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logo

NTDB id 1034084 AB6A22 RS16695 WP 024085865.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRINRFIEKEHITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                      *****    !   !*      !!!!!*!**!!!  !  *!   *!!!!*!!   ! !! !*!!!!*!! *!  ** **

logo

NTDB id 1034084 AB6A22 RS16695 WP 024085865.1  RQITYCRACVMMGRADELTSLYSWNQAPENSWEPVKLSWEGTLTDGQKQAAAALTDAIKERQELLVWAVCGSGKTEMLFP   156
NTDB id 108 BSU 35470 NP 391427.1              KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                      **  !!! !!!!!!  !  *!!!!   *!  ! **!!*!*! !* !!  !!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 1034084 AB6A22 RS16695 WP 024085865.1  GIEFALNQGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF   236
NTDB id 108 BSU 35470 NP 391427.1              GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                      !!! !!!!!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo

NTDB id 1034084 AB6A22 RS16695 WP 024085865.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV   316
NTDB id 108 BSU 35470 NP 391427.1              PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                      !*!!! !! !!! !!!!!!! !!!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 1034084 AB6A22 RS16695 WP 024085865.1  TDWVRQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT   396
NTDB id 108 BSU 35470 NP 391427.1              KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                        !*  **    !!!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!!

logo

NTDB id 1034084 AB6A22 RS16695 WP 024085865.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVLFHFGMTNGMKKAKKHIELMNKLAQKSKLLD   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