logo
NTDB id 385252 F0Q04 RS07700 WP 182345106.1 MFSFFKKKSPAADAAPSPSAAEPAPAPAPAADVPPPAPQVPSAPLTPIRPVA.....AEPTKTGWLRGL..... 64
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAAQVQ.....ETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEM 75
consensus
logo
NTDB id 385252 F0Q04 RS07700 WP 182345106.1 .GMGGKAAAPAPTAAETVTKNPVTQAPQAPVAPI.TIASEPASSRDSWMNRLKSGLRKIG....SSIATVFTGTKIDEQL 138
NTDB id 1118 NGFG RS11455 WP 003696286.1 PSEAGEAAERVESAKEA.....VAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDL 150
consensus
logo
NTDB id 385252 F0Q04 RS07700 WP 182345106.1 YEELEEALLMADTGVKATQHLLKDLKQRVKDSKTTDPAAVKDLLASALADLLAPLEKPLVIGE.HSPTVIMVAGVNGAGK 217
NTDB id 1118 NGFG RS11455 WP 003696286.1 YEELETVLITGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGK 230
consensus
logo
NTDB id 385252 F0Q04 RS07700 WP 182345106.1 TTSIGKLTKHLADAGQSVLLAAADTFRAAAREQLGVWATRNTVEIISQEGGDPAAVSFDAVTAGKARGKDVVLVDTAGRL 297
NTDB id 1118 NGFG RS11455 WP 003696286.1 TTSIGKLAKYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRL 310
consensus
logo
NTDB id 385252 F0Q04 RS07700 WP 182345106.1 PTQLHLMEELKKIKRVVTKADGSAPHEVLLVIDGNTGQNALNQVRAFDDALQLTGLIVTKLDGTAKGGVLAAIAQERPIP 377
NTDB id 1118 NGFG RS11455 WP 003696286.1 PTQLHLMEEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVP 390
consensus
logo
NTDB id 385252 F0Q04 RS07700 WP 182345106.1 VYFIGVGEKVEDLETFSAKEFAQALLA 404
NTDB id 1118 NGFG RS11455 WP 003696286.1 VRYIGVGEGIDDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved