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logo

NTDB id 1113248 ABCQ42 RS16170 WP 024428879.1  MFSFFKRFKKAPDAAPAEPQQAPDAPRDASRAPASPDAARVDTPAAPQPRDERSENHDRPEHDETPTAEHSRSGAQPAAR   80
NTDB id 1118 NGFG RS11455 WP 003696286.1       MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGR...........AESAVETVSGAVEQVK   69
consensus                                      !!!!!*! !! * *!* !*!  * !**  !  *  *  * ! *  * *  !*********** **! ** !!! *  *

logo

NTDB id 1113248 ABCQ42 RS16170 WP 024428879.1  ATPPASAAASEAPVGQPRAAAARASEPAPSVVMTVTPSSNGRHGVVETVEIVPPPAPEPAAKKSWIARLKSGLAKTSS..  158
NTDB id 1118 NGFG RS11455 WP 003696286.1       E......TVAEMPSEAGE.AAERVESAKEAVAETV....GEAVG.....QVQEAVATTEEHKLGWAARLKQGLAKSRDKM  133
consensus                                       ******   ! !   * *!! !   * * !  !!****   *!***** * ***!* * *!  ! !!!! !!!!*  **

logo

NTDB id 1113248 ABCQ42 RS16170 WP 024428879.1  ..SITNVFVNTKIDDALYEELETALLMSDAGIDATEHLLDALREKVRAGRLTDPQQVKDALRGLLVELLAPLEKSLVLGR  236
NTDB id 1118 NGFG RS11455 WP 003696286.1       AKSLAGVFGGGQIGEDLYEELETVLITGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPE  213
consensus                                      **!*  !!    ! * !!!!!!! !*  ! !**!!!*!*  *! *!    ! !** ** !!*  ! *!* !!!!*!!!*

logo

NTDB id 1113248 ABCQ42 RS16170 WP 024428879.1  .AQPLVMMIAGVNGAGKTTSIGKLAKHLQSFDQSVLLAAGDTFRAAAREQLAIWGERNNVTVVQQESGDPAAVIFDAVSA  315
NTDB id 1118 NGFG RS11455 WP 003696286.1       TKEPFVIMLAGINGAGKTTSIGKLAKYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQA  293
consensus                                      *  ! !*!*!!*!!!!!!!!!!!!!!!* !    !!!!!!!!!!!!!!!!!!  !! !!!!!!* ! *!!*!!!*!!!! !

logo

NTDB id 1113248 ABCQ42 RS16170 WP 024428879.1  ARARNIDVMMADTAGRLPTQLHLMEELRKVKRVIGKAHDGAPHEVLLVIDANTGQNALAQVKAFDDALGLTGLIVTKLDG  395
NTDB id 1118 NGFG RS11455 WP 003696286.1       AKARGIDIVLADTAGRLPTQLHLMEEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDG  373
consensus                                      !*!! !!***!!!!!!!!!!!!!!!!**!!!!!* !!**!!!!!***!*!!! !!!!* !!!!!!!!!!!!!!!!!!!!

logo

NTDB id 1113248 ABCQ42 RS16170 WP 024428879.1  TAKGGILAAIARQRPIPVYFIGIGEKVEDLQPFSAEEFADALLG   439
NTDB id 1118 NGFG RS11455 WP 003696286.1       TAKGGILAALASDRPVPVRYIGVGEGIDDLRPFDARAFVDALLD   417
consensus                                      !!!!!!!!!*!  !!*!! *!!*!! **!! !! !  ! !!!!
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X non conserved

X similar

X $\geq$ 50% conserved