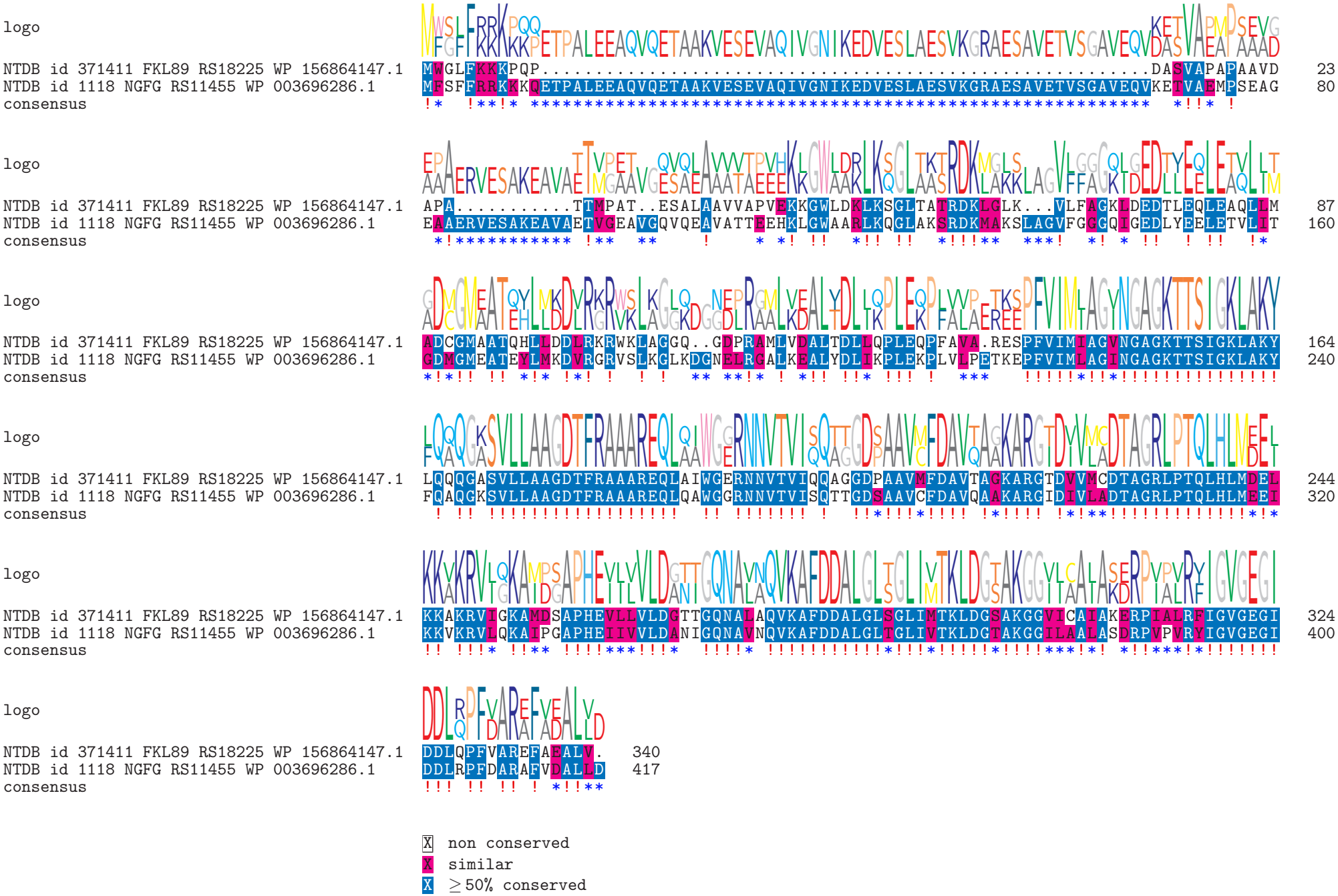
logo
NTDB id 371411 FKL89 RS18225 WP 156864147.1 MWGLFKKKPQP.....DASVAPAPAAVD 23
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG 80
consensus
logo
NTDB id 371411 FKL89 RS18225 WP 156864147.1 APA.....TTMPAT..ESALAAVVAPVEKKGWLDKLKSGLTATRDKLGLK...VLFAGKLDEDTLEQLEAQLLM 87
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLIT 160
consensus
logo
NTDB id 371411 FKL89 RS18225 WP 156864147.1 ADCGMAATQHLLDDLRKRWKLAGGQ..GDPRAMLVDALTDLLQPLEQPFAVA.RESPFVIMIAGVNGAGKTTSIGKLAKY 164
NTDB id 1118 NGFG RS11455 WP 003696286.1 GDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAKY 240
consensus
logo
NTDB id 371411 FKL89 RS18225 WP 156864147.1 LQQQGASVLLAAGDTFRAAAREQLAIWGERNNVTVIQQAGGDPAAVMFDAVTAGKARGTDVVMCDTAGRLPTQLHLMDEL 244
NTDB id 1118 NGFG RS11455 WP 003696286.1 FQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEEI 320
consensus
logo
NTDB id 371411 FKL89 RS18225 WP 156864147.1 KKAKRVIGKAMDSAPHEVLLVLDGTTGQNALAQVKAFDDALGLSGLIMTKLDGSAKGGVICAIAKERPIALRFIGVGEGI 324
NTDB id 1118 NGFG RS11455 WP 003696286.1 KKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEGI 400
consensus
logo
NTDB id 371411 FKL89 RS18225 WP 156864147.1 DDLQPFVAREFAEALV. 340
NTDB id 1118 NGFG RS11455 WP 003696286.1 DDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved