```
logo
NTDB id 299143 DOU34 RS15765 WP 061047045.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRIKRFTEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !   !*       !!!!!*!**!!!  !  *    !!!!!*!!   ! !!  !*!!!!*!! *!   ** **

logo
NTDB id 299143 DOU34 RS15765 WP 061047045.1  RQITYCRACVVMGRADELTSLYYWNQASENSWEPVKLSWEGTLTDGQKRAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    **  !!! !!*!!!  !  *!! !    !  ! **!!*!*! !* !! *!!  ! *!!  * !!!*!!!!! !!!!!!!!

logo
NTDB id 299143 DOU34 RS15765 WP 061047045.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!!!!*!!!!!! !!!*!!*!   !!!!!!!!!!!

logo
NTDB id 299143 DOU34 RS15765 WP 061047045.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKKAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!*!!  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo
NTDB id 299143 DOU34 RS15765 WP 061047045.1  TDWVRQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !*  **    !!!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!!

logo
NTDB id 299143 DOU34 RS15765 WP 061047045.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGITNGMKKAKKHIEHMNKLAQKSKLLD   461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
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X non conserved

X similar

X ≥ 50% conserved