```
logo
NTDB id 984777 NYE36 RS18060 WP 265451073.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRIKRFTEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !   !*       !!!!!*!**!!!  !  *    !!!!!*!!   ! !!  !*!!!!*!! *!   ** **

logo

NTDB id 984777 NYE36 RS18060 WP 265451073.1  RQITYCRACVVMGRADELTSLYSWNQAYENSWEPVKLSWEGTLTDGQKRAAAALTDAIKERQELLVWAVCGSGKTEMLFP  156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    **  !!! !!*!!!  !  *!!!!    !  ! **!!*!*! !* !! *!!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 984777 NYE36 RS18060 WP 265451073.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF  236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo

NTDB id 984777 NYE36 RS18060 WP 265451073.1  PFSADETLGFAVDKARKKNSALVYVTATPSDTLKKKAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV  316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!*!!  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 984777 NYE36 RS18060 WP 265451073.1  TDWVRQKLQSHLPVFLFVPSVHILKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGLLDLLVTTTILERGVTAPKVQT  396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !*  **  * !!!!!!!!!!*!! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!! !!!!!

logo

NTDB id 984777 NYE36 RS18060 WP 265451073.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGITSGMKKAKKHIEHMNKLAQKSKLLD  461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
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X non conserved

X similar

X ≥ 50% conserved