```
logo

NTDB id 1358 HI 0366 AAC22024.1                  ..MKTISKQLSAVIFPFIFSACVSQ...SASSLNHQTAAKARVELALSYLQQNNPQLAKINLDKALQHDKNYYLVHSALA   75
NTDB id 1115307 MIDG2331 RS06435 WP 039709242.1  MNLAKFLRNLSACMLLSVLFGCSSQLPTSQTTFNRSEAVKARINLALAYLDQHDLPKAKENIDKALSHDQNDYLPHSVLA   80
NTDB id 1386 A4U84 RS02735 WP 005710402.1        MTFAKFFRNLTACSVALWLVACANQ..TTQVDFNRSEAVKARINLALAYLEQSDFPKAKENIDKALEHDVKDYLPHSVLA   78
consensus                                        * ***** **!*!***  ** *! *!  ******!***!*!!!**!!!*!!*! * **!!*!*!!!! !! **!!*!!*!!

logo

NTDB id 1358 HI 0366 AAC22024.1                  HYYQQQGQIENAFREYEIAVNLN.......HKQGDVHNNFGTFLCSQKKFEQAQQQFELALNS.PNYYHQADTFENIVLC   147
NTDB id 1115307 MIDG2331 RS06435 WP 039709242.1  YYYQQIGDQVHAEQAYQQALKSS.......DNCPDVLNNYGTFLCKQAKFDQAYQQFEQAVKSEQPYYHQADSLENIVLC   153
NTDB id 1386 A4U84 RS02735 WP 005710402.1        YYYQQTGDNQKAEEAYQQALKLSKTQSKNNQVRPDVLNNYGTFLCKQKLFDKAYQQFETALTSQEAYYNQADTLENIALC   158
consensus                                        *!!!! !**  !* *!**!****          *!!*!!*!!!!!*!**!**!*!!!! !* !   !!*!!!**!!!*!!

logo

NTDB id 1358 HI 0366 AAC22024.1                  AYSAQKMDIYQQTLEKLRQIDGKRAEKFNSLK...   179
NTDB id 1115307 MIDG2331 RS06435 WP 039709242.1  AKQEPNLAKANEALSQLEKLDKSRAAALL......   182
NTDB id 1386 A4U84 RS02735 WP 005710402.1        ANMKKDIEKQKTALSQLEKIDKSRAERLYNFMEIR   193
consensus                                        !      *** * *!**!***!**!!***
```

X non conserved

X similar

X $\geq$ 50% conserved