYINELARSERIVDLNALLNPSHSVGT...G.

YP\_009054936.1 YESTHVFSG.METYLARGGFVVFVAYQPLLSSNLARLYLNELVRSNRTYDKSILQHSNDV...AS

AMB16079.1 YESTHVFSG.VEYLANGGFLIAYQPLMISNELARLYLNELVRSNRTYDLKLNLLNPNANHN...T.

YP\_006273012.1 YESTHVFSG.VEYLANGGFLIAYQPLMISNELARLYLNELVRSNRTYDLKLNLLNPNANHN...N.

YP\_002333514.1 YESTHVFSG.VEYLANGGFLIAYQPLMISNELARLYLNELVRSNRTYDLKLNLLNPNANHN...N.

ATI81366.1 YESTHVFSG.VEYLANGGFLIAYQPLMISNELARLYLNELVRSNRTYDLKLNLLNPNANHN...N.

YP\_009176910.1 YKDTHLRVNE.TQYLANGGFLIMYQPLIAKSIADLAANO.....K.....

AEM64049.1

500      510      520      530

..AARRARRSPGP.....AGTPEPPAVNGTGHRLRITGSAEFAR

AAF04615.1 ..GASAN..ASVERIKTTSSIEFAR

ADG45133.1 ..EAPSAN..ASVERIKTTSSIEFAR

AAP32845.1 TRNTRSRRSVVPV.....ELRANRTITTTSSVEFAM

YP\_003933812.1 ..P.....TTPAPEAAGSRGTLSTTQSVFAR

AAD11960.1 ..P.....KGPQATNTSAYRMIKTSSIEFAR

AGC54689.1 ..P.....QQ.N.....ERHVIKTTSSIEFAR

AAD11961.1 ..P.....KQ.NEDPKTERHVIKTTSSIEFAR

YP\_009230158.1 ..P.....K.NATEVISITSSVEFAR

BAC58067.1 ..P.....KPSADP.PDVERIKTTSSVEFAR

AAA85648.1 ..P.....GPSADP.PSVERIKTTSSVEFAR

AAA88010.1 ..P.....GPSVDP.PSVERIKTTSSVEFAR

BAE47051.1 ..P.....DAPSAN..ASVERIKTTSSIEFAR

YP\_009342376.1 DNS.....TVNGRNN.....GRGRSS.....TSRSRGRDIDTTSTGNNTIIKTTTTVFAM

YP\_003084394.1 DGRSRHARSVDGGPD.....GLIRGARNIDPYKNYTVRSARVARNADPYKNTTVKRSVMSAQFAM

YP\_009046525.1 GG.....GAA.....GKRKK.....RAAAAVDANKIDENTMIRTTSSAQYAM

NP\_073321.1 AT.....SVS.....RLRRD.....LHRASSGKAILNDSVIRSTASVQFAM

YP\_001033956.1 AT.....SLS.....RLRRD.....IRNAPNRKITLDDTTAKSTSSVQFAM

NP\_077446.1 SNG.RQRR.....SLIVNKTTTSSVEFAM

BAM99305.1 ..SASSL.....PIGGEKGTPAYKITTTGAEFAA

AAD46114.2 ALRRARRAAP.....GGGGAGRVTTVSSAEFAA

AAD46113.2 QGPRRARRSAPAARG.....D.....APEAEAAALERTVSSAEFAA

AAD46115.2 PGPRRARRAAPDEPA.....A.....GGERVTTVSSAEFAA

AFB76670.1 PGPRRARRAAPSAPG.....GPGAANGPAGDGDAGGRVTTVSSAEFAA

AAD46112.2 PVPRRARRASPTPP.....AP.AASGDGDGDANKRVTTVSSAEFAA

AP015888.1 PVPRRARRASPTPP.....AP.AASGGGD.DANKRVTTVSSAEFAA

ANG65542.1 ..RTRRSVPS.....NQHHSRRSTIEG.....GIENVNNSLLKTTSSVEFAM

AEK27122.1 ..RKRRSVEE.....NKRSK.RNIEG.....GIENVNNTIIKTTSSVHFAM

CAA92272.1 ..RKRRSIET.....ETLGRSK.RDVG.....GVQNVNNTLIKTTSSVHFAM

YP\_009054936.1 SEGKRTRRSLLSVAEAVPAAQPS.GGHELHRLRRRAADAATQA.GKDGKDAQLELIKTTSSVEFAM

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YP\_006273012.1 ..TTRRRSLLSIPEPTQDSGHRQILHRLHKRAVEATGTDSSNVTAKQLELIKTTSSVEFAM

YP\_002333514.1 ..NTRRRSLLSVPEPQPTQDGGHREQILHRLHKRAVEATGTDSSNVTAKQLELIKTTSSVEFAM

ATI81366.1 ..NTRRRSLLSVPEPQPTQDGVHREQILHRLHKRAVEATGTDSSNVTAKQLELIKTTSSVEFAM

YP\_009176910.1 PPSRVRREA.....EEPSTGLIESVRTAFLQ

AEM64049.1

α6 α7 β26 β27

540 550 560 570 580 590 600

AEM64049.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
AAF04615.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
ADG45133.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
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BAC58067.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
AAA85648.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
AAA88010.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
BAE47051.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
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NP\_077446.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
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AAD46113.2 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
AAD46115.2 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
AFB76670.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
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APO15888.1 LQFTYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
ANG65542.1 LQFAYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
AEK27122.1 LQFAYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
CAA92272.1 LQFAYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
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AIT81366.1 LQFAYDHIQAHVNDMLGRVIAIAWCELONKDRTEWSEMSRLNPSAVATAALGQRRVSAARMLGDDVMAVTS  
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2

AEM64049.1

β28 β29 β30 β31 β32 β33

610 620 630 640 650

AEM64049.1 RQVEVRRGCVYVQNSMRVPG... ERGT CYSRRLVTFEHN... TGVIEGQGLGDDNELLISRDL  
AAF04615.1 RQVEVRAADNVIVQNSMRVSS... RPGA CYSRRLVTFRYEDQ... GPLVEGQGLGENNLRRLRDA  
ADG45133.1 TQVVPVAPDNVIVQNSMRVSS... RPGT CYSRRLVTFRYEDQ... GPLIEGQGLGENNLRRLRDA  
AAP32845.1 NGPELGS DTRILQNSMRVSG... STTR CYSRRLVTFRYEDQ... SGTVVEGQGLGDDNELLIMSRL  
YP\_003933812.1 TCIAVAPHNVIMQNSMRVPA... RPKT CYARLVTFRYADE... GELIEGQGLGDDNELLIRLEQNN  
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AGC54689.1 TCRPIKA DNVIMQNSMRVPG... KPGT CYSRRLVTFKQEDN... GPLIEGQGLGDDNELLIRLDRS  
AAD11961.1 TCRPIKA DNVIMQNSMRVPG... KPGT CYSRRLVTFKQEDN... GPLIEGQGLGDDNELLIRLDRS  
YP\_009230158.1 TCVAVPA ENVIMQNSMRVPA... KPGT CYSRRLVTFKYADG... GDIVEGQGLGENNLRRLRDA  
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AAA85648.1 TQVVPVAPDNVIMQNSMRVPA... RPGT CYSRRLVTFRYEDG... GPLVEGQGLGDDNELLIRLDRDA  
AAA88010.1 TQVVPVAPDNVIMQNSMRVAA... RPGT CYSRRLVTFRYEAD... GPLVEGQGLGDDNELLIRLDRDA  
BAE47051.1 TQVVPVAPDNVIVQNSMRVSS... RPGT CYSRRLVTFRYEDQ... GPLIEGQGLGENNLRRLRDA  
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YP\_009046525.1 SCIKVRP EDVVLQNSMKVPT... STSS CYSRRLVTLFVSYEAK... QEKVTGQGLGDDNELLIPTRDA  
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YP\_001033956.1 SCTAIDA ESVTLQNSMRVIT... STNT CYSRRLVTLFVSYGEN... QGNIQGLGDDNELLPTLEA  
NP\_077446.1 YGPKLGTDRVVLQNSMRVSG... DSKR CYSRRLVTLFVSYLNT... SGVIEGQGLGDDNELLMLTRNL  
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AAD46114.2 YGRELGA GRVFIENS MRAPG... GAA CYSRRLVTFVAYGNE... SEPLIEGQGLGDDNELLTDRSL  
AAD46113.2 YGHELGA GRVFIENS MRAPG... GAA CYSRRLVTFVAVGNA... SEPVEGQGLGDDNELLTPGREL  
AAD46115.2 YGRELGE GRVFIENS MRAPG... GAA CYSRRLVTFVAFGNE... SEPVEGQGLGDDNELLTPGREL  
AFB76670.1 YGHELGE GRVFIENS MRAPG... GAA CYSRRLVTFVAFGNE... SEPVEGQGLGDDNELLTPGREL  
AAD46112.2 YGHELGE GRVFIENS MRAPG... GAA CYSRRLVTFVAFGNE... SEPVEGQGLGDDNELLTPGREL  
APO15888.1 YGHELGE GRVFIENS MRAPG... GAA CYSRRLVTFVAFGNE... SEPVEGQGLGDDNELLTPGREL  
ANG65542.1 QGVNISS GHVYIQNSMRVVTG... SSTT CYSRRLVTFVFRALND... SEYIEGQGLGENNELLVERKLI  
AEK27122.1 QCVNISG SSVFIQNSMRVLTG... STTT CYSRRLVTFVFRALND... TNYIEGQGLGENNELLVERKLI  
CAA92272.1 QCVNIEG SNVFIQNSMRVVTG... STTT CYSRRLVTFVFRALND... TDYIEGQGLGENNELLVDRKLI  
YP\_009054936.1 QCVKIEG EVVFLQNSMRVTG... DGHS CYSRRLVTFVFRALND... GGTIEGQGLGDDNELLIERKLI  
AMB16079.1 HCAKIEG NVYLLQNSMRSS... DSNT CYSRRLVTFVFRALND... GGTIEGQGLGDDNELLIERKLI  
YP\_006273012.1 HCAKIEG NVYLLQNSMRSM... DSNT CYSRRLVTFVFRALND... GGTIEGQGLGDDNELLIERKLI  
YP\_002333514.1 HCAKIEG NVYLLQNSMRAM... DSNT CYSRRLVTFVFRALND... GGTIEGQGLGDDNELLIERKLI  
AIT81366.1 HCAKIEG NVYLLQNSMRSV... DSNT CYSRRLVTFVFRALND... GGTIEGQGLGDDNELLIERKLI  
YP\_009176910.1 DGLTIPR NNVRLI NSMYITKGNLVGSGV CYSRRLVTVTFGNS... TESLYGHLGENNELLIPYVGLI

1 5



$\beta$ 34                     $\beta$ 35                     $\beta$ 36                     $\beta$ 37                     $\alpha$ 8  
 AEM64049.1            660                    670                    680                    690                    700                    710                    720

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AEM64049.1  I E P C T G N H R R Y F F K L G S G V Y Y E D Y S Y V R M V E V P . . E T I S T R V T L N L T L L E D R E F L P E V Y T R H E I K
AAF04615.1  I E P C T V G H R R Y F F T F G G G V Y Y F E E Y A Y S H Q L S R A D I T T V S T F I D L N I T M L E D H E F V P E V Y T R H E I K
ADG45133.1  L E P C T V S H R R Y F I F G G G V Y Y F E E Y A Y S H Q L S R A D V T T V S T F I D L N I T M L E D H E F V P E V Y T R H E I K
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BAC58067.1  L E P C T V G H R R Y F T F G A G V Y Y F E D Y A Y S H Q L G R A D V T T V S T F I N L N L T M L E D H E F V P E V Y T R Q E I K
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AAD46112.2  V E P C A L N H K R Y F R F G A D V Y Y E N Y A Y V R R V P L A E L E V I S T F V D L N L T V L E D R E F L P E V Y T R A E L A
APO15888.1  V E P C A L N H K R Y F R F G A D V Y Y E N Y A Y V R R V P L A E L E V I S T F V D L N L T V L E D R E F L P E V Y T R A E L A
ANG65542.1  I E P C T V N N K R Y F K F G A D V Y Y F E D Y A Y V R K V P L S E I E L I S A Y V D L N L T L L E D R E F L P E V Y T R A E L E
AEK27122.1  I E P C T A N H K R Y F K F G V D V Y Y F E N Y V Y I R K V P L N E I E M I S A Y V D L N I T L L E D R E F L P E V Y T R A E L E
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BAE47051.1	LSSKVTN...MVLKRRN.K....	TRYSPHNEDEAGDEDEL.....
YP_009342376.1	LTAKLAN...MALRSRKQ....	PKYSKLENSDSDSDEGDF.V.....
YP_003084394.1	LSNHLSN...LRSRS.NG....	KKYSKVEDEYEDGDSADE.TEILVTDREV.....
YP_009046525.1	LADHLTG...LRLRN.KS....	PKYERLRDTGSEDDPDDN.YKDVI.....
NP_073321.1	LSDHLSN...MRLMN.GH....	RKYDKLNDTSETDDEIV.....
YP_001033956.1	LSDHLAK...MRIKN.SN....	PKYDKLPITYSDEDDAV.....
NP_077446.1	LSSRLTQ...LALKNRGK....	SRYSRVSTEDT.GV.....
BAM99305.1	INSRIID...MAMRRRG....	PKYQRLPDTETDVGKQPL.YP.....
AAD46114.2	LANRLTQ...LALQRAR....	PAYQQLPMSDVGGA.....
AAD46113.2	LANRLTQ...LALRRRPP....	PAYQQLPMSDVGGA.....
AAD46115.2	LATRLTQ...LALRRRAP....	PAYQQLPMDVGGGA.....
AFB76670.1	LATRLTQ...LALRRRAP....	PEYQQLPMDVGGGA.....
AAD46112.2	LATRLTQ...LALRRRAP....	PEYQQLPMDVGGGA.....
AP015888.1	LANRLTQ...LALRRRAP....	PAYQQLPMSDVGEP.....
ANG65542.1	LTSHLTN...MALRRRG....	PKYQRLNNDSGDDTETN.LV.....
AEK27122.1	LASHITN...LSLKHG.....	PKYKRLKNVNEVESKV.....
CAA92272.1	LANRVAN...LALKHKG.....	PKYKRLKNMDDENDEV.....
YP_009054936.1	IANHVSN...LALKRG.....	PKYTAVPSEDEAESYTVV.....
AMB16079.1	IASNVSK...LALRRRG....	PKYTRLREDPMSEKVM.....
YP_006273012.1	IASNVSK...LALRRRG....	PKYTRLQONDMEDEKVM.....
YP_002333514.1	IASNVSK...LALRRRG....	PKYTRLQONDMEDEKVM.....
AII81366.1	IASNVSK...LALRRRG....	PKYTRLQONDMEDEKVM.....
YP_009176910.1	KRRNL..PKFLGRFRHR.....	NGYSKLIDEDELTELHEIDDS.SQ.....