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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 41528 M3B RS08530 WP 002991052.1 .MTKKILIIEDEKNLARFVSLELQHEGYEVIVEVNGREGLETALEKEFDLILLDLMLPEMDGFEVTRRLQTEKTTYIMMMTARDS   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 41528 M3B RS08530 WP 002991052.1 IMDVVAGLDRGADDYIVKPFAIEELLARIRAIFRRQDIESEKKV.....PSQ.GIYRDLVLNPQNRSVNRGDDEISLTKREYDLL   163
NTDB id 471 HSISS4 RS01430 WP 002883757.1 IMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNA.....PAKASTYRDLKLDVQNRTVVRGDEAIPLTKREFDLL   164
consensus                                *!*!*!!**!!!!!**!!!***!!*!!**!  *!!  *                     **!!  *  *  ****  **  ****!!*!!!**!!
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logo
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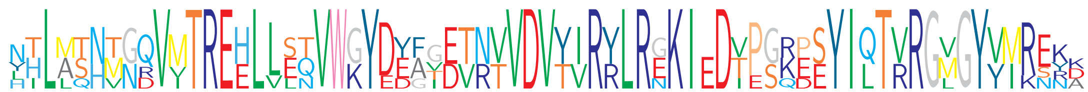

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NTDB id 413 AAK55817.1 141..845( )      YHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA*   234
NTDB id 374 SMU RS06885 WP 002262930.1  HHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.   235
NTDB id 606 V4T04 RS01910 WP 003130756.1 LTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 41528 M3B RS08530 WP 002991052.1 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 $\geq 50\%$ conserved