```
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 1052184 ACE2AN RS05845 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 1052184 ACE2AN RS05845 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 1052184 ACE2AN RS05845 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                                    !*********!!!!***!****!!**************!**!!!*******!**!!*!!!!!*!!**!!***!!!**!!!
```

```
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 1052184 ACE2AN RS05845 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                                       *!!***!*!**!*****!!******!***!****!!*!!!******!*******
```

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