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logo

NTDB id 606 V4T04 RS01910 WP 003130756.1    MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRK.EKDTPIIMMTARD   84
NTDB id 471 HSISS4 RS01430 WP 002883757.1   .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQ.EKDTYIMMMTARD   83
NTDB id 95240 QML87 RS09465 WP 000166475.1  .MTKQVLLVDDEEHILKLLDYHLSKEGFSTQLVTNGRKALALAETEPFDFILLDIMLPQLDGMEVCKRLRAKGVKTPIMMVSAKS   84
NTDB id 374 SMU RS06885 WP 002262930.1      ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRK.NSHVPIIMLSAKD   82
NTDB id 413 AAK55817.1 141..845( )          ..MKKILIVDDEKPISDIIKFNMTKEGYEVVTAFNGREALEQFEAEQPDIIILDLMLPEIDGLEVAKTIRK.TSSVPILMLSAKD   82
consensus                                     *!**!***!!* * *** * * *!!*****  *!!**!* ** * *!*!*!!*!!!**!!*!!******     **!*!**!**

logo

NTDB id 606 V4T04 RS01910 WP 003130756.1    STMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ER.....AENTSFRDLVIDKTNRTVHRGKKVIDLTRREYDL   163
NTDB id 471 HSISS4 RS01430 WP 002883757.1   SIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAP.....AKASTYRDLKLDVQNRTVVRGDEAIPLTKREFDL   163
NTDB id 95240 QML87 RS09465 WP 000166475.1  DEFDKVLALELGADDYLTKPFSPRELLARVKAVLRRTKGEQEGD.DSDNIADDSWLFGTLKVYPERHEVYKANKLLSLTPKEFEL   168
NTDB id 374 SMU RS06885 WP 002262930.1      SEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEVELTHREFEL   167
NTDB id 413 AAK55817.1 141..845( )          SEFDKVIGLELGADDYVTKPFSNRELQARVKALLRRSQPMPVDGQ.EADSKPQPIQIGDLEIVPDAYVAKKYGEELDLTHREFEL   166
consensus                                   ***!*!**!**!!!!!**!!!* *!!*!!**! *!!**                  ***! * **   * **   **!! *!**!

   <0

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NTDB id 606 V4T04 RS01910 WP 003130756.1    LLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKID.VEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 471 HSISS4 RS01430 WP 002883757.1   LNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKID.VPGKESYIQTVRGMGYVIREK..   229
NTDB id 95240 QML87 RS09465 WP 000166475.1  LLYLMKHPNMTLTRERLLERIWGYDFGQETRLVDVHIGKLREKIEDNPKAPQFIRTIRGYGYKFKEL..   235
NTDB id 374 SMU RS06885 WP 002262930.1      LHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.   235
NTDB id 413 AAK55817.1 141..845( )          LYHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA*   234
consensus                                   !  !*** ***!!!*!** *!*!*** ****!!! ***!!*!!** * ** *! !*!!*!! ***
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X non conserved

X similar

X $\geq$ 50% conserved