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logo
NTDB id 1361 HI 0985 AAC22646.1          MNDITYTLLRLMQVPKLGGVGIDKILSNITLNELLNYDDV......AFRQMGWGA.IQIRRWFKPEAKFIEPALV...WSQKEGN   75
NTDB id 626 LCA RS04960 WP 011374694.1   MLTKNQLLLKVHLAAGFGTISELR.........LAAWLSTSHNWALSALEIAQIARLPERYWPTFQASFQSTTLQRQCIDHEVRT   76
NTDB id 599 KW2 RS05940 WP 021037268.1   .MITNFDLFRW.KKAGMTNLGVNK.........LLKFFRK.YDRKISLRQMGQVAQVK..SIPNFIEQYKNQDVK.KLRADYKKF   70
NTDB id 525 SMSK321 RS06295 WP 000705298.1 MKITNYEIYKL.KKSGLTNQQILK.........VLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLEKEFKKI   71
NTDB id 267 KZH43 RS05590 WP 000705306.1 MKITNYEIYKL.KKSGLTNQQILK.........VLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLSKEFQKF   71
NTDB id 226 SPD RS05990 WP 000705306.1   MKITNYEIYKL.KKSGLTNQQILK.........VLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLSKEFQKF   71
NTDB id 192 SPR RS05715 WP 000705306.1   MKITNYEIYKL.KKSGLTNQQILK.........VLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLSKEFQKF   71
NTDB id 157 SP RS06205 WP 000705306.1    MKITNYEIYKL.KKSGLTNQQILK.........VLEYGEN.VDQELLLGDIADISGCR..NPAVFMERYFQIDDA.HLSKEFQKF   71
NTDB id 497 SM12261 RS05565 WP 000705318.1 MKITNYEIYKL.KKSGLTNQQVLA.........VLEYGEN.VDQELLLGDIAEISGCR..NPAVFMERYFQIDDA.HLEKEFQKF   71
NTDB id 140402 RDF RS05295 WP 001015250.1 ..MNHFELFKL.KKAGLTNLNINN.........IINYLKKNSLTSLSVRNMAVVSKCK..NPTFFIENYKQLDLK.KLRQEFKKF   70
NTDB id 407 SMU RS04605 WP 002262865.1   ..MDNFQLFKL.KKAGLTNLNILN.........IIDYEER.TQKSLSLRDMAVVSKNK..KPLIFMEHYKNLDSK.ALRKEFNRF   69
consensus                                *********** ***********          *******  ****************   ***************  **  ******

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NTDB id 1361 HI 0985 AAC22646.1          HLVNYFSPFYPFLLKQTASFPPLLFVKGNLTALSQRQMAMVGSRYCTTYGEYWAKHFATELSLAGFTITSGLALGIDGHCHQAVV  160
NTDB id 626 LCA RS04960 WP 011374694.1   TYLTILDKDYPQRLLETYLPPVLLFYRGDLRLLKQPCLAVVGARQATHYSKQSLEQLLQGLT.A.TTIISGLAQGADAMAHEVAL  159
NTDB id 599 KW2 RS05940 WP 021037268.1   SSFSILDDLYPERLREIYNPPVLIFYQGNIDLLKNPKLAFVGSRLAGQSGIKSVQKIVTELN.QSFTIVSGLAKGIDTASHLSAI  154
NTDB id 525 SMSK321 RS06295 WP 000705298.1 PSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRSCSKQGAKSVEKIIQGLE.NELVIVSGLAKGIDTAAHMAAL  155
NTDB id 267 KZH43 RS05590 WP 000705306.1 PSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKGIDTAAHMAAL  155
NTDB id 226 SPD RS05990 WP 000705306.1   PSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKGIDTAAHMAAL  155
NTDB id 192 SPR RS05715 WP 000705306.1   PSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKGIDTAAHMAAL  155
NTDB id 157 SP RS06205 WP 000705306.1    PSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKGIDTAAHMAAL  155
NTDB id 497 SM12261 RS05565 WP 000705318.1 PSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKGIDTAAHMAAL  155
NTDB id 140402 RDF RS05295 WP 001015250.1 PVLSILDSNYPLELKEIYNPPVLLFYQGNIELLSKPKLAVVGARQASQIGCQSVKKIIKETN.NQFVIVSGLARGIDTAAHVSAL  154
NTDB id 407 SMU RS04605 WP 002262865.1   PSLSILDKEYPLELKNIYNPPVLLFYQGDLDLLARPKLAVVGSRNASQMGVAAVKKIIQDLS.KQFVIISGLARGIDTAAHLASL  153
consensus                                *********!!**!******!*!*!**!****!*****!*!!*! ***************** ****!*!!!!*!*!***!****

logo
NTDB id 1361 HI 0985 AAC22646.1          NIQGQTIAVLGSGLEQIYPSKHQRLSAQIIENNGALVSEFLPNQAPIAANFPRRNRIISGLSVGTLVVEATEKSGSLITARYALE  245
NTDB id 626 LCA RS04960 WP 011374694.1   QRGLAPIGVIGTGINCSYPPQNEHLQ.QVVAEKGLLLSEYALGTPARRYQFPARNKIIAGLCHSLIVTEARHKSGSLITANLALQ  243
NTDB id 599 KW2 RS05940 WP 021037268.1   KTKTPTIAVIGTGLDIFYPLENRKIQ.EYLAKYQLVLSEYSLGEKPLKYHFPERNRIIAGLSRGVVVVEAKLRSGSLITCERALE  238
NTDB id 525 SMSK321 RS06295 WP 000705298.1 QNGGKTIAVIGTGLDVFYPKANKRLQ.DYISNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCERAME  239
NTDB id 267 KZH43 RS05590 WP 000705306.1 QNGGKTIAVIGTGLDVFYPKANKRLQ.DYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCERAME  239
NTDB id 226 SPD RS05990 WP 000705306.1   QNGGKTIAVIGTGLDVFYPKANKRLQ.DYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCERAME  239
NTDB id 192 SPR RS05715 WP 000705306.1   QNGGKTIAVIGTGLDVFYPKANKRLQ.DYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCERAME  239
NTDB id 157 SP RS06205 WP 000705306.1    QNGGKTIAVIGTGLDVFYPKANKRLQ.DYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCERAME  239
NTDB id 497 SM12261 RS05565 WP 000705318.1 QNGGKTIAVIGTGLDVFYPKANKRLQ.DYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGSLITCERAME  239
NTDB id 140402 RDF RS05295 WP 001015250.1 KNGGSSIAVIGSGLDVYYPTENKKLQ.EYMSYNHLVLSEYFTGEQPLKFHFPERNRIIAGLCQGIVVAEAKMRSGSLITCERALE  238
NTDB id 407 SMU RS04605 WP 002262865.1   KSGGATIAVIGTGLDVHYPKENRRLQ.DYIAKNHLLLSEYEAQSQPLKYHFPERNRIIAGLSQGVMVAEAKIRSGSLITCERAME  237
consensus                                ******!*!*!*!****!!******* **********!!***********!*!!*!!*!!*****!*!!***!!!!!!***!**
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logo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
NTDB id 1361 HI 0985 AAC22646.1             QNREVFAVPGNIQNKSSQGCHRLIKQGAMLVENAKDILETLYQHSIHSQTEIDFDQIAVPNYTPPPDPRRLVEAPSHPKLYSRIG   330
NTDB id 626 LCA RS04960 WP 011374694.1      ANRNVYAIPGRIDQSLSQGCNQLIAAGATPLLDKNILIEELRYFD........................................   288
NTDB id 599 KW2 RS05940 WP 021037268.1      EGRDIFAIPGNIADGTSDGCNHLIQQGAKLVYQAQDILEEYLYN..........................................   282
NTDB id 525 SMSK321 RS06295 WP 000705298.1  EGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF...........................................   282
NTDB id 267 KZH43 RS05590 WP 000705306.1    EGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF...........................................   282
NTDB id 226 SPD RS05990 WP 000705306.1      EGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF...........................................   282
NTDB id 192 SPR RS05715 WP 000705306.1      EGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF...........................................   282
NTDB id 157 SP RS06205 WP 000705306.1       EGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF...........................................   282
NTDB id 497 SM12261 RS05565 WP 000705318.1  EGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF...........................................   282
NTDB id 140402 RDF RS05295 WP 001015250.1   EGREVFAIPGNIIDGKSDGCHHLIQEGAKCIISGKDILSEYQ............................................   280
NTDB id 407 SMU RS04605 WP 002262865.1      EGRDVFVVPGNILDGQSEGCHHLIQEGAKCITSGFDILNEFNF...........................................   280
consensus                                   **!*****!!*!****!*!!**!!**!!**************
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logo
                                            YTPVSIDDLAEEFNLSVDVLLVQLLDLELQDLIISENGLYKRV
NTDB id 1361 HI 0985 AAC22646.1             YTPVSIDDLAEEFNLSVDVLLVQLLDLELQDLIISENGLYKRV   373
NTDB id 626 LCA RS04960 WP 011374694.1      ..........................................   288
NTDB id 599 KW2 RS05940 WP 021037268.1      ..........................................   282
NTDB id 525 SMSK321 RS06295 WP 000705298.1  ..........................................   282
NTDB id 267 KZH43 RS05590 WP 000705306.1    ..........................................   282
NTDB id 226 SPD RS05990 WP 000705306.1      ..........................................   282
NTDB id 192 SPR RS05715 WP 000705306.1      ..........................................   282
NTDB id 157 SP RS06205 WP 000705306.1       ..........................................   282
NTDB id 497 SM12261 RS05565 WP 000705318.1  ..........................................   282
NTDB id 140402 RDF RS05295 WP 001015250.1   ..........................................   280
NTDB id 407 SMU RS04605 WP 002262865.1      ..........................................   280
consensus
```

X non conserved
X similar
X $\geq$ 50% conserved