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logo

NTDB id 26038 SPT RS07505 WP 001839487.1  MPTTRNNDMMVYCSFCGKSQEEVQKIIAGNNAFICNECVELAQEIIREELVEEVLADLSEVPKPIELLHILNHYVIGQDRAKRAL   85
NTDB id 379 SMU RS04375 WP 002262816.1    MAGNRTNDVTVHCSFCGKNQDEVKKIIAGNGVFICNECVELSQEIIREELAEEVLADLSEVPKPKELLAILDSYVIGQDRAKRAL   85
consensus                                 !*  ! !!* !*!!!!!! !*!! !!!!!!  !!!!!!!!! !!!!!!!! !!!!!!!!!!!! !!!*!! *!!!!!!!!!!!!

logo

NTDB id 26038 SPT RS07505 WP 001839487.1  AVAVYNHYKRINFHDTREESEDVDLQKSNILMIGPTGSGKTFLAQTLAKSLNVPFAIADATALTEAGYVGEDVENILLKLLQAAD   170
NTDB id 379 SMU RS04375 WP 002262816.1    AVAVYNHYKRISFTESQ.DDQDVDLQKSNILMIGPTGSGKTFLAQTLAKSLNVPFAIADATALTEAGYVGEDVENILLKLIQAAD   169
consensus                                 !!!!!!!!!!! !*** **  !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!

logo

NTDB id 26038 SPT RS07505 WP 001839487.1  FNIERAERGIIYVDEIDKIAKKSENVSITRDVSGEGVQQALLKIIEGTVASVPPQGGRKHPQQEMIQVDTKNILFIVGGAFDGIE   255
NTDB id 379 SMU RS04375 WP 002262816.1    YNVERAERGIIYVDEIDKIAKKGENVSITRDVSGEGVQQALLKIIEGTVASVPPQGGRKHPQQEMIQIDTKNILFIVGGAFDGIE   254
consensus                                 *!*!!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 26038 SPT RS07505 WP 001839487.1  EIVKQRLGEKVIGFGQNNKAIDENSSYMQEIIAEDIQKFGIIPELIGRLPVFAALEQLTVDDLVRILKEPRNALVKQYQTLLSYD   340
NTDB id 379 SMU RS04375 WP 002262816.1    DIVKQRLGEKIIGFGQNNKKIDDQSSYMQEIISEDIQKFGLIPEFIGRLPVLAALEQLTVDDLVKILTEPKNALVKQYQTLLSYD   339
consensus                                 *!!!!!!!!!*!!!!!!!! !!**!!!!!!!! !!!!!!!*!!! !!!!!! !!!!!!!!!!!!*!! !!*!!!!!!!!!!!!!!!

logo

NTDB id 26038 SPT RS07505 WP 001839487.1  DVELEFDDEALQEIANKAIERKTGARGLRSIIEETMLDVMFEVPSQENVKLVRITKEAVDGTDKPILETA.   410
NTDB id 379 SMU RS04375 WP 002262816.1    GVELEFDQEALQAIAQKAIERKTGARGLRSIIEETMLDLMFEIPSQEDVTCVRITKKAVEGTDKPILETAS   410
consensus                                  !!!!!! !!!! !!*!!!!!!!!!!!!!!!!!!!!!!!!*!!!*!!!! ! *!!!!! !!*!!!!!!!!!!*
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X non conserved

X similar

X $\geq$ 50% conserved