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logo

NTDB id 1102305 ACNFKI RS18435 WP 418134191.1  ....MAEGASEFSEVRDFFYGRHLLRSEIPFSDHRIKRFIEKAYITAEPSIIRRKNRYVCQRCGQSDQACFATFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                      *****    !   !*      !!!!!*!**!!!* !  *!  *!!!!!*!!   ! !! !*!!!!*!! *!  ** **

logo

NTDB id 1102305 ACNFKI RS18435 WP 418134191.1  RQITYCRACVMMGRADELTSLYSWNQAPENRWRPVKLSWEGTLTDGQKQAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1              KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                      **  !!! !!!!!!  !  *!!!!   *!  !***!!*!*! !* !!  !!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 1102305 ACNFKI RS18435 WP 418134191.1  GIEFALNQGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTAHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1              GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                      !!! !!!!!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo

NTDB id 1102305 ACNFKI RS18435 WP 418134191.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1              PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                      !*!!! !! !!! !!!!!!! !!!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 1102305 ACNFKI RS18435 WP 418134191.1  TDWVRQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1              KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                        !*  **    !!!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!!

logo

NTDB id 1102305 ACNFKI RS18435 WP 418134191.1  CVLGAEAPIFTESALVQIAGRTGRHYKYFSGDVVLFHFGITVGMKKAKKHIEHMNKLAQKSKLLD   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