```
logo
                                          MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG
NTDB id 176119 A4F89 RS10910 WP 071539811.1  ..............................................................................  0
NTDB id 1118 NGFG RS11455 WP 003696286.1     MFSFFRRKKKQETPALEEAQVQETAAKVESEVAQIVGNIKEDVESLAESVKGRAESAVETVSGAVEQVKETVAEMPSEAG  80
consensus                                    ******************************************************************************

logo
                                                                                                  RFKMRKTLGSVFKTSQTGEDWYETLETVLIT
                                          EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSMDGLAKSLAGLFGGGKIDLALFDELESLIQ
NTDB id 176119 A4F89 RS10910 WP 071539811.1  ...................................................MFGLRKTLGSLFKTSKTDEAWFDTLEESLIQ  31
NTDB id 1118 NGFG RS11455 WP 003696286.1     EAAERVESAKEAVAETVGEAVGQVQEAVATTEEHKLGWAARLKQGLAKSRDKMAKSLAGVFGGGQIGEDLYEELETVLIT  160
consensus                                    ************************************************   * !*!* *!      !  ** !!  !!

logo
                                          SDVGMPTTEYLMKKVRKRVSSKKLSSPNELRGLKQEVYT SLKDNPNPLVTQKTKLDEVWMVYGYNGAGKTTTIGK
                                          GDMGLEATEQLTIDLGAAKLDGAKDGELQAALIEALSDLLGLTETLEKLFLDPETHEEEVILLAYNGAGKTTSIGK
NTDB id 176119 A4F89 RS10910 WP 071539811.1  SDVGLPTTEQLIIKLRKAAKSDKASSPEELQALLIQEVSTLLGSLEPNPNPLFTDQKIHIPEVWLVVGVNGAGKTTTIGK  111
NTDB id 1118 NGFG RS11455 WP 003696286.1     GDMGMEATEYLMKDVRGRVSLKGLKDGNELRGALKEALYD...LIKPLEKPLVL.PETKEPFVIMLAGINGAGKTTSIGK  236
consensus                                     !*!** !! !*  *!          * !! * !   *  *** * ! * !!  **  * ! ! ** !*!!!!!!!*!!!

logo
                                          LCKYFQSQGKSVLLAAGDTFRAAARNQLQEWGGRNQVTVITQTTGDSAAVCHDAVQAANSRKSDIYLIDTAGRLATQDHL
                                          LAKLFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQDGGDAAVAFDAIHAKARGIDILTADTAGRLATQDHL
NTDB id 176119 A4F89 RS10910 WP 071539811.1  LCKLFQSQGKSVLLAAGDTFRAAARNQLQEWGGRNQVDVITQDGGDAAVAHDAIHAANSRKSDILIIDTAGRLATQDHL  191
NTDB id 1118 NGFG RS11455 WP 003696286.1     LAKYFQAQGKSVLLAAGDTFRAAAREQLQAWGGRNNVTVISQTTGDSAAVCFDAVQAAKARGIDIVLADTAGRLPTQLHL  316
consensus                                    !*! !! !!!!!!!!!!!!!!!!!! !!! !!!!!*! !!*!  !! !!!**!!**!!  !  !!** !!!!!!*!! !!

logo
                                          MEELKKVKRVLGKALPGAPHHTLLVLDGNTGQNGLSQVKAFHAALGLTGLIVTKLDGTAKGGVICALAHTLKDEPKPAVL
                                          MEEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASD...RP.VPVR
NTDB id 176119 A4F89 RS10910 WP 071539811.1  MEELKKVKRVIGKALPGAPHHTLLVLDGNTGQNGLSQVKAFHAALGLTGLIVTKLDGTAKGGVICALAHTLKDEPKPAVL  271
NTDB id 1118 NGFG RS11455 WP 003696286.1     MEEIKKVKRVLQKAIPGAPHEIIVVLDANIGQNAVNQVKAFDDALGLTGLIVTKLDGTAKGGILAALASD...RP.VPVR  392
consensus                                    !!!*!!!!!!* !!*!!!!!* **!!!*! !!!** !!!!!* !!!!!!!!!!!!!!!!!!!***!!!* *** !***!

logo
                                          YLGVGEGIDDLVPFTARQYVSELLN
                                          ATGKGEGIDDLRPFDAHAFSDALFD
NTDB id 176119 A4F89 RS10910 WP 071539811.1  ALGKGEGIDDLVPFTAHQYSSELFN  296
NTDB id 1118 NGFG RS11455 WP 003696286.1     YIGVGEGIDDLRPFDARAFVDALLD  417
consensus                                     *! !!!!!!! !! !* *   !
```

X non conserved

X similar

X ≥ 50% conserved