```
logo
NTDB id 606 V4T04 RS01910 WP 003130756.1      MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRK.EKDTPIIM   79
NTDB id 471 HSISS4 RS01430 WP 002883757.1     .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQ.EKDTYIMM   78
NTDB id 109004 ACAM23 RS10360 WP 000166475.1 .MTKQVLLVDDEEHILKLLDYHLSKEGFSTQLVTNGRKALALAETEPFDFILLDIMLPQLDGMEVCKRLRAKGVKTPIMM   79
NTDB id 374 SMU RS06885 WP 002262930.1       ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRK.NSHVPIIM   77
NTDB id 413 AAK55817.1 141..845( )            ..MKKILIVDDEKPISDIIKFNMTKEGYEVVTAFNGREALEQFEAEQPDIIILDLMLPEIDGLEVAKTIRK.TSSVPILM   77
consensus                                       *!**!***!!* * *** * * *!!******* *!!**!* ** * *!*!*!!*!!!**!!*!!******    **!*!
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logo
NTDB id 606 V4T04 RS01910 WP 003130756.1      MTARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ER.....AENTSFRDLVIDKTNRTVHRGKKV   153
NTDB id 471 HSISS4 RS01430 WP 002883757.1     MTARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAP.....AKASTYRDLKLDVQNRTVVRGDEA   153
NTDB id 109004 ACAM23 RS10360 WP 000166475.1 VSAKSDEFDKVLALELGADDYLTKPFSPRELLARVKAVLRRTKGEQEGD.DSDNIADDSWLFGTLKVYPERHEVYKANKL   158
NTDB id 374 SMU RS06885 WP 002262930.1       LSAKDSEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTE   157
NTDB id 413 AAK55817.1 141..845( )            LSAKDSEFDKVIGLELGADDYVTKPFSNRELQARVKALLRRSQPMPVDGQ.EADSKPQPIQIGDLEIVPDAYVAKKYGEE   156
consensus                                     **!*****!*!**!**!!!!!**!!!* *!!*!!**! *!!**                ***! * **   * **
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<0
logo
NTDB id 606 V4T04 RS01910 WP 003130756.1      IDLTRREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKID.VEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 471 HSISS4 RS01430 WP 002883757.1     IPLTKREFDLLNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKID.VPGKESYIQTVRGMGYVIREK..   229
NTDB id 109004 ACAM23 RS10360 WP 000166475.1 LSLTPKEFELLLYLMKHPNMTLTRERLLERIWGYDFGQETRLVDVHIGKLREKIEDNPKAPQFIRTIRGYGYKFKEL..   235
NTDB id 374 SMU RS06885 WP 002262930.1       VELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.   235
NTDB id 413 AAK55817.1 141..845( )            LDLTHREFELLYHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA   234
consensus                                     **!! *!**!!  !*** ***!!!*!** *!*!*** *****!!! ****!*!!** * ** *! !*!!*!! ***
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X non conserved

X similar

X ≥ 50% conserved