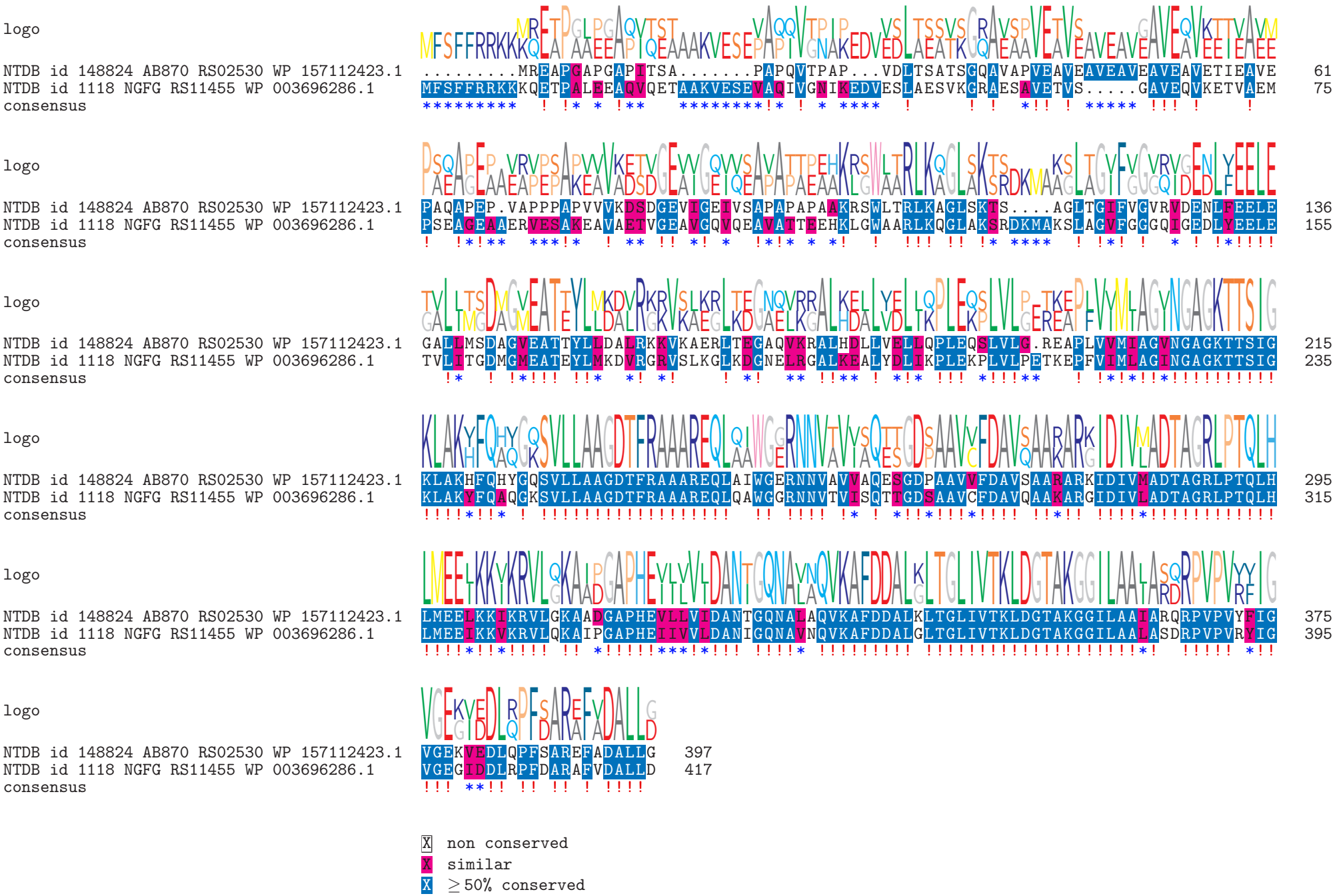
logo
NTDB id 148824 AB870 RS02530 WP 157112423.1 .....MREAPGAPGAPITSA.....PAPQVTPAP...VDLTSATSGQAVAPVEAVEAVEAVEAVEAVETIEAVE 61
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVS.....GAVEQVKETVAEM 75
consensus
NTDB id 148824 AB870 RS02530 WP 157112423.1 PAQAPEP.VAPPPAPVVVKDSDGEVIGEIVSAPAPAPAAKRSWLTRLKAGLSKTS....AGLTGIFVGVRVDENLFEELE 136
NTDB id 1118 NGFG RS11455 WP 003696286.1 PSEAGEAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELE 155
consensus
NTDB id 148824 AB870 RS02530 WP 157112423.1 GALLMSDAGVEATTYLLDALRKKVKAERLTEGAQVKRALHDLLVELLQPLEQSLVLG.REAPLVVMIAGVNGAGKTTSIG 215
NTDB id 1118 NGFG RS11455 WP 003696286.1 TVLITGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIG 235
consensus
NTDB id 148824 AB870 RS02530 WP 157112423.1 KLAKHFQHYGQSVLLAAGDTFRAAAREQLAIWGERNNVAVVAQESGDPAAVVFDAVSAARARKIDIVMADTAGRLPTQLH 295
NTDB id 1118 NGFG RS11455 WP 003696286.1 KLAKYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLH 315
consensus
NTDB id 148824 AB870 RS02530 WP 157112423.1 LMEELKKIKRVLGKAADGAPHEVLLVIDANTGQNALAQVKAFDDALKLTGLIVTKLDGTAKGGILAAIARQRPVPVYFIG 375
NTDB id 1118 NGFG RS11455 WP 003696286.1 LMEEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIG 395
consensus
logo
NTDB id 148824 AB870 RS02530 WP 157112423.1 VGEKVEDLQPFSAREFADALLG 397
NTDB id 1118 NGFG RS11455 WP 003696286.1 VGEGIDDLRPFDARAFVDALLD 417
consensus
X non conserved
X similar
X ≥ 50% conserved