```
logo
NTDB id 290065 DDT10 RS16880 WP 053574011.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRIKRFIEKEYITAEPSIIRRKNRYVCQRCGQFDQACFAAFWASSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    *****    !   !*      !!!!!*!**!!!  !  *!   !!!!!*!!   ! !!  !*!!!! !! *!  ** !**

logo
NTDB id 290065 DDT10 RS16880 WP 053574011.1  RQITYCRACVMMGRADELTSLYSWNQASENSWEPVKLFWEGTLTDGQKRAAAALTDAIKERQELLVWAVCGSGKTEMLFP  156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    **  !!! !!!!!!  !  *!!!!   !  ! **!! !*! !* !! *!!  ! *!!  * !!!*!!!!! !!!!!!!!

logo
NTDB id 290065 DDT10 RS16880 WP 053574011.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF  236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo
NTDB id 290065 DDT10 RS16880 WP 053574011.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV  316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo
NTDB id 290065 DDT10 RS16880 WP 053574011.1  TDWVCQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGIHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT  396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !** **     !!!!!!!!!!**! !   *!  ***!   *!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!

logo
NTDB id 290065 DDT10 RS16880 WP 053574011.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGMTNGMKKAKKHIEHMNKLAQKSKLLD  461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
```

X non conserved

X similar

X ≥ 50% conserved