```
logo
NTDB id 107449 AABA74 RS17040 WP 058906395.1  ....MAEGASEFSEVRDFFYGRHLLRSEIPFSDHCIKRFIEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1             MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                     *****    !   !*      !!!!!*!**!!!**!  *!   !!!!!*!!   ! !! !*!!!!*!! *!  ** **

logo
NTDB id 107449 AABA74 RS17040 WP 058906395.1  RQITYCRACVMMGRADELTSLYSWNQAPENSWEPVKLSWEGTLTDGQKQAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1             KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                     **  !!! !!!!!!  !  *!!!!   *!  ! **!!*!*! !* !!  !!  ! *!!  * !!!*!!!!! !!!!!!!!

logo
NTDB id 107449 AABA74 RS17040 WP 058906395.1  GIKFALNQGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTAHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1             GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                     !!  !!!!!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo
NTDB id 107449 AABA74 RS17040 WP 058906395.1  PFSADETLRFAVDKARKKNSALIYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPHFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1             PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                     !*!!! !! !!! !!!!!!! !*!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!*!*!!!!!!!!!** !*!* !

logo
NTDB id 107449 AABA74 RS17040 WP 058906395.1  TDWVRQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1             KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                       !*  **     !!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!!

logo
NTDB id 107449 AABA74 RS17040 WP 058906395.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVLFHFGITNGMKKAKKHIEHMNKLAQKSKLLD   461
NTDB id 108 BSU 35470 NP 391427.1             GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                     *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
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X non conserved

X similar

X ≥50% conserved