```
logo
NTDB id 65508 ANG RS02970 WP 003035572.1   MKKYIFMRILRSLVSIFMVTTLTYTIIYTMVPRKLIFKQDPNYNKIATTPDKKTNYENTIFERMGYIDYYDTKELQEKASKENSS   85
NTDB id 476 HSISS4 RS06995 WP 013990225.1 MKKYILLRTLRSLLSIFVVTALTYTIIYTMVPRRLIFRQDPNYNKIAKTADSKANYENTIYERMGYIDYYDTKELQEKASSLDKS   85
NTDB id 325 STU RS16125 WP 002946410.1    MKKYILLRTLRSLLSIFVVTALTYTIIYTMVPRRLIFRQDPNYNKIAKTADSKANYENTIYERLGYIDYYDTKELQEKASSLDKS   85
NTDB id 293 STER RS06925 WP 011681416.1   MKKYILLRTLRSLLSIFVVTALTYTIIYTMVPRRLIFRQDPNYNKIAKTADSKANYENTIYERLGYIDYYDTKELQEKASSLDKS   85
consensus                                 !!!!!**!*!!!!*!!!*!!*!!!!!!!!!!!!!*!!!*!!!!!!!!!*!*!*!*!!!!!!*!!!*!!!!!!!!!!!!!!!****!

logo
NTDB id 65508 ANG RS02970 WP 003035572.1   VTVEPTNANKKIYEAYIKKLGRGWKLQQFKESKQFYATREVPVYERVLGFYGNLIQIDHTGAVKDASNPNLKRYIRIENDPAIGW   170
NTDB id 476 HSISS4 RS06995 WP 013990225.1 VTTKPTKENKAIYQKYVDSLGHGWRLHQFKQSKQFYATRDVPVLERVFGFYTHLFEFDNTGWVKDKTNPNLKRYIRIENDPAIGW   170
NTDB id 325 STU RS16125 WP 002946410.1    VTTKPTKENKAIYQKYVDSLGRGWRLHQFKQSKQFYATRDVPVLERVFGFYTHLFEFDNTGWVKDKTNPNLKRYIRIENDPAIGW   170
NTDB id 293 STER RS06925 WP 011681416.1   VTTKPTKENKAVYQKYVDSLGRGWRLHQFKQSKQFYATRDVPVLERVFGFYTHLFEFDNTGWVKDKTNPNLKRYIRIENDPAIGW   170
consensus                                 !!**!!**!!**!**!***!!*!!*!*!!!*!!!!!!!!*!!!*!!!*!!!**!***!*!!*!!!**!!!!!!!!!!!!!!!!!!

logo
NTDB id 65508 ANG RS02970 WP 003035572.1   SVVGSGTKHKYLLYFNSQFPFIHQNFVRLNLGTSYPTYANLPVLQVISQGQGQTKTSEVQFPTGKKTSSVNIYTRTYKSPKQADA   255
NTDB id 476 HSISS4 RS06995 WP 013990225.1 SVVGSGTKHKYLLYFNSQFPFVHQNFVKMNLGTSYPTYAEQGVLDVITQGQGQTQSSEVNFPTGKKVSSVDIYSRTYKSPSQADA   255
NTDB id 325 STU RS16125 WP 002946410.1    SVVGSGTKHKYLLYFNSQFPFVHQNFVKMNLGTSYPTYAEQGVLDVITQGQGQTKSSVVNFPTGKKISSVDIYSRTYKSPSQADA   255
NTDB id 293 STER RS06925 WP 011681416.1   SVVGSGTKHKYLLYFNGQFPFVHQNFVKMNLGTSYPTYAGQGVLDVITQGQGQTKSSVVNFPTGKKISSVDIYSRTYKSPSQADA   255
consensus                                 !!!!!!!!!!!!!!!!!*!!!!*!!!!!**!!!!!!!!!!***!!*!!*!!!!!!**!  !*!!!!!!*!!!*!!*!!!!!!*!!!!

logo
NTDB id 65508 ANG RS02970 WP 003035572.1   RDVANYGKDDPYTATESNYQYPSMIVSSSIVGLIGLALSYLIAVPLGSYMARFKNTLFDSISTGALTFLMSLPTIALVYIIRLIG   340
NTDB id 476 HSISS4 RS06995 WP 013990225.1 RDRSYYG.DDPYTATKSRYQYPSMVTSSAIAGLIGLVLSYALAIPLGSYMARFKNTLFDSVSTGILTFLLSLPTIALVYIIRLIG   339
NTDB id 325 STU RS16125 WP 002946410.1    RDRSYYG.NDPYTATKSRYQYPSMVTSSAIAGLIGLVLSYALAIPLGSYMALFKNTIFDSVSTGVLTFLLSLPTIALVYIIRLIG   339
NTDB id 293 STER RS06925 WP 011681416.1   RDRSYYG.NDPYTATKSRYQYPSMVTSSAIAGLIGLVLSYALAIPLGSYMALFKNTLFDSVSTGVLTFLLSLPTIALVYIIRLIG   339
consensus                                 !!***!!  !!!!!!*!*!!!!!!**!!*!*!!!!!*!!!**!*!!!!!!!  !!!!*!!!*!!!*!!!!*!!!!!!!!!!!!!!!

logo
NTDB id 65508 ANG RS02970 WP 003035572.1   SAIGLPDSFPILGAGDWRSYVLPAVILGLLSAPWTAVWIRRYMIDLQSQDFVRFARAKGLSEKEISNKHIFKNAMVPLVSSIPGA   425
NTDB id 476 HSISS4 RS06995 WP 013990225.1 SEIGLPDSFPILGAGDWRSYVLPSVILGLLSTPGLAIWIRRYMIDLQSQDFVRFARAKGLSEQEISNKHIFKNAMVSLVSGIPAS   424
NTDB id 325 STU RS16125 WP 002946410.1    SEIGLPDSFPILGAGDWRSYVLPSVILGLLSTPGLAIWIRRYMIDLQSQDFVRFARAKGLSEQEISNKHILKNAMVSLVSGIPAS   424
NTDB id 293 STER RS06925 WP 011681416.1   SEIGLPDSFPILGAGDWRSYVLPSVILGLLSTPGLAIWIRRYMIDLQSQDFVRFARAKGLSEQEISNKHILKNAMVSLVSGIPAS   424
consensus                                 !*!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!*!**!*!!!!!!!!!!!!!!!!!!!
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X non conserved
X similar
X $\geq$50% conserved