```
logo
NTDB id 179858 A1D33 RS11895 WP 040238815.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRIKRFIEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWASSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    *****    !   !*       !!!!!*!**!!!  !   *!   !!!!!*!!   ! !!  !*!!!!*!! *!   ** !**

logo

NTDB id 179858 A1D33 RS11895 WP 040238815.1  RQITYCRACVMMGRADELTSLYSWNQASENSWEPVKLSWEGTLTDGQKKAAAALTDAIKERQELLVWAVCGSGKTEMLFP  156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    **  !!! !!!!!!  !  *!!!!    !  ! **!!*!*! !* !! !!!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 179858 A1D33 RS11895 WP 040238815.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF  236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!!!!*!!!!!! !!!*!!*!   !!!!!!!!!!!

logo

NTDB id 179858 A1D33 RS11895 WP 040238815.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKKAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV  316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!*!!  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 179858 A1D33 RS11895 WP 040238815.1  TDWVCQKLQSQLPVFLFVPSVDVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT  396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !** **     !!!!!!!!! *! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!

logo

NTDB id 179858 A1D33 RS11895 WP 040238815.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGMTNGMKKAKKHIEHMNKLAQKSKLLD  461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
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X non conserved

X similar

X ≥ 50% conserved