```
logo

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 1074864 ACI1SY RS04850 WP 019291673.1  .MIKNFEILRLK.KAGMSNLGILKLIDYQR.RHEARLTLRQLSRIAEV..KTVPNFIESYKSQDVKRL.REQYKIFPSFS   74
NTDB id 599 KW2 RS05940 WP 021037268.1         .MITNFDLFRWK.KAGMTNLGVNKLLKFFR.KYDRKISLRQMGQVAQV..KSIPNFIEQYKNQDVKKL.RADYKKFSSFS   74
consensus                                       ****!*******  **!**************  *****************  *****!***********  **********

logo

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 1074864 ACI1SY RS04850 WP 019291673.1  ILDDIYPEWLRETYNPPALLFYRGDLKLLSLPKLGFVGSREMSKEAPRIIHKLIEELKQNFVIVSGLARGVDTSSHVAAV   154
NTDB id 599 KW2 RS05940 WP 021037268.1         ILDDLYPERLREIYNPPVLIFYQGNIDLLKNPKLAFVGSRLAGQSGIKSVQKIVTELNQSFTIVSGLAKGIDTASHLSAI   154
consensus                                       !!!**!!**!***!**!*!!*!***!!**!****!!*!****************!*****!*!!!!*!*!***!****

logo

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 1074864 ACI1SY RS04850 WP 019291673.1  KQKTPTIAVIGNGLDISYPKENRKLQEYLAAHELVLSEYLVGEQPLKFHFPERNRIIAGLSRGVVVVEAKQRSGSLITSR   234
NTDB id 599 KW2 RS05940 WP 021037268.1         KTKTPTIAVIGTGLDIFYPLENRKIQEYLAKYQLVLSEYSLGEKPLKYHFPERNRIIAGLSRGVVVVEAKLRSGSLITCE   234
consensus                                       ******!*!!!*!****!!**!***!*******!*!!!!**********!!*!!*!!!!!*****!*!!***!!!!!!**
```

```
logo

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 1074864 ACI1SY RS04850 WP 019291673.1 YALEGNREVFAVPGDILNRNASGCNQLIQQGAAKLVTHGQDILDEFYLYEGNFFP   289
NTDB id 599 KW2 RS05940 WP 021037268.1        RALEEGRDIFAIPGNIADGTSDGCNHLIQQGAK.LVYQAQDILEEYLYN......   282
consensus                                     *!****!*****!!*!******!!**!!**!!* **********!***
```

X non conserved

X similar

X $\geq$ 50% conserved