```
logo
NTDB id 324047 EEB07 RS07185 WP 123117468.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRIKRFIEKEYITAEPSIIRRKNGYVCQRCGQSDQACFAAFWASSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    *****    !   !*      !!!!!*!**!!!  !  *!   !!!!!*!!   !  ! !*!!!!*!! *!  ** !**

logo

NTDB id 324047 EEB07 RS07185 WP 123117468.1  RQITYCRACVMMGRADELTSLYSWNQASENSWEPVKLSWEGTLTDGQKKAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    **  !!! !!!!!!  !  *!!!!   !  ! **!!*!*! !* !! !!!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 324047 EEB07 RS07185 WP 123117468.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!!!!*!!!!!! !!!*!!*!   !!!!!!!!!!!

logo

NTDB id 324047 EEB07 RS07185 WP 123117468.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKKAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!*!!  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 324047 EEB07 RS07185 WP 123117468.1  TDWVCQKLQSQLPVFLFVPSVDVLKKTTDYFRKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                     !** **    !!!!!!!!! *! !   *!* ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!

logo

NTDB id 324047 EEB07 RS07185 WP 123117468.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGMTNGMKKAKKHIEHMNKLAQKSKLLD   461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
```

X non conserved

X similar

X $\geq$ 50% conserved