```
logo
NTDB id 374 SMU RS06885 WP 002262930.1        ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKNSHVPIIML   78
NTDB id 413 AAK55817.1 141..845( )            ..MKKILIVDDEKPISDIIKFNMTKEGYEVVTAFNGREALEQFEAEQPDIIILDLMLPEIDGLEVAKTIRKTSSVPILML   78
NTDB id 606 V4T04 RS01910 WP 003130756.1      MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKEKDTPIIMM   80
NTDB id 1171338 DYB47 RS08445 WP 003082300.1 .MAKSILIIEDEKNLAKFVSLELQHEGYEVEVEHDGRSGLNKALEKDYDLILLDLMLPEMDGYEVTRRLQLEKTTYVIMV   79
NTDB id 471 HSISS4 RS01430 WP 002883757.1    .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQEKDTYIMMM   79
consensus                                       !*!!!**!!!********** *!!!***** *!!**!* * ****!*!*!!!!!!!*!!*!!******** ****!*

logo
NTDB id 374 SMU RS06885 WP 002262930.1        SAKDSEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEV   158
NTDB id 413 AAK55817.1 141..845( )            SAKDSEFDKVIGLELGADDYVTKPFSNRELQARVKALLRRSQPMPVDGQ.EADSKPQPIQIGDLEIVPDAYVAKKYGEEL   157
NTDB id 606 V4T04 RS01910 WP 003130756.1      TARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ERA.....ENTSFRDLVIDKTNRTVHRGKKVI   154
NTDB id 1171338 DYB47 RS08445 WP 003082300.1 TARDSVMDIVTGLDRGADGYIVKPFAIEELLARVRAIFRRQDIEKAKYVTK.....PDGTYRDLQLDVHNRAAIRNGETI   154
NTDB id 471 HSISS4 RS01430 WP 002883757.1    TARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPA.....KASTYRDLKLDVQNRTVVRGDEAI   154
consensus                                    *!*!! *!*! !!**!!!*!**!!!***!!*!!**! *!! *   *            ***!! **  ** * * ** *

   <0
logo
NTDB id 374 SMU RS06885 WP 002262930.1        ELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.   235
NTDB id 413 AAK55817.1 141..845( )            DLTHREFELLYHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA*   234
NTDB id 606 V4T04 RS01910 WP 003130756.1      DLTRREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 1171338 DYB47 RS08445 WP 003082300.1 PLTKREFDLLSVLMENINQVMTREELLAHVWKYDQEAETNVVDVYIRYLRGKI.DVPGKESYVQTVRGMGYVIRDK..   229
NTDB id 471 HSISS4 RS01430 WP 002883757.1    PLTKREFDLLNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKI.DVPGKESYIQTVRGMGYVIREK..   229
consensus                                    *!!*!!**!!  !******!*!!!*!*  !!*!*  *****!!!**!*!! !! !******!**!*!!*!!*****
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X non conserved

X similar

X $\geq$ 50% conserved