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logo
NTDB id 71569 URS RS03940 WP 004985578.1   MLNNLNPHHYHTIAVWYLVQHSLSAFQKIKHHFGDCEQAMLPQHLAQWSQLGLHASHLKRVQEYQSDAGQQDFARLINLVKQYTD   85
NTDB id 1043 HON27 RS16615 WP 168727007.1  MLTQLSSHQYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHLKRVNEFQTPQGQAQFEQLVQQVRQHTD   85
NTDB id 1073 ABD1 RS00865 WP 015451369.1   MLTQLSSHHYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHLKRVNEFQTTQGQAQFEQLVQQVRQHTD   85
NTDB id 1021 ACIAD RS00975 WP 004930462.1  MITILSSHHYHTIKVWYVLQHSLSGFKKLIHYFGDCETALQPQRLSDWQKLGLHANHLKRLEEVHTLQGQQQFEKMLAQLQTHTD   85
consensus                                  !***!**!*!!!**!!!**!!!! *!*!****!! !!*!**! *!**!**!!!!!*!!!!**!*** *!! *!**********!!

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NTDB id 71569 URS RS03940 WP 004985578.1   FIVTPDDTLYPSQLLPYEDRPPIIFGQGKVDALLQPQIAIVGSRKPSPHGRQVAYDFAFYLSEKGFFVSSGLAHGIDEAAHQGGL   170
NTDB id 1043 HON27 RS16615 WP 168727007.1  FILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGLAYGIDEAAHQGAS   170
NTDB id 1073 ABD1 RS00865 WP 015451369.1   FILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGLAYGIDEAAHQGAS   170
NTDB id 1021 ACIAD RS00975 WP 004930462.1  FIVTPDDPAYPSQLIPYQDRPPILFGQGSIQSLIQPQIAVVGSRKPSPHGRQVAYDFSYFLSEKGFYITSGLAHGIDEAAHQGSL   170
consensus                                  !!*!!!!**!!*!!*!!*!*!!!*!! !****!*!!!!!*!!!!!!!!!!!!!!!!!!***!!!!!!***!!!!*!!!!!!!!!*

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NTDB id 71569 URS RS03940 WP 004985578.1   QHQRSIAVMGTGLDTTYPTANQDLRQQIA.QQGAVISEFLPQTLPLQRHFPRRNRIVSGLSLGVLVVEAKQQSGSLITANEAAKQ   254
NTDB id 1043 HON27 RS16615 WP 168727007.1  THQRTIAVTGTGLDTTYPAQNKKLAEHILAKNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLVVEATLKSGSLITANKAAEQ   255
NTDB id 1073 ABD1 RS00865 WP 015451369.1   AHQRTIAVTGTGLDTTYPAQNKKLAEYILAQNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLVVEATLKSGSLITANKAAEQ   255
NTDB id 1021 ACIAD RS00975 WP 004930462.1  VHHRAIAVVGTGLDLCYPSGNKALKQHIRDQGGAIVSEFLPGTPPLQAHFPRRNRIVSGLSLGVLVVEATLKSGSLITANKAAEQ   255
consensus                                   !*!*!!!*!!!!!**!!**!**!* *!****!!***!!!!*!*!!!*!!!!!!!!!!!!!!!!!!!!!!***!!!!!!!!*!!*!

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NTDB id 71569 URS RS03940 WP 004985578.1   GKLIFAIPGHIYSEFHQGCHQLIREGAILVDHPEQIIEDLALPTQWQINQQVQPD......STEQTHHIPEHLIGLYQQLDWIGQ   333
NTDB id 1043 HON27 RS16615 WP 168727007.1  GKTVFAIPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDLALPTQWQSQQQNQT.....EETNTNTPEIPEHLIDLYQSLDWVGQ   335
NTDB id 1073 ABD1 RS00865 WP 015451369.1   GKTVFAIPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDLALPTQWQSQQQNQT.....EEANTNTPEIREHLIDLYQSLDWVGQ   335
NTDB id 1021 ACIAD RS00975 WP 004930462.1  GKVVFAIPGHIYSEFHQGCHQLIREGAILVDHPEQIIEDLALPTHWHSQSTASGEANADDSGKIDDADLPDDLLPLYQLLDWQGQ   340
consensus                                  !!**!!!!!!!!!!!!!!!!!!!
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