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logo

NTDB id 1055506 ACFDAU RS09530 WP 413436697.1  MKRSLLVL.LVVLLA...GCGLLPKTVDETQGWSAQRLYAEAKDQLNSGGYEKAIKYFETLEARYPYGRYAQQAQLEVAY   76
NTDB id 1102 NMB RS03635 WP 002244053.1        MKKILLTVSLGLALSACATQGTVDKDAQITQDWSVEKLYAEAQDELNSSNYTRAVKLYEILESRFPTSRHAQQSQLDTAY   80
NTDB id 1106 NGFG RS01495 WP 003687645.1       MKKILLTVSLGLALSACATQGTADKDAQITQDWSVEKLYAEAQDELNSSNYTRAVKLYEILESRFPTSRHARQSQLDTAY   80
consensus                                      !!**!!***!***!******!**!****!!*!!***!!!!!*!*!!!**!**!*!**!*!!*!*!**!*!*!*!!**!!

logo

NTDB id 1055506 ACFDAU RS09530 WP 413436697.1  AYYKDNEPVSAIAACDRFIKLHPEHPNVDYAYYLRGLANFTEDQGLLGRIGDQDMTERDPKAASESFDSFQQLVTRFPNS  156
NTDB id 1102 NMB RS03635 WP 002244053.1        AYYKDDEKDKALAAIDRFRRLHPQHPNMDYALYLRGLVLFNEDQSFLNKLASQDWSDRDPKANREAYQAFAELVQRFPNS  160
NTDB id 1106 NGFG RS01495 WP 003687645.1       AYYKDDEKDKALAAIERFRRLHPQHPNMDYALYLRGLVLFNEDQSFLNKLASQDWSDRDPKANREAYQAFAELVQRFPNS  160
consensus                                      !!!!!*!***!*!!**!!**!!!*!!!*!!!*!!!!!**!*!!!**!*****!!***!!!!!**!****!**!!*!!!!!

logo

NTDB id 1055506 ACFDAU RS09530 WP 413436697.1  KYTPDALARMKYLVDSLASHEVHVALYYYKRGAYVAASKRAQYAIEHYPNAPAIEQALAILVKSYDKMGINDLRDDALRV  236
NTDB id 1102 NMB RS03635 WP 002244053.1        KYAADATARMVKLVDALGGNEMSVARYYMKRGAYIAAANRAQKIIGSYQNTRYVEESLAILELAYKKLDKPRLAADTRRV  240
NTDB id 1106 NGFG RS01495 WP 003687645.1       KYAADATARMVKLVDALGGNEMSVARYYMKRGAYIAAANRAKKIIGSYQNTRYVEESLAILELAYKKLDKPQLAADTRRV  240
consensus                                      !!**!!*!!!**!!!*!***!**!!*!!*!!!!!*!!**!!***!**!*!****!**!!!!***!*!**** !**!**!!

logo

NTDB id 1055506 ACFDAU RS09530 WP 413436697.1  LQKNFPNSKYVSGNFD.KSKPWWRFWQL   263
NTDB id 1102 NMB RS03635 WP 002244053.1        LETNFPKSPFLKQPWRSDDMPWWRYWH.   267
NTDB id 1106 NGFG RS01495 WP 003687645.1       LETNFPKSPFLTHAWQPDDMPWWRYWH.   267
consensus                                      !**!!!*!****   *   ***!!!!*!*
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X non conserved

X similar

X ≥ 50% conserved