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logo

NTDB id 1038797 ACBW56 RS16380 WP 043867470.1  ....MAEGASEFSEVRDFFYGRHLLRSEIPFSDHCIKRFIEKEYITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                      *****    !   !*      !!!!!*!**!!!**!  *!   !!!!!*!!   ! !! !*!!!!*!! *!  ** **

logo

NTDB id 1038797 ACBW56 RS16380 WP 043867470.1  RQITYCRACVMMGRADELTLLYSWNQAPENRWKPVKLSWEGTLTDGQKQAAAALTDAIKERQELLVWAVCGSGKTEMLFP  156
NTDB id 108 BSU 35470 NP 391427.1              KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                      **  !!! !!!!!!  !  *!!!!   *!  !!**!!*!*! !* !!  !!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 1038797 ACBW56 RS16380 WP 043867470.1  GIEFALNQGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF  236
NTDB id 108 BSU 35470 NP 391427.1              GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                      !!! !!!!!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo

NTDB id 1038797 ACBW56 RS16380 WP 043867470.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV  316
NTDB id 108 BSU 35470 NP 391427.1              PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                      !*!!! !! !!! !!!!!!! !!!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 1038797 ACBW56 RS16380 WP 043867470.1  TDWVRQELQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT  396
NTDB id 108 BSU 35470 NP 391427.1              KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                        !*  **    !!!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!!

logo

NTDB id 1038797 ACBW56 RS16380 WP 043867470.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVLFHFGITVGMKKAKKHIEHMNKLAQKSKLLD   461
NTDB id 108 BSU 35470 NP 391427.1              GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                      *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!! *!! !! !  * !
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X non conserved

X similar

X $\geq$ 50% conserved