logo
NTDB id 291239 DEH84 RS10860 WP 109036869.1 MFSFIKKKLGWGQSAPEAPAEQPAAAPATPAA.PETAPLPPA..PAPAPVASPPTSPI.........VPAPAAAVPAAAP 68
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG 80
consensus
logo
NTDB id 291239 DEH84 RS10860 WP 109036869.1 TPAAAPAPVAQAPAAAPAPVSVA.EAAAPRAPEPERRSWLDKLRQGLKKTG....SGIAQVFTGTRIDDALYEELESALLM 143
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLIT 160
consensus
logo
NTDB id 291239 DEH84 RS10860 WP 109036869.1 ADAGVAATEHLLHDLKRRVKETKATEPAQVKALLIDAITELLAPLEKSLEVGH.TTPTVIMVAGVNGAGKTTTIGKLTRH 222
NTDB id 1118 NGFG RS11455 WP 003696286.1 GDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAKY 240
consensus
logo
NTDB id 291239 DEH84 RS10860 WP 109036869.1 LADARQRVLLAAADTFRAAAREQLGVWADRNQVDIVSQEGGDPAAVTFDAVQAGKARGCDVVIADTAGRLATQLHLMEEL 302
NTDB id 1118 NGFG RS11455 WP 003696286.1 FQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEEI 320
consensus
logo
NTDB id 291239 DEH84 RS10860 WP 109036869.1 RKIKRVIGKAMDTAPHEVLLVVDGNTGQNALAQVKAFDEALGLTGLIVTKLDGTAKGGVLAAIALWSRQRQAPVPVYFIG 382
NTDB id 1118 NGFG RS11455 WP 003696286.1 KKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALA.....SDRPVPVRYIG 395
consensus
logo
NTDB id 291239 DEH84 RS10860 WP 109036869.1 VGEKLEDLQTFSAREFAHALLS 404
NTDB id 1118 NGFG RS11455 WP 003696286.1 VGEGIDDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved