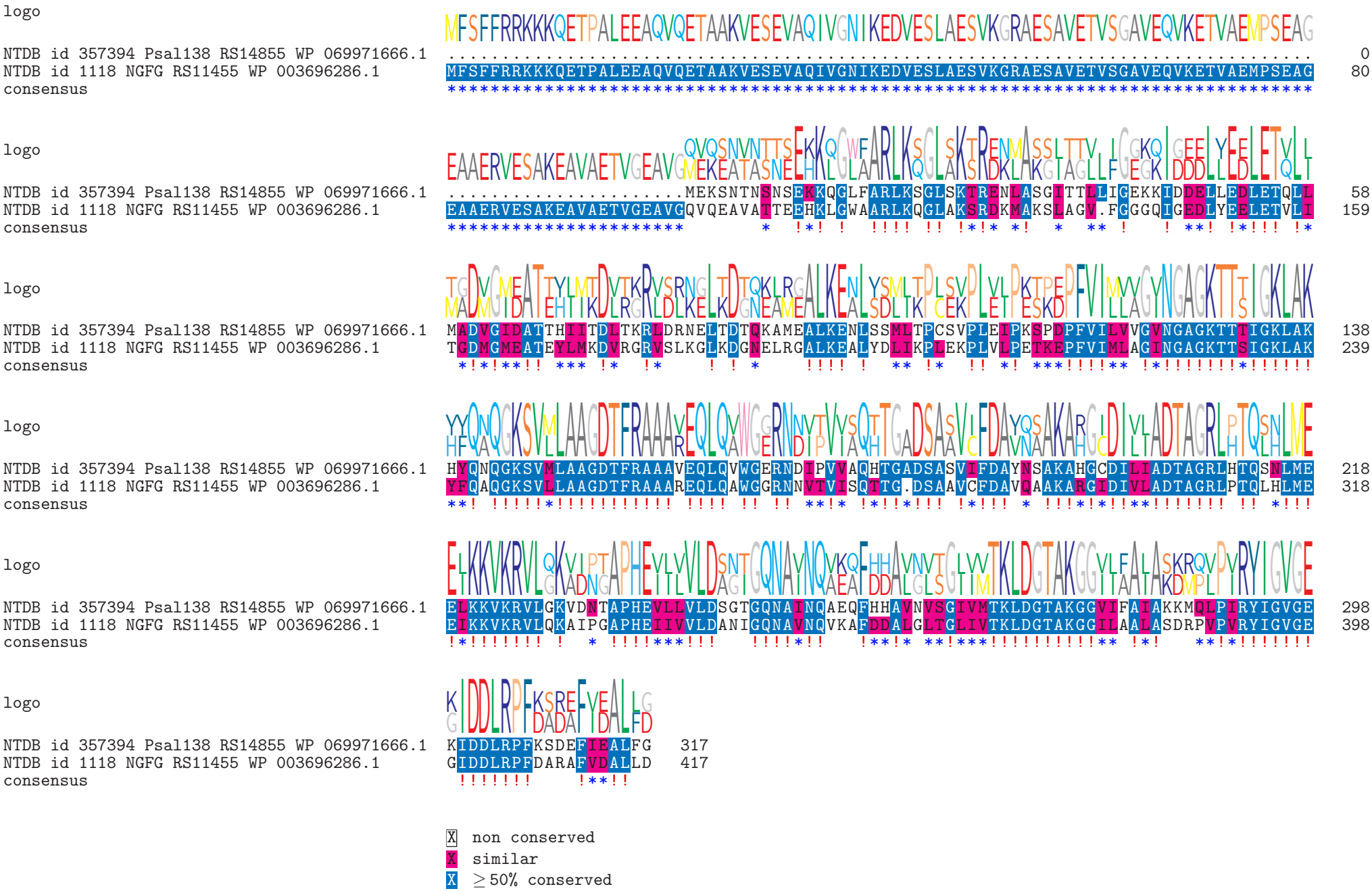
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NTDB id 1118 NGFG RS11455 WP 003696286.1 MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG 80
consensus **********
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NTDB id 357394 Psal138 RS14855 WP 069971666.1 .....MEKSNTNSNSEKKQGLFARLKSGLSKTRENLASGITTLLIGEKKIDDELLEDLETQLL 58
NTDB id 1118 NGFG RS11455 WP 003696286.1 EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGV.FGGGQIGEDLYEELETVLI 159
consensus ********** * !*! ! !!!! !! !*!* *! * ** ! ! **! !*!!! !*
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NTDB id 357394 Psal138 RS14855 WP 069971666.1 MADVGIDATTHIITDLTKRLDRNELTDTQKAMEALKENLSSMLTPCSVPLEIPKSPDPFVILVVGVNGAGKTTTIGKLAK 138
NTDB id 1118 NGFG RS11455 WP 003696286.1 TGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAK 239
consensus *!*!**!! *** !* !* ! ! * !!!! ! ** !* !! *! ***!!!!** !*!!!!!!!*!!!!!!
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NTDB id 357394 Psal138 RS14855 WP 069971666.1 HYQNQGKSVMLAAGDTFRAAAVEQLQVWGERNDIPVVAQHTGADSASVIFDAYNSAKAHGCDILIADTAGRLHTQSNLME 218
NTDB id 1118 NGFG RS11455 WP 003696286.1 YFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTG.DSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLME 318
consensus **! !!!!!*!!!!!!!!!!!! !!!! !! !! **!* !*!!*!!! !*!!! * !!!*!*!!**!!!!!!! !! *!!!
logo
NTDB id 357394 Psal138 RS14855 WP 069971666.1 ELKKVKRVLGKVDNTAPHEVLLVLDSGTGQNAINQAEQFHHAVNVSGIVMTKLDGTAKGGVIFAIAKKMQLPIRYIGVGE 298
NTDB id 1118 NGFG RS11455 WP 003696286.1 EIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGE 398
consensus !*!!!!!!! ! * !!!!***!!! !!!!*!! !**!* **!***!!!!!!!!!** !*! **!*!!!!!!!
logo
NTDB id 357394 Psal138 RS14855 WP 069971666.1 KIDDLRPFKSDEFIEALFG 317
NTDB id 1118 NGFG RS11455 WP 003696286.1 GIDDLRPFDARAFVDALLD 417
consensus !!!!!!! !**!!
X non conserved
X similar
X ≥ 50% conserved