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logo

NTDB id 995325 AAVC46 RS11660 WP 307500336.1  ......MNMDKAMELRQQLQSRHLLTAETRSSQSDLDWLEEKGFVIRTPAIERKANGLTCCRCGISKKRYFAHTPCDMCQ   74
NTDB id 108 BSU 35470 NP 391427.1             MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                     ****** !     !! ! ! !!!!! !   !   **!*   !**   * !        !*!!! *  !!! *  ** *

logo

NTDB id 995325 AAVC46 RS11660 WP 307500336.1  KDCVYCRSCIMMGKTTECGFLYEWTGPQMEETCHTELTWQGNLSKGQKRASEKLIEAIKNKSDLLIWAVCGAGKTEVLFY   154
NTDB id 108 BSU 35470 NP 391427.1             KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                     ! **!!!!!*!!!* *!* *!! !  **    **  !!! ! !! !! *!   !!!!!  ! *!!!!!!!!!!!!!*!!*

logo

NTDB id 995325 AAVC46 RS11660 WP 307500336.1  GIEYALHQGMSVCIATPRTDVVLELEPRLKKAFQGMKIAVLYGGSPQRFQIAPLVIATTHQLMRYKHAFDVLIIDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1             GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                     !!! !!*!!* !!!!!!!!!!!!!! !!!! !!!!  !  !!!!!* *  * !!*! !!!!!*!!!*! !!*!!!!!!!!

logo

NTDB id 995325 AAVC46 RS11660 WP 307500336.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMKRDVSRGQLEAIKIPLRFHQQPLPVPSFQWIGHWKKKLKKNQLPPKV   314
NTDB id 108 BSU 35470 NP 391427.1             PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                     !!! !  !!!!! !! *!    !!!!!!!*! *!!    !!!* **!! !*!  !!! ! ! !*!*!!!!! *! *!! !

logo

NTDB id 995325 AAVC46 RS11660 WP 307500336.1  MNWMQKHITKKRRILLFVPSISTMKKITKVLREHRLNVEGVSADDPDRKQKVQHFRDYKYDVLVTTTILERGVTIPNVQV   394
NTDB id 108 BSU 35470 NP 391427.1             KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                       !*  !*   !** !!!!!*! * !   * * ***    !*!*!**!! !!!*!!!   !*!*!!!!!!!!!!*! !!

logo

NTDB id 995325 AAVC46 RS11660 WP 307500336.1  GVLGAESTIFTESALVQISGRAGRHPDFFKGDVIFFHFGLTRSMKQAKKHIVKMNDTAAKEFSEK   459
NTDB id 108 BSU 35470 NP 391427.1             GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                     !!!!!!!*!!!!!!!!!!! !! !!!***  !!!!*!!!! !*!!  !*!!!  !!* !!!   *
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X non conserved

X similar

X ≥50% conserved