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logo

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 304824 DV130 RS01380 WP 000705304.1  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                                    ************************************ **  ****************   ****!*********  ***

logo

NTDB id 25 SA RS06185 WP 000593194.1          YIIYMDSEYPVLLKEIYQFPLLLFYKGNIKLINNMHHLAVVGARDSISYTQQSLEFLLSNDKSKYLTIVSGLAQGADAMA  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 304824 DV130 RS01380 WP 000705304.1  SFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKF.PKVAVVGSRACSKQGAKSVEKVI.QGLENELVIVSGLAKGIDTAA  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                                    *****!**!!**!**!!**!*!*!!*!***!***  ***!*!!*!**************  ********!*!!!!*!*!***

logo

NTDB id 25 SA RS06185 WP 000593194.1          HQIALKYNLPTIAVLAFGHQTHYPKSTLALRNKIEEKGLVISEYPPHTPIAKYRFPERNRIISGLSKGVLITEAKEQSGS  238
NTDB id 599 KW2 RS05940 WP 021037268.1        HLSAIKTKTPTIAVIGTGLDIFYPLENRKIQEYLAKYQLVLSEYSLGEKPLKYHFPERNRIIAGLSRGVVVVEAKLRSGS  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 304824 DV130 RS01380 WP 000705304.1  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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logo

NTDB id 25 SA RS06185 WP 000593194.1          HITIDFALEGNRNVYVLPGSMFNPMTKGNLLRIQEGAKVVLNANDIFEDYYI.   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 304824 DV130 RS01380 WP 000705304.1  LITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLLTSGQDVLAEFEF.   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