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logo
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NTDB id 25 SA RS06185 WP 000593194.1          .MI.KLFLLKLYWAHFSTKQIHQFLMAYPNVIKEEGRKKDSYLCEWVNREENVLLLRKYYAFIKLDHNDIIKELQKLKVS   78
NTDB id 599 KW2 RS05940 WP 021037268.1        .MITNFDLFRWKKAGMTNLGVNKLLKFFRKYDRKISL.RQ..MGQVAQVKSIPNFIEQ...YKNQDVKKLRADYK..KFS   71
NTDB id 407 SMU RS04605 WP 002262865.1        ..MDNFQLFKLKKAGLTNLNILNIIDYEERTQKSLSL.RD..MAVVSKNKKPLIFMEH...YKNLDSKALRKEFN..RFP   70
NTDB id 525 SMSK321 RS06295 WP 000705298.1    MKITNYEIYKLKKSGLTNQQILKVLEYGENVDQELLL.GD..IADISGCRNPAVFMER...YFQIDDAHLEKEFK..KIP   72
NTDB id 497 SM12261 RS05565 WP 000705318.1    MKITNYEIYKLKKSGLTNQQVLAVLEYGENVDQELLL.GD..IAEISGCRNPAVFMER...YFQIDDAHLEKEFQ..KFP   72
NTDB id 25979 SP70585 RS06600 WP 000705310.1 MKITNYEIYKLKKSGLTNQQILKVLEYGENVDQELLL.GD..IADISGCRNPAVFMER...YFQIDDAHLSKEFQ..KFP   72
NTDB id 267 KZH43 RS05590 WP 000705306.1     MKITNYEIYKLKKSGLTNQQILKVLEYGENVDQELLL.GD..IADISGCRNPAVFMER...YFQIDDAHLSKEFQ..KFP   72
NTDB id 226 SPD RS05990 WP 000705306.1       MKITNYEIYKLKKSGLTNQQILKVLEYGENVDQELLL.GD..IADISGCRNPAVFMER...YFQIDDAHLSKEFQ..KFP   72
NTDB id 192 SPR RS05715 WP 000705306.1       MKITNYEIYKLKKSGLTNQQILKVLEYGENVDQELLL.GD..IADISGCRNPAVFMER...YFQIDDAHLSKEFQ..KFP   72
NTDB id 157 SP RS06205 WP 000705306.1        MKITNYEIYKLKKSGLTNQQILKVLEYGENVDQELLL.GD..IADISGCRNPAVFMER...YFQIDDAHLSKEFQ..KFP   72
consensus                                    ************************************ **  ***************   ****!**********  ***
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NTDB id 25 SA RS06185 WP 000593194.1          YITYMDSEYPVLLKEIYQFPLLLFYKGNIKLINNMHHLAVVGARDSISYTQQSLEFLLSNDKSKYLTIVSGLAQGADAMA   158
NTDB id 599 KW2 RS05940 WP 021037268.1        SFSILDDLYPERLREIYNPPVLIFYQGNIDLLKN.PKLAFVGSRLAGQSGIKSVQKIV.TELNQSFTIVSGLAKGIDTAS   149
NTDB id 407 SMU RS04605 WP 002262865.1        SLSILDKEYPLELKNIYNPPVLLFYQGDLDLLAR.PKLAVVGSRNASQMGVAAVKKII.QDLSKQFVIISGLARGIDTAA   148
NTDB id 525 SMSK321 RS06295 WP 000705298.1    SFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRSCSKQGAKSVEKII.QGLENELVIVSGLAKGIDTAA   150
NTDB id 497 SM12261 RS05565 WP 000705318.1    SFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVI.QGLENELVIVSGLAKGIDTAA   150
NTDB id 25979 SP70585 RS06600 WP 000705310.1 SFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVI.QGLENELVIVSGMAKGIDTAA   150
NTDB id 267 KZH43 RS05590 WP 000705306.1     SFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVI.QGLENELVIVSGLAKGIDTAA   150
NTDB id 226 SPD RS05990 WP 000705306.1       SFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVI.QGLENELVIVSGLAKGIDTAA   150
NTDB id 192 SPR RS05715 WP 000705306.1       SFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVI.QGLENELVIVSGLAKGIDTAA   150
NTDB id 157 SP RS06205 WP 000705306.1        SFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVI.QGLENELVIVSGLAKGIDTAA   150
consensus                                    *****!**!!**!**!!**!*!*!!*!***!*** ***!*!!*!************** ********!*!!*!*!*!***
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NTDB id 25 SA RS06185 WP 000593194.1          HQIALKYNLPTIAVLAFGHQTHYPKSTLALRNKIEEKGLVISEYPPHTPIAKYRFPERNRIISGLSKGVLITEAKEQSGS   238
NTDB id 599 KW2 RS05940 WP 021037268.1        HLSALKTKTPTIAVIGTGLDIFYPLENRKIQEYLAKYQLVLSEYSLGEKPLKYHFPERNRIIAGLSRGVVVVEAKLRSGS   229
NTDB id 407 SMU RS04605 WP 002262865.1        HLASLKSGGATIAVIGTGLDVHYPKENRRLQDYIAKNHLLLSEYEAQSQPLKYHFPERNRIIAGLSQGVMVAEAKIRSGS   228
NTDB id 525 SMSK321 RS06295 WP 000705298.1    HMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYISNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGS   230
NTDB id 497 SM12261 RS05565 WP 000705318.1    HMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGS   230
NTDB id 25979 SP70585 RS06600 WP 000705310.1 HMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGS   230
NTDB id 267 KZH43 RS05590 WP 000705306.1     HMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGS   230
NTDB id 226 SPD RS05990 WP 000705306.1       HMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGS   230
NTDB id 192 SPR RS05715 WP 000705306.1       HMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGS   230
NTDB id 157 SP RS06205 WP 000705306.1        HMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSGS   230
consensus                                    !*********!!!!***!****!!************!**!!!*******!**!!*!!!!!*!!**!!***!!!**!!!
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NTDB id 25 SA RS06185 WP 000593194.1      HITIDFALEQNRNVYVLPGSMFNPMTKGNLLRIQEGAKVVLNANDIFEDYYI.   290
NTDB id 599 KW2 RS05940 WP 021037268.1    LITCERALEEGRDIFAIPGNIADGTSDGCNHLIQQGAKLVYQAQDILEEYLYN   282
NTDB id 407 SMU RS04605 WP 002262865.1    LITCERAMEEGRDVFVVPGNILDGQSEGCHHLIQEGAKCITSGFDILNEFNF.   280
NTDB id 525 SMSK321 RS06295 WP 000705298.1 LITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.   282
NTDB id 497 SM12261 RS05565 WP 000705318.1 LITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.   282
NTDB id 25979 SP70585 RS06600 WP 000705310.1 LITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.   282
NTDB id 267 KZH43 RS05590 WP 000705306.1  LITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.   282
NTDB id 226 SPD RS05990 WP 000705306.1    LITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.   282
NTDB id 192 SPR RS05715 WP 000705306.1    LITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.   282
NTDB id 157 SP RS06205 WP 000705306.1     LITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.   282
consensus                                 *!!***!*!**!*****!!********!****!!*!!!******!*******
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X non conserved

X similar

X $\geq$ 50% conserved