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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 255787 CTW00 RS00170 WP 037583387.1 .MTKKILIVEDEKNLARFVSLELQHEGYEVTVEVNGREGLDTALEKDFDLILLDLMLPEMDGFEVTRRLQTEKTTYIMMM    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 TARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAVE......RAENTSFRDLVIDKTNRTVHRGKKVI   154
NTDB id 255787 CTW00 RS00170 WP 037583387.1 TARDSIMDVVAGWDRGADDYIVKPFAIEELLARIRAIFRRQDIETEKKS.....PN.QGIYRDLVLNPQNRSVNRGDEEI   153
NTDB id 471 HSISS4 RS01430 WP 002883757.1 TARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNA.....PAKASTYRDLKLDVQNRTVVRGDEAI   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 DLTREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKID.VEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 255787 CTW00 RS00170 WP 037583387.1 SLTKREYDLLNILMSNMNRVMTREELLSNVWKYDEAVETNVVDVYIRYLRGKID.MQGRESYIQTVRGMGYVIREK..   228
NTDB id 471 HSISS4 RS01430 WP 002883757.1 PLTKREFDLLNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKID.VPGKESYIQTVRGMGYVIREK..   229
consensus                                 *!!*!!**!!  !******!*!!!*!* *!!*!*** ****!!!**!*!! !!* ******!!*!*!!*!!*****
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X non conserved

X similar

X $\geq$ 50% conserved