```
logo
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 283 SP RS06670 WP 000782668.1         MKMKQISDTTLKITISLEDLMDRGMEIADFLVPQEKTEEFFYAILDELEMPDSFLDTGMLSFRVTPKPDKVDVFVTKSKI   80
NTDB id 299 STER RS01050 WP 011680667.1       MEMKQISETTLKIMITMEDLEEHGMELKDFLIPQEKTEEFFYTVMDELDLPDNFKNSGMLSFRVTPRKDRVDVFVTKSDL   80
NTDB id 331 STU RS10485 WP 011225365.1        MEMKQINETTLKIMITMEDLEEHGMELKDFLIPQEKTEEFFYTVMDELDLPDNFKNSGMLSFRVTPRKDRVDVFVTKSDL   80
NTDB id 1116123 SP119 RS01390 WP 002986029.1 MEMKQISETTLKITISMDDLEERGMELKDFLIPQEKTEEFFYSVMDELDLPDNFKDSGMLSFRVTPRKDRLDVFVTKSEI   80
NTDB id 380 SMU RS01250 WP 002262749.1        MEMKQISETTLKITISMEDLEERGMELKDFLIPQEKTEEFFYTVMDELDLPENFKDSGMLSFRVTPRNDRIDVFVTKSEI   80
consensus                                     ! !!!!**!!!!!!*!***!! **!!!* !!!*!!!!!!!!!! **!!!**!* ! **!!!!!!!!!* !**!!!!!!! *

logo
NTDB id 286 KZH43 RS05975 WP 000782664.1      DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEAKEEEQ...........EQAEQEAESKK  149
NTDB id 285 SPD RS06395 WP 000782664.1        DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEAKEEEQ...........EQAEQEAESKK  149
NTDB id 284 SPR RS06100 WP 000782664.1        DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEAKEEEQ...........EQAEQEAESKK  149
NTDB id 283 SP RS06670 WP 000782668.1         DQNLDFEDLSDLPDMEELAQMSPDEFIKTLEKSIADKTKDDIEAIQSLEQVEVKEEEQ...........EQAEQEAESKK  149
NTDB id 299 STER RS01050 WP 011680667.1       KEDLDFNDLSDM...EDYSGLSPEEFLKALEDNFMDK..GDIEAHHKLEEHDKTLKEVDETMTE.....PAKEVAEETIR  150
NTDB id 331 STU RS10485 WP 011225365.1        KEALDFNDLSDM...EDYSGLSPEEFLKALEDNFMDK..GDIEAHHKLEEHDKTLKEVDETMTE.....PAKEVAEETIR  150
NTDB id 1116123 SP119 RS01390 WP 002986029.1 NKDINLEDLAEF...GDMSQMTPEDFFKSLEQSMREK..GDVKAHEKLEKIEEIMEDVVEATLANQSEAADPSTNHESEP  155
NTDB id 380 SMU RS01250 WP 002262749.1        NKNLNLEDLSDF...DDISKMSPEDFFNTLEETMREK..GDAAALDKLAEIEKREEEK...........TQQEKGETKEK  144
consensus                                       *****!!***   *** ***!**!***!! ** *!   !**!*  !* ** ****             * *   ** *

logo
NTDB id 286 KZH43 RS05975 WP 000782664.1      EPYIYYILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEY  228
NTDB id 285 SPD RS06395 WP 000782664.1        EPYIYYILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEY  228
NTDB id 284 SPR RS06100 WP 000782664.1        EPYIYYILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEY  228
NTDB id 283 SP RS06670 WP 000782668.1         EPYIYYILSFAKLADLVAFAKTV.TFEMETSELYKMNERYYLTILVDIENHPSPYPAWLLARMREFADDSDISRSVLQEY  228
NTDB id 299 STER RS01050 WP 011680667.1       EDYTHYVLAFSDFDQVVTFAQGLKNVSVEGSEFYKLGDVYYMTILLYLADEPDYYANNMYARFLEYANVADRTRPYLQEH  230
NTDB id 331 STU RS10485 WP 011225365.1        EDYTHYVLAFSDFDQVVTFAQGLKNVSVEGSEFYKLGDVYYMTILLYLADEPDYYANNMYARFLEYANVADRTRPYLQEH  230
NTDB id 1116123 SP119 RS01390 WP 002986029.1 LDYVHYVLDFSTITEAVAFAKTI.DFSIEASELYKGSNCYHMTILLDVQQQPSYFANVMYARLIEHANPGSKTRAYLQEH  234
NTDB id 380 SMU RS01250 WP 002262749.1        RDYVHFVLDFPNIQQVINFAKTV.DYDVEASELFKESDAYHMTVLLNLEDKPDYYADLMFARMLEHAGRGTKTRAYLLEH  223
consensus                                     * !* **! !  * ****!!***  ***! !!**!* * !**!*!***** !* *   * !!* !*!   * *!  !*!

logo
NTDB id 286 KZH43 RS05975 WP 000782664.1      GQVLMSHDAVLNLQKIG..  245
NTDB id 285 SPD RS06395 WP 000782664.1        GQVLMSHDAVLNLQKIG..  245
NTDB id 284 SPR RS06100 WP 000782664.1        GQVLMSHDAVLNLQKIG..  245
NTDB id 283 SP RS06670 WP 000782668.1         GQVLMSHDAVLNLQKIG..  245
NTDB id 299 STER RS01050 WP 011680667.1       ATILMEEDALPVLQATKWS  249
NTDB id 331 STU RS10485 WP 011225365.1        ATILMEEDALPVLQATKWS  249
NTDB id 1116123 SP119 RS01390 WP 002986029.1 GLQLMLDGAVEQLQKIELG  253
NTDB id 380 SMU RS01250 WP 002262749.1        GVQLIKADALQELQMIG..  240
consensus                                     * *!*  *!* *!!***
```

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