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NTDB id 626 LCA RS04960 WP 011374694.1      MLTKNQLLLKVHLAAGFGTISELRLAAWLSTSHNWALSALEIAQIARLPERYWPTFQASFQSTTLQRQCIDHEVRTTYLT  80
NTDB id 407 SMU RS04605 WP 002262865.1      ..MDNFQLFKLK.KAGLTNLNILNIIDYEE.RTQKSLSLRDMAVVSKN..KKPLIFMEHYKNLDSKAL.RKEFNRFPSLS  73
NTDB id 525 SMSK321 RS06295 WP 000705298.1  MKITNYEIYKLK.KSGLTNQQILKVLEYGE.NVDQELLLGDIADISGC..RNPAVFMERYFQIDDAHL.EKEFKKIPSFS  75
NTDB id 267 KZH43 RS05590 WP 000705306.1    MKITNYEIYKLK.KSGLTNQQILKVLEYGE.NVDQELLLGDIADISGC..RNPAVFMERYFQIDDAHL.SKEFQKFPSFS  75
NTDB id 226 SPD RS05990 WP 000705306.1      MKITNYEIYKLK.KSGLTNQQILKVLEYGE.NVDQELLLGDIADISGC..RNPAVFMERYFQIDDAHL.SKEFQKFPSFS  75
NTDB id 192 SPR RS05715 WP 000705306.1      MKITNYEIYKLK.KSGLTNQQILKVLEYGE.NVDQELLLGDIADISGC..RNPAVFMERYFQIDDAHL.SKEFQKFPSFS  75
NTDB id 157 SP RS06205 WP 000705306.1       MKITNYEIYKLK.KSGLTNQQILKVLEYGE.NVDQELLLGDIADISGC..RNPAVFMERYFQIDDAHL.SKEFQKFPSFS  75
NTDB id 497 SM12261 RS05565 WP 000705318.1  MKITNYEIYKLK.KSGLTNQQVLAVLEYGE.NVDQELLLGDIAEISGC..RNPAVFMERYFQIDDAHL.EKEFQKFPSFS  75
NTDB id 399196 GIG89 RS05190 WP 019291673.1 .MIKNFEILRLK.KAGMSNLGILKLIDYQR.RHEARLTLRQLSRIAEV..KTVPNFIESYKSQDVKRL.REQYKIFPSFS  74
NTDB id 599 KW2 RS05940 WP 021037268.1      .MITNFDLFRWK.KAGMTNLGVNKLLKFFR.KYDRKISLRQMGQVAQV..KSIPNFIEQYKNQDVKKL.RADYKKFSSFS  74
consensus                                   ****!*******  **!***************  ******************   *****!************   **********
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NTDB id 626 LCA RS04960 WP 011374694.1      ILDKDYPQRLLETYLPPVLLFYRGDLRLLKQPCLAVVGARQATHYSKQSLEQLLQGLTA.TTIISGLAQGADAMAHEVAL  159
NTDB id 407 SMU RS04605 WP 002262865.1      ILDKEYPLELKNIYNPPVLLFYQGDLDLLARPKLAVVGSRNASQMGVAAVKKIIQDLSKQFVIISGLARGIDTAAHLASL  153
NTDB id 525 SMSK321 RS06295 WP 000705298.1  ILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRSCSKQGAKSVEKIIQGLENELVIVSGLAKGIDTAAHMAAL  155
NTDB id 267 KZH43 RS05590 WP 000705306.1    ILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTAAHMAAL  155
NTDB id 226 SPD RS05990 WP 000705306.1      ILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTAAHMAAL  155
NTDB id 192 SPR RS05715 WP 000705306.1      ILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTAAHMAAL  155
NTDB id 157 SP RS06205 WP 000705306.1       ILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTAAHMAAL  155
NTDB id 497 SM12261 RS05565 WP 000705318.1  ILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTAAHMAAL  155
NTDB id 399196 GIG89 RS05190 WP 019291673.1 ILDDIYPEWLRETYNPPALLFYRGDLKLLSLPKLGFVGSREMSKEAPRIIHKLIEELKQNFVIVSGLARGVDTSSHVAAV  154
NTDB id 599 KW2 RS05940 WP 021037268.1      ILDDLYPERLREIYNPPVLIFYQGNIDLLKNPKLAFVGSRLAGQSGIKSVQKIVTELNQSFTIVSGLAKGIDTASHLSAI  154
consensus                                   !!!**!!**!***!**!*!*!!*!***!!**!****!!*!*****************!*****!*!!!!*!*!***!****
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NTDB id 626 LCA RS04960 WP 011374694.1      QRGLAPIGVIGTGINCSYPPQNEHLQQVVAEKGLLLSEYALGTPARRYQFPARNKIIAGLCHSLIVTEARHKSGSLITAN  239
NTDB id 407 SMU RS04605 WP 002262865.1      KSGGATIAVIGTGLDVHYPKENRRLQDYIAKNHLLLSEYEAQSQPLKYHFPERNRIIAGLSQGVMVAEAKIRSGSLITCE  233
NTDB id 525 SMSK321 RS06295 WP 000705298.1  QNGGKTIAVIGTGLDVFYPKANKRLQDYISNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCE  235
NTDB id 267 KZH43 RS05590 WP 000705306.1    QNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCE  235
NTDB id 226 SPD RS05990 WP 000705306.1      QNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCE  235
NTDB id 192 SPR RS05715 WP 000705306.1      QNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCE  235
NTDB id 157 SP RS06205 WP 000705306.1       QNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCE  235
NTDB id 497 SM12261 RS05565 WP 000705318.1  QNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCE  235
NTDB id 399196 GIG89 RS05190 WP 019291673.1 KQKTPTIAVIGNGLDISYPKENRKLQEYLAAHELVLSEYLVGEQPLKFHFPERNRIIAGLSRGVVVVEAKQRSGSLITSR  234
NTDB id 599 KW2 RS05940 WP 021037268.1      KTKTPTIAVIGTGLDIFYPLENRKIQEYLAKYQLVLSEYSLGEKPLKYHFPERNRIIAGLSRGVVVVEAKLRSGSLITCE  234
consensus                                   ******!*!!!*!****!!**!***!*******!*!!!!**********!!*!!*!!!!!*****!*!!***!!!!!!**
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NTDB id 626 LCA RS04960 WP 011374694.1      LALQANRNVYAIPGRIDQSLSQGCNQLIAAGATPLLDKNI.LIEELRYFD.....   288
NTDB id 407 SMU RS04605 WP 002262865.1      RAMEEGRDVFVVPGNILDGQSEGCHHLIQEGAK.CITSGFDILNEFNF.......   280
NTDB id 525 SMSK321 RS06295 WP 000705298.1  RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAK.LVTSGQDVLAEFEF.......   282
NTDB id 267 KZH43 RS05590 WP 000705306.1    RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAK.LVTSGQDVLAEFEF.......   282
NTDB id 226 SPD RS05990 WP 000705306.1      RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAK.LVTSGQDVLAEFEF.......   282
NTDB id 192 SPR RS05715 WP 000705306.1      RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAK.LVTSGQDVLAEFEF.......   282
NTDB id 157 SP RS06205 WP 000705306.1       RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAK.LVTSGQDVLAEFEF.......   282
NTDB id 497 SM12261 RS05565 WP 000705318.1  RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAK.LVTSGQDVLAEFEF.......   282
NTDB id 399196 GIG89 RS05190 WP 019291673.1 YALEGNREVFAVPGDILNRNASGCNQLIQQGAAKLVTHGQDILDEFYLYEGNFFP   289
NTDB id 599 KW2 RS05940 WP 021037268.1      RALEEGRDIFAIPGNIADGTSDGCNHLIQQGAK.LVYQAQDILEEYLYN......   282
consensus                                   *!****!*****!!*!******!!**!!**!!* **********!***
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X non conserved

X similar

X ≥ 50% conserved