```
logo

NTDB id 1152281 OC617 RS01265 WP 000520444.1  MGKSLVTGIDIGHHSIKAAVLKPMGDTYALVGYEELLVTADIFTDNHTLDYQKIVKKLKELKKGLPLFSHKVAIAIPDSA   80
NTDB id 1171 A1552VC RS12125 WP 000520444.1   MGKSLVTGIDIGHHSIKAAVLKPMGDTYALVGYEELLVTADIFTDNHTLDYQKIVKKLKELKKGLPLFSHKVAIAIPDSA   80
NTDB id 1404 DSB67 RS14000 WP 010643494.1     MDKLLVTGIDIGHNSLKAVVLKPNGNSYALLGYKEIILKEGIVAENNTINHQEIVKTLKEMKKELPFRARKVAISVPDNA   80
consensus                                     !*!*!!!!!!!!!!*!*!!*!!!!*!**!!!*!!*!******!***!*!***!*!!!*!!!*!!*!!****!!!!**!!*!

logo

NTDB id 1152281 OC617 RS01265 WP 000520444.1  VISKVLQIDSDLEQRELEFAVYQAFSHQSPFPVEELSLDFVKVTEKSLARSSTTTFQVYATKKDVVDSRLHAVKKAGFEP  160
NTDB id 1171 A1552VC RS12125 WP 000520444.1   VISKVLQIDSDLEQRELEFAVYQAFSHQSPFPVEELSLDFVKVTEKSLARSSTTTFQVYATKKDVVDSRLHAVKKAGFEP  160
NTDB id 1404 DSB67 RS14000 WP 010643494.1     VISKKLQIEQNLEESEKEFAVVQAFSHQSPFPVEELSLDFIKVDTDEQMR.GNDSYQVFATRKDVVETRVEALQKSGLKP  159
consensus                                     !!!!*!!!***!!**!*!!!!*!!!!!!!!!!!!!!!!!!!!*!!******!******!!*!!*!!!!**!**!**!*!**!

logo

VLMDVQVHSLLHLWQLASRAYRR.PDWMLVDIGYTQSSLCLDFPEKMPFYKDVPLGTRQLESEPSAVNSLNHPLLH...D  236
VLMDVQVHSLLHLWQLASRAYRR.PDWMLVDIGYTQSSLCLDFPEKMPFYKDVPLGTRQLESEPSAVNSLNHPLLH...D  236
VLVDVHSQSLGHIWKLVAKRFPEKNKYCLLDIRSLNSSFTMFTEQGELFHKEFPCGSRTTGSLF.....QQDPLVDDAQV  234
consensus                                     !!*!!***!!*!*!*!******* ****!*!!****!!**********!*!**!*!*!***!**********!!**   *

logo

PTQRFIQELVDKIARQIQLFTSVHGTQSLGGLWLSGGGATLSGLEDALYQRLSLPCEVLNPFSLFKNNVAKRKRPLVDGQ  316
PTQRFIQELVDKIARQIQLFTSVHGTQSLGGLWLSGGGATLSGLEDALYQRLSLPCEVLNPFSLFKNNVAKRKRPLVDGQ  316
ATEQFNRQIVERVKRQMQLYTSINGSQDIKGVWLSGEGAATPMLAEELSSQLALECELLNPLGLFEMKVSKRKRRAADWQ  314
consensus                                     *!**!****!****!!*!!*!!**!*!***!*!!!!*!!****!***!***!*!*!!*!!!**!!***!*!!!!***!*!

logo

NTDB id 1152281 OC617 RS01265 WP 000520444.1  RFSTAAGLALRGLAWLESEHVA..   338
NTDB id 1171 A1552VC RS12125 WP 000520444.1   RFSTAAGLALRGLAWLESEHVA..   338
NTDB id 1404 DSB67 RS14000 WP 010643494.1     HFTAAAGLAVRGIQWLGGDNAVSH   338
consensus                                     *!**!!!!!*!!**!!******
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X non conserved

X similar

X ≥ 50% conserved