

logo

NTDB id 1284 ACE17W RS12370 WP 010946666.1  
 NTDB id 1257 GC085 RS04855 WP 163621000.1  
 NTDB id 1408 DSB67 RS13980 WP 010643500.1  
 NTDB id 407241 GPY20 RS11650 WP 233976036.1  
 NTDB id 1186 GTF74 RS01320 WP 000788426.1  
 NTDB id 1175 A1552VC RS12105 WP 000788426.1  
 NTDB id 1193 PAKAF RS26665 WP 003161249.1  
 NTDB id 1009 ACIAD RS15175 WP 004923730.1  
 consensus

MRKIIAILILI..SASLSMAYSKDNSLISVKVLPLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDLFISTDMQIPSDQ 78  
 MRKIIAILILI..SASLSLAYSKDNSLISVKVLPLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDLFISTDMQIPSDQ 78  
 ..... 0  
 ..... 0  
 ..... 0  
 MNSGLSRLGIALAA.MFAPALLAADLEKLDVAALPGDRVELKLFDEPVA.APRGYTIEQPARIALDLPGVQNKLGTT.. 76  
 MKQIIRQFSIGTVAYAIMQVASAQVAITNVVPMNIPGGQTEIRVMFNGLPP.QPQAYQLEQPARLILDFDKAGQKLA.. 77

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 consensus

KTKTIQLGSLHSYNIVAVGDRVRAI...LELDRSVSYSGSTAGSYSLVINGKSNLDFENSKEVFIT.....NQV 145  
 KTKTIQLGSLHSYNIVAVGDRVRAI...LELDRSVSYSGSTAGSYSLVINGKSNLDFENSKEVFIT.....NQV 145  
 .....MKMRHGLTLTPRKLTLGFLSFLWFL...LL...A.PFVA.....AE 33  
 .....MIKGLNA..STAWGIRCLFVGA...CLLLSA.ATL.....AQ 31  
 .....MKNGLKT..YVAQTWLTWVGL...ALCASS.MVFS.....AE 32  
 .....MKNGLKT..YVAQTWLTWVGL...ALCASS.MVFS.....AE 32  
 KNRELSVGNTRSVTVVEAKDRTRLI...INLTTLSYTTIRVEGNLFFVVGNPAGASVASTAPVKASPAPASYAQPIKPKPY 156  
 SLIPVTTNEASSIDVSSDDKRARVV...VNLKDAAGAF...TTRVEGNVFILKINNIQSTATP.....VAT...SA..... 138

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VAAANQKN|DFR...NKKAGWVYVELSSP...SAYVDVQV...GLVLEL...LKT...KYPD...LLYRLDV...DF...STP...VESY...EVEFR...G...S...T  
 VNAKHEIKRIDFRGIEKQGGRRVLIDVSDTGIPIDVTQVVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV 225  
 VNAKHEIKRIDFRGIEKQGGRRVLIDVSDTGIPIDVTQVVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV 225  
 EVQSNLSKSIDFRINKDKDAVIVVELVSPAAIVDIKRVQEGLSIDLLNLSVKKDDQLYLLDVKDFSTVVESVEVFRDRTSTT 113  
 ESAANQLKNIDFRINKDKAAVLIVELASASAVVDVQKTEQGLNIELLKTIDVSDDKLYLLDVRDFATAVENIEVFRQRPST 111  
 SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKQVQEGLSIELLKTIDVADDKLYLLDVKDFSTPVESVEVFRKEPST 112  
 SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKQVQEGLSIELLKTIDVADDKLYLLDVKDFSTPVESVEVFRKEPST 112  
 VPAGRAIRNIDFRQGEKGEKNVIDLSDPTLSPDIQEQQGKIRLDFAKTQLP DALRVRLDVKDFATPVQFVNASASQSDRT 236  
 PAPQGIIGNIGFQRGAQGEGLVVIDLQGTNTPTVDVQQQGSKVVVRFPGIKIPHTLARRLNTTDFATPVASIDSYNDGNSG 218

logo

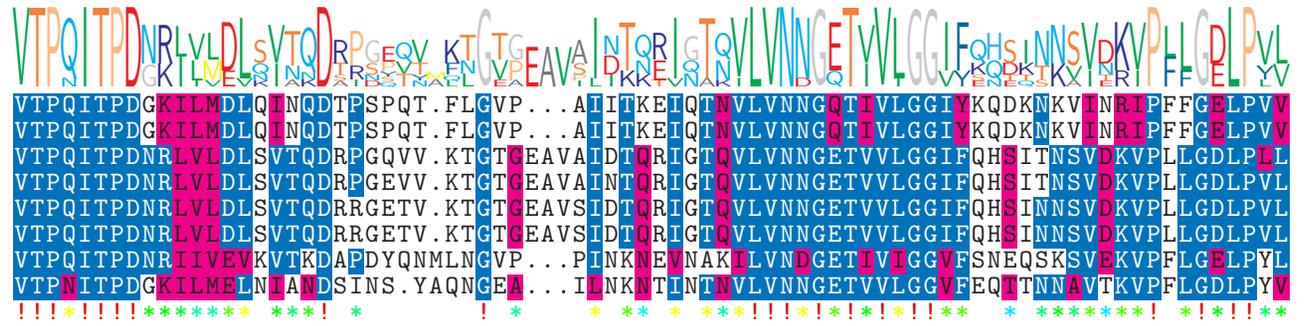
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RLVITVD...G...Y...H...Y...Q...K...K...Y...L...E...V...I...K...L...K...A...E...E...K...R...K...P...K...S...V...L...E...K...T...G...K...L...I...S...L...N...F...Q...D...I...V...R...V...L...Q...L...L...A...D...Y...T...G...F...N...L...W...S...D...S...V...G  
 RMTILSKGDYGHFVYQVNVKQFMVDVFPFLTAAEIRQAKLKKQVFTGKRISLNFQNISTRAVLQLLADFTGINMVVSDKVQG 305  
 RMTILSKGDYGHFVYQVNVKQFMVDVFPFLTAAEIRQAKLKKQVFTGKRISLNFQNISTRAVLQLLADFTGINMVVSDKVQG 305  
 RLVAVIDEDYSHDYRLTGRYLEVVKVGLKANEPD.KSILDKEGKLISINFQDIPVRNVLQLIADYNQFNLVVSDSVEG 192  
 LLVATVQGEFNYDYSLKGNYLEVVIRKLEKAEKAKP.KSVLEKEGKLISINFQDIPVRNVLQLIADYNEFNLVVSDSVRG 190  
 QLVVTVDGEFQHDYTLKGYLEVVISKLEKAEKPKP.KSVLEKEGKLISINFQDIPVRNVLQLIADYNGFNLVVSDSVVG 191  
 QLVVTVDGEFQHDYTLKGYLEVVISKLEKAEKPKP.KSVLEKEGKLISINFQDIPVRNVLQLIADYNGFNLVVSDSVVG 191  
 SITIEPSGLYDYLVTQDNRLTVISIKPMTTEAERRKKNDFAYTGEKLSLNFQDIDVRSVLQLIADFTDLNLVASTVQG 316  
 VISIQSTGSYEMAYQAENKLTISLKRPP.DNVRVLSKNNQNYTGKKSISLDFQDIEVRVRLQLIADFTNINMVTADSIVQG 297



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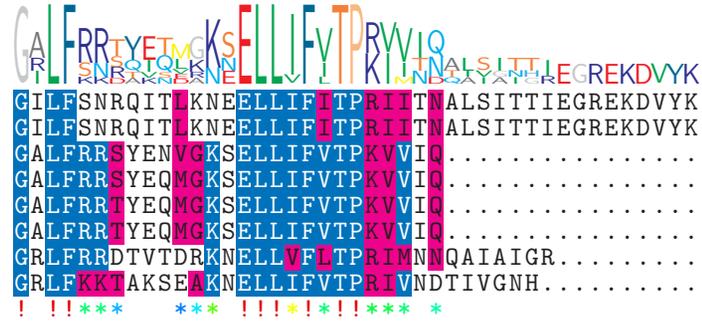
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655  
655  
553  
551  
544  
544  
680  
676

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698  
698  
580  
578  
571  
571  
714  
709

X non conserved  
 \* similar  
 ! ≥ 50% conserved