logo
NTDB id 106828 ACAM54 RS21325 WP 369648861.1 MFSFFKKKPPAESPAAPAPSRAVEPVPAPEPAPAPAAAP.ARSVFS.PSSWFGSKPAAEEAVPPPAAPDMAPPVAPPPAP 78
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAK.VESEVAQIVGNIKEDVESLAESVKGRAFSAVETVSG.AVFQVKETVAEMPSE 78
consensus
logo
NTDB id 106828 ACAM54 RS21325 WP 369648861.1 ..AAAPHLAPVPAAPVPTPAVPTVPPPPPAL.ATEVAMPAERKGWFDKLKTGLRKTG....TGIQAVFVNAQIDEALYEE 151
NTDB id 1118 NGFG RS11455 WP 003696286.1 AGEAAERVESAKE.AV....AETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEE 153
consensus
logo
NTDB id 106828 ACAM54 RS21325 WP 369648861.1 LESALLMADAGVKATEYLLEDLRGRVKRQMATDAAQVKRLLADAITDLLQPLEKPLVIGQ.FTPTVIMVAGVNGAGKTTS 230
NTDB id 1118 NGFG RS11455 WP 003696286.1 LETVLITGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTS 233
consensus
logo
NTDB id 106828 ACAM54 RS21325 WP 369648861.1 IGKLTKHLASEGASVLLAAADTFRAAAREQLLVWADRNTVEIVSQEGGDPSAVSFDAVTAGKARGKDVVLVDTAGRLPTQ 310
NTDB id 1118 NGFG RS11455 WP 003696286.1 IGKLAKYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQ 313
consensus
logo
NTDB id 106828 ACAM54 RS21325 WP 369648861.1 LHLMDELKKIKRVVTKADASAPHEVLLVIDGNTGQNALAQVRAFDETLGLTGLVVTKLDGTAKGGVLCAIARERPIPVYF 390
NTDB id 1118 NGFG RS11455 WP 003696286.1 LHLMEEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRY 393
consensus
logo
NTDB id 106828 ACAM54 RS21325 WP 369648861.1 IGVGEKLEDLETFNAREFAMALLG 414
NTDB id 1118 NGFG RS11455 WP 003696286.1 IGVGEGIDDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved