logo
NTDB id 40430 ALIDE2 RS04920 WP 013721532.1 MFSFFKKKSPSPAEPSS.APVPDAASAPAAD.....APTGGGALGWLRKSFGAQDAAA. 52
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAAETVSGAVEQVKETVAEMPSEAG 80
consensus
NTDB id 40430 ALIDE2 RS04920 WP 013721532.1 ..........PQAAPAADEAPPAVPEPAPKPKGTRQGWMERLKSGLRKTG....GSIATVFTGTQINDALYEELEDALLM 118
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATIEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLIT 160
consensus
NTDB id 40430 ALIDE2 RS04920 WP 013721532.1 ADTGVKATQHLLADLRRRVKEAKATEPAAVKALLADALADLLRPLEKPLVIGA.HQPTVIMVAGVNGAGKTTSIGKLTRH 197
NTDB id 1118 NGFG RS11455 WP 003696286.1 GDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAKY 240
consensus
NTDB id 40430 ALIDE2 RS04920 WP 013721532.1 LADHGESVLLAAADTFRAAAREQLGVWATRNTVEIISQEGGDPAAVSFDAVTAGRARGKDVVLVDTAGRLPTQLHLMEEL 277
NTDB id 1118 NGFG RS11455 WP 003696286.1 FQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEEI 320
consensus
NTDB id 40430 ALIDE2 RS04920 WP 013721532.1 KKIKRVVTKADATAPHEVLLVIDGNTGQNALAQVRAFDDALSLTGLIVTKLDGTAKGGVLAAIAQERPVPVYFIGVGEKV 357
NTDB id 1118 NGFG RS11455 WP 003696286.1 KKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEGI 400
consensus
NTDB id 40430 ALIDE2 RS04920 WP 013721532.1 EDLETFDAREFAQALLA 374
NTDB id 1118 NGFG RS11455 WP 003696286.1 DDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved