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logo

NTDB id 410667 GE573 RS07095 WP 190664622.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRIKRVTEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !   !*      !!!!!*!**!!!  !  *    !!!!!*!!   ! !!  !*!!!!*!! *!   ** **

logo

NTDB id 410667 GE573 RS07095 WP 190664622.1  RQITYCRACVMMGRADELTSLYYWNQAHENSWEPVKLSWEGTLTDGQKRAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    **  !!! !!!!!!  !  *!! !   *!  ! **!!*!*! !* !! *!!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 410667 GE573 RS07095 WP 190664622.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!!!!*!!!!!! !!!*!!*!   !!!!!!!!!!!

logo

NTDB id 410667 GE573 RS07095 WP 190664622.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKKAEANLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!*!!    !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 410667 GE573 RS07095 WP 190664622.1  TDWVRHKLQSQLPVFLFVPSVHILKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGLLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !* ***     !!!!!!!!!!*!! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!

logo

NTDB id 410667 GE573 RS07095 WP 190664622.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGMTNGMKKAKKHIEHMNKLAQKSKLLD   461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
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X non conserved

X similar

X ≥ 50% conserved