

logo

NTDB id 1272 LPP RS04360 WP 010946546.1
NTDB id 1249 GC085 RS04230 WP 010946546.1
NTDB id 1014 ACIAD RS13855 WP 004924483.1
NTDB id 493 SM12261 RS04300 WP 000387351.1
NTDB id 521 SMSK321 RS04960 WP 000443804.1
NTDB id 1159 ABDM36 RS04765 WP 001166105.1
NTDB id 1150 A1552VC RS08580 WP 001166105.1
NTDB id 1294 VP RS04495 WP 021449594.1
NTDB id 1086151 ACKWD1 RS22990 WP 043156043.1
NTDB id 1382 A4U84 RS07375 WP 062924234.1
NTDB id 1362 HI 1008 AAC22669.1
consensus

ME~~X~~IIEKIKEYKIIVICTGLGLLVGGFFLLKPAP~~R~~TPVKETNLQAEVVAISKDS~~X~~EK~~S~~VKKEEKEEP~~Y~~EQDLITVDVKG
.....
.....
.....
MEAIIEKIKEYKIIVICTGLGLLVGGFFLLKPAPQTPVKETNLQAEVVAISKDSVSEKEVKKEEKEEPLEQDLITVDVKG
MESIIEKIKEYKIIVICTGLGLLVGGFFLLKPAPHTPVKETNLQAEVVAISKDSSTEKDVKKEEKEEPVEQDLITVDVKG
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AVKSPGIYDL~~E~~VGSRVNDV~~N~~IA~~F~~EV~~E~~DS~~S~~TAT~~A~~QKVGD~~E~~SL~~A~~AK~~S~~AD~~E~~PAW~~K~~TER~~K~~ED~~T~~RLNS~~T~~AST~~E~~KK
.....MK.....ARLIA~~L~~...L...SFIVIPFSSQAE.....NEPQK
.....MK.....ARLIA~~L~~...L...SFIVIPFSSQAE.....NEPQK
.....MSIRHFFTFW.ATLLT~~L~~F...S.MQ~~I~~VFAQGFD~~Q~~QYDAWKTQQKAHDTRLNSSASHHSLS
AVKSPGIYDLPVGSRVNDVQKAGGLTEQADSKSLNLAQKVSDEALVYVPTK~~G~~EEAAS...Q.....QAGP
AVKSPGIYDLSVGSRVNDVQKAGGLTEQADSKSLNLAQKVSDEALVYVPTK~~G~~EEASAS...Q.....HTGS
.....MQIKTKIVTLF.....LS...LCLPT~~L~~PLLANA~~E~~ETAP...AA.....
.....MQIKTKIVTLF.....LS...LCLPT~~L~~PLLANA~~E~~ETAP...AA.....
.....MKWI.....LT...LCLV~~V~~FAPLSLA~~A~~D...T...KA.....
.....MNKKT.LIAAL.....LL...GCLP~~L~~LSQPLL~~A~~ADK~~A~~A...TK.....P
.....MKKLSRYTFSL.....LF...G...LFSATT~~F~~AEEKVT...TSTEH.....TPVVMQQ.
.....MKTL...FTSVV.....LC...G...ALV~~V~~SSSF~~A~~E~~E~~KAT...XQTAQ.....SVVTTQAE

27
27
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143
143
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32
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39

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TPAKQVL~~V~~KG~~K~~IN~~L~~NTADVSLTGSF~~K~~GIG~~K~~KRAE~~A~~IIAYRENHQQF~~K~~SLEELAEVKGIGQRF~~V~~DKNREKLKEIFVIN
TPAKQVL~~V~~KG~~K~~IN~~L~~NTADVSLTGSF~~K~~GIG~~K~~KRAE~~A~~IIAYRENHQQF~~K~~SLEELAEVKGIGQRF~~V~~DKNREKLKEIFVIN
KPTQQSGTGV~~K~~VNIN~~S~~ATA~~K~~ELQ.~~Q~~LHGVGEKKA~~L~~AIVEYRQ~~Q~~YGFASVDDLQKVKGIGPKF~~I~~EKNRDR~~L~~AI.....
GTASSTSKEK~~K~~VN~~L~~NKASLEELK.~~Q~~VKGLGGKRAQ~~D~~IIDHREANG~~K~~FKSVDELKKVSGIGAKTIEK~~L~~KDYVTVD....
GAPSSTSKDK~~K~~IN~~L~~NKASLEELK.~~Q~~VKGLGGKRAQ~~D~~IIDHREANG~~K~~FKSVDELKKVSGIGAKTIEK~~L~~KDYVTVD....
..QVEEG~~I~~VITVNINTASAEELATLLKGIGLKKQAIVDYREANGPFT~~H~~IDDLTNVKGIGEATVRNNAARILL.....
..QVEEG~~I~~VITVNINTASAEELATLLKGIGLKKQAIVDYREANGPFT~~H~~IDDLTNVKGIGEATVRNNAARILL.....
..DKYEG~~I~~TEITVNINTASAE~~E~~IATMLKGIGEKKAQ~~S~~IVDYRTEHGP~~F~~KTAADLTNVKGIGEATIKKNEDRILL.....
VATTQVKESG~~K~~IN~~L~~NTASASELT.~~A~~LKGIGEKKAQ~~I~~IDHREK~~K~~QGF~~T~~SVDQLADVSGIGPATLEANRDMIIVK....
VAATQKVNANV~~V~~NINTATASE~~I~~QDKLVGIGAKKAQ~~A~~IVYREK~~N~~GKFLNVEQLTEVSGIGKATLEKNRDCIVIE....
AQVAPAV~~V~~SD~~K~~LNINTATASE~~I~~QKSLTGIGAKKAQ~~A~~IVYREKHGNFXNAEQ~~L~~LEVQ~~G~~IGKATLEKNRDR~~I~~IF.....

105
105
128
216
216
103
103
94
105
113
112

 non conserved
 similar
 ≥ 50% conserved