```
logo
NTDB id 34628 SSU RS07770 WP 012027645.1   .MAKKILIAGKERNLSHFVSMELQKKDYLVDYASTGKEAMSLAHETDFDLILMSFQLSDMSSKELATELLAIKPATVMIVVVEPT   84
NTDB id 471 HSISS4 RS01430 WP 002883757.1  .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQEKDTYIMMMTARDS   84
NTDB id 606 V4T04 RS01910 WP 003130756.1   MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKEKDTPIIMMTARDS   85
consensus                                   **!*!!!***!*!!**!!!*!!****! ** ***!*****!* **!*!!!!****!******!****!   *!** *********

logo
NTDB id 34628 SSU RS07770 WP 012027645.1   EVSQYGEEVLSYAVSYVVKPFVISDLVEQISAIFRGRDFIDNNCKQVHMHAAYRDLKVDFQNRTVTRGDELINLTRREYDLLATL   169
NTDB id 471 HSISS4 RS01430 WP 002883757.1  IM.DIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAA.KNAPAKASTYRDLKLDVQNRTVVRGDEAIPLTKREFDLLNTL   167
NTDB id 606 V4T04 RS01910 WP 003130756.1   TM.DRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHA.V.ERAENTSFRDLVIDKTNRTVHRGKKVIDLTRREYDLLLTL   167
consensus                                   * * ***** *!**!**!!!*!**!*****! !!* *   *     *  ***!!!**! *!!!! !!***! !!*!!*!!! !!

logo
NTDB id 34628 SSU RS07770 WP 012027645.1   MNS.PEPVSREQLLERVWKYEAASETNVVDVYIRYLRGKLDLPHQDSYIKTVRGVGYAMRD..   229
NTDB id 471 HSISS4 RS01430 WP 002883757.1  LSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKIDVPGKESYIQTVRGMGYVIREK.   229
NTDB id 606 V4T04 RS01910 WP 003130756.1   MQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKIDVEGQDSYIQTVRGLGYVMRERK   230
consensus                                  **** ****!! !* *!!*!***!!!!!!!!!!!!!*!*!*****!!!*!!!!*!!**!**
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X non conserved

X similar

X $\geq$ 50% conserved