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logo

NTDB id 235428 SE071780 RS05180 WP 012515548.1  ..MIKLLLVEDDLSLSNSIF.DFLDDFADVTQVFDGDEGLYEAESGIYDLILLDLMLPEKDGFQVLKALREKDIKIPVLI   77
NTDB id 362 SMU RS05200 WP 002262214.1          ..MIKLLLVEDDLSLSNSIF.DFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 258 KZH43 RS03475 WP 000590640.1        ..MIKILLVEDDLGLSNSVF.DFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 217 SPD RS03775 WP 000590640.1          ..MIKILLVEDDLGLSNSVF.DFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 183 SPR RS03560 WP 000590640.1          ..MIKILLVEDDLGLSNSVF.DFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 147 SP RS03905 WP 000590640.1           ..MIKILLVEDDLGLSNSVF.DFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 606 V4T04 RS01910 WP 003130756.1        MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKE.KDTPIIM   79
NTDB id 471 HSISS4 RS01430 WP 002883757.1       .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQE.KDTYIMM   78
consensus                                         ****!**!!** !***** ***************!**!!**!*****!!!!!!!!!!!**!!*!***!***********

logo

NTDB id 235428 SE071780 RS05180 WP 012515548.1  MTAKESIDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRVGKF.....NDKSLKFGNLTVDTTRKEVQVNGQAIELLG   152
NTDB id 362 SMU RS05200 WP 002262214.1          MTAKEGLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKF.....NENNLTYGELTVDTATNTTMVNGKEVELLG   152
NTDB id 258 KZH43 RS03475 WP 000590640.1        MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKF.....NENTLTYGNIVVNLSTNTVKVEDTPVELLG   152
NTDB id 217 SPD RS03775 WP 000590640.1          MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKF.....NENTLTYGNIVVNLSTNTVKVEDTPVELLG   152
NTDB id 183 SPR RS03560 WP 000590640.1          MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKF.....NENTLTYGNIVVNLSTNTVKVEDTPVELLG   152
NTDB id 147 SP RS03905 WP 000590640.1           MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKF.....NENTLTYGNIVVNLSTNTVKVEDTPVELLG   152
NTDB id 606 V4T04 RS01910 WP 003130756.1        MTARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ERAENTSFRDLVIDKTNRTVHRGKKVIDLTR   158
NTDB id 471 HSISS4 RS01430 WP 002883757.1       MTARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKASTYRDLKLDVQNRTVVRGDEAIPLTK   158
consensus                                       !!!*****!***!***!!!!!**!!!**!!!**!**!***!****     ************ ****** * *   **!**

logo

NTDB id 235428 SE071780 RS05180 WP 012515548.1  KELDLLIYILQNQNVILPKSQIFDRIWGFDSDTTISVVEVYVSKIRKKLKGTDFVNHLQTLRSVGYILKANE   224
NTDB id 362 SMU RS05200 WP 002262214.1          KEFDLLVYFLQNQNVILPKSQIFDRIWGFDSDTTISVVEVYVSKIRKKLKDTTFGKNLQTLRSVGYILKDAN   224
NTDB id 258 KZH43 RS03475 WP 000590640.1        KEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTTFAENLQTLRSVGYLLKDVQ   224
NTDB id 217 SPD RS03775 WP 000590640.1          KEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTTFAENLQTLRSVGYLLKDVQ   224
NTDB id 183 SPR RS03560 WP 000590640.1          KEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTTFAENLQTLRSVGYLLKDVQ   224
NTDB id 147 SP RS03905 WP 000590640.1           KEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTTFAENLQTLRSVGYLLKDVQ   224
NTDB id 606 V4T04 RS01910 WP 003130756.1        REYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKIDVEGQDSYIQTVRGLGYVMRERK   230
NTDB id 471 HSISS4 RS01430 WP 002883757.1       REFDLLNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKIDVPGKESYIQTVRGMGYVIREK.   229
consensus                                       *!*!!!*****!*************!*********!!*!!****!*!******* **!!*!**!!**** *
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X non conserved

X similar

X ≥50% conserved