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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 358804 E8M05 RS09125 WP 003066186.1   .MSKKILIIEDEKNLARFVSLELQHEGYSVVVETNGRLGLQTALDDDFDLILLDLMLPDMDGFEITRRLRLEKETSIIMM    79
NTDB id 471 HSISS4 RS01430 WP 002883757.1     .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQEKDTYIMMM    79
consensus                                       *!*!!!**!!!********** *!!!***** *!!**!* * ****!*!*!!!!!!*!!*!**********!*!*

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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      TARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAVER......AENTSFRDLVIDKTNRTVHRGKKVI   154
NTDB id 358804 E8M05 RS09125 WP 003066186.1   TARDSIMDIVAGLDRGADDYIVKPFAIEELLARVRAVFRRQDVEFKREQ....GNQGKEGLLGLRLNPQNRSAVRGDDEI   155
NTDB id 471 HSISS4 RS01430 WP 002883757.1     TARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNA....PA.KASTYRDLKLDVQNRTVVRGDEAI   154
consensus                                     *!*!! *!*!*!!**!!!!!**!!!***!!*!!**! *!! *                 * *! * * **** ** ***

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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      DLTREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 358804 E8M05 RS09125 WP 003066186.1   SLTKREYDLLSVLLSNVNRVMTREELLANVWRYDTDIETNVVDVYIRYLRGKV.DIPGKESYIQTVRGMGYIIREK..   230
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