```
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 1159101 QOR62 RS08295 WP 000516681.1 .MGKKILIIEDEKNLARFVSLELLHEGYDVVVETNGREGLDTALEKDFDLILLDLMLPEMDGFEITRRLQAEKTTYIMMM   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    TARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHA.VERAENT.....SFRDLVIDKTNRTVHRGKKVI   154
NTDB id 1159101 QOR62 RS08295 WP 000516681.1 TARDSVMDIVAGLDRGADDYIVKPFAIEELLARVRAIFRRQEIETKTKEKGDSG.....SFRDLSLNTHNRSAMRGDEEI   154
NTDB id 471 HSISS4 RS01430 WP 002883757.1   TARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKAS.....TYRDLKLDVQNRTVVRGDEAI   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 1159101 QOR62 RS08295 WP 000516681.1 SLTKREFDLLNVLMTNMNRVMTREELLEHVWKYDVAAETNVVDVYIRYLRGKI.DIPGRESYIQTVRGMGYVIREK..   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