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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 1106634 ACN6MY RS10510 WP 419883881.1  ....MDAEIIAVGSELLLGQIANTNGQFLSRQFAEMGINVFYHTVAGDNAGRLKSAIEAAEKRANLIVFTGGLGPTKDDL   76
NTDB id 124 BSU 16930 NP 389575.2               MEFPKKAEIIAVGSELLLGQIANTNAQFISKQLAEIGVNVFYHTAVGDNPERLKQVIRIAEERSDFIIFSGGLGPTKDDL   80
consensus                                           ***!*!!!!*!*!*!!!*!!!*!!*!***!!*!**!***!**!!!* !!******!**!*******!!!!*!*!!!
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NTDB id 462 GPW51 RS00385 WP 012774894.1        TKQTLATFLGRNLVFDELAMAKLDRFFASRPGRVRTPNNERQAQIVEGSQALQNPAGLAVGGMIEQDGVTYIVLPGPPSE   156
NTDB id 412 SMU RS09535 WP 002262393.1          TKQTLAKFLKRELVFDKTAQERLDEFFASRPTSMRTPNNECQAQIIAGSQPLSNKTGLAVGGLLEADGVTYVVLPGPPSE   156
NTDB id 170 SP RS09755 WP 000642718.1           TKQTLAKFLGKALVFDPQAQEKLDIFFTLRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE   156
NTDB id 280 KZH43 RS08670 WP 000642700.1        TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE   156
NTDB id 205 SPR RS08830 WP 000642700.1          TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE   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 1106634 ACN6MY RS10510 WP 419883881.1  TKETISKHLGKKLVYDEAALASIKAYFQ.KTGREMTENNKKQALILEGSEVLPNDHGMAPGMVLDSNGKSYMLLPGPPKE   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        LKAMFSESLLPLLS...QSQQQLYSRVLRFFGIGESQLVTVLADVIDKQTDPTLAPYAKVGEVTLRLSTKATSQEEANLR   233
NTDB id 412 SMU RS09535 WP 002262393.1          LKPMVNKELLPYLS...KTSEKLYSRVLRFFGIGESHLVTLLHDLIAEQTDPTIAPYAKTGEVTIRLSTKAHRQKEADSK   233
NTDB id 170 SP RS09755 WP 000642718.1           LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA   232
NTDB id 280 KZH43 RS08670 WP 000642700.1        LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA   232
NTDB id 205 SPR RS08830 WP 000642700.1          LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA   232
NTDB id 239 SPD RS09270 WP 000642701.1          LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA   232
NTDB id 510 SM12261 RS08320 WP 000642690.1      LKPMVLNQLLPKLM....TGSKLHSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV   232
NTDB id 538 SMSK321 RS11060 WP 000642686.1      LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV   232
NTDB id 1106634 ACN6MY RS10510 WP 419883881.1  MNPMFVSYGHKSLMGKLDKHEIIESKVLRFFGIGEALLETRIADLLDGQGNPTIAPLASDGEVTLRITAKNESREKCAEL   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          LDKLEKKITTID.....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 1106634 ACN6MY RS10510 WP 419883881.1  IQQAEKSIME.......RVGKYYYGEGD.TSLIKELVKEMTARGLTIASAESLTGGMFQEQLTTIPGAGKIFKGGVVAYS   307
NTDB id 124 BSU 16930 NP 389575.2               LKETEAVILE.......RVGEFFYGYDD.TSLVKELSIACKEKGITISAAESFTGGLFSEWLTDHSGASKLFAGGVVCYT   311
consensus                                       ****!**!** ************!******!!*************!!***!**!*!******* *******!*!!*****

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NTDB id 462 GPW51 RS00385 WP 012774894.1        LGIES.................GWLS.EEADCIRQELQADLGLAVSVLIKPESTEDNVLAKVYLTLATPSGISQKEIDLG   370
NTDB id 412 SMU RS09535 WP 002262393.1          IEEKARMLGIPFEDLQLHGVVSAFTAEKMAERSRQLTQADLAISLTGVAGPDSLEGQPAGTVFIGLSSSKRTMAIKVLIG   388
NTDB id 170 SP RS09755 WP 000642718.1           LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNIG   392
NTDB id 280 KZH43 RS08670 WP 000642700.1        LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNIG   392
NTDB id 205 SPR RS08830 WP 000642700.1          LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNIG   392
NTDB id 239 SPD RS09270 WP 000642701.1          LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNIG   392
NTDB id 510 SM12261 RS08320 WP 000642690.1      LEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARIKTQSDFGLSLTGVAGPDSLEGHPAGTVFIGLAQEQGTEVIKVNIG   392
NTDB id 538 SMSK321 RS11060 WP 000642686.1      LEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPAGTVFIGLAQEHGTKVIKVNIG   392
NTDB id 1106634 ACN6MY RS10510 WP 419883881.1  TEVKEKVLKITPETISSHGVVSMECAGEMAVNIRTMMDADVGISFTGVAGPDEQEGKPVGTVFIGISIGDKKPIIERLNL   387
NTDB id 124 BSU 16930 NP 389575.2               NDVKQNVLGVKKETLDRFGAVSKECASELAKGVQKLTGSDIGISFTGVAGPDAQEGHEPGHVFIGISANGKEE.VHEFHF   390
consensus                                       *********** * ***************!*********!***********!***!******!******************

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NTDB id 462 GPW51 RS00385 WP 012774894.1        GYSWQYLRQLACLQAWDFVRNTL.......   393
NTDB id 412 SMU RS09535 WP 002262393.1          GRSRSDVRYIAVLHAFNLVRQTLLSHKNLV   418
NTDB id 170 SP RS09755 WP 000642718.1           GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 280 KZH43 RS08670 WP 000642700.1        GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 205 SPR RS08830 WP 000642700.1          GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 239 SPD RS09270 WP 000642701.1          GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 510 SM12261 RS08320 WP 000642690.1      GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 538 SMSK321 RS11060 WP 000642686.1      GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 1106634 ACN6MY RS10510 WP 419883881.1  SGSRAQIRMRSVKYGCRFLIRRLKDLI...   414
NTDB id 124 BSU 16930 NP 389575.2               AGSRTGIRKRGAKYGCHLILKLLEQK....   416
consensus                                       **!****!**************!***
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X non conserved

X similar

X ≥ 50% conserved