```
logo
NTDB id 211549 BUN12 RS13420 WP 013353785.1  ....MSGGASEFSKVRDFFYGRHLLRSEIPFSDQCIKRFIEKEYITAEPSVIRRKNRYVCRRCGQSDQARFAVFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !    *       !!!!!*!**!!! *!   *!   !!!!!*!*   ! !! ! !!!!*!!   !   ** **

logo
NTDB id 211549 BUN12 RS13420 WP 013353785.1  RHITYCRSCVVMGRADELTSLYSWNLAAENSWEPIKLSWEGTLTDGQKQAAEALIEAIKEKQELLVWAVCGSGKTEMLFP  156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    **  !!!!!!*!!!  !  *!!!!   !  ! *!!!*!*! !* !!  !!  !!!!!  ! !!!*!!!!! !!!!!!!!

logo
NTDB id 211549 BUN12 RS13420 WP 013353785.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGSLTPLMISTTHQLMRYRDIFDVMIIDEVDAF  236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!! !*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo
NTDB id 211549 BUN12 RS13420 WP 013353785.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKRAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLEKGKLPRSV  316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!**!  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!! * !*!* !

logo
NTDB id 211549 BUN12 RS13420 WP 013353785.1  TDWVRQKLQSRLPVFLFVPSVHILRKTTDYFQKLNIRAEGVHAEDTCRKDKVKRFREGRFDLLVTTTILERGVTVPKVQT  396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !*  **     !!!!!!!!!!*!! !   *!  ***!   !!!!!  !!*!!  !!*!  !!!*!!!!!!!!!!!!!!!!

logo
NTDB id 211549 BUN12 RS13420 WP 013353785.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGMTNGMKKAKKHIEYMNKLAQKNKLLD  461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!!  !! !! !  * !
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X non conserved

X similar

X ≥ 50% conserved