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logo

NTDB id 1078067 ACJ1CH RS17385 WP 024085865.1  ....MSEGASEFSEVRDFFYGRHLLRSEIPFSDQRINRFIEKEHITAEPSIIRRKNRYVCQRCGQSDQACFAAFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                       *****    !   !*      !!!!!*!**!!!  !  *!   *!!!!*!!   ! !! !*!!!!*!! *!  ** **

logo

NTDB id 1078067 ACJ1CH RS17385 WP 024085865.1  RQITYCRACVMMGRADELTSLYSWNQAPENSWEPVKLSWEGTLTDGQKQAAAALTDAIKERQELLVWAVCGSGKTEMLFP  156
NTDB id 108 BSU 35470 NP 391427.1               KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                       **  !!! !!!!!!  !  *!!!!   *!  ! **!!*!*! !* !!  !!  ! *!!  * !!!*!!!!! !!!!!!!!

logo

NTDB id 1078067 ACJ1CH RS17385 WP 024085865.1  GIEFALNQGLRVCVATPRTDVVLELLPRLKKAFEKVDVSALYGGSEDKGRLTPLMISTTHQLMRYRDIFDVMIIDEVDAF  236
NTDB id 108 BSU 35470 NP 391427.1               GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                       !!! !!!!!!!!!*!!!!!!!!!!! !!!! !!   !*!!!!!!!*!!!!!*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo

NTDB id 1078067 ACJ1CH RS17385 WP 024085865.1  PFSADETLRFAVDKARKKNSALVYVTATPSDTLKKNAEAGLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLQKGKLPRSV  316
NTDB id 108 BSU 35470 NP 391427.1               PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                       !*!!! !! !!! !!!!!!! !!!**!!!*  !!* !  ! !*!!!!!!!*!!!!!!!!!!*!!!!!!!!!** !*!* !

logo

NTDB id 1078067 ACJ1CH RS17385 WP 024085865.1  TDWVRQKLQSQLPVFLFVPSVHVLKKTTDYFQKLNIRAEGVHAEDTFRKDKVKRFRDGRLDLLVTTTILERGVTVPKVQT  396
NTDB id 108 BSU 35470 NP 391427.1               KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                         !*  **    !!!!!!!!!!**! !   *!  ***!   !!!!! *!!*!!  !!!! !!!!*!!!!!!!!!!!!!!!!!

logo

NTDB id 1078067 ACJ1CH RS17385 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