```
logo
NTDB id 1043769 ACEI37 RS12630 WP 373379167.1  MFSFWKKRKAEPAPIEAPAPAPAPTPEVPAPAPA.............PSPTPT.PTPTPSPSPAPAPVPVPVPVPVPAQV   66
NTDB id 1118 NGFG RS11455 WP 003696286.1       MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETV.AEMPSEA   79
consensus                                      !!!!****!  * !   *!* * * * !* * * **************!* * **** ***!*!* *!* *!* **!

logo
NTDB id 1043769 ACEI37 RS12630 WP 373379167.1  P.........PPAPAPVAAEAL.ELVPPPAPSAEARQGWMQRLRTGLSKTSR....NLGTLFVGVKVDEDLFEELETALL  132
NTDB id 1118 NGFG RS11455 WP 003696286.1       GEAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLI  159
consensus                                      ************!*!*  *!!** * ***!** !** !!  !!* !! !*  **** !* *! !  * !!!*!!!!! !*

logo
NTDB id 1043769 ACEI37 RS12630 WP 373379167.1  MADAGVEATEYLLGELRKRVRSERIETAEGVKAALRELLTQLLRPLEKTMALG.REQPLVMMIAGVNGAGKTTSIGKLCK  211
NTDB id 1118 NGFG RS11455 WP 003696286.1       TGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAK  239
consensus                                       *! !*!!!!!!* **! !!    *  *  ***!!*! !  !**!!!** !**   ! !*!*!!*!!!!!!!!!!!!!*!

logo
NTDB id 1043769 ACEI37 RS12630 WP 373379167.1  HFQRYDQKVLLAAGDTFRAAAREQLTIWGERNNVTVVAQESGDPAAVIFDAVNAAKARGIDIVMADTAGRLPTQLHLMEE  291
NTDB id 1118 NGFG RS11455 WP 003696286.1       YFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEE  319
consensus                                      *!!     !!!!!!!!!!!!!!!!!  !! !!!!!!* ! *!!*!!!*!!!!*!!!!!!!!!!*!!!!!!!!!!!!!!!!!

logo
NTDB id 1043769 ACEI37 RS12630 WP 373379167.1  LKKVKRVISKAMPSAPHEVLLVIDANTGQNALQQTRAFDDALGLTGLIVTKLDGTAKGGILAAIARQRPVPVYFIGVGEK  371
NTDB id 1118 NGFG RS11455 WP 003696286.1       IKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEG  399
consensus                                      *!!!!!!* !!*! !!!!***!*!!! !!!!**! *!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!  !!!!! *!!!!!

logo
NTDB id 1043769 ACEI37 RS12630 WP 373379167.1  VEDLQPFKAEEFAEALLG   389
NTDB id 1118 NGFG RS11455 WP 003696286.1       IDDLRPFDARAFVDALLD   417
consensus                                      **!! !! !  ! *!!!
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X non conserved

X similar

X ≥ 50% conserved