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NTDB id 462 GPW51 RS00385 WP 012774894.1          ....MKAELIAVGTEILTGQIINTNAQFLSEKCAELGIDVYFHTAVGDNEGRLLSTLEVASKRSNMVVLCGGLGPTEDDL   76
NTDB id 412 SMU RS09535 WP 002262393.1            ....MKSEIIAVGTEILTGQIVNTNSQFLSEKFAELGIDVYFQTAVGDNEERLLSVLKIAKERSDLIVLCGGLGPTEDDL   76
NTDB id 170 SP RS09755 WP 000642718.1             ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEVRLLSLLEIASQRSSLVILTGGLGPTEDDL   76
NTDB id 280 KZH43 RS08670 WP 000642700.1          ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEVRLLSLLEIASQRSSLVILTGGLGATEDDL   76
NTDB id 205 SPR RS08830 WP 000642700.1            ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEVRLLSLLEIASQRSSLVILTGGLGATEDDL   76
NTDB id 239 SPD RS09270 WP 000642701.1            ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEVRLLSLLEIASQRSSLVILTGGLGATEDDL   76
NTDB id 510 SM12261 RS08320 WP 000642690.1        ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEARLLSLLEIASQRSSLVILTGGLGPTEDDL   76
NTDB id 538 SMSK321 RS11060 WP 000642686.1        ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEARLLSLLEIASQRSSLVILTGGLGPTEDDL   76
NTDB id 79338 KH172YL63 RS08050 WP 173105619.1    ....MNAEIIAVGSELLLGQIVNSNAQYISEELAGIGVNVYYHTSVGDNPKRLLEAVKVAQGRADLLIFTGGLGPTKDDL   76
NTDB id 124 BSU 16930 NP 389575.2                 MEFPKKAEIIAVGSELLLGQIANTNAQFISKQLAEIGVNVFYHTAVGDNPERLKQVIRIAEERSDFIIFSGGLGPTKDDL   80
consensus                                              ***!*!!!!*!*!*!!!*!*!*!**!***!**!**!***!*!!!!* !!*******!**!*******!!!!*!*!!!
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NTDB id 462 GPW51 RS00385 WP 012774894.1          TKQTLATFLGRNLVFDELAMAKLDRFFASRPGRVRTPNNERQAAQIVEGSQALQNPAGLAVGGMIEQDGVTYIVLPGPPSE   156
NTDB id 412 SMU RS09535 WP 002262393.1            TKQTLAKFLKRELVFDKTAQERLDEFFASRPTSMRTPNNECQAAQIIAGSQPLSNKTGLAVGGLLEADGVTYVVLPGPPSE   156
NTDB id 170 SP RS09755 WP 000642718.1             TKQTLAKFLGKALVFDPQAQEKLDIFFTLRPDYARTPNNERQAAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE   156
NTDB id 280 KZH43 RS08670 WP 000642700.1          TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQAAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE   156
NTDB id 205 SPR RS08830 WP 000642700.1            TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQAAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE   156
NTDB id 239 SPD RS09270 WP 000642701.1            TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQVQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE   156
NTDB id 510 SM12261 RS08320 WP 000642690.1        TKQTLAKFLGKELVFDPQAQEKLDVFFAQRPDYARTPNNERQAQLVEGAIPLPNETGLAVGGILEVDGVTYVVLPGPPSE   156
NTDB id 538 SMSK321 RS11060 WP 000642686.1        TKQTLAKFLGKELVFDPQAQEKLDVFFAQRPDYARTPNNERQAQIVEGATPLPNETGLAVGGILEVDGVTYVVLPGPPSE   156
NTDB id 79338 KH172YL63 RS08050 WP 173105619.1    TKETIADALGTSLTMDGEALDSIRNYFR.KVNRTMTPNNEKQALILQGSDVLKNDHGMAPGMLLIKDGKAYMLLPGPPSE   155
NTDB id 124 BSU 16930 NP 389575.2                 TKETIANTLGRPLVLNDEAFQSIEDYFK.RTKRTMSPNNRKQALVIEGSDVLANHFGMAPGMLTEHESRYYMLLPGPPSE   159
consensus                                         !!*!*!**!** !*****!******!* *******!!!**!*****!***!*!**!*!*!**********!**!!!!!!!
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NTDB id 462 GPW51 RS00385 WP 012774894.1          LKAMFSESL...LPLLSQSQQQLYSRVLRFFGIGESQLVTVLADVIDKQTDPTLAPYAKVGEVTLRLSTKATSQEEANLR   233
NTDB id 412 SMU RS09535 WP 002262393.1            LKPMVNKEL...LPYLSKTSEKLYSRVLRFFGIGESHLVTLLHDLIAEQTDPTIAPYAKTGEVTIRLSTKAHRQKEADSK   233
NTDB id 170 SP RS09755 WP 000642718.1             LKPMVLNQL...LPKLM.TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA   232
NTDB id 280 KZH43 RS08670 WP 000642700.1          LKPMVLNQL...LPKLM.TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA   232
NTDB id 205 SPR RS08830 WP 000642700.1            LKPMVLNQL...LPKLM.TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA   232
NTDB id 239 SPD RS09270 WP 000642701.1            LKPMVLNQL...LPKLM.TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA   232
NTDB id 510 SM12261 RS08320 WP 000642690.1        LKPMVLNQL...LPKLM.TGSKLHSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV   232
NTDB id 538 SMSK321 RS11060 WP 000642686.1        LKPMVLNQL...LPKLM.TGSKLYSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV   232
NTDB id 79338 KH172YL63 RS08050 WP 173105619.1    MRPMFSAYGKQAIYALLKKKEIIHSRVLRFFGIGEAQLETELEELIDQQSNPTIAPLAADGEVTLRLTAKHESEDVAGKL   235
NTDB id 124 BSU 16930 NP 389575.2                 LRPMFENEAKPLLLKKMGSNEKIVSTVLRFFGIGESQLEADLEDIIDAQTNPTIAPLAADGEVTLRLTAKHADEKETERL   239
consensus                                         ***!*****    ***** ******!*!!!!!!!!!**!***!***!**!**!!!*!!*!**!!!!*!!**!*********
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NTDB id 462 GPW51 RS00385 WP 012774894.1      LNQLEEDILQHD.....KLADYFYAYGEDNSLVKTVATRLAEKRQTIAIVEQGTGGLLQAELSLALADQPYFSGGKVVGQ  308
NTDB id 412 SMU RS09535 WP 002262393.1        LDKLEKKIITID.....NLADYFYGYGEENSLPQVVFDLLKEKGKTITAAESLTAGLFQARLADFAGASDIFKGGFITYS  308
NTDB id 170 SP RS09755 WP 000642718.1         LDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFKGGFVTYS  312
NTDB id 280 KZH43 RS08670 WP 000642700.1      LDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTYS  312
NTDB id 205 SPR RS08830 WP 000642700.1        LDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTYS  312
NTDB id 239 SPD RS09270 WP 000642701.1        LDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTYS  312
NTDB id 510 SM12261 RS08320 WP 000642690.1    LDILENQILGRQTFEGLSLRDLCYGYGEETSLASIVVEELKRQGKTITSAESLTAGLFQARVADFSGASSIFKGGFVTYS  312
NTDB id 538 SMSK321 RS11060 WP 000642686.1    LDILENQILGRQTFEGLSLRDLCYGYGEEASLASIVVEELKKQGKTITAAESLTAGLFQATVADFSGASSIFKGGFVTYS  312
NTDB id 79338 KH172YL63 RS08050 WP 173105619.1 LDDVEEEIMKV.......AGEYFYGYNE.DSLVGVGFNLMKEKKLTLSCAESLTGGLFQSQLASLKGASSVLNGGVVCYQ  307
NTDB id 124 BSU 16930 NP 389575.2             LKETEAVILER.......VGEFFYGYDD.TSLVKELSIACKEKGITISAAESFTGGLFSEWLTDHSGASKLFAGGVVCYT  311
consensus                                     !***!**!** ************!*!****!!**************!****!**!*!!****** ********* !!*****
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NTDB id 462 GPW51 RS00385 WP 012774894.1      LGIES.................GWLS.EEADCIRQELQADLGLAVSVLIKPESTEDNVLAKVYLTLATPSGI.SQKEIDL  369
NTDB id 412 SMU RS09535 WP 002262393.1        IEEKARMLGIPFEDLQLHGVVSAFTAEKMAERSRQLTQADLAISLTGVAGPDSLEGQPAGTVFIGLSSSKRT.MAIKVLI  387
NTDB id 170 SP RS09755 WP 000642718.1         LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGT.EVIKVNI  391
NTDB id 280 KZH43 RS08670 WP 000642700.1      LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGT.EVIKVNI  391
NTDB id 205 SPR RS08830 WP 000642700.1        LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGT.EVIKVNI  391
NTDB id 239 SPD RS09270 WP 000642701.1        LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGT.EVIKVNI  391
NTDB id 510 SM12261 RS08320 WP 000642690.1    LEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARIKTQSDFGLSLTGVAGPDSLEGHPAGTVFIGLAQEQGT.EVIKVNI  391
NTDB id 538 SMSK321 RS11060 WP 000642686.1    LEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPAGTVFIGLAQEHGT.KVIKVNI  391
NTDB id 79338 KH172YL63 RS08050 WP 173105619.1 DEVKTKVLSVRESTLKTHSAVSEQCAKELAENVRVLLASDIGISFTGVAGPGEHEGHPSGTVWIGLAQDGQPTKAFKLNL  387
NTDB id 124 BSU 16930 NP 389575.2             NDVKQNVLGVKKETLDRFGAVSKECASELAKGVQKLTGSDIGISFTGVAGPDAQEGHEPGHVFIGISANGKE.EVHEFHF  390
consensus                                     ********** * ****************!**********!**********!***!*******!********** *******
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NTDB id 462 GPW51 RS00385 WP 012774894.1      GGYSWQYLRQLACLQAWDFVRNTL.......   393
NTDB id 412 SMU RS09535 WP 002262393.1        GGRSRSDVRYIAVLHAFNLVRQTLLSHKNLV   418
NTDB id 170 SP RS09755 WP 000642718.1         GGRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 280 KZH43 RS08670 WP 000642700.1      GGRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 205 SPR RS08830 WP 000642700.1        GGRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 239 SPD RS09270 WP 000642701.1        GGRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 510 SM12261 RS08320 WP 000642690.1    GGRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 538 SMSK321 RS11060 WP 000642686.1    GGRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 79338 KH172YL63 RS08050 WP 173105619.1 AG.GRNGNRLRATKFGWHYLIKSLS......   411
NTDB id 124 BSU 16930 NP 389575.2             AG.SRTGIRKRGAKYGCHLILKLLEQK....   416
consensus                                     *!******!***************!***
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X non conserved
X similar
X ≥ 50% conserved