logo

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NTDB id 29295 SALIVB RS04210 WP 013990465.1  ..MIKILLVEDDLSLSNSV.FDFLDDFADVMQVFDGDEGLYEAESGVYDLILLDLMLPEKDGFTVLRELRDKGVTTPVLI   77
NTDB id 258 KZH43 RS03475 WP 000590640.1     ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 217 SPD RS03775 WP 000590640.1       ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 183 SPR RS03560 WP 000590640.1       ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 147 SP RS03905 WP 000590640.1        ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 362 SMU RS05200 WP 002262214.1       ..MIKLLLVEDDLSLSNST.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 606 V4T04 RS01910 WP 003130756.1     MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKE.KDTPIIM   79
NTDB id 374 SMU RS06885 WP 002262930.1       ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKN.SHVPIIM   77
consensus                                      **!*!***!**  *****  ***************!***!*********!!!*!!!!!!!**!**!****!******!***
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NTDB id 29295 SALIVB RS04210 WP 013990465.1  MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFD.....QNT.....LSFGDVRVNLATNSTFVGDKE   147
NTDB id 258 KZH43 RS03475 WP 000590640.1     MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFN.....ENT.....LTYGNIVVNLSTNTVKVEDTP   147
NTDB id 217 SPD RS03775 WP 000590640.1       MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFN.....ENT.....LTYGNIVVNLSTNTVKVEDTP   147
NTDB id 183 SPR RS03560 WP 000590640.1       MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFN.....ENT.....LTYGNIVVNLSTNTVKVEDTP   147
NTDB id 147 SP RS03905 WP 000590640.1        MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFN.....ENT.....LTYGNIVVNLSTNTVKVEDTP   147
NTDB id 362 SMU RS05200 WP 002262214.1       MTAKEGLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFN.....ENN.....LTYGELTVDTATNTTMVNGKE   147
NTDB id 606 V4T04 RS01910 WP 003130756.1     MTARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAVERAENT.SFRDLVI.....DKTNRTVHRGKKV   153
NTDB id 374 SMU RS06885 WP 002262930.1       LSAKDSEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTE   157
consensus                                    **!*****!***!***!!!!!*!!!!***!!**!**!***!*****      *!*     ****  *  **********  **
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NTDB id 29295 SALIVB RS04210 WP 013990465.1  VELLGKEFDLLVYFLQNQNVILPKSQIFDRLWGFDSDTTVSVVEVYVSKIRKKLKGT.DFAANLQTLRSVGYILKHAD   224
NTDB id 258 KZH43 RS03475 WP 000590640.1     VELLGKEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ   224
NTDB id 217 SPD RS03775 WP 000590640.1       VELLGKEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ   224
NTDB id 183 SPR RS03560 WP 000590640.1       VELLGKEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ   224
NTDB id 147 SP RS03905 WP 000590640.1        VELLGKEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ   224
NTDB id 362 SMU RS05200 WP 002262214.1       VELLGKEFDLLVYFLQNQNVILPKSQIFDRIWGFDSDTTISVVEVYVSKIRKKLKDT.TFGKNLQTLRSVGYILKDAN   224
NTDB id 606 V4T04 RS01910 WP 003130756.1     IDLTRREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKIDV.EGQDSYIQTVRGLGYVMRERK   230
NTDB id 374 SMU RS06885 WP 002262930.1       VELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD   235
consensus                                    **!***!**!!*********************!!**********!*!*****!*!****  *******!*!**!!****  *
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X non conserved

X similar

X ≥ 50% conserved