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logo
NTDB id 995120 AAVD42 RS09220 WP 345808233.1  ......MNMDKAMELGQYLQSRHLLTAETRCSQSDLDWLEEKGLVIRTPAIERKANGLICCRCGVSKNRYFAHSPCDKCQ   74
NTDB id 108 BSU 35470 NP 391427.1             MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                     ****** !     !! ! ! !!!!!  !  *!   **!*   ! *   * !        !*!!! * *!!! *  ** *

logo
NTDB id 995120 AAVD42 RS09220 WP 345808233.1  KDCVYCRSCIMMGKTTECGFLYEWTGPQMEEACHSELTWQGDLSKGQKRASEKLIEAIKHKSDLLIWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1             KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                     ! **!!!!!*!!!* *!* *!! !  **    **  !!! ! !! !! *!   !!!!! *! *!!!!!!!!!!!!!*!!

logo
NTDB id 995120 AAVD42 RS09220 WP 345808233.1  GIEFALHQGMSVCIATPRTDVVLELEPRLKKAFQGMKIAVLYGGSPQRFQIAPLVIATTHQLMRYKHAFDVLIIDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1             GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                     !!!  !!*!!* !!!!!!!!!!!!!! !!!! !!!!  !  !!!!!* *  * !!*! !!!!!*!!!*! !!*!!!!!!!!

logo
NTDB id 995120 AAVD42 RS09220 WP 345808233.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMIRDVSRGQLEAVKIPLRFHQQPLPVPSFQWIGHWKKKLKKNQLPPKV   314
NTDB id 108 BSU 35470 NP 391427.1             PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                     !!! !  !!!!! !! *!    !!!!!!!*! * !    !!!* !*!! !*!  !!! ! ! !*!*!!!!! *! *!! !

logo
NTDB id 995120 AAVD42 RS09220 WP 345808233.1  MNWMQKHITKKRRVLLFVPSISTMKKVTKVLRKHHLNVEGVSADDPDRKQKVQQFRDDKYDVLVTTTILERGVTIPNVQV   394
NTDB id 108 BSU 35470 NP 391427.1             KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                       !*  !*   !*! !!!!!*! * !   * * *!*    !*!*!**!! !!!!!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 995120 AAVD42 RS09220 WP 345808233.1  GVLGAESTIFTESALVQISGRAGRHPDFFKGDVFFFHFGLTRSMKQAKKHIVKMNDTAEKEFSEK   459
NTDB id 108 BSU 35470 NP 391427.1             GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                     !!!!!!!*!!!!!!!!!!! !! !!!***  !!! *!!!! !*!!  !*!!!  !!* ! !  *
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X non conserved

X similar

X ≥ 50% conserved