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logo
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NTDB id 413 AAK55817.1 141..845( )   ..MKKILIVDDEKPISDIIKFNMTKEGYEVVTAFNGREALEQFEAEQPDIIILDLMLPEIDGLEVAKTIRKTSSVPILMLSAKDS   83
NTDB id 374 SMU RS06885 WP 002262930.1   ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKNSHVPIIMLSAKDS   83
NTDB id 606 V4T04 RS01910 WP 003130756.1   MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKEKDTPIIMMTARDS   85
NTDB id 71270 Q426 RS00485 WP 012516253.1   .MTKKILIIEDEKNLARFVSLELQHEGYEVTVEVNGREGLETALEKDFDLILLDLMLPEMDGFEVTRRLQTEKTTYIMMMTARDS   84
NTDB id 471 HSISS4 RS01430 WP 002883757.1   .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQEKDTYIMMMTARDS   84
consensus   *!*!!!**!!!**********  *!!!*****  *!!**!*  *  ****!*!*!!!!!!!*!!*!!********  **!*!**!*!!
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logo
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NTDB id 413 AAK55817.1 141..845( )   EFDKVIGLELGADDYVTKPFSNRELQARVKALLRRSQPMPVDGQ.EADSKPQPIQIGDLEIVPDAYVAKKYGEELDLTHREFELL   167
NTDB id 374 SMU RS06885 WP 002262930.1   EFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEVELTHREFELL   168
NTDB id 606 V4T04 RS01910 WP 003130756.1   TMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAVE......RAENTSFRDLVIDKTNRTVHRGKKVIDLTRREYDLL   164
NTDB id 71270 Q426 RS00485 WP 012516253.1   IMDVVAGLDRGADDYIVKPFAIEELLARIRAIFRRQDIESEKKT.....PSQ.GVYRDLVLNPQNRSVNRGDDEISLTKREYDLL   163
NTDB id 471 HSISS4 RS01430 WP 002883757.1   IMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNA.....PAKASTYRDLKLDVQNRTVVRGDEAIPLTKREFDLL   164
consensus   *!*!*!!**!!!!!**!!!***!!*!!**!  *!!  *                **!!  *  *  ****  **  ****!!*!!**!!
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logo
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NTDB id 413 AAK55817.1 141..845( )   YHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA*   234
NTDB id 374 SMU RS06885 WP 002262930.1   HHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.   235
NTDB id 606 V4T04 RS01910 WP 003130756.1   LTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 71270 Q426 RS00485 WP 012516253.1   NILMTNMNRVMTREELLSNVWKYDEAVETNVVDVYIRYLRGKI.DIPGKESYIQTVRGMGYVIREK..   228
NTDB id 471 HSISS4 RS01430 WP 002883757.1   NTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKI.DVPGKESYIQTVRGMGYVIREK..   229
consensus   !******!*!!!!*!* *!!*!*** ****!!!**!*!! !! !******!!*!*!!*!!*****
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X non conserved
X similar
X ≥ 50% conserved