logo
NTDB id 362403 FAY22 RS14575 WP 146330877.1 MFSFFKRKSKDT.PAVEPAPEALATPPAAE.....SAPVAEAPVAT 40
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQE.TAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEA 79
consensus
logo
NTDB id 362403 FAY22 RS14575 WP 146330877.1 AP.....EAEIIEEIVTAAPLRAEQKRSWLQKLKAGLSKTST....NLTTLFVGAKIDDDLYDELESALL 101
NTDB id 1118 NGFG RS11455 WP 003696286.1 GEAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLI 159
consensus
logo
NTDB id 362403 FAY22 RS14575 WP 146330877.1 VSDAGVEATQFLLDALKKKVKSEKLTEAQQVKDALRALLVEMLAPLQKPMVLGR.HQPLVMMIAGVNGAGKTTTIGKLAK 180
NTDB id 1118 NGFG RS11455 WP 003696286.1 TGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAK 239
consensus
logo
NTDB id 362403 FAY22 RS14575 WP 146330877.1 HMQTHHQSVLLAAGDTFRAAAREQLAIWGARNDVTVIAQESGDPAAVAFDAVQSAKARNVNVVMVDTAGRLPTQLHLMEE 260
NTDB id 1118 NGFG RS11455 WP 003696286.1 YFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEE 319
consensus
logo
NTDB id 362403 FAY22 RS14575 WP 146330877.1 LKKIKRVIGKGMESAPHELLLVIDGNTGQNALAQVKAFDDALQLTGLIVTKLDGTAKGGILAAIAKTRPVPVYFIGVGEQ 340
NTDB id 1118 NGFG RS11455 WP 003696286.1 IKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEG 399
consensus
logo
NTDB id 362403 FAY22 RS14575 WP 146330877.1 IEDLQPFNAEEFVDALLS 358
NTDB id 1118 NGFG RS11455 WP 003696286.1 IDDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved