

Est_p1 β1 → β2 → β3 → TT →

1 *Est_p1* 1 M ANIANGIOIEYDTFGNPDEPP .
 ACL67850 1 M AITNANGIOIEYDTFGKSGEPA .
 YP_001310323 1 M ARINANGIOIEYETFGKEKNTPT .
 2 10QZ_A 1 S E RTVPSGDVLWSDDFGDPADPA .
 AAA99002 1 P TRMITNDEVTLLWSEGLGDPADAP .
 AAB16939 1 P TRMITKDEVTLLWSEGLGDPADAP .
 3 AAC21862 1 MIFIFISLFAKIFFNY NDDFTNSHVKIMA KSLLNQYFHQVKQTINTPV
 ZP_05914249 1 MTDIASKLIGSTGKR .
 4 CAA37863 1 MLLKRLGLAALFSLSMVGCTTAPNTLAVNTTQKIIQYERSKSDLEVXSLTSLASGDKMYYAENDVTGEP .
 CAA47949 1 MLLKRLCFAALFSLSMVGCTNAPNALAVNTTQKIIQYERNKSDLETKSLTSLASGDKMYYAENGNAVAGEP .

Est_p1 β4 → TT η1 α1 β5 TT TT β6 TT β7 →

1 *Est_p1* 24 LLLIMGLACQIHDEDLCEQLAR RGHYVIRFDMRDTGLSTKFAEAIPDIGOIIEARMKGEEFRPP
 ACL67850 24 LLLIVGLANQIHDEALCQQLAR RGHYVIRFDMRDAGLSTKLAEASIPDIGOIMEARKGEEKIPPP
 YP_001310323 24 ILLIAGNGAQNFPEDPCEMLAK ENLVIRFDMRDAGLSTKFDAAIPDMERYQAQKGKTIINVA
 2 10QZ_A 26 LLLVMGNNLSLGS PDEFARRLADG GLHVIRYDMRDTGRSTTRFAAIPVIDMSPMPYEGFGHKDVF
 AAA99002 26 LLLIAGNNLSKSPDEFVERLVAA GHFVIRYDMRDTGRSSRCFAAIPVIDMSPMPYEGFGHKDVF
 AAB16939 26 LLLIAGNNLSRS PDEFVERLVAA GHFVIRYDMRDTGRSSRCFAAIPVIDMSPMPYEGFGHKDVF
 3 AAC21862 49 LIFIHGLFG DMDNLGVIARAFSEHYSILRIDLRNHGSHF . SE K
 ZP_05914249 49 IVFLHGLFG RGNKFTSIAKALPDYSSLLVLPNHDSEW . TE D
 4 CAA37863 76 LLLIHFGFG NKDNFTRIADKLEGYHLIIPDLLGFGESKPTA D
 CAA47949 76 LLLIHFGFG NKDNFTRIARQLEGYHLIIPDLLGFGESKPTA D
 70 LLLIHFGFG NKDNFTRIARQLEGYHLIIPDLLGFGESKPTA D
 70 LLLIHFGFG NKDNFTRIARQLEGYHLIIPDLLGFGESKPTA D

Est_p1 α2 β8 α3 η2 β9 TTT

1 *Est_p1* 91 YTTEDMADDVAGLLDALEIEKA HVCGMSMGGMIAQTIIGLNHQQRVLSLISITYSHTGNPELPPTPEA
 ACL67850 91 YTTEDMADDVAGLLDALGIEAA HICGMSMGGMIAQTIALNHRQRVLSLISITYSHTGNPELPPEKPEA
 YP_001310323 91 YTTEDMADDVAGLLDALNIKKA HICGMSMGGMIAQVFAYKHPSPRIYLSISMSTGNPNPNSPET
 2 10QZ_A 75 YGFDLAADAVAVLDGQVORA HVVGLSMGATITQVIALDHHRDLSLTMMLGGGLDQDFDANIERY
 AAA99002 75 YGFDLAADALAVLDGQVRAA HVGVMGSGNTIGQLLADAPERILLTVMLGGLADVDQDFDLEAA
 AAB16939 75 YGFDLAADALAVLDGQVRAA HVGVMGSGNTIGQLLADAPERILLTVMLGGLADVDQDFDLEAA
 3 AAC21862 92 MNVYMDAEDVIAVIRHLNLSKV ILTHGMSGKKVAMKITALCPLEKVIDMSPMPYEGFGHKDVF
 ZP_05914249 95 FSYYVMDASVAAAMIAEMTAPDDLPVHLVHSGSGGKAVMVALRHPLELDRLVVVDIAPT AGGSLGVF
 4 CAA37863 114 YRADAQATRLHHELMQAKGLASN THVGNSMGGAISVAYAAKYPKEIKSLWLVD . TAGFWSAGVPKSL
 CAA47949 114 YRSEARQATRLHELLQAKGLASN IHVGNSSMGGAISVAYAAKYPKDVLSLWLVD . SAGFWSAGIPKSL

Est_p1 α4 α5

1 *Est_p1* 158 LEVLT P PPMEREANITYTLDVWRTFSGKFLPDEEDWNKIAAKAYDRAFY
 ACL67850 158 LEVLT R PPEERQANIEYALKVFRITLSGSFLPDEEWHNIAAAQAYDRAFY
 YP_001310323 158 LKLVTA M PPNGRDAYINITYLRMWNKLSWFLPEEREAIRYTESYDRSYY
 2 10QZ_A 142 MRGEPTLDGLPGPQFLDALALMNQPAEGRAAEVAKRVSKWRILSGTVFPFDDAEYARWEERAIDHAGG
 AAA99002 142 LKGEPSVSLGPVPSRRLDMMTMLLQQAETDEELLERRVEKRWLLNGEVPFDDAEFRRLLEAAGHAG .
 AAB16939 142 LKGEPSVSLGPVPSRRLDMMTMLLQQAETDEELLERRVEKRWLLNGEVPFDDAEFRRLLEAAGHAG .
 3 AAC21862 159 NGFLFAVNKAKPENRQAKPTLK QEINDEDVQFMKSFDM SADCFRNLTLFNNYA
 ZP_05914249 126 EHLLS L AELDLDEIESRSGANETLEAKIPEDTIRGFLQLNLRITTSAGY
 4 CAA37863 181 GATLEN N PLLINSKEDFYKMYDFVMY KPPYLPKSKVAFQERINNKA
 CAA47949 181 GATLEN N PLLIKSNEDFYKMYDFVMY KPPYLPKSKVAFQERINNKE

Est_p1 η3 η4 β10 α6 β11

1 *Est_p1* 209 PEG VARQMAAVLTQKNRKFELGSVTPTLVIHGADDP LVPVEGGKDTAEAIPIGAEIIIDGWMGHDL
 ACL67850 209 PEG VARQLAAVLQTKNKRSELGSCVPTLVIHGADDL LVPVEGGKDTAAVPIGAEIIIDGWMGHDL
 YP_001310323 209 PQG AVRQMAAVLVANGDRQHLSLLTVP LVIHGTADPLFPVEAGKDTARTIPNKAAGLIIIDGWMGHDL
 2 10QZ_A 212 VLA EPYAHVSLTLPPPSRAAELEVTVP LVIQAEHDPITAPAPHGKHLAGLIPTRALAEIPGMGHAL
 AAA99002 211 TFD EPTVHHMIPLPVPSRGAELSRVTP LVAIQAMCDPAAPPHARHLANRIPGARVVEIENMGHAL
 AAB16939 211 TFD EPTVHHMIPQPPVSRGAELARITTP LVAIQAMCDPAAPPHARHLANRIPGARVVEIENMGHAL
 3 AAC21862 217 NIM DWEKRVFTPT FIKGMSGKSYIKENSEKILEQPNATFTINGGHWV
 ZP_05914249 175 AWQPNLTLHESLPTDGVDFPMGEASFDGVPWMAGENSVDVDELDPLMRSLPRATLLTVKSGSHWV
 4 CAA37863 229 L DTKTLEQVTDNVNEERAKITAKYNIPTLVVWGDKDQVIKPETTELKEIIPQAGVIMNEDGHVP
 CAA47949 229 L DAKTLEQVTDNVNEERAKITAKYNIPTLVVWGDKDQVIKPETTELKEIIPQAGVIMNEDGHVP

Est_p1 α7

1 *Est_p1* 276 HGGAIPQIVDQIVNHTQKIFI
 ACL67850 276 HAGAIPQIIDIIVGHHTKAAARPKSRS
 YP_001310323 276 KGTGTCVIEAIALNVDTS
 2 10QZ_A 279 PSSVNGPLAEVILAHTRSA
 AAA99002 278 PLAVNEPLAAAIKAHTRAATV
 AAB16939 278 PLAVNEPLAAAIKAHTRAATV
 3 AAC21862 269 HAEKDFVIRAIKRLFNKN
 ZP_05914249 244 HSEQKTFISALQTFESRD
 4 CAA37863 295 MVEAKDTANDYKAF RDGLKK .
 CAA47949 295 MVEADETANDYKAF RSTLEAQR .