```
logo
NTDB id 27678 BMA10247 RS22985 WP 004195253.1  MFSFFKRFKKAPDAAPAEPQQAPDAPRDASRAPASPDAARVDAPAAPQPRDERSENHDRPEHDETPTAEHSRSGAQPAAR   80
NTDB id 1118 NGFG RS11455 WP 003696286.1       MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKG......R.....AESAVETVSGAVEQVK   69
consensus                                      !!!!!*! !! * *!* !*!  * !**  !  *  *  * ! *  * *   ******!***** **! ** !!! *  *

logo

NTDB id 27678 BMA10247 RS22985 WP 004195253.1  ATPPASAAASEAPVGQPRAAAARASEPAPSVVMTVTPSSNGRHGVVETVEIVPPPAPEPAAKKSWIARLKSGLAKTSS..  158
NTDB id 1118 NGFG RS11455 WP 003696286.1       E......TVAEMPSEAGE.AAERVESAKEAVAETV....GEAVG.....QVQEAVATTEEHKLGWAARLKQGLAKSRDKM  133
consensus                                       ******   ! !   * *!! !   * * !  !!****   *!***** * ***!* * *!  ! !!!! !!!!*  **

logo

NTDB id 27678 BMA10247 RS22985 WP 004195253.1  ..SITNVFVNTKIDDALYEELETALLMSDAGIDATEHLLDALREKVRAGRLTDPQQVKDALRGLLVELLAPLEKSFVLGR  236
NTDB id 1118 NGFG RS11455 WP 003696286.1       AKSLAGVFGGGQIGEDLYEELETVLITGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPE  213
consensus                                      **!*  !!    ! * !!!!!!! !*  ! !**!!!*!*  *! *!    ! !** ** !!*  ! *!* !!!!* !!*

logo

NTDB id 27678 BMA10247 RS22985 WP 004195253.1  .AQPLVMMIAGVNGAGKTTSIGKLAKHLQSFDQSVLLAAGDTFRAAAREQLAIWGERNNVTVVQQESGDPAAVIFDAVSA  315
NTDB id 1118 NGFG RS11455 WP 003696286.1       TKEPFVIMLAGINGAGKTTSIGKLAKYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQA  293
consensus                                      *  ! !*!*!!*!!!!!!!!!!!!!!!* !    !!!!!!!!!!!!!!!!!!  !! !!!!!!* ! *!!*!!!*!!!! !

logo

NTDB id 27678 BMA10247 RS22985 WP 004195253.1  ARARNIDVMMADTAGRLPTQLHLMEELRKVKRVIGKAHDGAPHEVLLVIDANTGQNALAQVKAFDDALGLTGLIVTKLDG  395
NTDB id 1118 NGFG RS11455 WP 003696286.1       AKARGIDIVLADTAGRLPTQLHLMEEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDG  373
consensus                                      !*!! !!***!!!!!!!!!!!!!!!!**!!!!!* !!**!!!!!***!*!!! !!!!* !!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 27678 BMA10247 RS22985 WP 004195253.1  TAKGGILAAIARQRPIPVYFIGIGEKVEDLQPFSAEEFADALLG   439
NTDB id 1118 NGFG RS11455 WP 003696286.1       TAKGGILAALASDRPVPVRYIGVGEGIDDLRPFDARAFVDALLD   417
consensus                                      !!!!!!!!!*!  !!*!! *!!*!! **!! !! !  ! !!!!
```

X non conserved

X similar

X $\geq$ 50% conserved