```
logo

NTDB id 1018882 ABX013 RS03375 WP 037391728.1  MKNLFLAVALGLLLSACASTSTVDKDSQITQDWSVQRLYNEAHDELMHRNYTHAEKLYEILQARFPYGSYAEQAQLDTAY   80
NTDB id 1102 NMB RS03635 WP 002244053.1        MKKILLTVSLGLALSACATQGTVDKDAQITQDWSVEKLYAEAQDELNSSNYTRAVKLYEILESRFPTSRHAQQSQLDTAY   80
NTDB id 1106 NGFG RS01495 WP 003687645.1       MKKILLTVSLGLALSACATQGTADKDAQITQDWSVEKLYAEAQDELNSSNYTRAVKLYEILESRFPTSRHARQSQLDTAY   80
consensus                                      !!***!*!*!!!*!!!!!***!*!!!*!!!!!!!!!**!!*!!*!!!***!!!*!*!!!!!!**!!!****!  !*!!!!!!

logo

NTDB id 1018882 ABX013 RS03375 WP 037391728.1  AYYKDDENDKALVAIEQFQRLYPQHPNMDYALYLKALIQLNEDKSFVSKLAKQDWSDRDPKANREAYATFALLVQYFPQS  160
NTDB id 1102 NMB RS03635 WP 002244053.1        AYYKDDEKDKALAAIDRFRRLHPQHPNMDYALYLRGLVLFNEDQSFLNKLASQDWSDRDPKANREAYQAFAELVQRFPNS  160
NTDB id 1106 NGFG RS01495 WP 003687645.1       AYYKDDEKDKALAAIERFRRLHPQHPNMDYALYLRGLVLFNEDQSFLNKLASQDWSDRDPKANREAYQAFAELVQRFPNS  160
consensus                                      !!!!!!!*!!!!*!!**!*!!*!!!!!!!!!!!!!**!***!!!*!!**!!!*!!!!!!!!!!!!!!!**!!*!!!*!!*!

logo

NTDB id 1018882 ABX013 RS03375 WP 037391728.1  KYADDARAKMQKLLDALGGNELSVARYYMKRGAWLAAVGRAQTVISQFQNTPNVEEALAIMVSAYANLGEQKLSDDTKRV  240
NTDB id 1102 NMB RS03635 WP 002244053.1        KYAADATARMVKLVDALGGNEMSVARYYMKRGAYIAAANRAQKIIGSYQNTRYVEESLAILELAYKKLDKPRLAADTRRV  240
NTDB id 1106 NGFG RS01495 WP 003687645.1       KYAADATARMVKLVDALGGNEMSVARYYMKRGAYIAAANRAKKIIGSYQNTRYVEESLAILELAYKKLDKPQLAADTRRV  240
consensus                                      !!!*!!*!*!*!!*!!!!!!!!*!!!!!!!!!!!!**!!**!***!***!!!**!!!*!!!***!!**!***!**!!*!!

logo

NTDB id 1018882 ABX013 RS03375 WP 037391728.1  LAQNFPNSPYLQKPWQDHNTIPWWRYWK  268
NTDB id 1102 NMB RS03635 WP 002244053.1        LETNFPKSPFLKQPWRS.DDMPWWRYWH  267
NTDB id 1106 NGFG RS01495 WP 003687645.1       LETNFPKSPFLTHAWQP.DDMPWWRYWH  267
consensus                                      !**!!!*!!*!  *!*  ***!!!!!!*
```

X non conserved

X similar

X $\geq$ 50% conserved