```
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 1136080 DQL11 RS07770 WP 002991052.1 .MTKKILIIEDEKNLARFVSLELQHEGYEVIVEVNGREGLETALEKEFDLILLDLMLPEMDGFEVTRRLQTEKTTYIMMM    79
NTDB id 471 HSISS4 RS01430 WP 002883757.1   .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQEKDTYIMMM    79
consensus                                     *!*!!!**!!!********** *!!!***** *!!**!* * ****!*!*!!!!!!!*!!*!!******** **!*!*

logo

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 1136080 DQL11 RS07770 WP 002991052.1 TARDSIMDVVAGLDRGADDYIVKPFAIEELLARIRAIFRRQDIESEKKV.....PSQ.GIYRDLVLNPQNRSVNRGDDEI   153
NTDB id 471 HSISS4 RS01430 WP 002883757.1   TARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNA.....PAKASTYRDLKLDVQNRTVVRGDEAI   154
consensus                                   *!*!! *!*!*!!**!!!!!**!!!***!!*!!**! *!! *                **!! * * **** ** ***

   <0

logo

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    DLTRREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 1136080 DQL11 RS07770 WP 002991052.1 SLTKREYDLLNILMTNMNRVMTREELLSNVWKYDEAVETNVVDVYIRYLRGKI.DIPGKESYIQTVRGMGYVIREK..   228
NTDB id 471 HSISS4 RS01430 WP 002883757.1   PLTKREFDLLNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKI.DVPGKESYIQTVRGMGYVIREK..   229
consensus                                   *!!*!!**!!  !******!*!!!*!* *!!*!*** ****!!!**!*!! !! !******!!*!*!!*!!*****
```

X non conserved

X similar

X $\geq$ 50% conserved