logo

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NTDB id 21399 SPS RS05605 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                                    ****!***!** ***** ***************!***!*********!*!!!!!!!**!**!*******************!**
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NTDB id 21399 SPS RS05605 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.EADSKPQPIQIGDLEIVPDAYVAKKYGEELDLTHREFRL  166
NTDB id 374 SMU RS06885 WP 002262930.1     SEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEVELTHREFEL  167
NTDB id 606 V4T04 RS01910 WP 003130756.1   STMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ERAENTS.....FRDLVIDKTNRTVHRGKKVIDLTRREYDL  163
NTDB id 471 HSISS4 RS01430 WP 002883757.1  SIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKAST.....YRDLKLDVQNRTVVRGDEAIPLTKREFDL  163
consensus                                  ***!***!***!!!!!**!!!***!!**!**!***!*******          ********  ***********  **!***!**!
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NTDB id 21399 SPS RS05605 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