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logo

NTDB id 124 BSU 16930 NP 389575.2              MEFPKKAEIIAVGSELLLGQIANTNAQFISKQLAEIGVNVFYHTAVGDNPERLKQVIRIAEERSDFIIFSGGLGPTKDDL   80
NTDB id 1045090 ACEPSM RS10515 WP 395321105.1  ....MQAEIIAVGTEILLGQVVDTNSAYIAQGLADAGIEVYYHSLVGDNADRLTTVVNQARSRSDLVVISGGLGPTKDDL   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              TKETIANTLGRPLVLNDEAFQSIEDYFKRT.KRTMSPNNRKQALVIEGSDVLANHFGMAPGMLTE.HESRYYMLLPGPPS  158
NTDB id 1045090 ACEPSM RS10515 WP 395321105.1  TKQTVAQLLGVKLVEDAPAMAKIQRHFATT.GQKLTPNNRLQALYLAGSTLLKNSTGMAVGSFYRDPHGADLMLLPGPPS  155
NTDB id 462 GPW51 RS00385 WP 012774894.1       TKQTLATFLGRNLVFDELAMAKLDRFFASRPGRVRTPNNERQAQIVEGSQALQNPAGLAVGGMIE.QDGVTYIVLPGPPS  155
NTDB id 412 SMU RS09535 WP 002262393.1         TKQTLAKFLKRELVFDKTAQERLDEFFASRPTSMRTPNNECQAQIIAGSQPLSNKTGLAVGGLLE.ADGVTYVVLPGPPS  155
NTDB id 170 SP RS09755 WP 000642718.1          TKQTLAKFLGKALVFDPQAQEKLDIFFTLRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLE.VDGVTYVVLPGPPS  155
NTDB id 280 KZH43 RS08670 WP 000642700.1       TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLE.VDGVTYVVLPGPPS  155
NTDB id 205 SPR RS08830 WP 000642700.1         TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLE.VDGVTYVVLPGPPS  155
NTDB id 239 SPD RS09270 WP 000642701.1         TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQVQIVEGAIPLPNETGLAVGGKLE.VDGVTYVVLPGPPS  155
NTDB id 538 SMSK321 RS11060 WP 000642686.1     TKQTLAKFLGKELVFDPQAQEKLDVFFAQRPDYARTPNNERQAQIVEGATPLPNETGLAVGGILE.VDGVTYVVLPGPPS  155
NTDB id 510 SM12261 RS08320 WP 000642690.1     TKQTLAKFLGKELVFDPQAQEKLDVFFAQRPDYARTPNNERQAQLVEGAIPLPNETGLAVGGILE.VDGVTYVVLPGPPS  155
consensus                                      !!*!*!**!** !!*****!*******!* *******!!!**!*****!***!*!**!*!*!**** ********!!!!!!

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NTDB id 124 BSU 16930 NP 389575.2              ELRPMFENEAKPLLLKKMGSNEKIVSTVLRFFGIGESQLEADLEDIIDAQTNPTIAPLAADGEVTLRLTAKHADEKETER  238
NTDB id 1045090 ACEPSM RS10515 WP 395321105.1  ELEPMFENEALPRLEQAYRRQEFLVSRVLRFFGIGEAELVTQLADLIDEQTNPTIAPYAKVNEVTLRLTAAASSTAACNQ  235
NTDB id 462 GPW51 RS00385 WP 012774894.1       ELKAMFSESLLPLLSQS...QQQLYSRVLRFFGIGESQLVTVLADVIDKQTDPTLAPYAKVGEVTLRLSTKATSQEEANL  232
NTDB id 412 SMU RS09535 WP 002262393.1         ELKPMVNKELLPYLSKT...SEKLYSRVLRFFGIGESHLVTLLHDLIAEQTDPTIAPYAKTGEVTIRLSTKAHRQKEADS  232
NTDB id 170 SP RS09755 WP 000642718.1          ELKPMVLNQLLPKLM.T...GSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQ  231
NTDB id 280 KZH43 RS08670 WP 000642700.1       ELKPMVLNQLLPKLM.T...GSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQ  231
NTDB id 205 SPR RS08830 WP 000642700.1         ELKPMVLNQLLPKLM.T...GSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQ  231
NTDB id 239 SPD RS09270 WP 000642701.1         ELKPMVLNQLLPKLM.T...GSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQ  231
NTDB id 538 SMSK321 RS11060 WP 000642686.1     ELKPMVLNQLLPKLM.T...GSKLYSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQ  231
NTDB id 510 SM12261 RS08320 WP 000642690.1     ELKPMVLNQLLPKLM.T...GSKLHSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQ  231
consensus                                      !!**!******!*!* *   *****!*!!!!!!!!!!**!***!*!*!**!**!!*!!*!***!!!*!!************
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NTDB id 124 BSU 16930 NP 389575.2                LLKETEAVILE.......RVGEFFYGYDD.TSLVKELSIACKEKGITISAAESFTGGLFSEWLTDHSGASKLFAGGVVCY   310
NTDB id 1045090 ACEPSM RS10515 WP 395321105.1    LLDDMTATIQN.......RVGDFLYGYGDDNSLAQVVVNTLIDRHLTITAAESLTAGKFQSTLGDVPGVSAVFPGGFVTY   308
NTDB id 462 GPW51 RS00385 WP 012774894.1         RLNQLEEDILQHD.....KLADYFYAYGEDNSLVKTVATRLAEKRQTIAIVEQGTGGLLQAELSLALADQPYFSGGKVVG   307
NTDB id 412 SMU RS09535 WP 002262393.1           KLDKLEKKIITID.....NLADYFYGYGEENSLPQVVFDLLKEKGKTITAAESLTAGLFQARLADFAGASDIFKGGFITY   307
NTDB id 170 SP RS09755 WP 000642718.1            ALDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFKGGFVTY   311
NTDB id 280 KZH43 RS08670 WP 000642700.1         ALDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTY   311
NTDB id 205 SPR RS08830 WP 000642700.1           ALDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTY   311
NTDB id 239 SPD RS09270 WP 000642701.1           ALDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTY   311
NTDB id 538 SMSK321 RS11060 WP 000642686.1       VLDILENQILGRQTFEGLSLRDLCYGYGEEASLASIVVEELKKQGKTITAAESLTAGLFQATVADFSGASSIFKGGFVTY   311
NTDB id 510 SM12261 RS08320 WP 000642690.1       VLDILENQILGRQTFEGLSLRDLCYGYGEETSLASIVVEELKRQGKTITSAESLTAGLFQARVADFSGASSIFKGGFVTY   311
consensus                                         !******!** ************!*!****!!**************!!***!**!*!***************!  !!****

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NTDB id 124 BSU 16930 NP 389575.2                TNDVKQNVLGVKKETLDRFGAVSKECASELAKGVQKLTGSDIGISFTGVAGPDAQEGHEPGHVFIGISANGKEEVHEFHF   390
NTDB id 1045090 ACEPSM RS10515 WP 395321105.1    ANDAKRDLLGIPQQVIDTDGVVSEHTAQEMAERSREKLNTDFALSFTGVAGPDALEGQPAGTVWLGLAQRNQAPQAKLVH   388
NTDB id 462 GPW51 RS00385 WP 012774894.1         QLGIES.................GWLS.EEADCIRQELQADLGLAVSVLIKPESTEDNVLAKVYLTLATPSGISQKEIDL   369
NTDB id 412 SMU RS09535 WP 002262393.1           SIEEKARMLGIPFEDLQLHGVVSAFTAEKMAERSRQLTQADLAISLTGVAGPDSLEGQPAGTVFIGLSSSKRTMAIKVLI   387
NTDB id 170 SP RS09755 WP 000642718.1            SLEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNI   391
NTDB id 280 KZH43 RS08670 WP 000642700.1         SLEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNI   391
NTDB id 205 SPR RS08830 WP 000642700.1           SLEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNI   391
NTDB id 239 SPD RS09270 WP 000642701.1           SLEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNI   391
NTDB id 538 SMSK321 RS11060 WP 000642686.1       SLEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPAGTVFIGLAQEHGTKVIKVNI   391
NTDB id 510 SM12261 RS08320 WP 000642690.1       SLEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARIKTQSDFGLSLTGVAGPDSLEGHPAGTVFIGLAQEQGTEVIKVNI   391
consensus                                        ************ * ***************!*********!***********!***!******!******************

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NTDB id 124 BSU 16930 NP 389575.2                .AGSRTGIRKRGAKYGCHLILKLLEQK....   416
NTDB id 1045090 ACEPSM RS10515 WP 395321105.1    LTGNRAKVRERAVMQALDWLRRILRDQK...   416
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 538 SMSK321 RS11060 WP 000642686.1       GGRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 510 SM12261 RS08320 WP 000642690.1       GGRSRADVRHIAVMHAFNLVRKALLSD....   418
consensus                                        ********!**************!***
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X non conserved

X similar

X ≥ 50% conserved