```
logo
NTDB id 313952 D3C60 RS17080 WP 007407482.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRIKRFTEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !   !*       !!!!!*!**!!!  !  *    !!!!!*!!   ! !!  !*!!!!*!! *!   ** **

logo
NTDB id 313952 D3C60 RS17080 WP 007407482.1  RQITYCRACVVMGRADELTSLYSWNQAHENSWEPVKLSWEGTLTDGQKRAAAALTDAIKERQELLVWAVCGSGKTEMLFP  156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    **  !!! !!*!!!  !  *!!!!   *!  ! **!!*!*! !* !! *!!  ! *!!  * !!!*!!!!! !!!!!!!!

logo
NTDB id 313952 D3C60 RS17080 WP 007407482.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF  236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo
NTDB id 313952 D3C60 RS17080 WP 007407482.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKKAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV  316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!*!!  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo
NTDB id 313952 D3C60 RS17080 WP 007407482.1  TDWVRQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT  396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !*  **     !!!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!

logo
NTDB id 313952 D3C60 RS17080 WP 007407482.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGMTNGMKKAKKHIEHMNKLAQKSKLLD  461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
```

X non conserved

X similar

X $\geq$ 50% conserved