logo
NTDB id 68468 GsYM18 RS05630 WP 119332202.1 .....MAEERKGFFKGLWGKVAGGDR..... 21
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG 80
consensus
logo
NTDB id 68468 GsYM18 RS05630 WP 119332202.1 .......DQEEAVNETTS.AVAD.VAAPPEQEDRRPGFFERLKQGLSKTRDSLVGRIDRLVLGKKEIDADTLEELEEILI 92
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAG.VFGGGQIGEDLYEELETVLI 159
consensus
logo
NTDB id 68468 GsYM18 RS05630 WP 119332202.1 TADLGVQTTVELIRGLEQRLSRNELKDGEALREALKEDIHGRLARDAHQL.DVTGASPFVIMVIGVNGVGKTTTIGKLAA 171
NTDB id 1118 NGFG RS11455 WP 003696286.1 TGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAK 239
consensus
logo
NTDB id 68468 GsYM18 RS05630 WP 119332202.1 RFTAQGKKVILAAGDTFRAAAAEQLQIWGERTGVDVIRHKEGADPSAVVFDSIKAAVARGADILIVDTAGRLHTKVNLME 251
NTDB id 1118 NGFG RS11455 WP 003696286.1 YFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTG.DSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLME 318
consensus
logo
NTDB id 68468 GsYM18 RS05630 WP 119332202.1 ELKKVRRIMSREIPGAPHETLLVLDAATGQNALSQAKLFKEAAQVTGIALTKLDGTAKGGIVVAICNEFRIPVRYIGVGE 331
NTDB id 1118 NGFG RS11455 WP 003696286.1 EIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGE 398
consensus
logo
NTDB id 68468 GsYM18 RS05630 WP 119332202.1 GIDDLRDFDPSQFVDALFQ 350
NTDB id 1118 NGFG RS11455 WP 003696286.1 GIDDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved