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NTDB id 124 BSU 16930 NP 389575.2              MEFPKKAEIIAVGSELLLGQIANTNAQFISKQLAEIGVNVFYHTAVGDNPERLKQVIRIAEERSDFIIFSGGLGPTKDDL   80
NTDB id 250061 CO995 RS13580 WP 002296026.1    ....MKAEIIAVGTELLLGQVVNTNATFLSEQLADLGIEVYYQTVVGDNQQRLEELIALAETRSELILLCGGLGPTEDDL   76
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 538 SMSK321 RS11060 WP 000642686.1     ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEARLLSLLEIASQRSSLVILTGGLGPTEDDL   76
NTDB id 510 SM12261 RS08320 WP 000642690.1     ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEARLLSLLEIASQRSSLVILTGGLGPTEDDL   76
consensus                                       *!*!*!!!!*!*!*!!**!!!**!*!***!**!**!***!*!!!!* !!*******!**!!******!!!!*!*!!!
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NTDB id 124 BSU 16930 NP 389575.2              TKETIANTLGRPLVLNDEAFQSIEDYFKRTKR.TMSPNNRKQALVIEGSDVLANHFGMAPGMLTEHESRYYMLLPGPPSE   159
NTDB id 250061 CO995 RS13580 WP 002296026.1    TKEATAAHLGKSLIQNTEGYKKLLAYFETTHR.KMTKNNLQQSQIIEGGVPLPNRTGLALGTFYQTDTHAYILLPGPPNE   155
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 538 SMSK321 RS11060 WP 000642686.1     TKQTLAKFLGKELVFDPQAQEKLDVFFAQRPDYARTPNNERQAQIVEGATPLPNETGLAVGGILEVDGVTYVVLPGPPSE   156
NTDB id 510 SM12261 RS08320 WP 000642690.1     TKQTLAKFLGKELVFDPQAQEKLDVFFAQRPDYARTPNNERQAQLVEGAIPLPNETGLAVGGILEVDGVTYVVLPGPPSE   156
consensus                                       !!***!**!** !*************!* ********!!**!*****!***!*!**!*!*!**********!**!!!!!*!
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NTDB id 124 BSU 16930 NP 389575.2              LRPMFENEAKPLLLKKMGSNEKIVSTVLRFFGIGESQLEADLEDIIDAQTNPTIAPLAADGEVTLRLTAKHADFKETERL   239
NTDB id 250061 CO995 RS13580 WP 002296026.1    LKPMFVEQVRPLLEERFPSEEKLISKVLRFYGIGESRLVTELKDLIETQINPTIAPYAKPNEVTLRLTVKTNDVQAGNQA   235
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 538 SMSK321 RS11060 WP 000642686.1     LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV   232
NTDB id 510 SM12261 RS08320 WP 000642690.1     LKPMVLNQLLPKLM....TGSKLHSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV   232
consensus                                       !**!******!*!*     *****!*!!!!*!!!!!*!***!*!*!**! *!!*!!*!**!!!*!!**!*********
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NTDB id 124 BSU 16930 NP 389575.2                LKETEAVILE.......RVGEFFYGYDD.TSLVKELSIACKEKGITISAAESFTGGLFSEWLTDHSGASKLFAGGVVCYT   311
NTDB id 250061 CO995 RS13580 WP 002296026.1      LLALEEKIQF.......RVGEYFYGYGDDNSLAKVVVELLKENKQTVTAAESLTAGAFQAALGDIAGVSEVFPGGFVTYS   308
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 538 SMSK321 RS11060 WP 000642686.1       LDILENQILGRQTFEGLSLRDLCYGYGEEASLASIVVEELKKQGKTITAAESLTAGLFQATVADFSGASSIFKGGFVTYS   312
NTDB id 510 SM12261 RS08320 WP 000642690.1       LDILENQILGRQTFEGLSLRDLCYGYGEETSLASIVVEELKRQGKTITSAESLTAGLFQARVADFSGASSIFKGGFVTYS   312
consensus                                        !***!**!** ***************!*!****!!***************!****!**!*!****************!  !!*****
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NTDB id 124 BSU 16930 NP 389575.2                NDVKQNVLGVKKETLDRFGAVSKECASELAKGVQKLIGSDIGISFTGVAGPDAQEGHEPGHVFIGISANGKEEVHEFHFA   391
NTDB id 250061 CO995 RS13580 WP 002296026.1      LQTKAGFLEIDPELLAEYGTVSKECVEQMAIQAREIARTDYSVAFTGVAGPDTLEGQSAGTVWIAISSKDGVVSEKYHF.   387
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 538 SMSK321 RS11060 WP 000642686.1       LEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPAGTVFIGLAQEHGTKVIKVNIG   392
NTDB id 510 SM12261 RS08320 WP 000642690.1       LEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARIKTQSDFGLSLTGVAGPDSLEGHPAGTVFIGLAQEQGTEVIKVNIG   392
consensus                                        ********** * ***************!*********!**********!***!******!*******************
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NTDB id 124 BSU 16930 NP 389575.2                GS.RTGIRKRGAKYGCHLILKLLEQK....   416
NTDB id 250061 CO995 RS13580 WP 002296026.1      ARDRAAIRYNAVMQGFDLLRKQLLRK....   413
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 538 SMSK321 RS11060 WP 000642686.1       GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 510 SM12261 RS08320 WP 000642690.1       GRSRADVRHIAVMHAFNLVRKALLSD....   418
consensus                                        *******!**************!***
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X non conserved

X similar

X ≥ 50% conserved