logo



```
NTDB id 283 SP RS06670 WP 000782668.1        MKMKQISDTTLKITISLEDLMDRGMEIADFLVPQEKTEEFFYAILDELEMPDSFLDTGMLSFRVTPKPDKVDVFVTKSKI   80
NTDB id 67093 AABA08 RS04195 WP 000782676.1  MKMKQISDTTLKITMSLEDLMDRGMEIADFLVPQEKTEEFFYAILDELEMPDSFLDTGMLSFRVTPKPDKVDVFVTKSKI   80
NTDB id 286 KZH43 RS05975 WP 000782664.1     MKMKQISDTTLKITISLEDLMDRGMEIADFLVPQEKTEEFFYAILDELEMPDSFLDTGMLSFRVTPKPDKVDVFVTKSKI   80
NTDB id 285 SPD RS06395 WP 000782664.1       MKMKQISDTTLKITISLEDLMDRGMEIADFLVPQEKTEEFFYAILDELEMPDSFLDTGMLSFRVTPKPDKVDVFVTKSKI   80
NTDB id 284 SPR RS06100 WP 000782664.1       MKMKQISDTTLKITISLEDLMDRGMEIADFLVPQEKTEEFFYAILDELEMPDSFLDTGMLSFRVTPKPDKVDVFVTKSKI   80
NTDB id 380 SMU RS01250 WP 002262749.1       MEMKQISETTLKITISMEDLEERGMELKDFLIPQEKTEEFFYTVMDELDLPENFKDSGMLSFRVTPRNDRIDVFVTKSEI   80
NTDB id 299 STER RS01050 WP 011680667.1      MEMKQISETTLKIMITMEDLEEHGMELKDFLIPQEKTEEFFYTVMDELDLPDNFKNSGMLSFRVTPRKDRVDVFVTKSDL   80
NTDB id 331 STU RS10485 WP 011225365.1       MEMKQINETTLKIMITMEDLEEHGMELKDFLIPQEKTEEFFYTVMDELDLPDNFKNSGMLSFRVTPRKDRVDVFVTKSDL   80
consensus                                    !*!!!!**!!!!!*****!!!***!!!**!!!*!!!!!!!!!!!***!!!**!*!***!!!!!!!!!**!**!!!!!!!**
```

logo



```
NTDB id 283 SP RS06670 WP 000782668.1        DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEVKEEEQ......EQAEQEAESKKEPYIY   154
NTDB id 67093 AABA08 RS04195 WP 000782676.1  DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEAKEEEQ......EQAEQEAESKKEPYIY   154
NTDB id 286 KZH43 RS05975 WP 000782664.1     DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEAKEEEQ......EQAEQEAESKKEPYIY   154
NTDB id 285 SPD RS06395 WP 000782664.1       DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEAKEEEQ......EQAEQEAESKKEPYIY   154
NTDB id 284 SPR RS06100 WP 000782664.1       DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEAKEEEQ......EQAEQEAESKKEPYIY   154
NTDB id 380 SMU RS01250 WP 002262749.1       NKNLNLEDLSD...FDDISKMSPEDFFNTLEETMREK..GDAAALDKLAEIEKREEEK......TQQEKGETKEKRDYVH   149
NTDB id 299 STER RS01050 WP 011680667.1      KEDLDFNDLSD...MEDYSGLSPEEFLKALEDNFMDK..GDIEAHHKLEEHDKTLKEVDETMTEPAKEVAEETIREDYTH   155
NTDB id 331 STU RS10485 WP 011225365.1       KEALDFNDLSD...MEDYSGLSPEEFLKALEDNFMDK..GDIEAHHKLEEHDKTLKEVDETMTEPAKEVAEETIREDYTH   155
consensus                                    ***!***!!!!!**********!!**!***!!*****!***!**!***!****  ***!*      ***!**********!**
```

logo



```
NTDB id 283 SP RS06670 WP 000782668.1        YILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEYGQVLM   233
NTDB id 67093 AABA08 RS04195 WP 000782676.1  YILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEYGQVLM   233
NTDB id 286 KZH43 RS05975 WP 000782664.1     YILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEYGQVLM   233
NTDB id 285 SPD RS06395 WP 000782664.1       YILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEYGQVLM   233
NTDB id 284 SPR RS06100 WP 000782664.1       YILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEYGQVLM   233
NTDB id 380 SMU RS01250 WP 002262749.1       FVLDFPNIQQVINFAKTV.DYDVEASELFKESDAYHMTVLLNLEDKPDYYADLMFARMLEHAGRGTKTRAYLLEHGVQLI   228
NTDB id 299 STER RS01050 WP 011680667.1      YVLAFSDFDQVVTFAQGLKNVSVEGSEFYKLGDVYYMTILLYLADEPDYYANNMYARFLEYANVADRTRPYLQEHATILM   235
NTDB id 331 STU RS10485 WP 011225365.1       YVLAFSDFDQVVTFAQGLKNVSVEGSEFYKLGDVYYMTILLYLADEPDYYANNMYARFLEYANVADRTRPYLQEHATILM   235
consensus                                    **!*!*******!!*** ****!*!!**!****!**!*!******!**!*****!!**!*!******!**!*!****!*
```

logo



```
NTDB id 283 SP RS06670 WP 000782668.1        SHDAVLNLQKIG..   245
NTDB id 67093 AABA08 RS04195 WP 000782676.1  SHDAVLNLQKIG..   245
NTDB id 286 KZH43 RS05975 WP 000782664.1     SHDAVLNLQKIG..   245
NTDB id 285 SPD RS06395 WP 000782664.1       SHDAVLNLQKIG..   245
NTDB id 284 SPR RS06100 WP 000782664.1       SHDAVLNLQKIG..   245
NTDB id 380 SMU RS01250 WP 002262749.1       KADALQELQMIG..   240
NTDB id 299 STER RS01050 WP 011680667.1      EEDALPVLQATKWS   249
NTDB id 331 STU RS10485 WP 011225365.1       EEDALPVLQATKWS   249
consensus                                    **!!***!!***
```

X non conserved

X similar

X $\geq$ 50% conserved