logo

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NTDB id 378 SMU RS02690 WP 002263569.1          .....................................MLCQNCKLNEATIHLYAN.............VNGQQKQI.DL   28
NTDB id 85 BSU 00860 NP 387967.1                ..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGIAAKALQALGLGSEKIQKEVESLIGR........   70
NTDB id 610 V4T04 RS10165 WP 012897346.1        MKFENIKYTPTLDRILEKAEEYAHQYQYGTIESAHLLAAMATTSGSIAYSLLAGMNVDSSDLLI........DLEDLSSH   72
NTDB id 290 KZH43 RS10025 WP 001109677.1        .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLEE.....VALELTETDYS   70
NTDB id 289 SPD RS10700 WP 001109677.1          .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLEE.....VALELTETDYS   70
NTDB id 287 SP RS11210 WP 001109712.1           .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLEE.....VALELTETDYS   70
NTDB id 329 STU RS10020 WP 011225298.1          ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLS   76
NTDB id 297 STER RS00545 WP 011680614.1         ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLS   76
NTDB id 233330 CCZ24 RS00685 WP 000020286.1     ....MSHYSIKLQEVFRLAQFQAARYESHYLESWHLLLAMVLVHDSVAGLTFAEYESEVAIEEYEAATILALGRAPKEEI   76
NTDB id 377 SMU RS09275 WP 002262344.1          ....MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSSS   76
consensus                                             **********  ***  ****    ************  * ****  **  **   **   **       *****     * *
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NTDB id 378 SMU RS02690 WP 002263569.1          CQNCYQIMKTDPENGPLNHLSQ.......................Q..............NSSSINPFFFDDFFGDLNNF   70
NTDB id 85 BSU 00860 NP 387967.1                GQEMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNNLGVSLNKARQQVLQLL.........   141
NTDB id 610 V4T04 RS10165 WP 012897346.1        VKVKRSTLRFSPRAEEVMTAASFLAIHNNSEAVGTEHLLYALLQVEDGFGLQLLKL.........QKINIVSLRKELEKR   143
NTDB id 290 KZH43 RS10025 WP 001109677.1        QDETFTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER   150
NTDB id 289 SPD RS10700 WP 001109677.1          QDETFTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER   150
NTDB id 287 SP RS11210 WP 001109712.1           QDETFTELPFSRRLQVLFDEAEYVASVVHAKVLGTEHVLYAILHDSNALATRILERAGFSYEDKKDQVKIAALRRNLEER   150
NTDB id 329 STU RS10020 WP 011225298.1          ESDIIDLRAQSPALEAMLQEAQGIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSDKPRIIDLRRSLERN   156
NTDB id 297 STER RS00545 WP 011680614.1         ESDIIDLRAQSPALEAMLQEAQEIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSDKPRIIDLRRSLERN   156
NTDB id 233330 CCZ24 RS00685 WP 000020286.1     ..TNYQFLEQSPALKKILKLAENISIVVGAEDVGTEHVLLAMLVNKDLLATRILELVGFRGQDDGESVRMVDLRKALERH   154
NTDB id 377 SMU RS09275 WP 002262344.1          ..NDIMLLEQSHALKRTLAEAAAISQVTHAKEVGTEHVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVIERY   154
consensus                                         * *  * *****  ** **  ***** *  ************  ************** * *  ********** ***
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NTDB id 378 SMU RS02690 WP 002263569.1          RAFNNQDLPN.....TPPTQAGGGNGNGGNNRRPGGPQQQASQKPNGLLEEFGINLTDIARKGEIDPVIGRDEEITRVIE   145
NTDB id 85 BSU 00860 NP 387967.1                LGSNETG.....................................SSAAGTNSNANTPTLDSLARDLTAIAKEDSLDPVIGRSKEIQRVIE   194
NTDB id 610 V4T04 RS10165 WP 012897346.1        TGLKVPESKKAVTPMSKRKMAKGV.....................AENSTTPTLDSVSSDLTEEARLGKLDPMIGREAEIDRLIH   207
NTDB id 290 KZH43 RS10025 WP 001109677.1        AGWTREDLKA.LRQRHRT.VADKQN.........SMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQ   220
NTDB id 289 SPD RS10700 WP 001109677.1          AGWTREDLKA.LRQRHRT.VADKQN.........SMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQ   220
NTDB id 287 SP RS11210 WP 001109712.1           AGWTREDLKA.LRQRHRT.VADKQN.........SMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQ   220
NTDB id 329 STU RS10020 WP 011225298.1          AGLSKQDLKA.IHDLRKPKKSKASA.........NFANMMQPPQSSTGELADYTKDLTALAESGNLDPIIGRDEEISRMIQ   227
NTDB id 297 STER RS00545 WP 011680614.1         AGLSKQDLKA.IHDLRKPKKSKASA.........NFANMMQPPQSSTGELADYTKDLTALAESGNLDPVIGRDEEISRMIQ   227
NTDB id 233330 CCZ24 RS00685 WP 000020286.1     AGFTKDDIKA.IYELRNPKKAKSGA.........SFSDMMKPP.STAGDLADFTRDLSQMAVDGEIEPVIGRDKEISRMVQ   224
NTDB id 377 SMU RS09275 WP 002262344.1          AGFSKEDIKA.IFEMRKPKKVKNSS.........SFSDLMKPP.SVTGELADFTRDLTELARQGRLEPVIGREQEISRMVQ   224
consensus                                       ********** *  * *** **           * ****  *** **  !******!***!******!*!!!**!!*!***
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NTDB id 378 SMU RS02690 WP 002263569.1      ILNRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPQKLHGKNVIRLDVVSLVQGTGIRGQFEERMQKLMEEIRQRQDV  225
NTDB id 85 BSU 00860 NP 387967.1            VLSRRTKNNPVLIGEPGVGKTAIAEGLAQQIINNEVPEILRDKRVMTLDMGTVVAGTKYRGEFEDRLKKVMDEIRQAGNI  274
NTDB id 610 V4T04 RS10165 WP 012897346.1    ILSRRTKNNPVLVGEPGVGKSAIIEGLAQRIVNGQVPIGLMNSRIMALNMATVVAGTKFRGEFEDRLTAIVEEVSSDPDV  287
NTDB id 290 KZH43 RS10025 WP 001109677.1    ILSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQV  300
NTDB id 289 SPD RS10700 WP 001109677.1      ILSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQV  300
NTDB id 287 SP RS11210 WP 001109712.1       ILSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQV  300
NTDB id 329 STU RS10020 WP 011225298.1      VLSRKTKNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEADGKI  307
NTDB id 297 STER RS00545 WP 011680614.1     VLSRKTKNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEADGKI  307
NTDB id 233330 CCZ24 RS00685 WP 000020286.1 VLSRKTKNNPVLVGDAGVGKTALAYGLAQRIANGNIPYELRDMRVLELDMMSVVAGTRFRGDFEERMNQIIADIEEDGHI  304
NTDB id 377 SMU RS09275 WP 002262344.1      ILSRKTKNNPVLVGDAGVGKTALAYGLAQRIVDSAVPFELADMKVLELDMMSVVAGTRFRGDFEERMNQIIADIEADGHI  304
consensus                                   *!*!*!!!!!!!*!**!!!!*!***!!!!*!*****! **********!*****!*!!**!!*!!*!********** **  *
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NTDB id 378 SMU RS02690 WP 002263569.1      ILFIDEIHEIVGAGSAGDGNMDAGNILKPALARGELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPSVAETITILKG  304
NTDB id 85 BSU 00860 NP 387967.1            ILFIDELHTLIGAGG.AEGAIDASNILKPSLARGELQCIGATTLDEYRKYIEKDAALERRFQPIQVDQPSVDESIQILQG  353
NTDB id 610 V4T04 RS10165 WP 012897346.1    IIFIDELHTIIGAGGGMDSVNDAANILKPALARGDFQMVGATTYHEYQKYIEKDEALERRLARINVDEPSPDEAIAILQG  367
NTDB id 290 KZH43 RS10025 WP 001109677.1    ILFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQG  380
NTDB id 289 SPD RS10700 WP 001109677.1      ILFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQG  380
NTDB id 287 SP RS11210 WP 001109712.1       ILFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQG  380
NTDB id 329 STU RS10020 WP 011225298.1      ILFIDELHTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAIDILNG  387
NTDB id 297 STER RS00545 WP 011680614.1     ILFIDELHTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAIDILNG  387
NTDB id 233330 CCZ24 RS00685 WP 000020286.1 ILFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTIGATTQEEYQKHIEKDAALSRRFAKVLVEEPNLEDAYEILLG  384
NTDB id 377 SMU RS09275 WP 002262344.1      VLFIDELHTIMGSGSGIDSTLDAANILKPALARGSLRTIGATTQEEYQKHIEKDAALSRRFAKVTIEEPSEEEAYQILLG  384
consensus                                   **!!!!*!***!*!********!!*!!!!!*!!!!*****!!!!**!!***!!!!*!!*!!*********!** ***  !!*!
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NTDB id 378 SMU RS02690 WP 002263569.1      IQPKYEDYHHVKYTDEAIEAAANLSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFV..DPKEIDHRLIEAENLKAQATRD  382
NTDB id 85 BSU 00860 NP 387967.1            LRDRYEAHHRVSITDDAIEAAVKLSDRYISDRFLPDKAIDLIDEAGSKVRLRSFTTPPNLKELEQKLDEVRKEKDAAVQS  433
NTDB id 610 V4T04 RS10165 WP 012897346.1    LREKFEDYHQVKFTDQAIKSAVMLSVRYMTSRKLPDKAIDLLDEAAAAVKISVKNQQTKRLDLEKELAEAQEELSEAVIK  447
NTDB id 290 KZH43 RS10025 WP 001109677.1    LKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL....S....PADKALMD  452
NTDB id 289 SPD RS10700 WP 001109677.1      LKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL....S....PADKALMD  452
NTDB id 287 SP RS11210 WP 001109712.1       LKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL....S....PADKALMD  452
NTDB id 329 STU RS10020 WP 011225298.1      LRSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EAKREI....T....PLDEALIS  457
NTDB id 297 STER RS00545 WP 011680614.1     LRSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EDKREI....T....PLDEALIS  457
NTDB id 233330 CCZ24 RS00685 WP 000020286.1 LKPAYEAFHNVTISDEAVMTAVKVAHRYLTSKNLPDSAIDLLDEASATVQMMIKK..NAPSLL....T....EVDQAILD  454
NTDB id 377 SMU RS09275 WP 002262344.1      LKKSYETYHHVIISDAAVMAAVKGAHRYLSGKNLPDSAIDLLDEASATVQGLVKK..KAPAYL....T....DLDHALIT  454
consensus                                   **  **!  *!*!  **!*!***!**!***!!**** !!!*!!!!*!!!**********     *  **     *    ***  !***
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NTDB id 378 SMU RS02690 WP 002263569.1      EDYEKAAYFRDQIA.......KYKEMQSAKLDKENTPVITEKNIEVIVEQKTNIPVGELKEKEQSQLIHLADDLKTRVIG  455
NTDB id 85 BSU 00860 NP 387967.1            QEFEKAASLRDTEQRLREQVEDTKKSWKEK.QGQENSEVTVDDIAMVVSSWTGVPVSKIAQTETDKLLNMENILHSRVIG  512
NTDB id 610 V4T04 RS10165 WP 012897346.1    LDIKASRTKEKAVEKIADK......IYKFSVKEDKRQEVTDQAVVAVASTLTGVPITQMTKSESDRLINLEKELHKRVVG  521
NTDB id 290 KZH43 RS10025 WP 001109677.1    GKWKQAAQLIAKE..............EEVP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIG  516
NTDB id 289 SPD RS10700 WP 001109677.1      GKWKQAAQLIAKE..............EEVP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIG  516
NTDB id 287 SP RS11210 WP 001109712.1       GKWKQAAQLIAKE..............EEVP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIG  516
NTDB id 329 STU RS10020 WP 011225298.1      GDIGAAVKQYKAN..............QKAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVIG  522
NTDB id 297 STER RS00545 WP 011680614.1     GDIGAAVKQYKAN..............QKAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVIG  522
NTDB id 233330 CCZ24 RS00685 WP 000020286.1 DDMKSASKALKAS..............HKDKKHKPIAVTEDHIMATLSRLSGIPVEKLTQADSKKYLNLEKELHKRVIG  519
NTDB id 377 SMU RS09275 WP 002262344.1      NDYQLAKRLLKKE..............KKPLLKKRAEVKEEDILATLSKLSGIPVKKLTQADSKKYLNLERELHKRVIG  519
consensus                                   ****  **  ***  *              **    **  ********  *********!*  ***************  *!**!!*!
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NTDB id 378 SMU RS02690 WP 002263569.1      QDAAVDKIAKAIRRNRVGLGTPNRPIGSFLFVGPTGVGKTELSKQLAIELFGSEDSMIRFDMSEYMEKHAVAKLVGAPPG  535
NTDB id 85 BSU 00860 NP 387967.1            QDEAVVAVAKAVRRARAGLKDPKRPIGSFIFLGPTGVGKTELARALAESIFGDEESMIRIDMSEYMEKHSTSRLVGSPPG  592
NTDB id 610 V4T04 RS10165 WP 012897346.1    QEEAISAVSRAIRRARSGVADSRRPMGSFMFLGPTGVGKTELAKALADSVFGSEDNMIRVDMSEFMEKHSTSRLIGAPPG  601
NTDB id 290 KZH43 RS10025 WP 001109677.1    QDQAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPG  596
NTDB id 289 SPD RS10700 WP 001109677.1      QDQAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPG  596
NTDB id 287 SP RS11210 WP 001109712.1       QDQAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPG  596
NTDB id 329 STU RS10020 WP 011225298.1      QDEAVSAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGAPPG  602
NTDB id 297 STER RS00545 WP 011680614.1     QDEAVSAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGAPPG  602
NTDB id 233330 CCZ24 RS00685 WP 000020286.1 QDDAVTAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPG  599
NTDB id 377 SMU RS09275 WP 002262344.1      QDDAVSSISRAIRRNQSGIRVGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPG  599
consensus                                   !**!******!*!!***!***  *!!*!!!*!*!!!!!!!!!!!***!!***!**!****!*!!!!*!!!******!*!*!!!
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NTDB id 378 SMU RS02690 WP 002263569.1      YVGYEEAGQLTEKVRRNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGK..SEANVG  613
NTDB id 85 BSU 00860 NP 387967.1            YVGYDEGGQLTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNKYVG  672
NTDB id 610 V4T04 RS10165 WP 012897346.1    YVGYDEGGQLTERVRNKPYSVVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDKTVG  681
NTDB id 290 KZH43 RS10025 WP 001109677.1    YVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVG  676
NTDB id 289 SPD RS10700 WP 001109677.1      YVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVG  676
NTDB id 287 SP RS11210 WP 001109712.1       YVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVG  676
NTDB id 329 STU RS10020 WP 011225298.1      YVGYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVG  682
NTDB id 297 STER RS00545 WP 011680614.1     YVGYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVG  682
NTDB id 233330 CCZ24 RS00685 WP 000020286.1 YVGYDEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVG  679
NTDB id 377 SMU RS09275 WP 002262344.1      YVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVG  679
consensus                                   !!!!*!*!*!!!*!!**!!!**!*!!*!!!!!!*****!!*!*!!**!!**!!*!*!**!!*!!!!!!*!*********!!
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NTDB id 378 SMU RS02690 WP 002263569.1       FGASREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFQALSKDNLLQIVSLMLDDVNQRLAVNAIHLDVTDKVKEKLV   688
NTDB id 85 BSU 00860 NP 387967.1             FNVQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKAKVA   752
NTDB id 610 V4T04 RS10165 WP 012897346.1     FGAKNITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLIKRLAEQDIHVKLTPSAVKLIA   761
NTDB id 290 KZH43 RS10025 WP 001109677.1     FGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLLA   756
NTDB id 289 SPD RS10700 WP 001109677.1       FGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLLA   756
NTDB id 287 SP RS11210 WP 001109712.1        FGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLTEKGIDLKLQASALKLLA   756
NTDB id 329 STU RS10020 WP 011225298.1       FGAQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLA   762
NTDB id 297 STER RS00545 WP 011680614.1      FGAQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLA   762
NTDB id 233330 CCZ24 RS00685 WP 000020286.1  FGAKDISHDYTAMQKRIMEELKKAYRPEFINRIDEKVVFHSLSQDNMREVVKIMVKPLILALKDKGMDLKFQPSALKHLA   759
NTDB id 377 SMU RS09275 WP 002262344.1       FGAKSFSQDYKAMESRILEELKKVYRPEFINRIDEKVVFHNLGQEDIRHIVKIMVAPLIAHLADQGITLKFQPSALKHLA   759
consensus                                    !******* *   **  ****!!*****!!!*!!*!****!**!* * * **!**!*****  !***** *********  **
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NTDB id 378 SMU RS02690 WP 002263569.1       DLGYDPKMGARPLRRTIQEHIEDAITDFYLEHPEQKEL.KAIMTSNGKIVIKASNKVETVTKATSD   753
NTDB id 85 BSU 00860 NP 387967.1             EEGVDLEYGARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN........   810
NTDB id 610 V4T04 RS10165 WP 012897346.1     EVGFDPEYGARPLRKALQKEVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV...........   816
NTDB id 290 KZH43 RS10025 WP 001109677.1     NQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA...........   810
NTDB id 289 SPD RS10700 WP 001109677.1       NQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA...........   810
NTDB id 287 SP RS11210 WP 001109712.1        NQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIGVKAGQLKFDIA...........   810
NTDB id 329 STU RS10020 WP 011225298.1       KDGYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV...........   816
NTDB id 297 STER RS00545 WP 011680614.1      KDGYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV...........   816
NTDB id 233330 CCZ24 RS00685 WP 000020286.1  EDGYDIEMGARPLRRTIQTQVEDHLSELLLANQVKEGQVIKIGVSKGKLKFDIAKS.........   815
NTDB id 377 SMU RS09275 WP 002262344.1       LAGYDAEMGARPLRRTLQTEVEDKLAELILSGKLASGQTLKIGIQKEKLKFDIV...........   813
consensus                                      !*!***!!!!!!***!***!!******! * ** ** ****** *******
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X non conserved

X similar

X ≥ 50% conserved