logo
NTDB id 1044432 ACEN8S RS03805 WP 413625674.1 MLKFWKKKPTEPTEPAAPEPQAPEDR..VDQSA.....DPA.....EAEIGAGVAEALAETAQPEPAAP 57
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQET.PALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEA 79
consensus
logo
NTDB id 1044432 ACEN8S RS03805 WP 413625674.1 .....EIEAE.....AEESAVVEAAREAEQPARRSWRERLSG.....SGFAKSLSSLFVRHPKLDDDLLDELETSL 118
NTDB id 1118 NGFG RS11455 WP 003696286.1 GEAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVF.GGGQIGEDLYEELETVL 158
consensus
logo
NTDB id 1044432 ACEN8S RS03805 WP 413625674.1 ITADVGVEASTRLVEDLRKRMHKREFADAGALLKALRAELVALLRPVEQPLDVA.TPSPFVILTVGINGVGKTTTIGKLA 197
NTDB id 1118 NGFG RS11455 WP 003696286.1 ITGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLA 238
consensus
logo
NTDB id 1044432 ACEN8S RS03805 WP 413625674.1 RRYADEGRSVMLAAGDTFRAAAVEQLKTWGERNKVPVVSQGQDADSASVIFDALQAARSRGTQVLIADTAGRLHTQGGLM 277
NTDB id 1118 NGFG RS11455 WP 003696286.1 KYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQT.TGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLM 317
consensus
logo
NTDB id 1044432 ACEN8S RS03805 WP 413625674.1 DELGKIGRVMKKLDASAPHEVLMVIDGTTGQNAISQVRQFRDTAGVTGLVVTKLDGTAKGGVMFALAREFGLPIRYVGLG 357
NTDB id 1118 NGFG RS11455 WP 003696286.1 EEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVG 397
consensus
logo
NTDB id 1044432 ACEN8S RS03805 WP 413625674.1 ETATDLRVFDAEAFVDGLLPPTIGA 382
NTDB id 1118 NGFG RS11455 WP 003696286.1 EGIDDLRPFDARAFVDALLD..... 417
consensus
X non conserved
X similar
X ≥ 50% conserved