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logo

NTDB id 46809 HPSA RS00215 WP 001213934.1  ...MRGFLLAFLLVFSALKADDFLEEFNEKASTNLNHPMQDLNAIQGSFFNKNRSTMSNTLNIDYFQGQTYKIRLRYAMATLLFF   82
NTDB id 1217 CAA10656.1 1440..2420( )      MRKVLYALMGFLLAFSALKADDFLEEANETAPANLNHPMQDLNAIQGSFFDKNRSKMSNTLNIDYFQGQTYKIRLRYAMATLLFF   85
consensus                                  ****    !**!!! !!!!!!!!!!!! !! !* !!!!!!!!!!!!!!!!! !!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 46809 HPSA RS00215 WP 001213934.1  SKPISDFVLGDKVGFDAKILESNDRILLIKPLQIGVDSNISVIDSEGKIFSFYVFSTTFTSSKHPNLQVFIEDKNYYSNAFMKPK   167
NTDB id 1217 CAA10656.1 1440..2420( )      SKPISDFVLGDKVGFDAKILESNDRILLIKPLQIGVDSNISVIDSEGKIFSFYVFSTTFTSSKHPNLQVFIEDKNYYSNAFLKPQ   170
consensus                                  !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!

logo

NTDB id 46809 HPSA RS00215 WP 001213934.1  KENTAENVTENTLEN...ANKPLKETKAAEETKEKEEEEVITIGDNTNAMKIVKKDIQRNYKALKSSQRKWYCLWLCSKKSKLSL   249
NTDB id 1217 CAA10656.1 1440..2420( )      NKEN...VLENALENTPTNNKPLKEK...KEETKEKEEETITIGDNTNAMKIVKKDIQKGYKALKSSQRKWYCLGICSKKSKLSL   249
consensus                                      ***! !! !!!*** !!!!!! *** !     !!! !!!!!!!!!!!!!!!!!!* !!!!!!!!!!!!!! *!!!!!!!!!

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logo

NTDB id 46809 HPSA RS00215 WP 001213934.1  MPKEIFNDKQFTYFKFDKRLALSKFPVIYKVVDGYDNPVNTRIVGDYIIAEDVSPKWTLRLGKDYLCIRLLTKGRDE.   326
NTDB id 1217 CAA10656.1 1440..2420( )      MPKEIFNDKQFTYFKFDKRLALSKFPVIYKVVDGYDNPVNTRIVGDYIIAEDVSTKWTLRLGKDYLCIRFVKKGKDE*   326
consensus                                  !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
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X non conserved

X similar

X $\geq$ 50% conserved