logo

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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 1111670 HMPREF9319 RS01305 WP 003063311.1  ..MTEETILQVKNLRVDFHTYAGEIKAIRDVSFDLKEGETLAIVGESGSGKSVTTKTLMGLSASNAE.VTGDIDF  72
NTDB id 361 SMU RS01310 WP 002262737.1         ..MSKEKILQVNNLHVNFHTYAGEVKAIRDVSFYLEKGETLAIVGESGSGKSVTTRTLMGLSAKNAE.IFGDIEF  72
consensus                                      *******!!*******!*!********!!!*!!**!**!!*!!*!!!!!!!!!!*!*!**!****!*****!*!**
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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 1111670 HMPREF9319 RS01305 WP 003063311.1  KGKRLIELK.EDEWIKVRGNEIAMIFQDPMTSLDPTMKIGQQIAEPIMIHEKVSKEEALKRALELMKNVGIPNAE  146
NTDB id 361 SMU RS01310 WP 002262737.1         KGHNLNDLK.EEDWVHIRGNDISMIFQDPMTSLDPTMRIGLQIAEPIIKHEKVTKKEALKRALDMMEKVGIPNAQ  146
consensus                                      *!**!***!****!* *!!**!**!!!!!!!!!*!***!!*!!*!*!**!*******!!*!*!***!**!!!!*!*
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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 1111670 HMPREF9319 RS01305 WP 003063311.1  EHINDYPHQWSGGMRQRAVIAIALAANPDILIADEPTTALDVTIQAQILNLMKQIQKERGSSIIFITHDLGVVAG  221
NTDB id 361 SMU RS01310 WP 002262737.1         EHINDYPHQWSGGMRQRAVIAIALATNPEILVADEPTTALDVTIQAQILHLMKEIQKNTDSSIIFITHDLGVVAG  221
consensus                                      ***!*!!*!*!!!!!!!*!!!!!!!**!**!**!!!!!!!!!!!!!!!!!**!*!********!*!!!!!!!!!!*
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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 1111670 HMPREF9319 RS01305 WP 003063311.1  MADRVAVMYAGKIIEYGTVDEVFYNPQHPYTWGLLNSMPTTDTEAGSLQSIPGTPPDLLNPPKGDAFAPRNEFAL  296
NTDB id 361 SMU RS01310 WP 002262737.1         MADRVAVMYAGKIVEYGTVDEVFYNPQHPYTWGLLNSMPTTNTASGSLHSIPGTPPDLLQPPQGDAFAPRNEFAL  296
consensus                                      *!!*!!!!!!!*!*!!*!!*!*!!*!*!!!!!*!!*!*!*!***** ! !*!!!!!!!*!**!**!!!!!*!***!*
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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 1111670 HMPREF9319 RS01305 WP 003063311.1  DIDYEEEPPMFKVSDTHFAATWLLDERAPKVTPPLPIQKRWAKWKELEGRKA.........  348
NTDB id 361 SMU RS01310 WP 002262737.1         DIDLKEEPPFFKVSDSHYAATWLLDDRAPKITPPERILQRWEKWKSLQGEKHND.......  350
consensus                                      *!!**!**!*!*!!!!*!*!*!!!!***!!!***!**!*****!*****!************
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X non conserved
X similar
X ≥ 50% conserved