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logo

NTDB id 25853 MGAS9429 RS05135 WP 002984519.1  ..MIKILLVEDDLSLSNSI.FDFLDDFADVMQVFDGDEGLYEAESGIYDLILLDLMLPEKNGFQVLKELREKDIKIPVLI   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         ..MIKLLLVEDDLSLSNSI.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLI   77
NTDB id 413 AAK55817.1 141..845( )             ..MKKILIVDDEKPISDIIKFNMTKEGYEVVTAFNGREALEQFEAEQPDIIILDLMLPEIDGLEVAKTIRKT.SSVPILM   77
NTDB id 374 SMU RS06885 WP 002262930.1         ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKN.SHVPIIM   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 25853 MGAS9429 RS05135 WP 002984519.1  MTAKEGLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRTGKFADK..........NISFGNLVVDLARKEVKVEGKV  147
NTDB id 258 KZH43 RS03475 WP 000590640.1       MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........TLTYGNIVVNLSTNTVKVEDTP  147
NTDB id 217 SPD RS03775 WP 000590640.1         MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........TLTYGNIVVNLSTNTVKVEDTP  147
NTDB id 183 SPR RS03560 WP 000590640.1         MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........TLTYGNIVVNLSTNTVKVEDTP  147
NTDB id 147 SP RS03905 WP 000590640.1          MTAKESLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........TLTYGNIVVNLSTNTVKVEDTP  147
NTDB id 362 SMU RS05200 WP 002262214.1         MTAKEGLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNEN..........NLTYGELTVDTATNTTMVNGKE  147
NTDB id 413 AAK55817.1 141..845( )             LSAKDSEFDKVIGLELGADDYVTKPFSNRELQARVKALLRRSQPMPVDGQ.EADSKPQPIQIGDLEIVPDAYVAKKYGEE  156
NTDB id 374 SMU RS06885 WP 002262930.1         LSAKDSEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTE  157
NTDB id 606 V4T04 RS01910 WP 003130756.1       MTARDSTMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ERAENTS.....FRDLVIDKTNRTVHRGKKV  153
NTDB id 471 HSISS4 RS01430 WP 002883757.1      MTARDSIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKAST.....YRDLKLDVQNRTVVRGDEA  153
consensus                                      **!*****!***!***!!!!!**!!!***!!**!**!***!*******          ********  ***********

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NTDB id 25853 MGAS9429 RS05135 WP 002984519.1  VELLGKEFDLLVYLLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYISKIRKKLKGTR.FVNRLQTLRSVGYILKNNE.  224
NTDB id 258 KZH43 RS03475 WP 000590640.1       VELLGKEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTT.FAENLQTLRSVGYLLKDVQ.  224
NTDB id 217 SPD RS03775 WP 000590640.1         VELLGKEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTT.FAENLQTLRSVGYLLKDVQ.  224
NTDB id 183 SPR RS03560 WP 000590640.1         VELLGKEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTT.FAENLQTLRSVGYLLKDVQ.  224
NTDB id 147 SP RS03905 WP 000590640.1          VELLGKEFDLLVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGTT.FAENLQTLRSVGYLLKDVQ.  224
NTDB id 362 SMU RS05200 WP 002262214.1         VELLGKEFDLLVYFLQNQNVILPKSQIFDRIWGFDSDTTISVVEVYVSKIRKKLKDTT.FGKNLQTLRSVGYILKDAN.  224
NTDB id 413 AAK55817.1 141..845( )             LDLTHREFELLYHLASHTGQVITREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMRNNA*  234
NTDB id 374 SMU RS06885 WP 002262930.1         VELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD.  235
NTDB id 606 V4T04 RS01910 WP 003130756.1       IDLTRREYDLLLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKI.DVEGQDSYIQTVRGLGYVMRERK.  230
NTDB id 471 HSISS4 RS01430 WP 002883757.1      IPLTKREFDLLNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKI.DVPGKESYIQTVRGMGYVIREK..  229
consensus                                      **!***!**!!** *****************!**********!*!*****!*!** ** ******!*!**!!****  *
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X non conserved

X similar

X $\geq$ 50% conserved