```
logo
NTDB id 51294 MYA RS12535 WP 011886072.1  MFSFFKRFKKTQEPDSAESQPADAPQPDEPSAAPAPAARAA........DTARAPAVVMT..............VTPTNDGS..D.   61
NTDB id 1118 NGFG RS11455 WP 003696286.1  MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAFSAVETVSGAVEQVKETVAEMPSEAGEAAER   85
consensus                                 !!!!!*! !!   !   ! !* * * * !*  !* **    ********  *!!*  ! !**************  !*  ! ****

logo
NTDB id 51294 MYA RS12535 WP 011886072.1  .........EVVEAVEI.VPPPTQDASAKKSWLSRLKSGLAKTG....SSITSVFVNTKIDEDLYEELETALLMSDAGVDATEY  131
NTDB id 1118 NGFG RS11455 WP 003696286.1  VESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLITGDMGMEATEY  170
consensus                                 ********** ! !!!  * ***     *!  !  !!! !!!!* **** !*  !!    ! !!!!!!!!! !*  ! !**!!!!

logo
NTDB id 51294 MYA RS12535 WP 011886072.1  LLGALREKVRVGRLTDPQQVKAALHDLLVELLQPLEKSLMLGR.AQPLVMMITGVNGAGKTTSIGKLAKHLQSFDQSVLLAAGDT  215
NTDB id 1118 NGFG RS11455 WP 003696286.1  LMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAKYFQAQGKSVLLAAGDT  255
consensus                                 !*  *! *! *  ! !** ***!!** ! *!* !!!!*!*!* *  ! !*!* !*!!!!!!!!!!!!!!* !    !!!!!!!!!

logo
NTDB id 51294 MYA RS12535 WP 011886072.1  FRAAAREQLAVWGERNNVTVVQQESGDPAAVIFDAVSAARARKIDVMMADTAGRLPTQLHLMEELKKVKRVIAKAHDGAPHEVLL  300
NTDB id 1118 NGFG RS11455 WP 003696286.1  FRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEEIKKVKRVLQKAIPGAPHEIIV  340
consensus                                 !!!!!!!!!  !! !!!!!!* ! *!!*!!!*!!!! !!*!! !!***!!!!!!!!!!!!!!!!!*!!!!!!* !!**!!!!!***

logo
NTDB id 51294 MYA RS12535 WP 011886072.1  VIDANTGQNALTQVKAFDDALGLTGLIVTKLDGTAKGGILAAIARQRPVPVYFIGVGEKVEDLQPFNAVEFADALLG  377
NTDB id 1118 NGFG RS11455 WP 003696286.1  VLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEGIDDLRPFDARAFVDALLD  417
consensus                                 !*!!! !!!!* !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!  !!!!! *!!!!! **!! !! !  ! !!!!
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X non conserved

X similar

X $\geq$ 50% conserved