```
logo
NTDB id 362 SMU RS05200 WP 002262214.1      ..MIKLLLVEDDLSLSNSI.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE   82
NTDB id 39329 SIR RS14120 WP 003036714.1    ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKDGFQVLKELREKGVTTPVLIMTAKE   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 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 362 SMU RS05200 WP 002262214.1      GLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NN.....LTYGELTVDTATNTTMVNGKEVELLGKEFDL   157
NTDB id 39329 SIR RS14120 WP 003036714.1    SLNDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LSYGDVTINLSTNTTLVDGNEVELLGKEFDL   157
NTDB id 258 KZH43 RS03475 WP 000590640.1    SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL   157
NTDB id 217 SPD RS03775 WP 000590640.1      SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL   157
NTDB id 183 SPR RS03560 WP 000590640.1      SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL   157
NTDB id 147 SP RS03905 WP 000590640.1       SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL   157
NTDB id 374 SMU RS06885 WP 002262930.1      SEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEVELTHREFEL   167
NTDB id 606 V4T04 RS01910 WP 003130756.1    STMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ERAENTSFRDLV.....IDKINRTVHRGKKVIDLTRREYDL   163
NTDB id 471 HSISS4 RS01430 WP 002883757.1   SIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKASTYRDLK.....LDVQNRTVVRGDEAIPLTKREFDL   163
consensus                                   ***!***!***!!!!!**!!!***!!**!**!***!******     **      **** * ************* **!***!**!

logo
NTDB id 362 SMU RS05200 WP 002262214.1      LVYFLQNQNVILPKSQIFDRIWGFDSDTTISVVEVYVSKIRKKLKDT.TFGKNLQTLRSVGYILKDAN   224
NTDB id 39329 SIR RS14120 WP 003036714.1    LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKIRKKLKGT.TFANNLQTLRSVGYILKDAE   224
NTDB id 258 KZH43 RS03475 WP 000590640.1    LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ   224
NTDB id 217 SPD RS03775 WP 000590640.1      LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ   224
NTDB id 183 SPR RS03560 WP 000590640.1      LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ   224
NTDB id 147 SP RS03905 WP 000590640.1       LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ   224
NTDB id 374 SMU RS06885 WP 002262930.1      LHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD   235
NTDB id 606 V4T04 RS01910 WP 003130756.1    LLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKID.VEGQDSYIQTVRGLGYVMRERK   230
NTDB id 471 HSISS4 RS01430 WP 002883757.1   LNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKID.VPGKESYIQTVRGMGYVIREK.   229
consensus                                   !********************!**********!*!*****!*!**** *******!*!**!!**** *
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X non conserved

X similar

X ≥50% conserved