```
logo
                                          MEDAFQNLKVMVIDDSKTIRRTAETLLQREGCEVITAVDGFEALSKIAEANPDIVFVDIMMPRLDGYQTCALIKNSQNYQ
NTDB id 374 SMU RS06885 WP 002262930.1    ......MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRK...NS    71
NTDB id 263742 C1H71 RS08060 WP 130106087.1 .MSKLAGIKVMVIDDSNTIRRSAEIFLGQAGCEVILAEDGFDALAKISDRLPDVIFVDVMMPRLDGYQTCSLIKKNPRYK    79
NTDB id 1047 HON27 RS03110 WP 000389061.1 MEDAFQNLKVMVIDDSKTIRRTAETLLQREGCEVITAVDGFEALSKIAEANPDIVFVDIMMPRLDGYQTCALIKNSQNYQ    80
consensus                                        *!****!!***!*****  !***!***!*! !!**!!*!* * *!!****!*!*!*!!!**** ****   *

logo
                                          HTPVIMLSSKDGLFDRARGRMVGSDEYLTKPFTKDSLLQAVSAHIRLD
NTDB id 374 SMU RS06885 WP 002262930.1    HVPIIMLSAKDSEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVA   151
NTDB id 263742 C1H71 RS08060 WP 130106087.1 MTPVIMLSSKDGLFDRARGRMVGSDEYLTKPFTKDSLLQAVSAHIRLD.............................   127
NTDB id 1047 HON27 RS03110 WP 000389061.1 NIPVIMLSSKDGLFDQAKGRVVGSDEYLTKPFSKDELLNAIRNHVSS.............................   127
consensus                                  *!*!!!!*!!**!!***!***!*!*!*!!!!****!!*****!**

logo
                                          KKRGTEVELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYM
NTDB id 374 SMU RS06885 WP 002262930.1    KKRGTEVELTHREFELLHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYM   231
NTDB id 263742 C1H71 RS08060 WP 130106087.1 ..................................................................................   127
NTDB id 1047 HON27 RS03110 WP 000389061.1 ..................................................................................   127
consensus

logo
                                          KSYD
NTDB id 374 SMU RS06885 WP 002262930.1    KSYD   235
NTDB id 263742 C1H71 RS08060 WP 130106087.1 ....   127
NTDB id 1047 HON27 RS03110 WP 000389061.1 ....   127
consensus
```

X non conserved
X similar
X ≥ 50% conserved