```
logo
NTDB id 23454 M6 RS04740 WP 002984519.1     ..MIKILLVEDDLSLSNSI.FDFLDDFADVMQVFDGDEGLYEAESGIYDLILLDLMLPEKNGFQVLKELREKDIKIPVLIMTAKE   82
NTDB id 258 KZH43 RS03475 WP 000590640.1    ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE   82
NTDB id 217 SPD RS03775 WP 000590640.1      ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE   82
NTDB id 183 SPR RS03560 WP 000590640.1      ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE   82
NTDB id 147 SP RS03905 WP 000590640.1       ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE   82
NTDB id 362 SMU RS05200 WP 002262214.1      ..MIKLLLVEDDLSLSNSI.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE   82
NTDB id 413 AAK55817.1 141..845( )          ..MKKILIVDDEKPISDIIKFNMTKEGYEVVTAFNGREALEQFEAEQPDIIILDLMLPEIDGLEVAKTIRKT.SSVPILMLSAKD   82
NTDB id 374 SMU RS06885 WP 002262930.1      ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKN.SHVPIIMLSAKD   82
NTDB id 606 V4T04 RS01910 WP 003130756.1    MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKE.KDTPIIMMTARD   84
NTDB id 471 HSISS4 RS01430 WP 002883757.1   .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQE.KDTYIMMMTARD   83
consensus                                    ****!***!** ***** ***************!***!********!*!!!!!!!**!**!******************!**

logo
NTDB id 23454 M6 RS04740 WP 002984519.1     GLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRTGKFADK..........NISFGNLVVDLARKEVKVEGKVVELLGKEFDL   157
NTDB id 258 KZH43 RS03475 WP 000590640.1    SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........TLTYGNIVVNLSTNTVKVEDTPVELLGKEFDL   157
NTDB id 217 SPD RS03775 WP 000590640.1      SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........TLTYGNIVVNLSTNTVKVEDTPVELLGKEFDL   157
NTDB id 183 SPR RS03560 WP 000590640.1      SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........TLTYGNIVVNLSTNTVKVEDTPVELLGKEFDL   157
NTDB id 147 SP RS03905 WP 000590640.1       SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........TLTYGNIVVNLSTNTVKVEDTPVELLGKEFDL   157
NTDB id 362 SMU RS05200 WP 002262214.1      GLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........NLTYGELTVDTATNTTMVNGKEVELLGKEFDL   157
NTDB id 413 AAK55817.1 141..845( )          SEFDKVIGLELGADDYVTKPFSNRELQARVKALLRRSQPMPVDGQ.EADSKPQPIQIGDLEIVPDAYVAKKYGEELDLTHREFEL   166
NTDB id 374 SMU RS06885 WP 002262930.1      SEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEVELTHREFEL   167
NTDB id 606 V4T04 RS01910 WP 003130756.1    STMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ERAENTS.....FRDLVIDKTNRTVHRGKKVIDLTREYDL   163
NTDB id 471 HSISS4 RS01430 WP 002883757.1   SIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKAST.....YRDLKLDVQNRTVVRGDEAIPLTKREFDL   163
consensus                                   ***!***!***!!!!!**!!!***!!**!**!***!*******          ******** *********** **!***!**!

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logo
NTDB id 23454 M6 RS04740 WP 002984519.1     LVYLLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYISKIRKKLKGTR.FVNRLQTLRSVGYILKNNE.   224
NTDB id 258 KZH43 RS03475 WP 000590640.1    LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTT.FAENLQTLRSVGYLLKDVQ.   224
NTDB id 217 SPD RS03775 WP 000590640.1      LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTT.FAENLQTLRSVGYLLKDVQ.   224
NTDB id 183 SPR RS03560 WP 000590640.1      LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTT.FAENLQTLRSVGYLLKDVQ.   224
NTDB id 147 SP RS03905 WP 000590640.1       LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTT.FAENLQTLRSVGYLLKDVQ.   224
NTDB id 362 SMU RS05200 WP 002262214.1      LVYFLQNQNVILPKSQIFDRIWGFDSDTTISVVEVYVSKIRKKLKDTT.FGKNLQTLRSVGYILKDAN.   224
NTDB id 413 AAK55817.1 141..845( )          LYHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA*   234
NTDB id 374 SMU RS06885 WP 002262930.1      LHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.   235
NTDB id 606 V4T04 RS01910 WP 003130756.1    LLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.   230
NTDB id 471 HSISS4 RS01430 WP 002883757.1   LNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKI.DVPGKESYIQTVRGMGYVIREK..   229
consensus                                   !** ****************!**********!*!*****!*!** ** ******!*!**!!**** *
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X non conserved

X similar

X ≥ 50% conserved