logo
NTDB id 331487 EJN92 RS11995 WP 126128038.1 MFSFFKKKPKDEPTSPAE..... 18
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG 80
consensus
NTDB id 331487 EJN92 RS11995 WP 126128038.1 .ATP.....ALNLTTAE.....PLAAPAAALDKPSWLSRLKAGLSKTS....SSLTTLFVGAKIDDDLYDELETALLI 81
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLIT 160
consensus
NTDB id 331487 EJN92 RS11995 WP 126128038.1 SDAGVEATQFLLNGLKKKVKEEKLTEAEQVKTALKMLLLELLRPLQKPLELGR.HQPLVMMISGVNGAGKTTTIGKLAKH 160
NTDB id 1118 NGFG RS11455 WP 003696286.1 GDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAKY 240
consensus
NTDB id 331487 EJN92 RS11995 WP 126128038.1 LQNHQQSVLLAAGDTFRAAAREQLTIWGERNNITVISQESGDPAAVAFDAVASAKARGTNVVMVDTAGRLPTQLHLMEEL 240
NTDB id 1118 NGFG RS11455 WP 003696286.1 FQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEEI 320
consensus
NTDB id 331487 EJN92 RS11995 WP 126128038.1 KKIKRVIGKGMDGAPQEILLVIDGNTGQNALAQVKAFDAALNLTGLIITKLDGTAKGGVLAAIAKSHPIPVYFIGIGEQI 320
NTDB id 1118 NGFG RS11455 WP 003696286.1 KKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEGI 400
consensus
NTDB id 331487 EJN92 RS11995 WP 126128038.1 EDLQAFNAQEFVDALFD 337
NTDB id 1118 NGFG RS11455 WP 003696286.1 DDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved