```
logo
NTDB id 258494 CU648 RS12705 WP 101195070.1  ...................MVAGKQLLLEELSSDLRRELSD.LKKKGEIICVQGIIKKASKYICQRCGNIEQRLFASFLCKR   62
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELS..FSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..   76
consensus                                    ***************** *  **!!  !!!**   !* *** ! ! ! * * !     *! !*!!!* *!! !  *****

logo
NTDB id 258494 CU648 RS12705 WP 101195070.1  CSKVCTYCRKCITMGRVSECAVLVRGIHERKGERELHSLQWKGSLSLGQELAAQGVIEAIKQKESFFIWAVCGAGKTEML   142
NTDB id 108 BSU 35470 NP 391427.1            SGKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEML   156
consensus                                    * ! * !!! !* !!!!!!* *!    *!       * ! ! ! !! !!  !!* *!!!!  !!   !!!!!!!!!!!!!

logo
NTDB id 258494 CU648 RS12705 WP 101195070.1  FYGIEEALQKGERVCIATPRTDVVLELAPRLQEVFPSINVAALYGGSVDREKDAALVVATTHQLLRYYRAFHVMIVDEID   222
NTDB id 108 BSU 35470 NP 391427.1            FPGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVD   236
consensus                                    !*!!! !!* ! !!!!!!!!!!!!!!!!!!!!   !*   * !!!!!! !* *  *!** !!!!!!!!  ! *!!!*!!*!

logo
NTDB id 258494 CU648 RS12705 WP 101195070.1  AFPYHADQMLQYAVQQAMKEKAARIYLTATPDEKWKRNFRRGKQKGIIVSGRYHRHPLPVPLFSWCGNWKKSLHHKKIPR   302
NTDB id 108 BSU 35470 NP 391427.1            AFPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPP   316
consensus                                    !!!!*!!! !!*!!! ! !     *!!*!!!*   !!    !  * * ***!*!!*!!! ! ! !!!!!!! !** !!!*

logo
NTDB id 258494 CU648 RS12705 WP 101195070.1  VLLQWLKMYVNKKYPIFLFVPHVRYIEEIGLLLKGLDHRIDGVHAEDPMRKEKVAEFRKGDIPLLVTTTILERGVTVKNL   382
NTDB id 108 BSU 35470 NP 391427.1            AVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKV   396
consensus                                     *  !*  *!    !*!!!!!*!  *!  * * !!** !   !!!!!**!!!!!  !! ! **!!*!!!!!!!!!!!* *

logo
NTDB id 258494 CU648 RS12705 WP 101195070.1  QVAVLGAEEEIFSESALVQIAGRAGRSFEEPYGEVVYFHYGKTESMVRAKRHIQSMNKSAKEQGLID   449
NTDB id 108 BSU 35470 NP 391427.1            QTGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    ! *!!!!!  !!*!!!!!!!!!! !!* ! * !*!*!!!*!!! !!* !**!!  !!  !    * !
```

X non conserved

X similar

X ≥ 50% conserved