```
logo
NTDB id 401448 GKC27 RS11260 WP 003217401.1  MYGIEYLGQELLEEACRMRASDVHIVPKEKKASVSFRVDSDLIQQRTIDKKSGERLIAHFKFLSSMDIGEKRRPQNGSLA   80
NTDB id 96 BSU 24730 NP 390353.1             MDSIEKVSKNLIEEAYLTKASDIHIVPRERDAIIHFRVDHALLKKRDMKKEECVRLISHFKFLSAMDIGERRKPQNGSLT   80
consensus                                    !  !! *   !*!!!*  *!!!*!!!!*!* ! **!!!!* !*  ! * !  * !!! !!!!!! !!!!!*!*!!!!!!

logo
NTDB id 401448 GKC27 RS11260 WP 003217401.1  VMLRRGQVFIRMSTLPTVNDESLVIRILPQDHVPKIKHLSLFPKASTRLLSFLNHSHGLILFTGPTNSGKTTTLYSLIQF  160
NTDB id 96 BSU 24730 NP 390353.1             LKLKEGNVHLRMSTLPTINEESLVIRVMPQYNIPSIDKLSLFPKTGATLLSFLKHSHGMLIFTGPTGSGKTTTLYSLVQY  160
consensus                                    * !* !*!**!!!!!!!*!*!!!!!!**!! **! ! *!!!!!!    !!!!! !!!!***!!!!! !!!!!!!!!!*!*

logo
NTDB id 401448 GKC27 RS11260 WP 003217401.1  AKKNFNRNIITLEDPVETRNEEVLQVQVNEKAGITYAAGLRAILRHDPDMIVLGEIRDAETARTAIRAALTGHLVMSTLH  240
NTDB id 96 BSU 24730 NP 390353.1             AKKHFNRNIVTLEDPVETRDEDVLQVQVNEKAGVTYSAGLKAILRHDPDMIILGEIRDAETAEIAVRAAMTGHLVLTSLH  240
consensus                                    !!!*!!!!!*!!!!!!!!! !*!!!!!!!!!!!*!! !!!*!!!!!!!!!!!*!!!!!!!!!  !*!!!*!!!!!***!!

logo
NTDB id 401448 GKC27 RS11260 WP 003217401.1  AKNAKGALYRMLEFGVTMNELEQTMVAIAAQRLIELTCPFCGETCQ.LYCKLNRPVRRTNVFELLFGKELRECIKEAKGE  319
NTDB id 96 BSU 24730 NP 390353.1             TRDAKGAIYRLLEFGINMNEIEQTVIAIAAQRLVDLACPFCENGCSSVYCRQSRNTRRASVYELLYGKNLQQCIQEAKGN  320
consensus                                     * !!!!*!!*!!!!* !!!*!!!**!!!!!!!**! !!!!   ! **!!*  !* !!  !*!!!*!! !  !! !!!!

logo
NTDB id 401448 GKC27 RS11260 WP 003217401.1  YAHSSYETLQRLIRKGVALGYLSKNTYHRWVYEEASL  356
NTDB id 96 BSU 24730 NP 390353.1             HANYQYQTLRQIIRKGIALGYLTTNNYDRWVYHEKD.  356
consensus                                    *!*  ! !!  *!!!!*!!!!!* ! !*!!!!*!  *
```

X non conserved

X similar

X $\geq$ 50% conserved