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logo

NTDB id 1039293 ACDJ02 RS01850 WP 151725291.1  MLSILNPHHYHTIAVWYLVQHSLSAFQKIKHHFGDCEQAMLPQHLTQWSQLGLHASHLKRVQEYQSDAGQQDFARLINLV   80
NTDB id 1043 HON27 RS16615 WP 168727007.1      MLTQLSSHQYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHLKRVNEFQTPQGQAQFEQLVQQV   80
NTDB id 1073 ABD1 RS00865 WP 015451369.1       MLTQLSSHHYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHLKRVNEFQTTQGQAQFEQLVQQV   80
NTDB id 1021 ACIAD RS00975 WP 004930462.1      MTTILSSHHYHTIKVWYVLQHSLSGFKKLIHYFGDCETALQPQRLSDWQKLGLHANHLKRLEEVHTLQGQQQFEKMLAQL   80
consensus                                      !** !**!*!!!**!!!**!!!! *!*!****!! !!*!**! *!**!**!!!!!*!!!!**!*** *!! *!*******

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NTDB id 1039293 ACDJ02 RS01850 WP 151725291.1  KQYTDFIVTPDDTLYPSQLLPYEDRPPIIFGQGKVDALLQPQLAIVGSRKPSPHGRQVAYDFAFYLSEKGFFVSSGLAHG  160
NTDB id 1043 HON27 RS16615 WP 168727007.1      RQHTDFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGLAYG  160
NTDB id 1073 ABD1 RS00865 WP 015451369.1       RQHTDFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGLAYG  160
NTDB id 1021 ACIAD RS00975 WP 004930462.1      QTHTDFIVTPDDPAYPSQLIPYQDRPPILFGQGSIQSLIQPQIAVVGSRKPSPHGRQVAYDFSYFLSEKGFYITSGLAHG  160
consensus                                      ***!!!!*!!!!**!!*!!*!!*!*!!!*!! !****!*!!!*!*!!!!!!!!!!!!!!!!!!***!!!!!!***!!!!*!

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NTDB id 1039293 ACDJ02 RS01850 WP 151725291.1  IDEAAHQGGLQHQRSIAVMGTGLDTTYPTANQDLRQQIA.QQGAVISEFLPQTLPLQRHFPRRNRIVSGLSLGVLVVEAK  239
NTDB id 1043 HON27 RS16615 WP 168727007.1      IDEAAHQGASTHQRTIAVTGTGLDTTYPAQNKKLAEHILAKNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLVVEAT  240
NTDB id 1073 ABD1 RS00865 WP 015451369.1       IDEAAHQGASAHQRTIAVTGTGLDTTYPAQNKKLAEYILAQNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLVVEAT  240
NTDB id 1021 ACIAD RS00975 WP 004930462.1      IDEAAHQGSLVHHRAIAVVGTGLDLCYPSGNKALKQHIRDQGGAIVSEFLPGTPPLQAHFPRRNRIVSGLSLGVLVVEAT  240
consensus                                      !!!!!!!!*  !*!*!!!*!!!!!**!!**!**!* *!****!!***!!!!*!*!!!*!!!!!!!!!!!!!!!!!!!!*

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NTDB id 1039293 ACDJ02 RS01850 WP 151725291.1  QQSGSLITANEAAKQGKLIFAIPGHIYSEFHQGCHQLIREGAILVDHPEQIIEDLALPTQWHINQQVQPD......STEQ  313
NTDB id 1043 HON27 RS16615 WP 168727007.1      LKSGSLITANKAAEQGKTVFAIPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDLALPTQWQSQQQNQT.....EETNTN  315
NTDB id 1073 ABD1 RS00865 WP 015451369.1       LKSGSLITANKAAEQGKTVFAIPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDLALPTQWQSQQQNQT.....EEANTN  315
NTDB id 1021 ACIAD RS00975 WP 004930462.1      LKSGSLITANKAAEQGKVVFAIPGHIYSEFHQGCHQLIREGAILVDHPEQIIEDLALPTHWHSQSTASGEANADDSGKID  320
consensus                                      **!!!!!!!!*!!*!!!**!!!!!!!!!!!!!!!!!!!
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