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logo

NTDB id 144907 AAV30 RS02690 WP 038460045.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRINGFIEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFGAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSS..G   78
consensus                                    *****    !   !*       !!!!!*!**!!!  !   *!   !!!!!*!!   ! !!  !*!!!!*!! *!   ** ***

logo

NTDB id 144907 AAV30 RS02690 WP 038460045.1  RQITYCRACVMMGRADEQTSLYSWNQAPENSWEPVKLSWEGTLTDGQKRAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    **  !!! !!!!!!  !  *!!!!   *!  ! **!!*!*! !* !! *!!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 144907 AAV30 RS02690 WP 038460045.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVVIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!*!!!!!!!!

logo

NTDB id 144907 AAV30 RS02690 WP 038460045.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 144907 AAV30 RS02690 WP 038460045.1  TDWVCQKLQLQLPVFLFVPSVHVLKKTTDYFQKLNIRTEGVHAEDTFRKDKVKRFRNCRLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !** **     !!!!!!!!!!**! !   *!  ***!!  !!!!! *!!*!!  !! ! !!!!*!!!!!!!!!!!!!!!!!

logo

NTDB id 144907 AAV30 RS02690 WP 038460045.1  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