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logo
NTDB id 626 LCA RS04960 WP 011374694.1          MLTKNQLLLKVHLAAGFGTISELRLAAWLSTSHNWALSALEIAQIARLPERYWPTFQASFQSTTLQRQCIDHEVRTTYLT   80
NTDB id 599 KW2 RS05940 WP 021037268.1          .MITNFDLFRW.KKAGMTNLGVNKLLKFFRK.YDRKISLRQMGQVAQVK..SIPNFIEQYKNQDVK.KLRADYKKFSSFS   74
NTDB id 525 SMSK321 RS06295 WP 000705298.1      MKITNYEIYKL.KKSGLTNQQILKVLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLEKEFKKIPSFS   75
NTDB id 267 KZH43 RS05590 WP 000705306.1        MKITNYEIYKL.KKSGLTNQQILKVLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLSKEFQKFPSFS   75
NTDB id 226 SPD RS05990 WP 000705306.1          MKITNYEIYKL.KKSGLTNQQILKVLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLSKEFQKFPSFS   75
NTDB id 192 SPR RS05715 WP 000705306.1          MKITNYEIYKL.KKSGLTNQQILKVLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLSKEFQKFPSFS   75
NTDB id 157 SP RS06205 WP 000705306.1           MKITNYEIYKL.KKSGLTNQQILKVLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLSKEFQKFPSFS   75
NTDB id 497 SM12261 RS05565 WP 000705318.1      MKITNYEIYKL.KKSGLTNQQVLAVLEYGEN.VDQELLLGDIAEISGCR..NPAVFMERYFQIDDA.HLEKEFQKFPSFS   75
NTDB id 1097373 ACM3HZ RS06000 WP 001015240.1  ..MNHFELFKL.KKAGLTNLNIHNIINYLKKNSLTSLSVRNMAVVSKCK..NPTFFIENYKQLDLK.KLRQEFKKFPVLS   74
NTDB id 407 SMU RS04605 WP 002262865.1          ..MDNFQLFKL.KKAGLTNLNILNIIDYEER.TQKSLSLRDMAVVSKNK..KPLIFMEHYKNLDSK.ALRKEFNRFPSLS   73
consensus                                       *********** ***!*************** ****************  ****!********** ** *********

logo
NTDB id 626 LCA RS04960 WP 011374694.1          ILDKDYPQRLLETYLPPVLLFYRGDLRLLKQPCLAVVGARQATHYSKQSLEQLLQGLTA.TTIISGLAQGADAMAHEVAL   159
NTDB id 599 KW2 RS05940 WP 021037268.1          ILDDLYPERLREIYNPPVLIFYQGNIDLLKNPKLAFVGSRLAGQSGIKSVQKIVTELNQSFTIVSGLAKGIDTASHLSAI   154
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 1097373 ACM3HZ RS06000 WP 001015240.1  ILDSNYPLELKEIYNPPVLLFYQGNIELLSKPKLAVVGARQASQIGCQSVKKIIKETNNQFVIVSGLARGIDTAAHVSAL   154
NTDB id 407 SMU RS04605 WP 002262865.1          ILDKEYPLELKNIYNPPVLLFYQGDLDLLARPKLAVVGSRNASQMGVAAVKKIIQDLSKQFVIISGLARGIDTAAHLASL   153
consensus                                       !!!**!!**!***!**!!!*!!*!***!!**!**!*!!*!**********************!*!!!!*!*!***!****

logo
NTDB id 626 LCA RS04960 WP 011374694.1          QRGLAPIGVIGTGINCSYPPQNEHLQQVVAEKGLLLSEYALGTPARRYQFPARNKIIAGLCHSLIVTEARHKSGSLITAN   239
NTDB id 599 KW2 RS05940 WP 021037268.1          KTKTPTIAVIGTGLDIFYPLENRKIQEYLAKYQLVLSEYSLGEKPLKYHFPERNRIIAGLSRGVVVVEAKLRSGSLITCE   234
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 1097373 ACM3HZ RS06000 WP 001015240.1  KNGGSSIAVIGSGLDVYYPTENKKLQEYMSYNHLVLSEYFTGEQPLKFHFPERNRIIAGLCQGIVVAEAKMRSGSLITCE   234
NTDB id 407 SMU RS04605 WP 002262865.1          KSGGATIAVIGTGLDVHYPKENRRLQDYIAKNHLLLSEYEAQSQPLKYHFPERNRIIAGLSQGVMVAEAKIRSGSLITCE   233
consensus                                       ******!*!!!*!****!!**!***!*******!*!!!!**********!!*!!*!!!!!*****!*!!***!!!!!!**
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logo

NTDB id 626 LCA RS04960 WP 011374694.1                LALQANRNVYAIPGRIDQSLSQGCNQLIAAGATPLLDKNILIEELRYFD   288
NTDB id 599 KW2 RS05940 WP 021037268.1                RALEEGRDIFAIPGNIADGTSDGCNHLIQQGAKLVYQAQDILEEYLYN.   282
NTDB id 525 SMSK321 RS06295 WP 000705298.1            RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 267 KZH43 RS05590 WP 000705306.1              RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 226 SPD RS05990 WP 000705306.1                RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 192 SPR RS05715 WP 000705306.1                RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 157 SP RS06205 WP 000705306.1                 RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 497 SM12261 RS05565 WP 000705318.1            RAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 1097373 ACM3HZ RS06000 WP 001015240.1         RALEEGREVFAIPGNIIDGKSDGCHHLIQEGAKCIISGKDILSEYQ...   280
NTDB id 407 SMU RS04605 WP 002262865.1                RAMEEGRDVFVVPGNILDGQSEGCHHLIQEGAKCITSGFDILNEFNF..   280
consensus                                             *!****!*****!!*!****!*!!**!!**!!***********!***
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X non conserved

X similar

X $\geq$ 50% conserved