```
logo

NTDB id 1016702 ABW387 RS10045 WP 038648650.1  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 1016702 ABW387 RS10045 WP 038648650.1  AYYKDDENDKALAAIEQFQRLYPQHPNMDYALYLKALIQLNEDKSFVSKLAKQDWSDRDPKANREAYATFALLVQYFPQS  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 1016702 ABW387 RS10045 WP 038648650.1  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 1016702 ABW387 RS10045 WP 038648650.1  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                                      !**!!!*!!*!  *!*  ***!!!!!!*
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X non conserved

X similar

X ≥ 50% conserved