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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 1158997 QOR45 RS08270 WP 000516681.1    .MGKKILIIEDEKNLARFVSLELLHEGYDVVVETNGREGLDTALEKDFDLILLDLMLPEMDGFEITRRLQAEKTTYIMMM    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        TARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHA.VERAENT.....SFRDLVIDKTNRTVHRGKKVI   154
NTDB id 1158997 QOR45 RS08270 WP 000516681.1    TARDSVMDIVAGLDRGADDYIVKPFAIEELLARVRAIFRRQEIETKTKEKGDSG.....SFRDLSLNTHNRSAMRGDEEI   154
NTDB id 471 HSISS4 RS01430 WP 002883757.1       TARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKAS.....TYRDLKLDVQNRTVVRGDEAI   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        DLTRREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 1158997 QOR45 RS08270 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 ≥ 50% conserved