```
logo

NTDB id 1023994 AB3G27 RS11280 WP 249118252.1  MYGIEYLGQELLEEACRMRASDVHIVPKEKEASVSFRVDSDLIQQRTIDKKSGERLIAHFKFLSSMDIGEKRRPQNGSLA   80
NTDB id 96 BSU 24730 NP 390353.1               MDSIEKVSKNLIEEAYLTKASDIHIVPRERDAIIHFRVDHALLKKRDMKKEECVRLISHFKFLSAMDIGERRKPQNGSLT   80
consensus                                      !  !! *   !*!!!*  *!!!*!!!!*!**! **!!!!* !*  ! * !  * !!! !!!!!! !!!!!*!*!!!!!!

logo

NTDB id 1023994 AB3G27 RS11280 WP 249118252.1  VMLRRGQVFIRMSTLPTVNDESLVIRILPQDHVPKIKHLSLFPKASTRLLSFLNHSHGLILFTGPTNSGKTTTLYSLIQF  160
NTDB id 96 BSU 24730 NP 390353.1               LKLKEGNVHLRMSTLPTINEESLVIRVMPQYNIPSIDKLSLFPKTGATLLSFLKHSHGMLIFTGPTGSGKTTTLYSLVQY  160
consensus                                      * !* !*!**!!!!!!!*!*!!!!!**!! **! ! *!!!!!!    !!!!! !!!!***!!!!! !!!!!!!!!!*!*

logo

NTDB id 1023994 AB3G27 RS11280 WP 249118252.1  AKKNFNRNIITLEDPVETRNEEVLQVQVNEKAGITYAAGLRAILRHDPDMIVLGEIRDAETARTAIRAALTGHLVMSTLH  240
NTDB id 96 BSU 24730 NP 390353.1               AKKHFNRNIVTLEDPVETRDEDVLQVQVNEKAGVTYSAGLKAILRHDPDMIILGEIRDAETAEIAVRAAMTGHLVLTSLH  240
consensus                                      !!!*!!!!!*!!!!!!!!! !*!!!!!!!!!!!*!! !!!*!!!!!!!!!!*!!!!!!!!!  !*!!!*!!!!!***!!

logo

NTDB id 1023994 AB3G27 RS11280 WP 249118252.1  AKNAKGALYRMLEFGVTMNELEQTMVAIAAQRLIELTCPFCGETCQ.LYCKLNRPVRRTNVFELLFGKELGECIKEAKGE  319
NTDB id 96 BSU 24730 NP 390353.1               TRDAKGAIYRLLEFGINMNEIEQTVIAIAAQRLVDLACPFCENGCSSVYCRQSRNTRRASVYELLYGKNLQQCIQEAKGN  320
consensus                                       * !!!!*!!*!!!!* !!!*!!!**!!!!!!!**! !!!!   ! **!!*  !* !!  !*!!!*!! !  !! !!!!

logo

NTDB id 1023994 AB3G27 RS11280 WP 249118252.1  YAHSSYETLHRLIRKGVALGYLSKNTYHRWVYEEASL  356
NTDB id 96 BSU 24730 NP 390353.1               HANYQYQTLRQIIRKGIALGYLTTNNYDRWVYHEKD.  356
consensus                                      *!*  ! !!* *!!!!*!!!!!* ! !*!!!!*!  *
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X non conserved

X similar

X $\geq$ 50% conserved