```
logo
NTDB id 32100 BCB4264 RS26180 WP 000225358.1  ..................MVAGKQLLLEELSSDLQRKLNDLKKKGEIVCVQGVKKKNSKYMCQRCGNVDRRLFASFLCKRC   63
NTDB id 108 BSU 35470 NP 391427.1             MNVPVEKNSSFSKELQQTLRSRHLLRTELSFS.DEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..S   77
consensus                                     **************** *  **!!  !!!  *   *  * ! ! ! * * *     *! !*!!!* ! ! !  ******

logo
NTDB id 32100 BCB4264 RS26180 WP 000225358.1  SKVCTYCRKCITMGRVSECAVLVRGIAERKREKNSNLLQWDGTLSTGQNLAAQGVIEAIKQKESFFIWAVCGAGKTEMLF   143
NTDB id 108 BSU 35470 NP 391427.1             GKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLF   157
consensus                                      ! * !!! !* !!!!!!* *!     !      !  ! !!! !!*!!* !!* *!!!!  !!   !!!!!!!!!!!!!!

logo
NTDB id 32100 BCB4264 RS26180 WP 000225358.1  YGINEALQKGERVCIATPRTDVVLELAPRLQEVFPYIKVAALYGGSVDKEKDAVLVVATTHQLLRYYRAFHVIVVDEIDA   223
NTDB id 108 BSU 35470 NP 391427.1             PGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDA   237
consensus                                     *!!  !!* ! !!!!!!!!!!!!!!!!!!!!    !*   * !!!!!! !! *  *!** !!!!!!!!  ! *!***!!*!!

logo
NTDB id 32100 BCB4264 RS26180 WP 000225358.1  FPYCADQMLQYAVKQAMKEKAARIYLTATPDETWKRKFRKGEQKGVIVSGRYHRHPLPVPLFCWCGNWKKSLNRERIPRV   303
NTDB id 108 BSU 35470 NP 391427.1             FPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRLPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPA   317
consensus                                     !!!*!!!  !!*!!  !  !     *!!*!!!*   !!!   !  * ! ***!*!!*!!! ! !*!!!!!!! !!!  *!!*

logo
NTDB id 32100 BCB4264 RS26180 WP 000225358.1  LLRWLKMHLNKKYPVFLFVPHVRYIEEISSLLKSLHNKVEGVHAEDPMRKEKVAAFRKGEIPLLVTTTILERGVTVKNLQ   383
NTDB id 108 BSU 35470 NP 391427.1             VKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQ   397
consensus                                     * !!*  !*    !!!!!!!*!  *!    * ! *!**   !!!!!**!!!!!  !! ! **!!*!!!!!!!!!!!!* *!

logo
NTDB id 32100 BCB4264 RS26180 WP 000225358.1  VAVLGAEEEIFSESALVQIAGRAGRSFEALYGEVIYFHYGKTEAMVRAKKHIQGMNKNAKEQGLID   449
NTDB id 108 BSU 35470 NP 391427.1             TGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                      *!!!!!  !!*!!!!!!!!!! !!* !   !*!!!!!*!!!  !* !*!!!  !!   !    * !
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X non conserved

X similar

X ≥ 50% conserved