```
logo
NTDB id 374 SMU RS06885 WP 002262930.1        ......MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKN...S   71
NTDB id 396466 PaeAG1 RS02545 WP 003084583.1  MEQQSDGLKVMVIDDSKTIRRTAETLLKKVGCDVITAIDGFDALAKIADTHPNIIFVDIMMPRLDGYQTCALIKNNSAFK   80
NTDB id 1047 HON27 RS03110 WP 000389061.1     MEDAFQNLKVMVIDDSKTIRRTAETLLQREGCEVITAVDGFEALSKIAEANPDIVFVDIMMPRLDGYQTCALIKNSQNYQ   80
consensus                                     **      *!****!!*!*!*******!  **!***!!!*!!**!!*!***  *!*****!*!*!*!!!**********   *

logo
NTDB id 374 SMU RS06885 WP 002262930.1        HVPIIMLSAKDSEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVA  151
NTDB id 396466 PaeAG1 RS02545 WP 003084583.1  STPVIMLSSKDGLFDKAKGRIVGSDQYLTKPFSKEELLGAIKAHVPSFTPVDAVS........................  135
NTDB id 1047 HON27 RS03110 WP 000389061.1     NIPVIMLSSKDGLFDQAKGRVVGSDEYLTKPFSKDELLNAIRNHVSS................................  127
consensus                                      *!*!!!!*!!**!!***!***!*!*!*!!!!!**!!!*****!* *    **

logo
NTDB id 374 SMU RS06885 WP 002262930.1        KKRGTEVELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYM  231
NTDB id 396466 PaeAG1 RS02545 WP 003084583.1  ........................................................................................  135
NTDB id 1047 HON27 RS03110 WP 000389061.1     ........................................................................................  127
consensus

logo
NTDB id 374 SMU RS06885 WP 002262930.1        KSYD   235
NTDB id 396466 PaeAG1 RS02545 WP 003084583.1  ....   135
NTDB id 1047 HON27 RS03110 WP 000389061.1     ....   127
consensus
```

X non conserved

X similar

X ≥50% conserved