```
logo
NTDB id 373216 FOG69 RS17315 WP 013353785.1  ....MSGGASEFSKVRDFFYGRHLLRSEIPFSDQCIKRFIEKEYITAEPSVIRRKNRYVCRRCGQSDQARFAVFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !    *       !!!!!*!**!!! *!   *!   !!!!!*!*   ! !! ! !!!!*!!   !   ** **

logo
NTDB id 373216 FOG69 RS17315 WP 013353785.1  RHITYCRSCVVMGRADELTSLYSWNLAAENSWEPIKLSWEGTLTDGQKQAAEALIEAIKEKQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    **  !!!!!!*!!!  !  *!!!!   !  ! *!!!*!*! !* !!  !!  !!!!!  ! !!!*!!!!! !!!!!!!!

logo
NTDB id 373216 FOG69 RS17315 WP 013353785.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGSLTPLMISTTHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!! !*!!!!!! !!!*!!*!   !!!!!!!!!!!

logo
NTDB id 373216 FOG69 RS17315 WP 013353785.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKRAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLEKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!**!  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!! * !*!* !

logo
NTDB id 373216 FOG69 RS17315 WP 013353785.1  TDWVRQKLQSRLPVFLFVPSVHILRKTTDYFQKLNIRAEGVHAEDTCRKDKVKRFREGRFDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !*  **     !!!!!!!!!!*!! !   *!  ***!   !!!!!  !!*!!  !!*!  !!!*!!!!!!!!!!!!!!!!

logo
NTDB id 373216 FOG69 RS17315 WP 013353785.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGMTNGMKKAKKHIEYMNKLAQKNKLLD   461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!!  !! !! !  * !
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X non conserved

X similar

X ≥ 50% conserved