```
logo
NTDB id 984991 MKX52 RS16000 WP 140404325.1  ......MNMDKAMKLGEQLQSRHLLTAETRCLQSELDWLEEKGLVIRRPAIERKANGLICCRCGVSKNQYFAHSPCDKCQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !      !  ! !!!!!  !  *    **!*   ! *   * !        !*!!! * * !! *  ** *

logo
NTDB id 984991 MKX52 RS16000 WP 140404325.1  KDCVYCRSCIMMGKTLECEFLYEWTGPPIEGTAHTELTWRGNLSKGQKRASEKLIEAIKHKSDLLIWAVCGAGKTEVLFQ  154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    ! **!!!!!*!!!*  !* *!! !  **     *  !!! ! !! !! *!   !!!!! *! *!!!!!!!!!!!!!*!!*

logo
NTDB id 984991 MKX52 RS16000 WP 140404325.1  GIEYALHQGMRVCIATPRTDVVLELEPRLKKAFHGLKIAALYGGSLQRFQIAPLVIATTHQLMRYKHAFDVLVIDEVDAF  234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!*!!*!!!!!!!!!!!!!!! !!!! !!*!  ! !!!!!!  *  * !!*! !!!!!*!!!*! !!**!!!!!!!

logo
NTDB id 984991 MKX52 RS16000 WP 140404325.1  PYSIDERLQFAVLKAMRKKGVRVYLSATPSKKMIRDVSRGQLEAIKIPLRFHQQPLPVPSFQWIGHWKKKLKKNQLPPIV  314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !!! !  !!!!! !! *!    !!!!!!!*! * !    !!!* **!! !*!  !!! ! ! !*!*!!!!! *! *!! !

logo
NTDB id 984991 MKX52 RS16000 WP 140404325.1  MNWMQNHIAKKRRVLLFVPSISTMKKVTKVLRKHHLNVEGVSADDPDRKQKVQQFRDDKYDVLVTTTILERGVTIPNVQV  394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !*  !*   !*! !!!!!*! * !   * * *!*    !*!*!**!! !!!!!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 984991 MKX52 RS16000 WP 140404325.1  GVLGAESTIFTESALVQISGRAGRHPDFFKGDVFFFHFGLTRSMKQAKDHIVKMNDTAEKEFSEK   459
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    !!!!!!!*!!!!!!!!!!! !! !!!***  !!! *!!!! !*!!  !* !!  !!* ! !  *
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X non conserved

X similar

X $\geq$ 50% conserved