```
logo
NTDB id 1106601 ACN6MY RS00180 WP 419882290.1  ....MKRDFPFLKELQKHLYGRSLLAEEIPFPLETIGYHQERGYVSGTPGVEKEKGRFVCRRCGCREQRLFYSFPCKRCG   76
NTDB id 108 BSU 35470 NP 391427.1              MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSG   78
consensus                                      ***** *  *! !!!! *!  !*!!  !**!* ! ! *!   !!*** * *   ! !* ! !!!* *!! !  * ** *!

logo
NTDB id 1106601 ACN6MY RS00180 WP 419882290.1  KMCSYCRSCIMMGRVSECSLLYSWSGDHYSFAVPENPMLWDGTLSQGQKTASEAVAEAVTRNEEVLVWAVCGAGKTEVLF   156
NTDB id 108 BSU 35470 NP 391427.1              KNKLYCRSCVMMGRVSEEVPLYSWKEENESN.WKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLF   157
consensus                                      ! * !!!!!*!!!!!!!* *!!!!  ** ! * *  ** !!! !! !!  !   * !!*** !!*!*!!!!!!!!!!*!!

logo
NTDB id 1106601 ACN6MY RS00180 WP 419882290.1  QGIETALKSKKRVCIATPRTDVVLELAPRLKQAFPGIDVAALYGGSEERHILAPLTVLTTHQLFRFQQAFDTIIIDEVDA   236
NTDB id 108 BSU 35470 NP 391427.1              PGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDA   237
consensus                                      *!!!*!!    !!!!!!!!!!!!!!!!!!!! !!*! !* !!!!!!**** ! !! * !!!!! !*  ! ! *!!!!!!!

logo
NTDB id 1106601 ACN6MY RS00180 WP 419882290.1  FPYSMDFSLQYAAEKSKKAQSSTIYLTATPSKKMQSSAKTGKLTHVTIPARYHRKPIPVPEMKWCGNYSKQFSKKVIPVP   316
NTDB id 108 BSU 35470 NP 391427.1              FPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPA   317
consensus                                      !!!! ! *!!*!  ! *! *!* *!!*!!!*! *   !  ! !**! !!!!*!!!!*! !   !!!!* !   *  !!**

logo
NTDB id 1106601 ACN6MY RS00180 WP 419882290.1  IKDWLKKRLEAETPILLFFPSIVMMESVLPLFQHLHEGLISVHSQDPERKEKVTALRKGEVLGLLTTTILERGVTIPRLD   396
NTDB id 108 BSU 35470 NP 391427.1              VKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQ   397
consensus                                      *! !*  **    !* !! !!* **!   **! **!*   !!!  !**!!!!!   ! ! *  !*!!!!!!!!!!*!**

logo
NTDB id 1106601 ACN6MY RS00180 WP 419882290.1  VAVIGAEHEVFSESALVQIAGRVGRSSQHYSGNVTFFHYGKTNSMMSAVHHISLMNSEAKKRGLLDE   463
NTDB id 108 BSU 35470 NP 391427.1              TGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD.   463
consensus                                       *!*!!!* *!*!!!!!!!!!! !!*  *  ! ! *!!*!!! !!* ! *!!  !!  ! !  * !*
```

X non conserved

X similar

X $\geq$ 50% conserved