logo
NTDB id 75138 MPB2EB RS07545 WP 185181713.1 MFSFFKKLHKSSTSAPEPA.....EA. 21
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG 80
consensus
NTDB id 75138 MPB2EB RS07545 WP 185181713.1 .....EHKTKNDTQDKNPSAPALTPDRPTSWVNRLKSGLAKTRNNF....TNLFTNVKIDEDFFEELEAALLM 85
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLIT 160
consensus
NTDB id 75138 MPB2EB RS07545 WP 185181713.1 ADTGLEASQFLLNALRQKVLAERLNDGEAVKAALRSLLADLLKPLEHTLVLD.RAQPLVMMITGVNGAGKTTSIGKLAQH 164
NTDB id 1118 NGFG RS11455 WP 003696286.1 GDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAKY 240
consensus
NTDB id 75138 MPB2EB RS07545 WP 185181713.1 LQRHGQSVLLAAGDTFRAAAHEQLALWGERNQINVISQQSGDPAAVIFDALNAARARKLDILMADTAGRLPTQLHLMEEL 244
NTDB id 1118 NGFG RS11455 WP 003696286.1 FQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEEI 320
consensus
NTDB id 75138 MPB2EB RS07545 WP 185181713.1 KKIKRVIAKAMADAPHEVLLVIDANTGQNALAQVKAFDDALGLTGLIVTKLDGTAKGGILAAIARQRPIPVYFIGVGEHI 324
NTDB id 1118 NGFG RS11455 WP 003696286.1 KKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEGI 400
consensus
NTDB id 75138 MPB2EB RS07545 WP 185181713.1 DDLQPFCAEEFANALLN 341
NTDB id 1118 NGFG RS11455 WP 003696286.1 DDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved