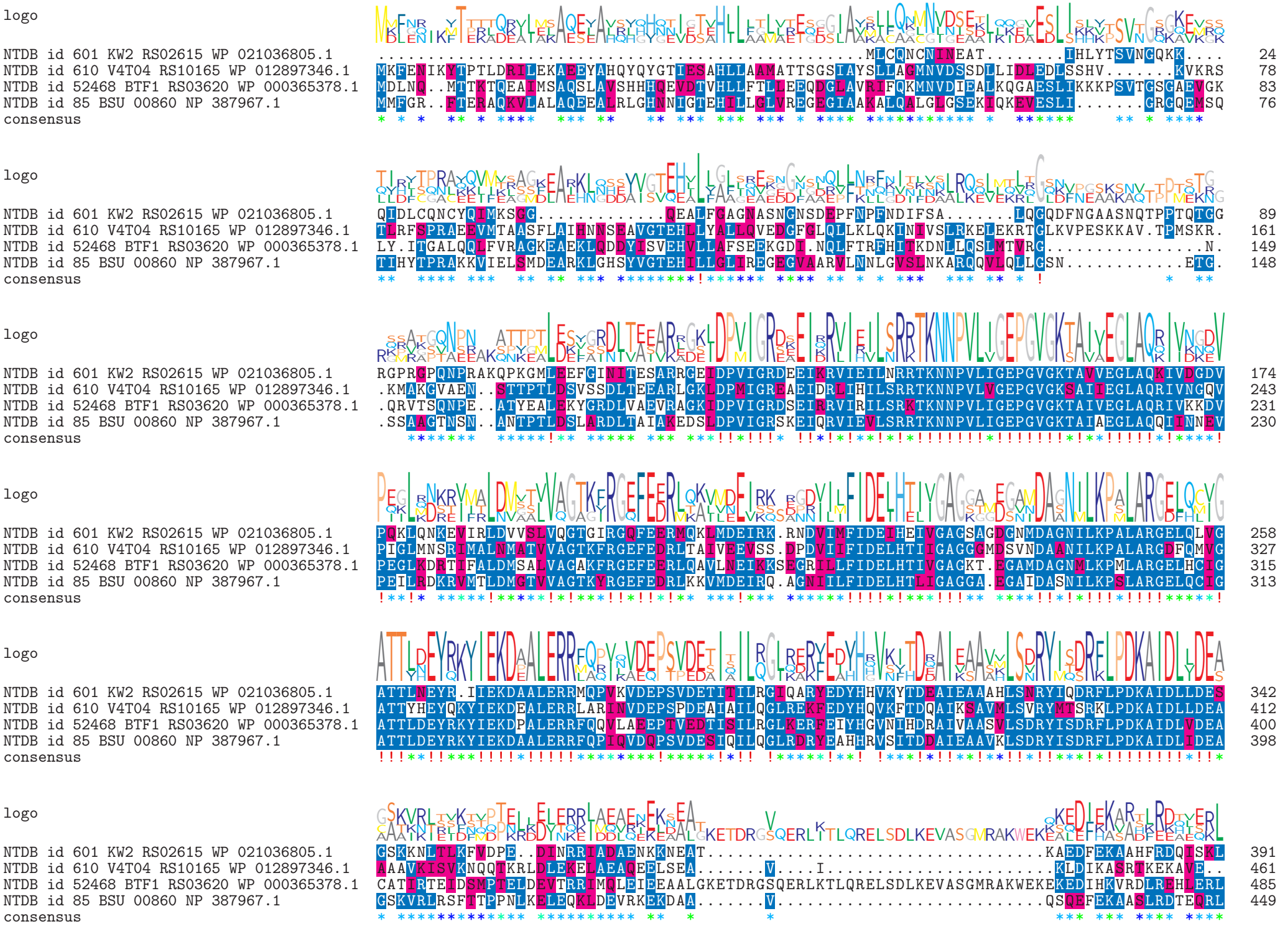
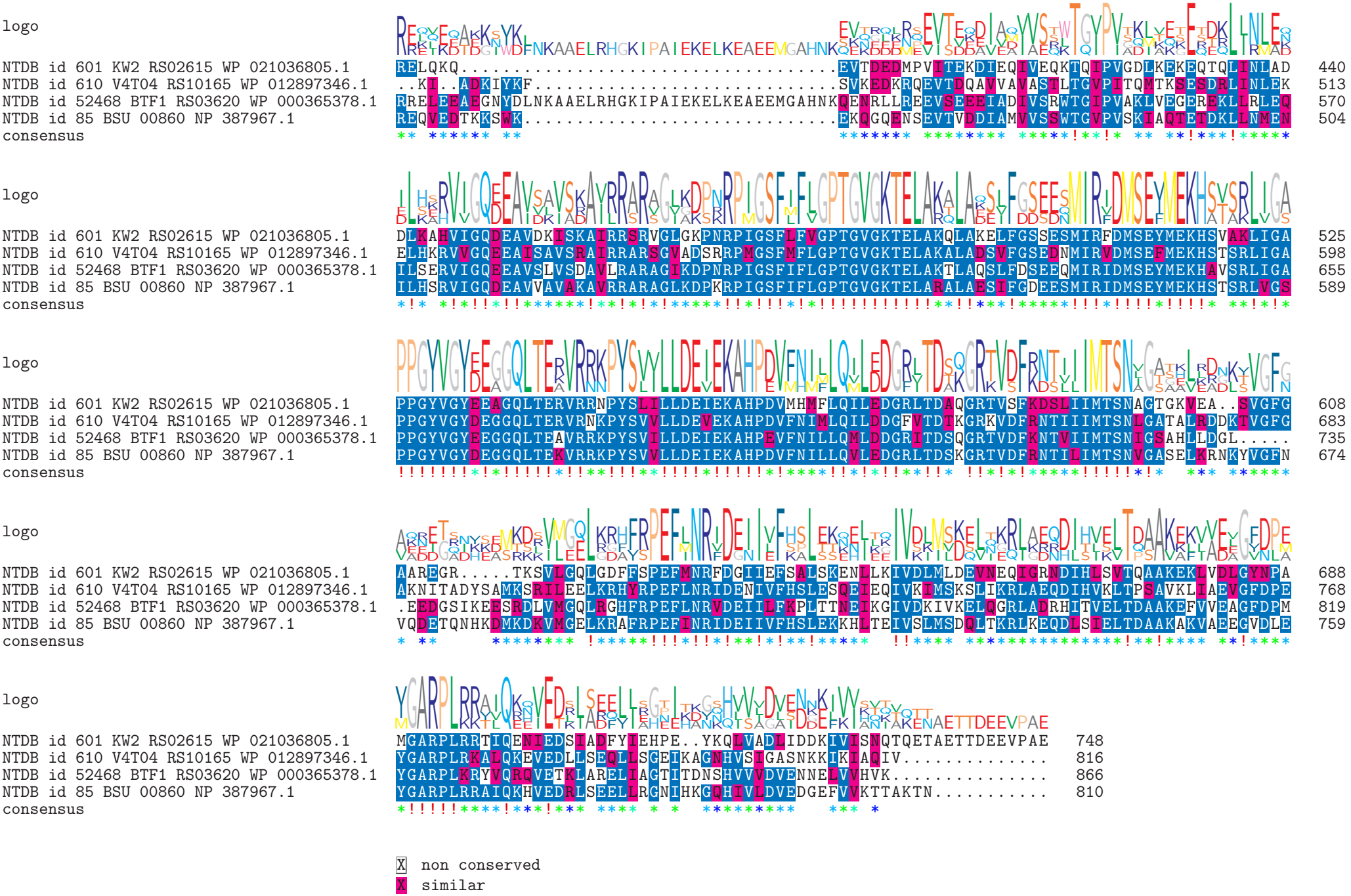

logo
NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 52468 BTF1 RS03620 WP 000365378.1
NTDB id 85 BSU 00860 NP 387967.1
consensus
logo
NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 52468 BTF1 RS03620 WP 000365378.1
NTDB id 85 BSU 00860 NP 387967.1
consensus
logo
NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 52468 BTF1 RS03620 WP 000365378.1
NTDB id 85 BSU 00860 NP 387967.1
consensus
logo
NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 52468 BTF1 RS03620 WP 000365378.1
NTDB id 85 BSU 00860 NP 387967.1
consensus
logo
NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 52468 BTF1 RS03620 WP 000365378.1
NTDB id 85 BSU 00860 NP 387967.1
consensus
logo
NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 52468 BTF1 RS03620 WP 000365378.1
NTDB id 85 BSU 00860 NP 387967.1
consensus


logo
NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 52468 BTF1 RS03620 WP 000365378.1
NTDB id 85 BSU 00860 NP 387967.1
consensus
RELQKQ.....EVTDEDMPVITEKDIEQIVEQKTQIPVGDLKEKEQTQLINLAD 440
..KI..ADKIYKF.....SVKEDKRQEVTDQAVVAVASTLTGVPITQMTKSESDRLINLEK 513
RRELEEAEGNYDLNKAAELRHGKIPAIEKELKEAEEMGAHNKQENRLLREEVSEEEIADIVSRWTGIPVAKLVEGEREKLLRLEQ 570
REQVEDTKKSWK.....EKQGQENSEVTVDDIAMVVSSWTGVPVSKIAQTETDKLLNMEN 504
DLKAHVIGQDEAVDKISKAIRRSRVGLGKPNRPIGSFLFVGPTGVGKTELAKQLAKELFGSSESMIRFDMSEYMEKHSVAKLIGA 525
ELHKRVVGQEEAISAVSRAIRRARSGVADSRRPMGSFMFLGPTGVGKTELAKALADSVFGSEDNMIRVDMSEFMEKHSTSRLIGA 598
ILSERVIGQEEAVSLVSDAVLRARAGIKDPNRPIGSFIFLGPTGVGKTELAKTLAQSLFDSEEQMIRIDMSEYMEKHAVSRLIGA 655
ILHSRVIGQDEAVVAVAKAVRRARAGLKDPKRPIGSFIFLGPTGVGKTELARALAESIFGDEESMIRIDMSEYMEKHSTSRLVGS 589
PPGYVGYEEAGQLTERVRRNPYSLILLDEIEKAHPDVFNILLQVLEDGRLTDSQGRTVDFRNTIIIMTSNAGTGKVEA..SVGFG 608
PPGYVGYDEGGQLTERVRNKPYSVVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDKTVGFG 683
PPGYVGYEEGGQLTEAVRRKPYSVILLDEIEKAHPEVFNILLQMLDDGRITDSQGRTVDFKNTVIIMTSNIGSAHLLDGL..... 735
PPGYVGYDEGGQLTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNKYVGFN 674
AARERGR.....TKSVLGQLGDFFSPEFMNRFDGIIEFSALSKENLLKIVDLMLDEVNEQIGRNDIHLSVTQAAKEKLVDLGYNPA 688
AKNITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLIKRLAEQDIHVKLTPSAVKLIAEVGFDPE 768
.EEDGSIKEFSRDLVMGQLRGHFRPEFLNRVDEIILFKPLTTNEIKGIVDKIVKELQGRLADRHITVELTDAAKEFVVEAGFDPM 819
VQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKAKVAEEGVDLE 759
MGARPLRRTIQENIEDSIADFYIEHPE..YKQLVADLIDDKIVISNQTQETAETTDEEVPAE 748
YGARPLRKALQKEVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV..... 816
YGARPLKRYVQRQVETKLARELIAGTITDNSHVVVDVENNELVVHVK..... 866
YGARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN..... 810
X non conserved
X similar
X ≥ 50% conserved