logo

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NTDB id 361 SMU RS01310 WP 002262737.1          ..MSKEKILQVNNLHVNFHTYAGEVKAIRDVSFYLEKGETLAIVGESGSGKSVTTRTLMGLSAKNAE.IFGDIEF   72
NTDB id 327 STU RS16115 WP 011226304.1          MTENKNVILSARDIVVEFDVRDRVLTAIRGVSLDLVEGEVLALVGESGSGKSVLTKTFTGMLEENGRVASGSIDY   75
NTDB id 295 STER RS06915 WP 011226304.1         MTENKNVILSARDIVVEFDVRDRVLTAIRGVSLDLVEGEVLALVGESGSGKSVLTKTFTGMLEENGRVASGSIDY   75
NTDB id 1111738 HMPREF9425 RS02790 WP 003096593.1 MTENKNVILSARDIVVEFDVRDRVLTAIRGVSLDLVEGEVLALVGESGSGKSVLTKTFTGMLEENGRVASGSIDY   75
NTDB id 478 HSISS4 RS06985 WP 021143811.1       MTENKNVILSARDIVVEFDVRDRVLTAIRGVSLDLVEGEVLALVGESGSGKSVLTKTFTGMLEENGRVASGSIDY   75
consensus                                       ****!**!!******!*!********!!!*!!**!**!!*!!*!!!!!!!!!!*!*!**!****!*****!*!**
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NTDB id 361 SMU RS01310 WP 002262737.1          KGHNLNDLK.EEDWVHIRGNDISMIFQDPMTSLDPTMRIGLQIAEPIIKHEKVTKKEALKRALDMMEKVGIPNAQ  146
NTDB id 327 STU RS16115 WP 011226304.1          RGKDLTKFKSHQDWAAIRGAKIATIFQDPMTSLNPIKTIGSQIIEVIVKHQGKTAKEAKKMAIDYMDKVGIPDAE  150
NTDB id 295 STER RS06915 WP 011226304.1         RGKDLTKFKSHQDWAAIRGAKIATIFQDPMTSLNPIKTIGSQIIEVIVKHQGKTAKEAKKMAIDYMDKVGIPDAE  150
NTDB id 1111738 HMPREF9425 RS02790 WP 003096593.1 RGQDLTKLKSHQDWAPIRGAKIATIFQDPMTSLDPIKTIGSQIVEVIVKHQGKSVKEAKKMAIDYMDKVGIPDAE  150
NTDB id 478 HSISS4 RS06985 WP 021143811.1       RGQDLTKLKSHQDWAHIRGAKIATIFQDPMTSLDPIKTIGSQIVEVIVKHQGKSAKEAKKMAIDYMDKVGIPDAE  150
consensus                                       *! *!***!***!!* !!!**!**!!!!!!!!!*!***!!*!!*!*!*!!*****!!!*!*!*!*!*!!!!!*!*
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NTDB id 361 SMU RS01310 WP 002262737.1          EHINDYPHQWSGGMRQRAVIAIALATNPEILVADEPTTALDVTIQAQILHLMKEIQKNTDSSIIFITHDLGVVAG  221
NTDB id 327 STU RS16115 WP 011226304.1          KRFNEYPFQYSGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVAS  225
NTDB id 295 STER RS06915 WP 011226304.1         KRFNEYPFQYSGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVAS  225
NTDB id 1111738 HMPREF9425 RS02790 WP 003096593.1 KRFNEYPFQYSGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVAS  225
NTDB id 478 HSISS4 RS06985 WP 021143811.1       KRFNEYPFQYSGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVAS  225
consensus                                       ***!*!!*!*!!!!!!!*!!!!!!!**!**!**!!!!!!!!!!!!!!!!!**!*!********!*!!!!!!!!!!*
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NTDB id 361 SMU RS01310 WP 002262737.1          MADRVAVMYACKIVEYGTVDEVFYNPQHPYTWGLLNSMPTTNTASGSLHSIPGTPPDLLQPPQGDAFAPRNEFAL  296
NTDB id 327 STU RS16115 WP 011226304.1          IADKVAVMYAGEIIEYATVEEIFYEPCHPYTWSLLSSLPQLADDNGKLFSIPGTPPSLYTPVVGDAFALRSDYAL  300
NTDB id 295 STER RS06915 WP 011226304.1         IADKVAVMYAGEIIEYATVEEIFYEPCHPYTWSLLSSLPQLADDNGKLFSIPGTPPSLYTPVVGDAFALRSDYAL  300
NTDB id 1111738 HMPREF9425 RS02790 WP 003096593.1 IADKVAVMYAGEIIEYATVEEIFYEPCHPYTWSLLSSLPQLADDKGELFSIPGTPPSLYTPVVGDAFALRSDYAM  300
NTDB id 478 HSISS4 RS06985 WP 021143811.1       IADKVAVMYAGEIIEYATVEEIFYEPCHPYTWSLLSSLPQLADDKGELFSIPGTPPSLYTPVVGDAFALRSDYAM  300
consensus                                       *!!*!!!!!!!*!*!!*!!*!*!!*!*!!!!!*!!*!*!*****  !  !*!!!!!!!*!**!**!!!!!*!***!*
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NTDB id 361 SMU RS01310 WP 002262737.1          DIDLKEEPPFFKVSDSHYAATWLLDDRAPKITPPERILQRWEKWKSLQGEKHND.......                 350
NTDB id 327 STU RS16115 WP 011226304.1          QIDFEEKAPQFQVSDTHWAKTWLLHEDAPKVDKPAVIQNLHEKILANMGFAHLGDEEEGNA                 361
NTDB id 295 STER RS06915 WP 011226304.1         QIDFEEKAPQFQVSDTHWAKTWLLHEDAPKVDKPAVIQNLHEKILANMGFAHLGDEEEGNA                 361
NTDB id 1111738 HMPREF9425 RS02790 WP 003096593.1 QIDFEEKAPQFQVSDTHWAKTWLLHEDAPKVEKPAVIQNLHEKIRANMGFAHLGDEEEGDA                 361
NTDB id 478 HSISS4 RS06985 WP 021143811.1       QIDFEEKAPQFQVSDTHWAKTWLLHEDAPKVEKPAVIQNLHEKIRANMGFAHLGDEEEGNA                 361
consensus                                       *!!**!**!*!*!!!*!*!*!!!!***!!!**!**!****!!*****!**!*********
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X non conserved
X similar
X ≥ 50% conserved