**S4 Fig. Sequence alignment of phenylalanine ammonia-lyase (PAL) proteins from *E. pseudowushanense* and various other plants, and phylogenetic relationships of phenylalanine ammonia-lyase (PAL) proteins from *E. pseudowushanense* and various other plants.**

\* 20 \* 40 \* 60 \* 80 \* 100   
P45726.pro : MDSTTAIG-----NGVGSGGSPGFCLK------------DPLNWGVAAEAMKGSHLEEVKGMVEEFRKPVVRLGGETLTISQVAAIAVR-G--SE-VAVE : 79  
O64963.pro : MATNSIKQNG---HKNGSVELPELCIKK-----------DPLNWGVAAETLKGSHLDEVKRMVAEYRKPVVKLGGESLTISQVAAIATHDS---G-VKVE : 82  
Q42667.pro : MELSHETCNGIKNDRNGGTSSLGLCTG-T----------DPLNWTVAADSLKGSHLDEVKRMIDEYRRPVVKLGGESLTIGQVTAIAAHDS---G-VKVE : 85  
P45729.pro : MAYVNG-TT----NGHANGNGLDLCMKKE----------DPLNWGVAAEALTGSHLDEVKRMVAEYRKPVVKLEGETLTISQVAAISARDD--SG-VKVE : 82  
P45730.pro : METVTKNG-----YQN--GSLESLCVNQR----------DPLSWGVAAEAMKGSHLDEVKRMVADYRKPVVKLGGETLTIAQVASIAGHDT---GDVKVE : 80  
P24481.pro : MENGNGATT----NGHVNGNGMDFCMKTE----------DPLYWGIAAEAMTGSHLDEVKKMVAEYRKPVVKLGGETLTISQVAAISARDG--SG-VTVE : 83  
P35513.pro : MAG-VA---------QNGHQEMDFCMK-V----------DPLNWEMAADSLKGSHLDEVKKMVAEFRKPVVKLGGETLTVAQVAAIAAKDN-VKT-VKVE : 77  
O23865.pro : MDCENK--------NVVLGNG--LCMQK-----------DPLNWGMAAEALTGSHLDEVKRMVAEFRKPMVQLGGETLTVSQVAAIAAG-----S-VKVE : 73  
P25872.pro : MASNGH---------VNGGENFELCKKSA----------DPLNWEMAAESLRGSHLDEVKKMVSEFRKPMVKLGGESLTVAQVAAIAVRDKSANG-VKVE : 80  
P45728.pro : MENGNGAIT----NGHVNGNGMDFCMKTE----------DPLYWGIAAEAMTGSHLDEVKKMVAEYRKPVVKLGGETLTISQVAAISARDG--SG-VTVE : 83  
TR2108|c0\_ : MATTTTTVH----HQNGNGSIDGLCMKS-----------DPLNWGLAAESLQGSHLDEVKRMVNEFHKPIVKLEGQSLTISQVAAVAMR-G--DG-IEIE : 81  
P27991.pro : MEATNG-------HQN-----GSFCLSTAKGN----N--DPLNWGAAAEAMKGSHLDEVKRMVAEYRKPVVRLGGETLTIAQVAAVAGHDH---G-VAVE : 78  
O49835.pro : METIVE---------NGNGKTMEFCMK------------DPLNWEMASESMKGSHLDEVKNMVAEFRKPVVQLAGKTLTIGQVAAIAARDD---G-VTVE : 75  
P45734.pro : MEVVAAAI-----LKNNINDYDSFCLTHANANNMKVNAADPLNWGVAAEAMKGSHLDEVKRMVEEYRKPVVRLGGETLTISQVAAIAAHD----G-ATVE : 90  
Q01861.pro : METVAAAI-----TKN--NGYESFCVTNAKNNNMKVNSADPLNWGVAAEAMKGSHLDEVKRMVEEYRKPVVRLGGETLTISQVAAIAAHDH---G-VKVE : 89  
TR575|c1\_g : ----MGSLV----QEN---SIA-LCLNK-----------DPLNWNMAAESMKGSHLDEVKRMVEEYRKGVVRLGGESLTISQVAAIASH-D--QG-VKVE : 73  
 m C DPLnW Aae 6 GSHLdEVK M6 e5r4p6V LgG 3LT6 QVaa6a g 6E   
   
 \* 120 \* 140 \* 160 \* 180 \* 200   
P45726.pro : LSESAREGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKEGGALQKELIRFLNAGIFGNGTES-CHTLPQSATRAAMLVRINTLLQGYSGIRFEILE : 178  
O64963.pro : LSESARAGVKASSDWVMDSMSKGTDSYGVTTGFGATSHRRTKQGAALQKELIRFLNAGVFGSTKES-GHTLPHQATRAAMLVRINTLLQGYSGIRFEILE : 181  
Q42667.pro : LAEAARAGVKASSDWVMDSMMKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNSGIFGNGTES-SHTLPHSATRAAMLVRVNTLLQGYSGIRFEILE : 184  
P45729.pro : LSEEARAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGSGAEAGNNTLPHSATRAAMLVRINTLLQGYSGIRFEILE : 182  
P45730.pro : LSESARPGVKASSDWVMDSMDKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTET-CHTLPHSATRAAMLVRINTLLQGYSGIRFEILE : 179  
P24481.pro : LSEAARAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGSD---NTLPHSATRAAMLVRINTLLQGYSGIRFEILE : 180  
P35513.pro : LSEGARAGVKASSDWVMDSMGKGTDSYGVTTGFGATSHRRTKNGGALQKELIRFLNAGVFGNGTES-CHTLPQSGTRAAMLVRINTLLQGYSGIRFEILE : 176  
O23865.pro : LAESARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGSGNDS-SNILPHSATRAAMLVRINTLLQGYSGIRFEILE : 172  
P25872.pro : LSEEARAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKNGGALQKELIRFLNAGVFGNGTET-SHTLPHSATRAAMLVRINTLLQGYSGIRFEILE : 179  
P45728.pro : LSEAARAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGSD---NTLPHSATRAAMLVRINTLLQGYSGIRFEILE : 180  
TR2108|c0\_ : LSESARAGVKASSDWVMDSMSKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGVFGNGTES-THTLPQTATRAAMLVRINTLLQGYSGIRFEIME : 180  
P27991.pro : LSESAREGVKASSEWVMNSMNNGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTES-SHTLPHTATRAAMLVRINTLLQGYSGIRFEILE : 177  
O49835.pro : LAEAAREGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTET-SHTLPHSATRAAMLVRINTLLQGYSGIRFEILE : 174  
P45734.pro : LSESARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTES-NHTLPHTATRAAMLVRINTLLQGYSGIRFEILE : 189  
Q01861.pro : LSESARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTES-SHTLPHTATRAAMLVRINTLLQGYSGIRFEILE : 188  
TR575|c1\_g : LNESSRAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTNQGGALQKELIRFLNAGVFGNGTET-SHTLPHSATRAAMLVRINTLLQGYSGIRFEILE : 172  
 L E aR GVKASSdWVM SM kGTDSYGVTTGFGATSHRRTk GgALQKELIRFLNaG6FGng e tLPh aTRAAMLVR6NTLLQGYSGIRFEI6E   
   
 \* 220 \* 240 \* 260 \* 280 \* 300   
P45726.pro : AISKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRHNSKAVGPTGEILHPKEAFRLAGVEGGFFELQPKEGLALVNGTAVGSGLASMVLFEANILA : 278  
O64963.pro : VITKFLNNNVTPCLPLRGTITASGDLVPLSYIAGMLTGRPNSKAVGPDGQTLSAAEAFEFVGINSGFFELQPKEGLALVNGTAVGSGLASTVLFDTNILA : 281  
Q42667.pro : TITKFLNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGSNGQVLNPTEAFNLAGVTSGFFELQPKEGLALVNGTAVGSGLAATVLFEANILA : 284  
P45729.pro : AITKFLNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGVTLSPEEAFKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFEANILA : 282  
P45730.pro : AITRLLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKATGPTGEVLDAAEAFKAAGIESGFFELQPKEGLALVNGTAVGSGLASMVLFETNVLA : 279  
P24481.pro : AITKFLNQNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGVILSPEEAFKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFEANILA : 280  
P35513.pro : AITKLLNHNVTPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPNGETLNAEEAFRVAGVNGGFFELQPKEGLALVNGTAVGSGLASMVLFDANVLA : 276  
O23865.pro : AITKFLNQNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGENLTAAEAFKLAGVDGGFFELQPKEGLALVNGTAVGSGMASMVLFETNILA : 272  
P25872.pro : AITKLINSNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPNGETLNAEEAFRVAGVNGGFFELQPKEGLALVNGTAVGSGMASMVLFDSNILA : 279  
P45728.pro : AITKFLNQNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGVILSPEEAFKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFEANILA : 280  
TR2108|c0\_ : AITKFLNNNITPCLPLRGTITASGDLVPLSYIAGILTGRPNSKAVGPKGEALTAQEAFNLAGIETGFFELQPKEGLALVNGTAVGSGLASMVLFDANILA : 280  
P27991.pro : AITKLLNNNVTPCLDLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPSGEVLNAKEAFELASINSEFFELQPKEGLALVNGTAVGSGLASMVLFEANILA : 277  
O49835.pro : AITKFLNTNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEKINAEEAFRLAGISTGFFELQPKEGLALVNGTAVGSGMASMVLYEANILA : 274  
P45734.pro : AITKLLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRSNSKAHGPSGEMLNAKEAFQLAGINAEFFELQPKEGLALVNGTAVGSGLASIVLFEANILA : 289  
Q01861.pro : AITKLINNNVTPCL-LRGTITASGDLVPLSYIAGLLTGRPNSKAHGTSGEILNAKEAFQSAEINDGFFELQPKEGLALVNGTAVGSGLASIVLFEANILA : 287  
TR575|c1\_g : AITKFLNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPKGEPLNAQEAFTLAGIDTGFFELQPKEGLAMVNGTAVGSGLASMVLFEANILA : 272  
 aI34 6N N6TPCLpLRGTITASGDLVPLSYIAG6LTGRpNSKAvGp G 6 EAF ag6 gFFELQPKEGLA6VNGTAVGSG6As VL5 N6LA   
   
 \* 320 \* 340 \* 360 \* 380 \* 400   
P45726.pro : VLSEVLSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAQKLHEMDPLQKPKQDRYALRTSPQWLGPLIEVIRSSTKSIEREINS : 378  
O64963.pro : LLSEILSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAKKLHEQDPLQKPKQDRYALRTSPQWLGPQIEVIRYSTKSIEREIDS : 381  
Q42667.pro : IMSEVLSAIFAEVMNGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAQKLHETDPLQKPKQDRYALRTSPQWLGPQIEVIRAATKMIEREINS : 384  
P45729.pro : VLAEVMSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSPQWLGPQIEVIRSSTKMIEREINS : 382  
P45730.pro : VLSELLSAIFAEVMNGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYMKAAKKLHETDPLQKPKQDRYALRTSPQWLGPQIEVIRFSTKSIEREINS : 379  
P24481.pro : VLAEVMSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSPQWLGPQIEVIRSSTKMIEREINS : 380  
P35513.pro : VFSEVLSAIFAEVMNGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAQKLHETDPLQKPKQDRYALRTSPQWLGPQIEVIRSATKMIEREINS : 376  
O23865.pro : VLAEVMSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAEKQHEMDPLQKPKQDRYALRTSPQWLGPQIEVIRSSTKMIEREINS : 372  
P25872.pro : VMSEVLSAIFAEVMNGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAQKLHEMDPLQKPKQDRYALRTSPQWLGPQIEVIRAATKMIEREINS : 379  
P45728.pro : VLAEVMSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSPQWLGPQIEVIRSSTKMIEREINS : 380  
TR2108|c0\_ : LLSEVISAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKSAQKLHETDPLQKPKQDRYALRTSPQWLGPLIEVIRFSTKSIEREINS : 380  
P27991.pro : VLSEVLSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYMKAAKKLHEIDPLQKPKQDRYALRTSPQWLGPLIEVIRFSTKSIEREINS : 377  
O49835.pro : VLSEVISAIFAEVMNGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSGYVKAAQKLHEMDPLQKPKQDRYALRTSPQWLGPQIEVIRSATKMIEREINS : 374  
P45734.pro : VLSEVLSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILHGSAYVKDAKKLHEMDPLQKPKQDRYALRTSPQWLGPLIEVIRFSTKSIEREINS : 389  
Q01861.pro : VLSEVLSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYVKAAKKLHEMDPLQKPKQDRYALRTSPQWLGPLIEVIRFSTKSIEREINS : 387  
TR575|c1\_g : VLSEVISAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILTGSSYVKAAEKLHEMDPLQKPKQDRYALRTSPQWLGPLIEVIRSSTKSIEREINS : 372  
 6 E66SAIFAEVM GKPEFTDHLTHKLKHHPGQIEAAAIMEHILdGS Y6KaA KlHE DPLQKPKQDRYALRTSPQWLGP IEVIR TK IEREI1S   
   
 \* 420 \* 440 \* 460 \* 480 \* 500   
P45726.pro : VNDNPLINVSRNKALHGGNFQGTPIGVSMDNTRLAVASIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHV : 478  
O64963.pro : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIASIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHV : 481  
Q42667.pro : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIASIGKLMFAQFSELVNDFYNNGLPSNLTGGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHV : 484  
P45729.pro : VNDNPLIDVSRNKAIHGGNFQGSPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHV : 482  
P45730.pro : VNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNVRLAIASIGKLLFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTTHV : 479  
P24481.pro : VNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHV : 480  
P35513.pro : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNARLALASIGKLMFGQFSELVNDYYNNGLPSNLTAGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHV : 476  
O23865.pro : VNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLGNPVTNHV : 472  
P25872.pro : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNARLALASIGKLMFAQFSELVNDYYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHV : 479  
P45728.pro : VNDNPLIDVSRNKAIHGGNFQGTPIGMSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHV : 480  
TR2108|c0\_ : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASIGKLLFAQFSELVNDLYNNGLPSNLSGGRNPSLDYGMKGAEIAMASYCSELQFLANPVTNHV : 480  
P27991.pro : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASIGKLMFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTTHV : 477  
O49835.pro : VNDNPLIDVSRNKALHGGNFQGTPIGVAMDNTRLAIASIGKLLFAQFSELVNDYYNNGLPSNLTGSRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHV : 474  
P45734.pro : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASIGKLLFAQFSELVNDFYNNGLPSNLSASRNPSLDYGFKGSEIAMASYCSELQYLANPVTTHV : 489  
Q01861.pro : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASIGKLLFAQFSELVNDFYNNGLPSNLSASRNPSLDYGFKGSEIAMASYCSELQYLANPVTTHV : 487  
TR575|c1\_g : VNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIGSIGKLLFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLSNPVTNHV : 472  
 VNDNPLI1VSRNKA6HGGNFQG3PIG6sMDNtRLA6a IGKL6FaQFSELVND YNNGLPSNL3 RNPSLDYGfKGaEIAMAsYCSELQ5LaNPVT HV   
   
 \* 520 \* 540 \* 560 \* 580 \* 600   
P45726.pro : QSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSTYLVALCQAVDLRHFEENLRNTVKSTVSQVAKRVLTMGVNGELHPSRFCEKDLLRVVDREYIFAYID : 578  
O64963.pro : QSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSTFLVALCQAIDLRHLEENLRNTVKNTVSQVAKRTLTTGVNGELHPSRFCEKDLLKVVDREYVFAYID : 581  
Q42667.pro : QSAEQHNQDVNSLGLNSSRKTAEAVDILKLMSSTFLVALCQAIDLRHLEENLKNTVKNTVSQVAKRVLTMGVNGELHPSRFCEKDLIKVVDREYVFAYID : 584  
P45729.pro : QSAEQHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSQVAKRVLTMGVNGELHPSRFCEKDLLRVVDREYIFAYID : 582  
P45730.pro : QSAEQHNQDVNSLGLISSRKTAEAVDILKLMSTTFLVALCQAIDLRHLEENLKSAVKNTVSQVSKRVLTTGANGELHPSRFCEKELLKVVDREYVFAYVD : 579  
P24481.pro : QSAEQHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSSVAKRVLTMGVNGELHPSRFCEKDLLRVVDREYIFAYID : 580  
P35513.pro : QSAEQHNQDVNSLDLISARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLRNAVKNTVSQVAKRTLTMGTNGELHPSRFCEKDLLRVVDREYVFAYAD : 576  
O23865.pro : QSAEQHNQDVNSLGLISSRKTAEAVEILKLMSTTFLVGLCQAVDLRHLEENLKSTVKNTVSQVAKKVLTMGVNGELHPSRFCELDLLRVVDREYIFAYID : 572  
P25872.pro : QSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLKNAVKNTVSQVAKRTLTMGANGELHPARFCEKELLRIVDREYLFAYAD : 579  
P45728.pro : QSAEQHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSSVAKRVLTMGVNGELHPSRFCEKDLLRFVDREYIFAYID : 580  
TR2108|c0\_ : QSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSTFLVGLCQAIDLRHLEENLKSAVKSTVSQVAKKVLTMGVNGELHPSRFCEKDLLQVVDREYVYAYID : 580  
P27991.pro : QSAEQHNQDVNSLGLISSRKTNEAIEILKLMSSTFLIALCQAIDLRHLEENLKNSVKNTVSQVSKRILTTGVNGELHPSRFCEKDLLKVVDREYIFSYID : 577  
O49835.pro : QSAEQHNQDVNSLGLISSRKTSEAVEILKLMSSSFLVALFQAVDLRHIEENVRLAVKNTVSQVAKRTLTTGVNGELHPSRFSEKDLLRVVDREYVFAYAD : 574  
P45734.pro : QSAEQHNQDVNSLGLISSRKTKEAIEILQLMSSTFLIALCQAIDLRHLEENLKNSVKNTVSQVAKKTLTIGVSGELHPSRFCEKDLLKVVDREHVFSYID : 589  
Q01861.pro : QSAEQHNQDVNSLGLISSRKTYEAIEILQLMSSTFLIALCQAVDLRHLEENLKNSVKNIVSQVAKRTLTTGVNGELHPSRFCEKDLLRVVDREHVFAYID : 587  
TR575|c1\_g : QSAEQHNQDVNSLGLISSRKTAESVEILKLMSSTFLVGLCQAIDLRFMEENLRSCVKSTVSQVAKKVLTMGVNGELHPSRFCEKDLLKVIDREYIFAYID : 572  
 QSAEQHNQDVNSLgLiSsRKT Ea6 ILkLMS335L6 LcQA6DLRh EEN64 VKntVSqVaK4 LT GvnGELHPsRFcEkdL6 6DREy65aY D   
   
 \* 620 \* 640 \* 660 \* 680 \* 700   
P45726.pro : DPCSATYPLMQKLRQVLVEHALKNGESEKNLSTSIFQKIRAFEEEIKTLLPKEVESTRAAIENGNSAIPNRIKECRSYPLYKFVREELGTELLTGEKVRS : 678  
O64963.pro : DPCSATYPLMQKLRQVLVEHALTNGENEKNASTSIFQKIVAFEEELKVLLPKEVDSARAALDSGSAGVPNRITECRSYPLYKFVREELGAEYLTGEKVRS : 681  
Q42667.pro : DPCSASSPLMQKLRQVLVDHALDNGDREKNSTTSIFQKIGAFEDELKTLLPKEVEIARTELESGNAAIPNRIKECRSYPLYKIVREDIGTSLLTGEKVRS : 684  
P45729.pro : DPCSATYPLMQKLRETLVEHALNNGDKERNLSTSIFQKIAAFEDELKALLPKEVETARAALESGNPAIPNRIKECRSYPLYKFVREELGTEYLTGEKVRS : 682  
P45730.pro : DPCSATYPLMQKLRQVFVDHALENGENEKNFSTSVFQKIEAFEEELKALLPKEVESARAAYDSGNSAIDNKIKECRSYPLYKFVREELGTVLLTGEKVQS : 679  
P24481.pro : DPCSATYPLMQKLRQTLVEHALKNGDNERNLSTSIFQKIATFEDELKALLPKEVESARAALESGNPAIPNRIEECRSYPLYKFVRKELGTEYLTGEKVTS : 680  
P35513.pro : DACSANYPLMQKLRQVLVDHALQNGENEKNANSSIFQKILAFEDELKAVLPKEVESARAALESGNPAIANRIKECRSYPLYRFVRGELGAELLTGEKVRS : 676  
O23865.pro : DPCSATYPLMQKLRQVLVEHALKNGETEKNLSTSIFQKIAAFEDELKALLPKEVESARAVVESGNPAIPNRIKECRSYPLYKFIREELGTVYLTGEKVTS : 672  
P25872.pro : DPCSCNYPLMQKLRQVLVDHAMNNGESEKNVNSSIFQKIGAFEDELKAVLPKEVESARAALESGNPAIPNRITECRSYPLYRFVRKELGTELLTGEKVRS : 679  
P45728.pro : DPCSATYPLMQKLRQTLVEHALKNGDNERNMNTSIFQKIATFEDELKALLPKEVESARAALESGNPAIPNRIEECRSYPLYKFVRKELGIEYLTGEKVTS : 680  
TR2108|c0\_ : DPCSAVYPLMQKLRQVLVEHALSNGENEKNSSTSIFQKISLFEEELKLLLPKEVESARSAVESDNAAIPNQIKDCRSYPLYRFIRGELGTALLTGEKVVS : 680  
P27991.pro : DPCSATYPLMQKLRQVLVDHALVNAECEKDVNSSIFQKIAIFEEELKNLLPKEVEGARAAYESGKAAIPNKIQECRSYPLYKFVREELGTGLLTGEKVRS : 677  
O49835.pro : DPCLTTYPLMQKLRETLVGHALDNGENEKDVNTSIFHKIAIFEEELKAILPKEVENARASVENGIPAISNRIEECRSYPLYKFVREELGTELLTGEKVRS : 674  
P45734.pro : DPCSATYPLAQKLRQVLVDHALVNGESEKNSNTSIFQKIATFEEELKTLLPKEVESARTAYENGNSTIANKINGCRSYPLYKFVREELGTSLLTGERVIS : 689  
Q01861.pro : DPCSATYPLMQKLRQVLVDHALVNGESEKNLNTSIFQKIATFEDELKTLLPKEVESTRAAYESGNPTVPNKINGCRSYPLYRFVRQELGTGLLTGEKVIS : 687  
TR575|c1\_g : DPCSATYPLMQKLRQVLVDHALLNGQNEKDLNTSIFQKISTFEEELKALLPKEVESMRTAIESGNPLIPNRIKECRSYPLYKFVREELGTELLTGEKVRS : 672  
TR575|c1\_g : DpCsa yPLmQKLR2 lV HA6 Ng E41 3S6FqKI FE E6K 6LPKEVe aR a esgn 6 N I eCRSYPLY4f6R e6Gt LTGE4V S   
   
 \* 720 \*   
P45726.pro : PGEEFDKVFTALCKGEMIDPLMDCLKEWNGAPLPIC-- : 714  
O64963.pro : PGEECDKVFTAICEGKIIDPILDCLEGWNGAPLPIC-- : 717  
Q42667.pro : PGEEFDKVFTAMCEGKLIDPMLECLKEWNGAPLPICQN : 722  
P45729.pro : PGEEFEKVFTAMSKGEIIDPLLECLESWNGAPLPIC-- : 718  
P45730.pro : PGEEFDKVFTAMCQGKIIDPMLECLGEWNGSPLPIC-- : 715  
P24481.pro : PGEEFEKVFIAMSKGEIIDPLLECLESWNGAPLPIC-- : 716  
P35513.pro : PGEECDKVFTAMCNGQIIDSLLECLKEWNGAPLPIC-- : 712  
O23865.pro : PGEEFDKVFTAMSKGEIIDPLLACLESWNGAPLPIA-- : 708  
P25872.pro : PGEECDKVFTAMCNGQIIDPMLECLKSWNGAPLPIC-- : 715  
P45728.pro : PGEEFDKVFIAMSKGEIIDPLLECLESWNGAPLPIC-- : 716  
TR2108|c0\_ : PGEEIDKVFTAMCEGKLIDPLLECLKEWNGAPLPIC-- : 716  
P27991.pro : PGEEFDKLFTAMCQGKIIDPLMECLGEWNGAPLPIS-- : 713  
O49835.pro : PGEELDKVFTAMCEGKLVDPLLACLEAWNGAPLPIC-- : 710  
P45734.pro : PGEECDKLFTAMCQGKIIDPLLKCLGEWNGAPLPIC-- : 725  
Q01861.pro : PGEECDKLFTAICQGKIIDPLLQCLGDWNGAPLPIS-- : 723  
TR575|c1\_g : PGEEIDKVFTAICQGKLIDPLLACVSEWNGSPLPIC-- : 708  
 PGEE dK6FtA6 G 66Dp66 C6 WNGaPLPIc

