```
logo
NTDB id 246034 CLI97 RS07935 WP 094247454.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRINRFIEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !   !*       !!!!!*!**!!!  !   *!   !!!!!*!!   ! !!  !*!!!!*!! *!   ** **

logo
NTDB id 246034 CLI97 RS07935 WP 094247454.1  RQITYCRACVMMGRADELTSLYSWNQAPENSWEPVKLSWEGTLTDGQKQAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    **  !!! !!!!!!  !  *!!!!   *!  ! **!!*!*! !* !!  !!  ! *!!  * !!!*!!!!! !!!!!!!!

logo
NTDB id 246034 CLI97 RS07935 WP 094247454.1  GIEFALNQGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!!!!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!   !!!!!!!!!!!

logo
NTDB id 246034 CLI97 RS07935 WP 094247454.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo
NTDB id 246034 CLI97 RS07935 WP 094247454.1  TDWVRQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGLLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !*  **     !!!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!

logo
NTDB id 246034 CLI97 RS07935 WP 094247454.1  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