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logo

NTDB id 235527 CEG11 RS16780 WP 003151388.1  ....MAEGASEFSEVRDFFYGRHLLRSEIPFSDHCIKRFIEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !   !*      !!!!!*!**!!!**!  *!   !!!!!*!!   ! !!  !*!!!!*!! *!   ** **

logo

NTDB id 235527 CEG11 RS16780 WP 003151388.1  RQITYCRACVMMGRADELTLLYSWNQAPENRWKPVKLSWEGTLTDGQKQAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    **  !!! !!!!!!  !  *!!!!   *!  !!**!!*!*! !* !!  !!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 235527 CEG11 RS16780 WP 003151388.1  GIEFALNQGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!!!!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo

NTDB id 235527 CEG11 RS16780 WP 003151388.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 235527 CEG11 RS16780 WP 003151388.1  TDWVRQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !*  **     !!!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!!

logo

NTDB id 235527 CEG11 RS16780 WP 003151388.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVLFHFGITNGMKKAKKHIEHMNKLAQKSKLLD   461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  *  !
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X non conserved

X similar

X ≥ 50% conserved