```
logo
NTDB id 296229 DM992 RS05835 WP 111016069.1  MFSFFKRFKKTQEPDPAESQSADASQTDEPSDAPTLEAPLAADVPQA..........PVQ...PAAPAVVMT..VTPTND   65
NTDB id 1118 NGFG RS11455 WP 003696286.1     MFSFFRRKKKQETPALEEAQVQETAAKVESE.VAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEA   79
consensus                                    !!!!!*! !!   ! * ! !  *     !* * * * ***  !!*  ***********! ****! * !  !**  !*

logo
NTDB id 296229 DM992 RS05835 WP 111016069.1  .........GRDEVVETVEI....V.PPPLQDASAKKSWLARLKTGLAKTG....SSITGVFVNTKIDEDLYEELETALL   127
NTDB id 1118 NGFG RS11455 WP 003696286.1     GEAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLI   159
consensus                                    ************ ! !!!  ****!****     *!  ! !!!! !!!!* **** !* !!!    ! !!!!!!!!! !*

logo
NTDB id 296229 DM992 RS05835 WP 111016069.1  MSDAGVDATEYLLDALREKVRTGRLTDPQQVKSALHDLLVELLKPLEKSLMLGR.AQPLVMMITGVNGAGKTTSIGKLAK   206
NTDB id 1118 NGFG RS11455 WP 003696286.1     TGDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYDLIKPLEKPLVLPETKEPFVIMLAGINGAGKTTSIGKLAK   239
consensus                                      ! !**!!!!!*  *! *!    ! !** ** !!** ! *!*!!!!!*!*!* *  ! !*!* !*!!!!!!!!!!!!!!

logo
NTDB id 296229 DM992 RS05835 WP 111016069.1  HLQSFDQSVLLAAGDTFRAAAREQLAVWGERNNVTVVQQESGDPAAVIFDAVSAARARKIDVMMADTAGRLPTQLHLMEE   286
NTDB id 1118 NGFG RS11455 WP 003696286.1     YFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHLMEE   319
consensus                                    * !    !!!!!!!!!!!!!!!!!!  !! !!!!!!* ! *!!*!!!*!!!! !!*!! !!***!!!!!!!!!!!!!!!!

logo
NTDB id 296229 DM992 RS05835 WP 111016069.1  LKKVKRVISKAHDGSPHEVLLVIDANTGQNALTQVKAFDDALGLTGLIVTKLDGTAKGGILAAIARQRPVPVYFIGVGEK   366
NTDB id 1118 NGFG RS11455 WP 003696286.1     IKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASDRPVPVRYIGVGEG   399
consensus                                    *!!!!!!* !!**! !!!***!*!!! !!!!* !!!!!!!!!!!!!!!!!!
```