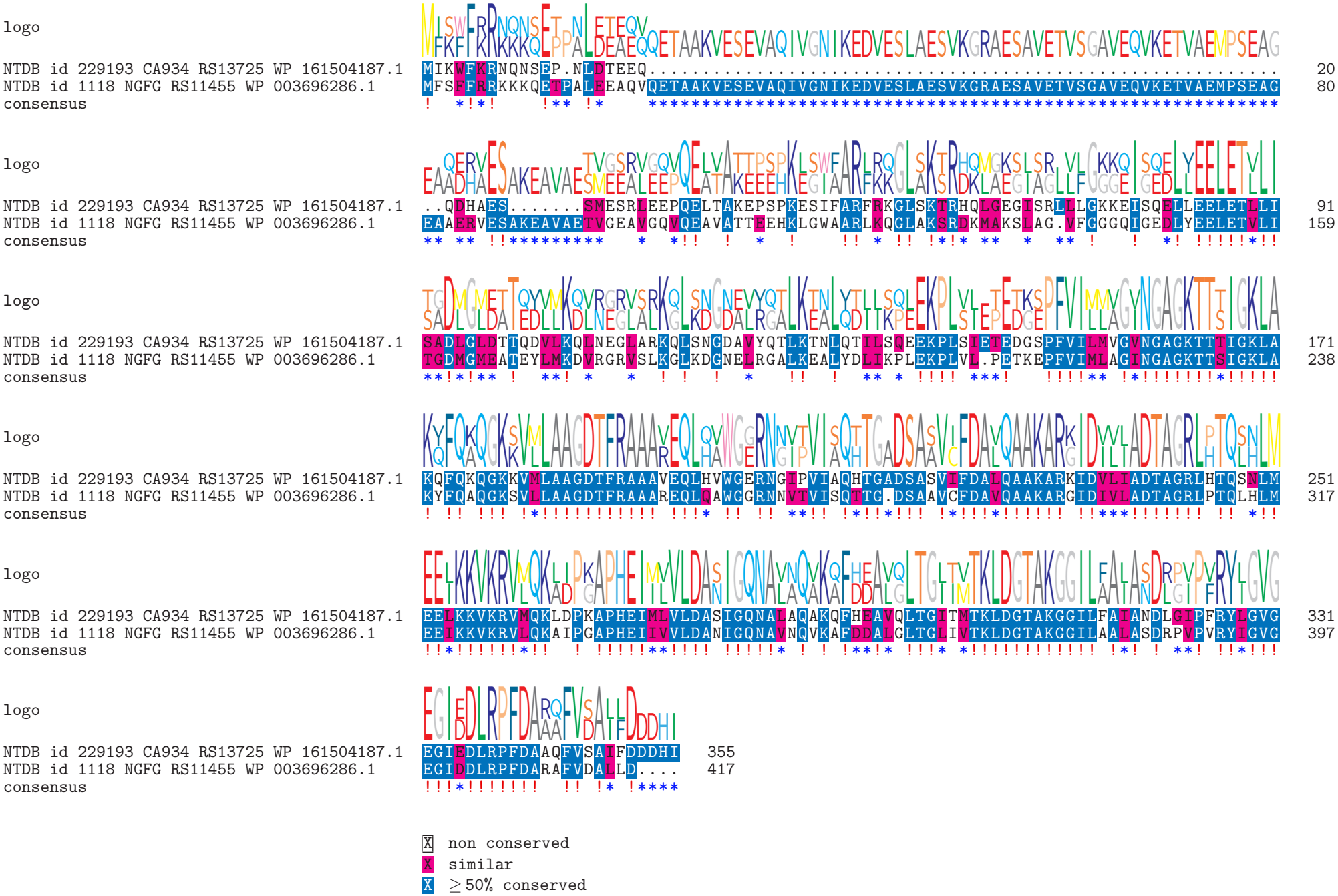

logo
NTDB id 229193 CA934 RS13725 WP 161504187.1 MIKWFKRNQNSEP.NLDTEEQ..... 20
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG 80
consensus
logo
NTDB id 229193 CA934 RS13725 WP 161504187.1 ..QDHAES.......SMESRLEEPQELTAKEPSPKESIFARFRKGLSKTRHQLGEGISRLLLGKKEISQELLEELETLLI 91
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAG.VFGGGQIGEDLYEELETVLI 159
consensus
logo
NTDB id 229193 CA934 RS13725 WP 161504187.1 SADLGLDTTQDVLKQLNEGLARKQLSNGDAVYQTLKTNLQTILSQEEKPLSIETEDGSPFVILMVGVNGAGKTTTIGKLA 171
NTDB id 1118 NGFG RS11455 WP 003696286.1 TGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVL.PETKEPFVIMLAGINGAGKTTSIGKLA 238
consensus
logo
NTDB id 229193 CA934 RS13725 WP 161504187.1 KQFQKQGKKVMLAAGDTFRAAAVEQLHVWGERNGIPVIAQHTGADSASVIFDALQAAKARKIDVLIADTAGRLHTQSNLM 251
NTDB id 1118 NGFG RS11455 WP 003696286.1 KYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTG.DSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLM 317
consensus
logo
NTDB id 229193 CA934 RS13725 WP 161504187.1 EELKKVKRVMQKLDPKAPHEIMLVLDASIGQNALAQAKQFHEAVQLTGITMTKLDGTAKGGILFAIANDLGIPFRYLGVG 331
NTDB id 1118 NGFG RS11455 WP 003696286.1 EEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVG 397
consensus
logo
NTDB id 229193 CA934 RS13725 WP 161504187.1 EGIEDLRPFDAAQFVSAIFDDDHI 355
NTDB id 1118 NGFG RS11455 WP 003696286.1 EGIDDLRPFDARAFVDALLD.... 417
consensus
X non conserved
X similar
X ≥ 50% conserved