```
logo
NTDB id 26230 H16 RS01785 WP 011614476.1  MFSFWKKRKAEPAPAEAPAPAPAPV.EVPAPVP....APAP....TPAPVPAPAPA...PVP..........AQVPPPAPAPVAA   63
NTDB id 1118 NGFG RS11455 WP 003696286.1  MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG.EAAE   84
consensus                                 !!!!****!  * !!  *!* * * * !* *!***** * ***** * *!***!* ****!***********! *!**!*** !

logo
NTDB id 26230 H16 RS01785 WP 011614476.1  PIPL....PAPAPAEA.LELVPPPAQTAEAKLGWMHRLRTGLSKTSRN....IGTLFVGVKVDEALREELETALLMADAGVEATE  139
NTDB id 1118 NGFG RS11455 WP 003696286.1  RVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLITGDMGMEATE  169
consensus                                 *** *****!* **!!*  * ***! ! !*!!!! *!!* !! !*   ****** *! !  * ! !*!!!!! !* *! !*!!!!

logo
NTDB id 26230 H16 RS01785 WP 011614476.1  YLLGELRKRVKAERIETAEGVKAALRELLTQLLRPLEKTMALG.REQPLVMMIAGVNGAGKTTSIGKLCKHFQRYDQKVLLAAGD  223
NTDB id 1118 NGFG RS11455 WP 003696286.1  YLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAKYFQAQGKSVLLAAGD  254
consensus                                 !!* **! !!    *  *  ***!!*! !  !**!!!** !**   ! !*!*!!*!!!!!!!!!!!!*!*!!     !!!!!!!

logo
NTDB id 26230 H16 RS01785 WP 011614476.1  TFRAAAREQLTIWGERNNVTVVAQESGDPAAVIFDAVNAAKARGIDIVMADTAGRLPTQLHLMEELKKVKRVISKAMPSAPHEVL  308
NTDB id 1118 NGFG RS11455 WP 003696286.1  TFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEEIKKVKRVLQKAIPGAPHEII  339
consensus                                 !!!!!!!!!!  !! !!!!!!* ! *!!*!!!*!!!!*!!!!!!!!!*!!!!!!!!!!!!!!!!!*!!!!!! !!*! !!!!**

logo
NTDB id 26230 H16 RS01785 WP 011614476.1  LVIDANTGQNALQQTRAFDDALGLTGLIVTKLDGTAKGGILAAIARQRPVPVYFIGVGEKVEDLQPFKADEFAEALLG  386
NTDB id 1118 NGFG RS11455 WP 003696286.1  VVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEGIDDLRPFDARAFVDALLD  417
consensus                                 *!*!!! !!!!**! *!!!!!!!!!!!!!!!!!!!!!!!!!!!*!  !!!!! *!!!!! **!! !! !  ! *!!!
```

X non conserved

X similar

X ≥ 50% conserved