```
logo
NTDB id 969576 MHB78 RS21435 WP 046130086.1  MEVIVIAGKQPASEYSRNLQSLLESRHLLKSELPFPDDVIDWHIQKGLIKAEKPIEETTKGFVCKRCGQDHQALFARYPC   80
NTDB id 108 BSU 35470 NP 391427.1            ....MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS   76
consensus                                    *****  *  * ! *!* !!  ! !!!!!**!!*!*!**!*!!!  ! ! !! *!    * * ! !!!! *!  !  ! *

logo
NTDB id 969576 MHB78 RS21435 WP 046130086.1  YACNQQCVYCRSCVMMGRVSECTPLLTWKGGDQSKWPPVRMVWEGILSAGQEKAARSIIEAIRKKEELLIWAVCGSGKTE  160
NTDB id 108 BSU 35470 NP 391427.1            S..GKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTE  154
consensus                                     **  ***!!!!!!!!!!!!!* !! *!!    ! !***** !*! !! !! !!!  *!!!! !!!!!!!!!!!! !!!!

logo
NTDB id 969576 MHB78 RS21435 WP 046130086.1  ILFQGIEFALNHGLRVCIATPRTDVVLELAPRVKKAFEGAEIAALYGGSPDRGMLSPLMISTTHQLFRYKEAFDVMVVDE  240
NTDB id 108 BSU 35470 NP 391427.1            MLFPGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDE  234
consensus                                    *!!*!!! !!!*!!!!!!!!!!!!!!!!!!!!*! !! !!*! !!!!!!*!*! !!!!!!!!!!!! !!!*! !!!**!!

logo
NTDB id 969576 MHB78 RS21435 WP 046130086.1  VDAFPYSYDQTLQYAVEKAGKRQSARIYLTATPSREMKKRAESGRLKAAHIPARYHRSPMPEPSFTWCGNWKKSLKCHII  320
NTDB id 108 BSU 35470 NP 391427.1            VDAFPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKI  314
consensus                                    !!!!!!! !!!!!*!! !! !**!  *!!*!!**!*!**!  ! !*  *!!!!*!! !*!!! ! !!!!!!! ! ** !

logo
NTDB id 969576 MHB78 RS21435 WP 046130086.1  PLAVKRWLFKHKEQKQPVFLFVPSIPALKSVVTLLKKEHFQIEGVYADDPDRNEKVKRFRDGTLDILVTTTILERGVTVQ  400
NTDB id 108 BSU 35470 NP 391427.1            PPAVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVP  394
consensus                                    !*!!!!!*  !     !!!!!!!!** !     * !  !*    !*!*!**! !!!  !!!! !!*!*!!!!!!!!!!!*

logo
NTDB id 969576 MHB78 RS21435 WP 046130086.1  KAQVGVLGAESAVFDESALVQISGRAGRHPQYTTGDVRFFHFGKTANMVAARRHIRRMNKMALLENLVD  469
NTDB id 108 BSU 35470 NP 391427.1            KVQTGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                    ! ! !!!!!!! *! !!!!!!! !! !!!* !  !!! *!!!!!!  !* !!*!!* !! *!    * !
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X non conserved

X similar

X $\geq$ 50% conserved