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logo
NTDB id 988698 AAFR80 RS12775 WP 011657978.1  MFSFFKRFKKTQESDSTESQSADALQPDE..............PSDAPAAD..ARQAIEAPPAP.........AQPQPAA   55
NTDB id 1118 NGFG RS11455 WP 003696286.1      MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG   80
consensus                                     !!!!!*! !!   *   ! !  *   * !***************! !*   **!  !*! *************  ! *!*

logo
NTDB id 988698 AAFR80 RS12775 WP 011657978.1  PAVVMTVTPTND.GSDDVVEAVEIV.PPPTQDASAKKSWLTRLKTGLAKTG....SSITGVFVNTKIDEDLYEELEAALL   129
NTDB id 1118 NGFG RS11455 WP 003696286.1      EAA.ERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLI   159
consensus                                     *! *  ! *  **  * ! !!!  !****     *!  !  !!! !!!!* **** !* !!!    ! !!!!!!!!  !*

logo
NTDB id 988698 AAFR80 RS12775 WP 011657978.1  MSDAGVDATEYLLGALREKVKTGRLTDPQQVKSALHDLLVELLKPLEKSLMLGR.AQPLVMMITGVNGAGKTTSIGKLAK   208
NTDB id 1118 NGFG RS11455 WP 003696286.1      TGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAK   239
consensus                                       ! !**!!!!!*  *! *!    ! !** ** !!** ! *!*!!!!!*!*!* *  ! !*!* !*!!!!!!!!!!!!!!!

logo
NTDB id 988698 AAFR80 RS12775 WP 011657978.1  HLQSFDQSVLLAAGDTFRAAAREQLAVWGERNNVTVVQQESGDPAAVIFDAVSAARARKIDVMMADTAGRLPTQLHLMEE   288
NTDB id 1118 NGFG RS11455 WP 003696286.1      YFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEE   319
consensus                                     * !    !!!!!!!!!!!!!!!!!!  !! !!!!!!* ! *!!*!!!*!!!! !!*!! !!***!!!!!!!!!!!!!!!!!

logo
NTDB id 988698 AAFR80 RS12775 WP 011657978.1  LKKVKRVISKAHDGAPHEVLLVIDANTGQNALTQVKAFDDALGLTGLIVTKLDGTAKGGILAAIARQRPVPVYFIGVGEK   368
NTDB id 1118 NGFG RS11455 WP 003696286.1      IKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEG   399
consensus                                     *!!!!!!* !!**!!!!!***!*!!! !!!!* !!!!!!!!!!!!!!!!!!
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