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logo

NTDB id 413 AAK55817.1 141..845( )      ..MKKILIVDDEKPISDIIKFNMTKEGYEVVTAFNGREALEQFEAEQPDIIILDLMLPEIDGLEVAKTIRKTSSVPILML   78
NTDB id 374 SMU RS06885 WP 002262930.1  ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKNSHVPIIML   78
NTDB id 606 V4T04 RS01910 WP 003130756.1 MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKEKDTPIIMM   80
NTDB id 1110961 ACNR93 RS07565 WP 021143010.1 .MSKKILIIEDEKNLARFVSLELQHEGYSVVVETNGRLGLQTALDDDFDLILLDLMLPDMDGFEITRRLRLEKETSIIMM   79
NTDB id 471 HSISS4 RS01430 WP 002883757.1 .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQEKDTYIMMM   79
consensus                                 *!*!!!**!!!********** *!!!***** *!!**!* * ****!*!*!!!!!!*!!*!**********!*!*

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NTDB id 413 AAK55817.1 141..845( )      SAKDSEFDKVIGLELGADDYVTKPFSNRELQARVKALLRRSQPMPVDGQ.EADSKPQPIQIGDLEIVPDAYVAKKYGEEL   157
NTDB id 374 SMU RS06885 WP 002262930.1  SAKDSEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEV   158
NTDB id 606 V4T04 RS01910 WP 003130756.1 TARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV..E....RAENTSFRDLVIDKTNRTVHRGKKVI   154
NTDB id 1110961 ACNR93 RS07565 WP 021143010.1 TARDSIMDIVAGLDRGADDYIVKPFAIEELLARVRAVFRRQEANSKHDKE....GQAKEGLLGLRLNPQNRSAVRGDDEI   155
NTDB id 471 HSISS4 RS01430 WP 002883757.1 TARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAP....AK.ASTYRDLKLDVQNRTVVRGDEAI   154
consensus                                *!*!! *!*!*!!**!!!!!**!!!***!!*!!**! *!! *       *    *     * *! * * **** ** ***

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NTDB id 413 AAK55817.1 141..845( )      DLTHREFELLYHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA*   234
NTDB id 374 SMU RS06885 WP 002262930.1  ELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.   235
NTDB id 606 V4T04 RS01910 WP 003130756.1 DLTREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 1110961 ACNR93 RS07565 WP 021143010.1 SLTKREYDLLSVLLSNVNRVMTREELLASVWRYDTDIETNVVDVYIRYLRGKI.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