```
logo
NTDB id 274670 C5Y82 RS16445 WP 012011432.1  ......MNMDKAMKLGEQLQSRHLLTAETRCLQSELDWLEEKGLVIRRTAIERKANGLICCRCGVSKNQYFAHSPCDKCQ   74
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                    ****** !      !  ! !!!!!  !  *    **!*   ! *     !        !*!!! * * !! *  ** *

logo
NTDB id 274670 C5Y82 RS16445 WP 012011432.1  KDCVYCRSCIMMGKTSECEFLYEWTGPPIEGTAHTELTWRGNLSKGQKRASEKLIEAIKHKSDLLIWAVCGAGKTEVLFH   154
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP   158
consensus                                    ! **!!!!!*!!!* !!* *!! !  **     *  !!! ! !! !! *!   !!!!! *! *!!!!!!!!!!!!!*!!

logo
NTDB id 274670 C5Y82 RS16445 WP 012011432.1  GIEYALHQGMRVCIATPRTDVVLELEPRLKKAFHGLKIAALYGGSLQRFQIAPLVIATTHQLMRYKHAFDVLVIDEVDAF   234
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF   238
consensus                                    !!! !!*!!*!!!!!!!!!!!!!!! !!!! !!*!  ! !!!!!!  *  * !!*! !!!!!*!!!*! !!**!!!!!!!

logo
NTDB id 274670 C5Y82 RS16445 WP 012011432.1  PYSMDERLHFAVLKAMRKKGVRVYLSATPSKKMIRDVSRGQLEAIKIPLRFHQQLLPVPSFQWIGHWKKKLKKNQLPPIV   314
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV   318
consensus                                    !!! !  !*!!! !! *!    !!!!!!!*! * !    !!!* **!! !*!  *!! ! ! !*!*!!!!! *! *!! !

logo
NTDB id 274670 C5Y82 RS16445 WP 012011432.1  MNWMQNHIAKKRRVLLFVPSISTMKKVTKVLRKHHLNVEGVSADDPDRKQKVQQFRDDKYDVLVTTTILERGVTIPNVQV   394
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT   398
consensus                                      !*  !*   !*! !!!!!*! * !   * * *!*    !*!*!**!! !!!!!!!   !*!*!!!!!!!!!!*! !!

logo
NTDB id 274670 C5Y82 RS16445 WP 012011432.1  GVLGAESTIFTESALVQISGRAGRHPDFFKGDVFFFHFGLTRSMKQAKNHIVKMNDTAEKEFSEK   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