logo

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NTDB id 37899 MSA RS02165 WP 000912307.1   MLKIENVTGGYVNIPVLKNISFEVNDGELVGLIGLNGAGKSTTINEIIGILRPYQGDITIDGISLEADQELYRKKIGFIPETPSL   85
NTDB id 481 STER RS07730 WP 002951673.1    MLKLEKVTGGYANIPVLKDVTFEVADGELVGLIGLNGAGKSTTINEIIGLLTPYGGQIAIDGLTIQQDPASYRQKIGYIPETPSL   85
NTDB id 473 HSISS4 RS07770 WP 021143710.1  MLKLEKVTGGYANIPVLKDVTFEVADGELVGLIGLNGAGKSTTINEIIGLLTPYGGQIAIDGLTIQQDPASYRQKIGYIPETPSL   85
consensus                                  !!!*!*!!!!!*!!!!!!***!!!*!!!!!!!!!!!!!!!!!!!!!!!!*!*!!*!*!*!!*****!***!!*!!!*!!!!!!!
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logo

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NTDB id 37899 MSA RS02165 WP 000912307.1   YEELTLREHLETVAMAYDIATDEVMARAQKLLEMFRLTDKLDWFPMHFSKGMKQKVMIICAFVVSPSLFIVDEPFLGLDPLAISD   170
NTDB id 481 STER RS07730 WP 002951673.1    YEELTLREHLETVLMAYGLDVTEGMARADKYLKLFRLDEKLDWFPTQFSKGMKQKVMIICAFIVNPSLFIVDEPFLGLDPLAISD   170
NTDB id 473 HSISS4 RS07770 WP 021143710.1  YEELTLREHLETVLMAYGLDVTEGMVRADKYLKLFRLDEKLDWFPTQFSKGMKQKVMIICAFIVNPSLFIVDEPFLGLDPLAISD   170
consensus                                  !!!!!!!!!!!!!!*!!!*****!*!*!!*!*!**!!!**!!!!!!**!!!!!!!!!!!!!!!!!*!*!!!!!!!!!!!!!!!!!!!
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logo

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NTDB id 37899 MSA RS02165 WP 000912307.1   LINLLAEEKAKGKSILMSTHVLDSAEKMCDRFVILHKGEIRAVGTLEELRAIFGDSNANLNDIYIALTKEV..   241
NTDB id 481 STER RS07730 WP 002951673.1    LIELLAEEKANGKSILMSTHVLDSAEKMCDRFVILHHGQILAQGTIDELRQTFGDSSASLNDIYMQLTKGELS   243
NTDB id 473 HSISS4 RS07770 WP 021143710.1  LIELLAEEKAKGKAILMSTHVLDSAEKMCDRFVILHHGQVLAQGTLEELRQTFGDDSASLNDIYMQLTKGELS   243
consensus                                  !!*!!!!!!!*!!*!!!!!!!!!!!!!!!!!!!!!!!!*!***!*!!**!!!**!!!**!*!!!!!**!!!****
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X non conserved

X similar

X ≥ 50% conserved