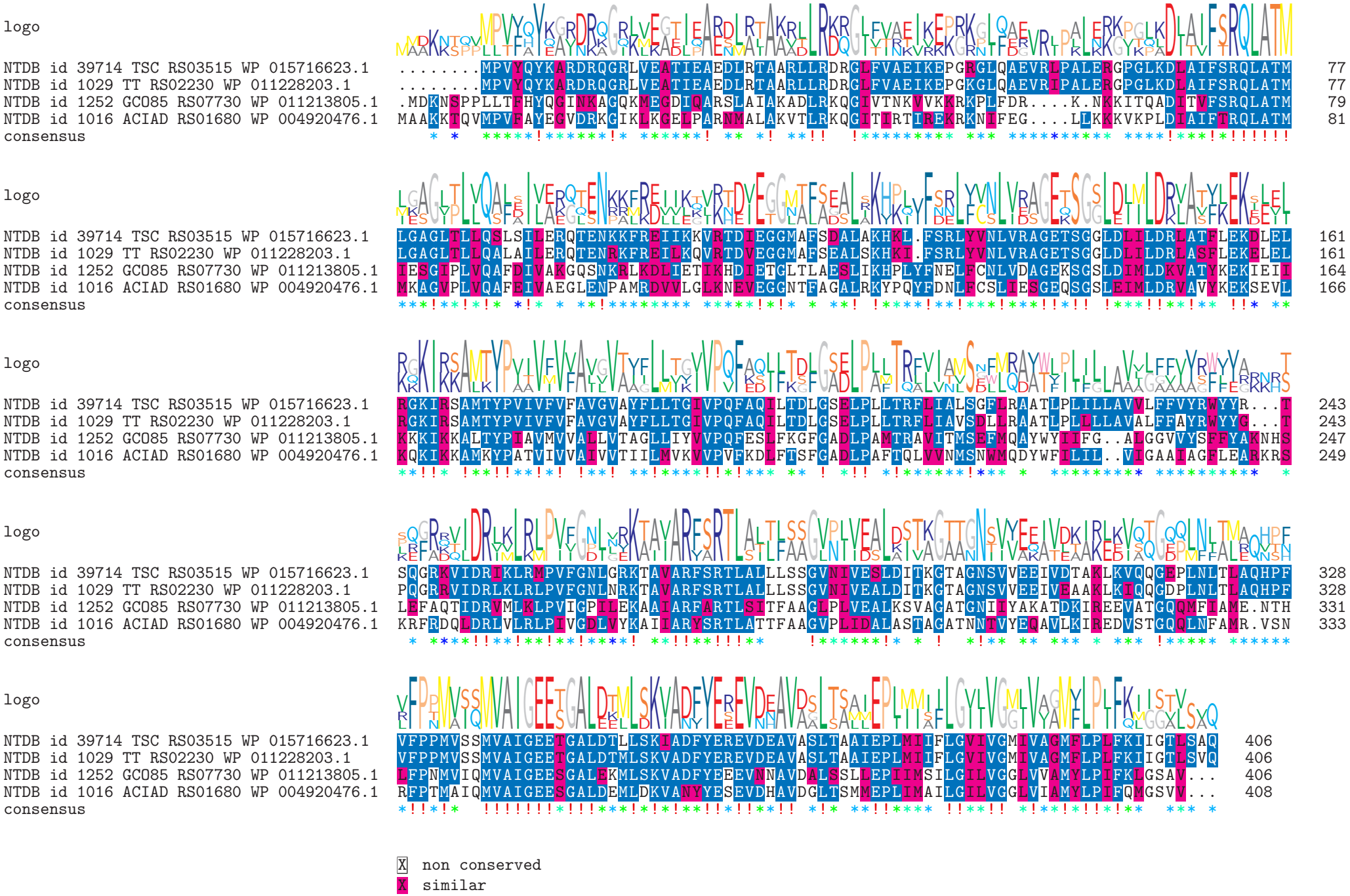
logo
NTDB id 39714 TSC RS03515 WP 015716623.1 ........MPVYQYKARDRQGRLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGRGLQAEVRLPALERGPGLKDLAIFSRQLATM 77
NTDB id 1029 TT RS02230 WP 011228203.1 ........MPVYQYKARDRQGRLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLKDLAIFSRQLATM 77
NTDB id 1252 GC085 RS07730 WP 011213805.1 .MDKNSPPLLTFHYQGINKAGQKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR....K.NKKITQADITVFSRQLATM 79
NTDB id 1016 ACIAD RS01680 WP 004920476.1 MAAKKTQVMPVFAYEGVDRKGIKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKVKPLDIAIFTRQLATM 81
consensus
logo
NTDB id 39714 TSC RS03515 WP 015716623.1 LGAGLTLLQSLSILERQTENKKFREIIKKVRTDIEGGMAFSDALAKHKL.FSRLYVNLVRAGETSGGLDLILDRLATFLEKDLEL 161
NTDB id 1029 TT RS02230 WP 011228203.1 LGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHKI.FSRLYVNLVRAGETSGGLDLILDRLASFLEKELEL 161
NTDB id 1252 GC085 RS07730 WP 011213805.1 IESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIMLDKVATYKEKIEII 164
NTDB id 1016 ACIAD RS01680 WP 004920476.1 MKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIMLDRVAVYKEKSEVL 166
consensus
logo
NTDB id 39714 TSC RS03515 WP 015716623.1 RGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIALSGFLRAATLPLILLAVVLFFVYRWYYR...T 243
NTDB id 1029 TT RS02230 WP 011228203.1 RGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATLPLLLLAVALFFAYRWYYG...T 243
NTDB id 1252 GC085 RS07730 WP 011213805.1 KKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG..ALGGVVYSFFYAKNHS 247
NTDB id 1016 ACIAD RS01680 WP 004920476.1 KQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFILIL..VIGAAIAGFLEARKRS 249
consensus
logo
NTDB id 39714 TSC RS03515 WP 015716623.1 SQGRKVIDRIKLRMPVFGNLGRKTAVARFSRTLALLLSSGVNIVESLDITKGTAGNSVVEEIVDTAKLKVQQGEPLNLTLAQHPF 328
NTDB id 1029 TT RS02230 WP 011228203.1 PQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVEEIVEAAKLKIQQGDPLNLTLAQHPF 328
NTDB id 1252 GC085 RS07730 WP 011213805.1 LEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATDKIREEVATGQQMFIAME.NTH 331
NTDB id 1016 ACIAD RS01680 WP 004920476.1 KRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVLKIREDVSTGQQLNFAMR.VSN 333
consensus
logo
NTDB id 39714 TSC RS03515 WP 015716623.1 VFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLGVIVGMIVACMFLPLFKIIGTLSAQ 406
NTDB id 1029 TT RS02230 WP 011228203.1 VFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLGVIVGMIVACMFLPLFKIIGTLSVQ 406
NTDB id 1252 GC085 RS07730 WP 011213805.1 LFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGGLVVAMYLPIFKLGSAV... 406
NTDB id 1016 ACIAD RS01680 WP 004920476.1 RFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVGGLVIAMYLPIFQMGSVV... 408
consensus
X non conserved
X similar
X ≥ 50% conserved