```
logo
                                        MRKVLYALMGFLLAFSALKADDFLEEANETAPANLNHPMQDLNAIQGSFFDKNRSKMSNTLNIDYFQGQTYKIRLRYAMATLLFF
NTDB id 96674 NHP RS07120 WP 265341559.1 ..............................................................................  0
NTDB id 1217 CAA10656.1 1440..2420( )    MRKVLYALMGFLLAFSALKADDFLEEANETAPANLNHPMQDLNAIQGSFFDKNRSKMSNTLNIDYFQGQTYKIRLRYAMATLLFF  85
consensus                                ******************************************************************************

logo
                                        SKPISDFVLGDKVGFDAKILESNDRILLIKPLQIGVDSNISVIDSEGKIFSFYVFSTTFTSSKHPNLQVFIEDKNYYSNAFLKPQ
NTDB id 96674 NHP RS07120 WP 265341559.1 ..............................................................................  0
NTDB id 1217 CAA10656.1 1440..2420( )    SKPISDFVLGDKVGFDAKILESNDRILLIKPLQIGVDSNISVIDSEGKIFSFYVFSTTFTSSKHPNLQVFIEDKNYYSNAFLKPQ  170
consensus                                ******************************************************************************

logo
                                                                                  MMLYVKSQMRRGYRVLKSSRRKWYCLWLCSVKSKLSLMPLEIF
                                        NKENVLENALENTPTNNKPLKEKKEETKEKEEETITIGDNTNALKIDIKDIQKGYKALGGKQRAWFCLGTCKKAFKAQIKPKDIF
NTDB id 96674 NHP RS07120 WP 265341559.1 ........................................MLLVDKSQMRRGYRVLGGKRRAWFCLWLCKVAFKAQIKPLDIF  43
NTDB id 1217 CAA10656.1 1440..2420( )    NKENVLENALENTPTNNKPLKEKKEETKEKEEETITIGDNTNAMKIVKKDIQKGYKALKSSQRKWYCLGICSKKSKLSLMPKEIF  255
consensus                                ****************************************** * * !  * *!!* !    ! !*!! *!    !  * ! *!!

   <0
                                        NDKQFTYFKFDSRRSLVKFPVLYKVVDGYDNPYNTRIVGDYLIAEDYSTKWTLRLGKVYLCYRKVSKTP
logo                                                KQLAGSKFPVAYKVVDGYDNPVNTRIVGDYIIAEDVSTKWTLRLGKDYLCIRFVKKGKDE
NTDB id 96674 NHP RS07120 WP 265341559.1 NDKHFTYFKFDSQRSGVKFPVAYKVVDGYDNPINTRIVGDYLIAEDIAPKWTLREGKVHACVRKVSKTP...  112
NTDB id 1217 CAA10656.1 1440..2420( )    NDKQFTYFKFDKRLALSKFPVIYKVVDGYDNPVNTRIVGDYIIAEDVSTKWTLRLGKDYLCIRFVKKGKDE*  326
consensus                                !!!*!!!!!!!      !!!! !!!!!!!!!!*!!!!!!!!*!!!!* *!!!!! !! * !*! ! ! ***
```

X non conserved

X similar

X $\geq$ 50% conserved