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logo

NTDB id 478 HSISS4 RS06985 WP 021143811.1          MTENKNVILSARDIVVEFDVRDRVLTAIRGVSLDLVEGEVLALVGESGSGKSVLTKTFTGMLEENGRVASGSIDY   75
NTDB id 327 STU RS16115 WP 011226304.1             MTENKNVILSARDIVVEFDVRDRVLTAIRGVSLDLVEGEVLALVGESGSGKSVLTKTFTGMLEENGRVASGSIDY   75
NTDB id 295 STER RS06915 WP 011226304.1            MTENKNVILSARDIVVEFDVRDRVLTAIRGVSLDLVEGEVLALVGESGSGKSVLTKTFTGMLEENGRVASGSIDY   75
NTDB id 1111771 HMPREF9425 RS08155 WP 037621603.1 ..MMKETILSVKNLHVNFHTYAGEVKAIRDVNFDLKKGETLAIVGESGSGKSVTTRTLMGLSDKNAKV.TGDITF   72
NTDB id 361 SMU RS01310 WP 002262737.1             ..MSKEKILQVNNLHVNFHTYAGEVKAIRDVSFYLEKGETLAIVGESGSGKSVTTRTLMGLSAKNAEI.FGDIEF   72
consensus                                          ****!**!******!*!********!!!*!***!**!!*!!*!!!!!!!!!!*!*!**!****!*****!*!**

logo

NTDB id 478 HSISS4 RS06985 WP 021143811.1          RGQDLTKLKSHQDWAHIRGAKIATIFQDPMTSLDPIKTIGSQIVEVIVKHQGKSAKEAKKMAIDYMDKVGIPDAE  150
NTDB id 327 STU RS16115 WP 011226304.1             RGKDLTKFKSHQDWAAIRGAKIATIFQDPMTSLNPIKTIGSQIIEVIVKHQGKTAKEAKKMAIDYMDKVGIPDAE  150
NTDB id 295 STER RS06915 WP 011226304.1            RGKDLTKFKSHQDWAAIRGAKIATIFQDPMTSLNPIKTIGSQIIEVIVKHQGKTAKEAKKMAIDYMDKVGIPDAE  150
NTDB id 1111771 HMPREF9425 RS08155 WP 037621603.1 KGHDMQALK.EEDWVKVRGNDIAMIFQDPMTSLDPTMKIGRQIAEPIMIHTKVSQKEALDMALQLMKDVGIPNAE  146
NTDB id 361 SMU RS01310 WP 002262737.1             KGHNLNDLK.EEDWVHIRGNDISMIFQDPMTSLDPTMRIGLQIAEPIIKHEKVTKKEALKRALDMMEKVGIPNAQ  146
consensus                                          *! *****!***!!* *!!**!**!!!!!!!!!*!***!!*!!*!*!**!*****!!!***!***!**!!!!*!*

logo

NTDB id 478 HSISS4 RS06985 WP 021143811.1          KRFNEYPFQYSGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVAS  225
NTDB id 327 STU RS16115 WP 011226304.1             KRFNEYPFQYSGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVAS  225
NTDB id 295 STER RS06915 WP 011226304.1            KRFNEYPFQYSGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVAS  225
NTDB id 1111771 HMPREF9425 RS08155 WP 037621603.1 EHINDYPHQWSGGMRQRAVIAIALAADPEILIADEPTTALDVTIQAQILHLMKKIQEERDSSIIFITHDLGVVAG  221
NTDB id 361 SMU RS01310 WP 002262737.1             EHINDYPHQWSGGMRQRAVIAIALATNPEILVADEPTTALDVTIQAQILHLMKEIQKNTDSSIIFITHDLGVVAG  221
consensus                                          ***!*!!*!*!!!!!!!*!!!!!!!**!**!**!!!!!!!!!!!!!!!!**!*!********!*!!!!!!!!!!!*

logo

NTDB id 478 HSISS4 RS06985 WP 021143811.1          IADKVAVMYAGEIIEYATVEEIFYEPCHPYTWSLLSSLPQLADDKGELFSIPGTPPSLYTPVVGDAFALRSDYAM  300
NTDB id 327 STU RS16115 WP 011226304.1             IADKVAVMYAGEIIEYATVEEIFYEPCHPYTWSLLSSLPQLADDNGKLFSIPGTPPSLYTPVVGDAFALRSDYAL  300
NTDB id 295 STER RS06915 WP 011226304.1            IADKVAVMYAGEIIEYATVEEIFYEPCHPYTWSLLSSLPQLADDNGKLFSIPGTPPSLYTPVVGDAFALRSDYAL  300
NTDB id 1111771 HMPREF9425 RS08155 WP 037621603.1 MADRVAVMYAGKIVEYGTVDEVFYNPQHPYTWGLLNSMPTTETESGSLEAIPGTPPDLLYPPKGDAFATRNVFAL  296
NTDB id 361 SMU RS01310 WP 002262737.1             MADRVAVMYAGKIVEYGTVDEVFYNPQHPYTWGLLNSMPTTNTASGSLHSIPGTPPDLLQPPQGDAFAPRNEFAL  296
consensus                                          *!!*!!!!!!!*!*!!*!!*!*!!*!*!!!!!*!!*!*!***** ! !**!!!!!!*!**!**!!!!!*!***!*

logo

NTDB id 478 HSISS4 RS06985 WP 021143811.1          QIDFEEKAPQFQVSDTHWAKTWLLHEDAPKVEKPAVIQNLHEKIRANMGFAHLGDEEEGNA  361
NTDB id 327 STU RS16115 WP 011226304.1             QIDFEEKAPQFQVSDTHWAKTWLLHEDAPKVDKPAVIQNLHEKILANMGFAHLGDEEEGNA  361
NTDB id 295 STER RS06915 WP 011226304.1            QIDFEEKAPQFQVSDTHWAKTWLLHEDAPKVDKPAVIQNLHEKILANMGFAHLGDEEEGNA  361
NTDB id 1111771 HMPREF9425 RS08155 WP 037621603.1 DIDYQEEPPMFKVSDTHFAATWLLDERAPKVTPPSPILKRWEKWSKMKEK..........  346
NTDB id 361 SMU RS01310 WP 002262737.1             DIDLKEEPPFFKVSDSHYAATWLLDDRAPKITPPERILQRWEKWKSLQGEKHND.......  350
consensus                                          *!!**!**!*!*!!!!*!*!*!!!!***!!!***!**!****!!* ****************
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X non conserved
X similar
X $\geq$ 50% conserved