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logo
NTDB id 393271 GCU53 RS07695 WP 152389817.1  MPKDSASLAGSVPSGNVLRLYHLYRLVIGLLLVLLISSNLDERLLQVAYPDLFRHGSWLYLILNILVAVLVHHP.KPLQL   79
NTDB id 1472 PAKAF RS23995 WP 016253893.1    MRAERL.RLSEEQGQRILRLYHLYRLTIGLVLVLLISSELEDQVLKLVHPELFHVGSWCYLVFNILVALFLPPSRQLLPI   79
consensus                                    !* *  *     *   *!!!!!!!!! !!!*!!!!!!! !** *! * *!*!!**!!!*!!* !!!!!* *  ** *!**

logo

NTDB id 393271 GCU53 RS07695 WP 152389817.1  FSLALVDVLLLSGLLYTAGGPSSGIGNLIIVSVAVANILLRGRIGLLIAAVAASGLVYMTFYLGLNRPAAATQYVHAGAL  159
NTDB id 1472 PAKAF RS23995 WP 016253893.1    FILALTDVLMLCGLFYAGGGVPSGIGSLLVVAVAIANILLRGRIGLVIAAAASLGLLYLTFFLSLSSPDATNHYVQAGGL  159
consensus                                    ! !!! !!**!*!! ! *!!**!!!! !**! !!*!!!!!!!!!!!*!!! !  !!*!*!!*! !  ! !  *!!*!!*!

logo

NTDB id 393271 GCU53 RS07695 WP 152389817.1  GSLCFAAALVVQSLTRRLQRSESLAERRAAEVADLQALNAQILERMRTGILVLDPQQQVLLANQSAFTLLGNPALVGQPL  239
NTDB id 1472 PAKAF RS23995 WP 016253893.1    GTLCFAAALVIQALVRRQEQTETLAEERAETVANLEELNALILQRMRTGILVWDSRQAILLANQAALGLLRQDDVQGASL  239
consensus                                    !*!!!!!!!**! ! !!   *!*!!! !!  !! !  !!! !! !!!!!!!!*!* ! *!!!!! !  !! ** * ! *!

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NTDB id 393271 GCU53 RS07695 WP 152389817.1  AGHCPALVERLKHWQQNPTLRPQDLHTLPHGPLVQPNFVPLTRGGKQSILVFLEDVSQIAQQAQQLKLASLGRLTAGIAH  319
NTDB id 1472 PAKAF RS23995 WP 016253893.1    GRHSPMLMHCMKQWRLNPSLRPPTLKVVPDGPTVQPSFISLNREDDQHVLIFLEDISQIAQQAQQMKLAGLGRLTAGIAH  319
consensus                                    * !*! !****!*!  !!*!!!* !* *!*!! !!! !**! !   !**!*!!!!*!!!!!!!!!*!!! !!!!!!!!!!

logo

NTDB id 393271 GCU53 RS07695 WP 152389817.1  EIRNPLGAISHAAQLLQESDDLDGPDRRLAQIIQDQSRRMNLVIENVLQLSRRRQAQPQLLDLKYWLHRFASEYRASAAP  399
NTDB id 1472 PAKAF RS23995 WP 016253893.1    EIRNPLGAISHAAQLLQESEELDAPDRRLTQIIQDQSKRMNLVIENVLQLSRRRQAEPQQLDLKEWLQRFVDEYPGRLRN  399
consensus                                    !!!!!!!!!!!!!!!!!!!**!!*!!!!! !!!!!!!*!!!!!!!!!!!!!!!!!! !! !!!! !!*!!  !!**    *

logo

NTDB id 393271 GCU53 RS07695 WP 152389817.1  NQILHLEIQSGSLKTRMDSNQLIQVLNNLVQNGLRYSAQCHPQGQVWLKLFRDPESDLPVLEVRDDGPGVPAAQIEHIFE  479
NTDB id 1472 PAKAF RS23995 WP 016253893.1    DSELHLQLGAGDIQTRMDPHQLNQVLSNLVQNGLRYSAQAHGRGQVWLSLARDPESDLPVLEIIDDGPGVPADKLNNLFE  479
consensus                                       !!! *  ! * !!!!**!! !!! !!!!!!!!!!!!*!* !!!!! ! !!!!!!!!!!!* !!!!!!!!  * **!!

logo

NTDB id 393271 GCU53 RS07695 WP 152389817.1  PFFTTESKGTGLGLYLSRELCESNQARLDYRGDEGKGGCFRITFAHPRKLS  530
NTDB id 1472 PAKAF RS23995 WP 016253893.1    PFFTTESKGTGLGLYLSRELCESNQARIDYRNREEGGGCFRITFAHPRKLS  530
consensus                                    !!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!  !  !!!!!!!!!!!!!!!
```

X non conserved
X similar
X $\geq$ 50% conserved