```
logo

NTDB id 1159648 QOR57 RS02675 WP 017647063.1  MKNKDPKRKHKSLLGLLKWWIIGFAFLLLVLASLVVRLPYYLEMPGGAYDIRSVLKVNKKADKAKGSYNFVAVSVSQATP   80
NTDB id 360 SMU RS02495 WP 002262039.1        ..........MKTNKKFKWWLISGISLILLLMVFFFPLPYYLEMPGGAYDIRSVVTVNHKEDKEKGSYNFVAVSLSKATP   70
consensus                                     **********       !!!*!    !*!*!     *!!!!!!!!!!!!!!!!!* !!*! !! !!!!!!!!!!*! !!!

logo

NTDB id 1159648 QOR57 RS02675 WP 017647063.1  AQVLYAWLTPFTELSSKEETTGGFSNDDYLRINQFYMETSQNESIYQALKLANKQVSLTYKGVYVLNLAKNSTFKDRLHL  160
NTDB id 360 SMU RS02495 WP 002262039.1        IQVLYAWLTPFTEITSAKETTGGVSDADYMRINQFYMETSQNGAIYKALSLAHKKASFNYMGVYVLQVSRNSTFKGVLNI  150
consensus                                      !!!!!!!!!!!!!**!  !!!!! !  !!*!!!!!!!!!!!!!  !! !! !!*!  !  ! !!!!!** *!!!!!   !**

logo

NTDB id 1159648 QOR57 RS02675 WP 017647063.1  ADTVTGVNGKSFKNSSQLIKYVAALHLGDKVKVQYTSQGKKKESVGKVIKLSNGKNGIGIGLTDHTEVSSDVPVDFNTEG  240
NTDB id 360 SMU RS02495 WP 002262039.1        ADTVTGVNDKTFHSSKELIKYVSGLKLGSKVSVQYTSENKKKTAKGKVIKLSNGKNGIGIGLVDHTKVTSDDKIEFSTNG  230
consensus                                     !!!!!!!! !*!* !  !!!!! *!*!! !! !!!!!  !!!   !!!!!!!!!!!!!!!!!! !!! !*!! ***! ! !

logo

NTDB id 1159648 QOR57 RS02675 WP 017647063.1  VGGPSAGLMFTLAIYDQLVKEDLRKGRKIAGTGTIEQNGHVGDIGGAGLKVVSAAKKGMDIFFVPNNPIDKKAKKGKTKV  320
NTDB id 360 SMU RS02495 WP 002262039.1        IGGPSAGLMFTLDIYDQLVKEDLRKGRIIAGTGTIGEDGSVGDIGGADMKVAAADRINADIFFVPNNPVSKATLKKNPKA  310
consensus                                     *!!!!!!!!!!!! !!!!!!!!!!!!!!! !!!!!!!   !*!!!!!!! *!!  ! *   !!!!!!!!!* !   !  *!

logo

NTDB id 1159648 QOR57 RS02675 WP 017647063.1  QTNYQEAKAAAKRLGTKMKIVPVQNVQQAIDYLKKTK  357
NTDB id 360 SMU RS02495 WP 002262039.1        LTNYQEAKQAAKKLGTKMKIVPVKNVQEAIDYLRKH.  346
consensus                                      !!!!!!! !!!*!!!!!!!!!! !!! !!!!!*!**
```

X non conserved

X similar

X $\geq$ 50% conserved