logo
NTDB id 370742 FKQ53 RS02470 WP 141572725.1 ..... MANVPT ..... SDA .... SETSEWLES..PESPESPESLA 29
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG 80
consensus
logo
NTDB id 370742 FKQ53 RS02470 WP 141572725.1 SSEVSASAAPVVVKDASGEAIGEIVSAPAPAPAAKRSWLTRLKAGLSKTS .... AGLTGIFVGVKVDENLFEELESALLM 105
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLIT 160
consensus
logo
NTDB id 370742 FKQ53 RS02470 WP 141572725.1 SDAGVEATTFLLDALRKKVKAERLTDGEQVKRALHDLLVELLQPLEQSLVLG.REAPLVVMIAGVNGAGKTTSIGKLAKH 184
NTDB id 1118 NGFG RS11455 WP 003696286.1 GDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAKY 240
consensus
logo
NTDB id 370742 FKQ53 RS02470 WP 141572725.1 FQHYGQSVLLAAGDTFRAAAREQLTIWGERNNVAVVSQESGDPAAVVFDAVNAARARKIDIVMADTAGRLPTQLHLMEEL 264
NTDB id 1118 NGFG RS11455 WP 003696286.1 FQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEEI 320
consensus
logo
NTDB id 370742 FKQ53 RS02470 WP 141572725.1 KKIKRVLGKAADGAPHEVLLVIDANTGQNALAQVKAFDDALQLTGLIVTKLDGTAKGGILAAIARQRPVPVYFIGVGEKV 344
NTDB id 1118 NGFG RS11455 WP 003696286.1 KKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEGI 400
consensus
logo
NTDB id 370742 FKQ53 RS02470 WP 141572725.1 EDLQPFSAREFADALLG 361
NTDB id 1118 NGFG RS11455 WP 003696286.1 DDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved