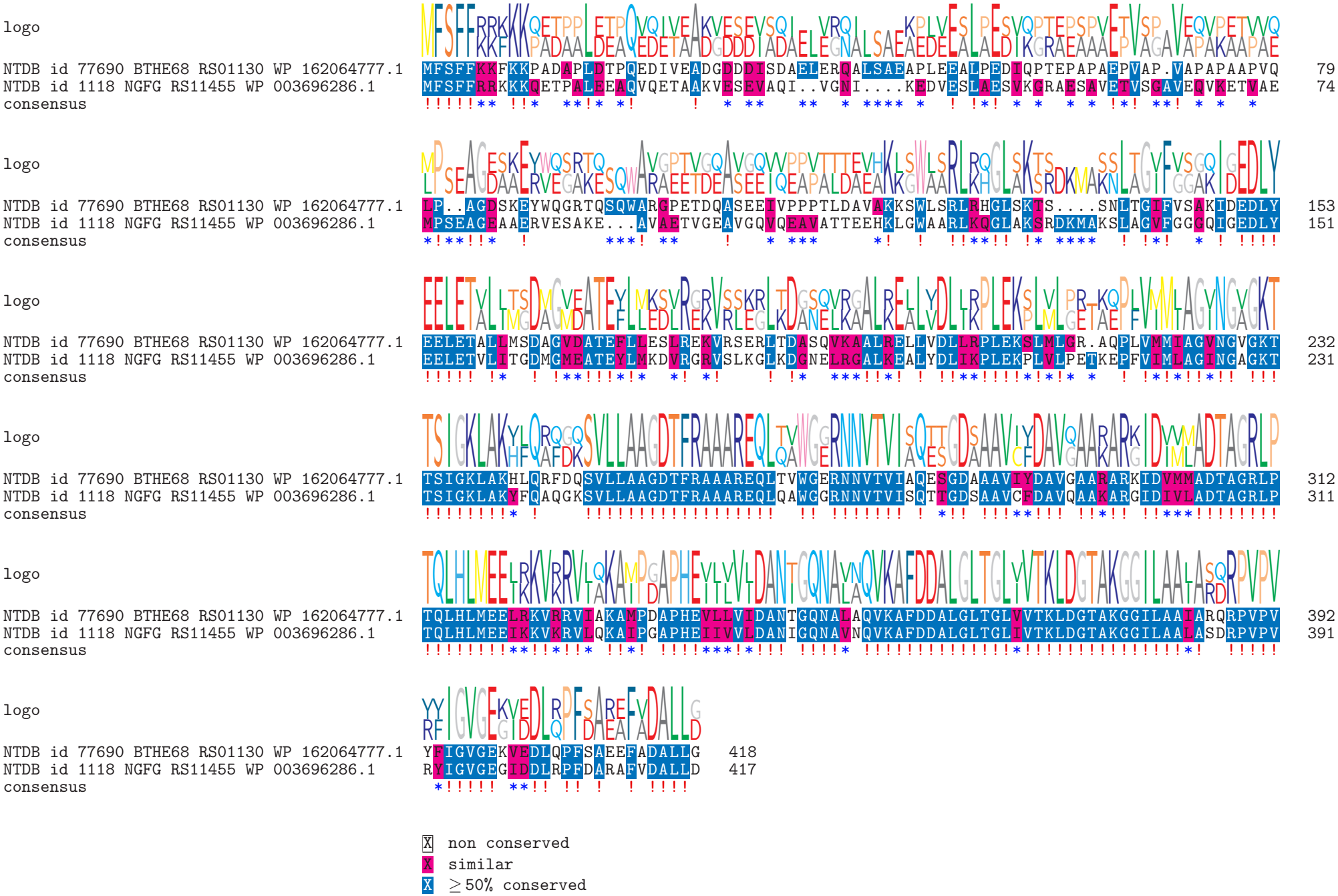
logo
NTDB id 77690 BTHE68 RS01130 WP 162064777.1 MFSFFKKFKKPADAPLDTPQEDIVEADGDDDISDAELERQALSAEAPLEEALPEDIQPTEPAPAEPVAP.VAPAPAAPVQ 79
NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQI..VGNI....KEDVESLAESVKGRAESAVETVSGAVEQVKETVAE 74
consensus !!!!!** !!* **!* *! ! * ** ** * **** * ! !*! * * * * !*! **! * * *
logo
NTDB id 77690 BTHE68 RS01130 WP 162064777.1 LP..AGDSKEYWQGRTQSQWARGPETDQASEEIVPPPTLDAVAKKSWLSRLRHGLSKTS....SNLTGIFVSAKIDEDLY 153
NTDB id 1118 NGFG RS11455 WP 003696286.1 MPSEAGEAAERVESAKE...AVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLY 151
consensus *!**!!* ! ***! ** ! * *** *! ! !!**!! !* **** ! !*! * ! !!!!
logo
NTDB id 77690 BTHE68 RS01130 WP 162064777.1 EELETALLMSDAGVDATEFLLESLREKVRSERLTDASQVKAALRELLVDLLRPLEKSLMLGR.AQPLVMMIAGVNGVGKT 232
NTDB id 1118 NGFG RS11455 WP 003696286.1 EELETVLITGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKT 231
consensus !!!!! !* ! !**!!!*!* *! *! ! !* ***!!*! ! !!**!!!!*!*!* * ! !*!*!!*!! !!!
logo
NTDB id 77690 BTHE68 RS01130 WP 162064777.1 TSIGKLAKHLQRFDQSVLLAAGDTFRAAAREQLTVWGERNNVTVIAQESGDAAAVIYDAVGAARARKIDVMMADTAGRLP 312
NTDB id 1118 NGFG RS11455 WP 003696286.1 TSIGKLAKYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLP 311
consensus !!!!!!!!* ! !!!!!!!!!!!!!!!!!! !! !!!!!!! ! *!! !!!**!!! !!*!! !!***!!!!!!!
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NTDB id 77690 BTHE68 RS01130 WP 162064777.1 TQLHLMEELRKVRRVIAKAMPDAPHEVLLVIDANTGQNALAQVKAFDDALGLTGLVVTKLDGTAKGGILAAIARQRPVPV 392
NTDB id 1118 NGFG RS11455 WP 003696286.1 TQLHLMEEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPV 391
consensus !!!!!!!!**!!*!!* !!*! !!!!***!*!!! !!!!* !!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!*! !!!!!
logo
NTDB id 77690 BTHE68 RS01130 WP 162064777.1 YFIGVGEKVEDLQPFSAEEFADALLG 418
NTDB id 1118 NGFG RS11455 WP 003696286.1 RYIGVGEGIDDLRPFDARAFVDALLD 417
consensus *!!!!! **!! !! ! ! !!!!
X non conserved
X similar
X ≥ 50% conserved