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logo
NTDB id 378 SMU RS02690 WP 002263569.1        ..................................................................................  0
NTDB id 85 BSU 00860 NP 387967.1              ..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGIAAKALQALGLGSEKIQKEVESLI........GR  70
NTDB id 399183 GIG89 RS02000 WP 029343521.1   MKFNEKDFTPQVVKVLEKSVDYAHKFNYAWVESSHLLAALAEVPASLAFTLLNSEKIDLEEMLIDI........EDFSSQ  72
NTDB id 610 V4T04 RS10165 WP 012897346.1      MKFENIKYTPTLDRILEKAEEYAHQYQYGTIESAHLLAAMATTSGSIAYSLLAGMNVDSSDLLIDL........EDLSSH  72
NTDB id 287 SP RS11210 WP 001109712.1         .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS  70
NTDB id 290 KZH43 RS10025 WP 001109677.1      .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS  70
NTDB id 289 SPD RS10700 WP 001109677.1        .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS  70
NTDB id 377 SMU RS09275 WP 002262344.1        ....MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSSS  76
NTDB id 329 STU RS10020 WP 011225298.1        ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLS  76
NTDB id 297 STER RS00545 WP 011680614.1       ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLS  76
consensus                                            *** ** *** * * * **   ***********   * **** *****  *** ** *    ****  * * *

logo
NTDB id 378 SMU RS02690 WP 002263569.1        ......MLCQNCKLNEATIHL...YANVNGQQKQIDLCQNCYQIMKTDPENGPLNHLSQQ.....NSSSINPFFDDFFGD  66
NTDB id 85 BSU 00860 NP 387967.1              GQEMSQTIHYTPRA.KKVIELSMDEARKLG.HSYVGTEHILLGLIRE..GEGVAARVLNNLGVSLNKARQQVLQL.....  141
NTDB id 399183 GIG89 RS02000 WP 029343521.1   VKTKKSEIKLSPRV.ETIIEQARALAQNND.KNRIGTEHLLYMLLAN..EASFAGQLLRE.........QDINIVNLRKK  139
NTDB id 610 V4T04 RS10165 WP 012897346.1      VKVKRSTLRFSPRA.EEVMTAASFLAIHNN.SEAVGTEHLLYALLQV..EDGFGLQLLKL.........QKINIVSLRKE  139
NTDB id 287 SP RS11210 WP 001109712.1         QDETFTELPFSRRL.QVLFDEAEYVASVVH.AKVLGTEHVLYAILHD..SNALATRILERAGFSYEDKKDQVKIAALRRN  146
NTDB id 290 KZH43 RS10025 WP 001109677.1      QDETFTELPFSRRL.QILFDEAEYVASVVH.AKVLGTEHVLYAILHD..GNALATRILERAGFSYEDKKDQVKIAALRRN  146
NTDB id 289 SPD RS10700 WP 001109677.1        QDETFTELPFSRRL.QILFDEAEYVASVVH.AKVLGTEHVLYAILHD..GNALATRILERAGFSYEDKKDQVKIAALRRN  146
NTDB id 377 SMU RS09275 WP 002262344.1        N..DIMLLEQSHAL.KRTLAEAAAISQVTH.AKEVGTEHVLFAMLLN..PNLLATRILELVGFHAKDDGESIRLLDLRKV  150
NTDB id 329 STU RS10020 WP 011225298.1        ESDIIDLRAQSPAL.EAMLQEAQGIASVTG.AVEVGSEHVLMAFLLH..KDLMVCRLLEVAGFQYKDDSDKPRIIDLRRS  152
NTDB id 297 STER RS00545 WP 011680614.1       ESDIIDLRAQSPAL.EAMLQEAQEIASVTG.AVEVGSEHVLMAFLLH..KDLMVCRLLEVAGFQYKDDSDKPRIIDLRRS  152
consensus                                       *  * * ***** * *****  ****   ** ***********    **** **** *** * *  ****** ***

logo
NTDB id 378 SMU RS02690 WP 002263569.1        LNNFRAFNNQDLPNTPPTQAGGGNGNGGNNRRPGGPQQQASQKPNGLLEEFGINLTDIARKGEIDPVIGRDEEITRVIEI  146
NTDB id 85 BSU 00860 NP 387967.1              ....LG...................SN...ETG.SSAAGTNSNANTPTLDSLARDLTAIAKEDSLDPVIGRSKEIQRVIEV  195
NTDB id 399183 GIG89 RS02000 WP 029343521.1   LEQKAYLRVPERRKAVTP.ASK..RN.......LSGK.VSETTTPTLDTVSTDLTKAAREGKLDPMIGREREVERLIHI  208
NTDB id 610 V4T04 RS10165 WP 012897346.1      LEKRTGLKVPESKKAVTP.MSK..RK.......MAKG.VAENSTTPTLDSVSSDLTEEARLGKLDPMIGREAEIDRLIHI  208
NTDB id 287 SP RS11210 WP 001109712.1         LEERAGWTREDLK.ALRQ.RHR..TV.ADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQI  221
NTDB id 290 KZH43 RS10025 WP 001109677.1      LEERAGWTREDLK.ALRQ.RHR..TV.ADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQI  221
NTDB id 289 SPD RS10700 WP 001109677.1        LEERAGWTREDLK.ALRQ.RHR..TV.ADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQI  221
NTDB id 377 SMU RS09275 WP 002262344.1        IERYAGFSKEDIK.AIFE.MRK..PKKVKNSSSFSDLMKPP.SVTGELADFTRDLTELARQGRLEPVIGREQEISRMVQI  225
NTDB id 329 STU RS10020 WP 011225298.1        LERNAGLSKQDLK.AIHD.LRK..PKKSKASANFANMMQPPQSSTGELADYTKDLTALAESGNLDPIIGRDEEISRMIQV  228
NTDB id 297 STER RS00545 WP 011680614.1       LERNAGLSKQDLK.AIHD.LRK..PKKSKASANFANMMQPPQSSTGELADYTKDLTALAESGNLDPVIGRDEEISRMIQV  228
consensus                                     ** ****** *** **     *           *****  *** ** !**** *!!**!******!*!!!**!**!****
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logo
NTDB id 378 SMU RS02690 WP 002263569.1        LNRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPQKLHGKNVIRLDVVSLVQGTGIRGQFEERMQKLMEEIRQRQDVI   226
NTDB id 85 BSU 00860 NP 387967.1              LSRRTKNNPVLIGEPGVGKTAIAEGLAQQIINNEVPEILRDKRVMTLDMGTVVAGTKYRGEFEDRLKKVMDEIRQAGNII   275
NTDB id 399183 GIG89 RS02000 WP 029343521.1   LSRRTKNNPVLVGEPGVGKSAIIEGFATRVAAGNVPVGLRGSRIMALNMAMVVAGTKFRGEFEDRLTAIVDEVTHDKDVI   288
NTDB id 610 V4T04 RS10165 WP 012897346.1      LSRRTKNNPVLVGEPGVGKSAIIEGLAQRIVNGQVPIGLMNSRIMALNMATVVAGTKFRGEFEDRLTAIVEEVSSDPDVI   288
NTDB id 287 SP RS11210 WP 001109712.1         LSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVI   301
NTDB id 290 KZH43 RS10025 WP 001109677.1      LSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVI   301
NTDB id 289 SPD RS10700 WP 001109677.1        LSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVI   301
NTDB id 377 SMU RS09275 WP 002262344.1        LSRKTKNNPVLVGDAGVGKTALAYGLAQRIVDSAVPFELADMKVLELDMMSVVAGTRFRGDFEERMNQIIADIEADGHIV   305
NTDB id 329 STU RS10020 WP 011225298.1        LSRKTKNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEADGKII   308
NTDB id 297 STER RS00545 WP 011680614.1       LSRKTKNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEADGKII   308
consensus                                     !*!*!!!!!!!*!**!!!!*!***!*!*******!! *** *****!*****!*!!**!!*!!*!********* ** **

logo
NTDB id 378 SMU RS02690 WP 002263569.1        LFIDEIHEIVGAGSAGDGNMDAGNILKPALARGELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPSVAETITILKGI   305
NTDB id 85 BSU 00860 NP 387967.1              LFIDELHTLIGAGG.AEGAIDASNILKPSLARGELQCIGATTLDEYRKYIEKDAALERRFQPIQVDQPSVDESIQILQGL   354
NTDB id 399183 GIG89 RS02000 WP 029343521.1   VFIDELHTIIGAGGGMDSVNDASNILKPALARGEFQLIGATTYQEYQKYIEKDEALERRFARVNVEEPSEEETVAILQGL   368
NTDB id 610 V4T04 RS10165 WP 012897346.1      IFIDELHTIIGAGGGMDSVNDAANILKPALARGDFQMVGATTYHEYQKYIEKDEALERRLARINVDEPSPDEAIAILQGL   368
NTDB id 287 SP RS11210 WP 001109712.1         LFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGL   381
NTDB id 290 KZH43 RS10025 WP 001109677.1      LFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGL   381
NTDB id 289 SPD RS10700 WP 001109677.1        LFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGL   381
NTDB id 377 SMU RS09275 WP 002262344.1        LFIDELHTIMGSGSGIDSTLDAANILKPALARGSLRTIGATTQEEYQKHIEKDAALSRRFAKVTIEEPSEEEAYQILLGL   385
NTDB id 329 STU RS10020 WP 011225298.1        LFIDELHTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAIDILNGL   388
NTDB id 297 STER RS00545 WP 011680614.1       LFIDELHTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAIDILNGL   388
consensus                                     *!!!!*!***!*!*******!!*!!!!!*!!!!** **!!!!**!!***!!!!*!!*!!********!!* *** !!*!*

logo
NTDB id 378 SMU RS02690 WP 002263569.1        QPKYEDYHHVKYTDEAIEAAANLSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNF..VDPKEIDHRLIEAENLKAQATRDE   383
NTDB id 85 BSU 00860 NP 387967.1              RDRYEAHHRVSITDDAIEAAVKLSDRYISDRFLPDKAIDLIDEAGSKVRLRSFTTPPNLKELEQKLDEVRKEKDAAVQSQ   434
NTDB id 399183 GIG89 RS02000 WP 029343521.1   KEKFEAYHIVKFEEGALERAVSLSNRYMPSRRLPDKAIDLLDEAAAKVKITSKTNYTKLDELKAELKAEELRLQKAVVAL   448
NTDB id 610 V4T04 RS10165 WP 012897346.1      REKFEDYHQVKFTDQAIKSAVMLSVRYMTSRKLPDKAIDLLDEAAAAVKISVKNQQTKRLDLEKELAEAQEELSEAVIKL   448
NTDB id 287 SP RS11210 WP 001109712.1         KATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL........SPADKALMDG   453
NTDB id 290 KZH43 RS10025 WP 001109677.1      KATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL........SPADKALMDG   453
NTDB id 289 SPD RS10700 WP 001109677.1        KATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL........SPADKALMDG   453
NTDB id 377 SMU RS09275 WP 002262344.1        KKSYETYHHVIISDAAVMAAVKGAHRYLSGKNLPDSAIDLLDEASATVQGLVKK..KAPAYL........TDLDHALITN   455
NTDB id 329 STU RS10020 WP 011225298.1        RSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EAKREI........TPLDEALISG   458
NTDB id 297 STER RS00545 WP 011680614.1       RSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EDKREI........TPLDEALISG   458
consensus                                     * **! *!*! ****!***!*****!!**** !!!*!!!!*!!!********* *  **        **** !** *
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logo
NTDB id 378 SMU RS02690 WP 002263569.1        DYEKAAYFRDQIAKYKEMQS......AKLDKENTPVITEKNIEVIVEQKTNIPVGELKEKEQSQLIHLADDLKTRVIGQD  457
NTDB id 85 BSU 00860 NP 387967.1              EFEKAASLRDTEQRLREQVEDTKKSWKEKQGQENSEVTVDDIAMVVSSWTGVPVSKIAQTETDKLLNMENILHSRVIGQD  514
NTDB id 399183 GIG89 RS02000 WP 029343521.1   DIVEAQGIEKDIEKLTHKIDNFT.....VSENDNPLVEESDVYAVVSNLTGIPLQQMTKTESERLINLEKELHKRVVGQE  523
NTDB id 610 V4T04 RS10165 WP 012897346.1      DIKASRTKEKAVEKIADKIYKFS.....VKEDKRQEVTDQAVVAVASTLTGVPITQMTKSESDRLINLEKELHKRVVGQE  523
NTDB id 287 SP RS11210 WP 001109712.1         KWKQAAQLIAKE.........EE.....VP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQD  518
NTDB id 290 KZH43 RS10025 WP 001109677.1      KWKQAAQLIAKE.........EE.....VP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQD  518
NTDB id 289 SPD RS10700 WP 001109677.1        KWKQAAQLIAKE.........EE.....VP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQD  518
NTDB id 377 SMU RS09275 WP 002262344.1        DYQLAKRLLKKE.........KK.....PLLKKRAEVKEEDILATLSKLSGIPVKKLTQADSKKYLNLERELHKRVIGQD  521
NTDB id 329 STU RS10020 WP 011225298.1        DIGAAVKQYKAN.........QK.....AKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVIGQD  524
NTDB id 297 STER RS00545 WP 011680614.1       DIGAAVKQYKAN.........QK.....AKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVIGQD  524
consensus                                     **  ** * * *                *    * **** *** ********!* ************** *!**!!*!!*

logo
NTDB id 378 SMU RS02690 WP 002263569.1        AAVDKIAKAIRRNRVGLGTPNRPIGSFLFVGPTGVGKTELSKQLAIELFGSEDSMIRFDMSEYMEKHAVAKLVGAPPGYV  537
NTDB id 85 BSU 00860 NP 387967.1              EAVVAVAKAVRRARAGLKDPKRPIGSFIFLGPTGVGKTELARALAESIFGDEESMIRIDMSEYMEKHSTSRLVGSPPGYV  594
NTDB id 399183 GIG89 RS02000 WP 029343521.1   EAISAVSRAIRRARSGIADTRRPLGSFMFLGPTGVGKTELAKALAESVFGSEENMIRVDMSEFMEKFSTSRLIGAPPGYV  603
NTDB id 610 V4T04 RS10165 WP 012897346.1      EAISAVSRAIRRARSGVADSRRPMGSFMFLGPTGVGKTELAKALADSVFGSEDNMIRVDMSEFMEKHSTSRLIGAPPGYV  603
NTDB id 287 SP RS11210 WP 001109712.1         QAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYV  598
NTDB id 290 KZH43 RS10025 WP 001109677.1      QAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYV  598
NTDB id 289 SPD RS10700 WP 001109677.1        QAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYV  598
NTDB id 377 SMU RS09275 WP 002262344.1        DAVSSISRAIRRNQSGIRVGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYV  601
NTDB id 329 STU RS10020 WP 011225298.1        EAVSAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGAPPGYV  604
NTDB id 297 STER RS00545 WP 011680614.1       EAVSAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGAPPGYV  604
consensus                                     *!******!*!!***!*** *!!*!!!*!*!!!!!!!!!!***!!***!**!****!*!!!!*!!!*****!*!*!!!!!

logo
NTDB id 378 SMU RS02690 WP 002263569.1        GYEEAGQLTEKVRRNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGK..SEANVGFG  615
NTDB id 85 BSU 00860 NP 387967.1              GYDEGGQLTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNKYVGFN  674
NTDB id 399183 GIG89 RS02000 WP 029343521.1   GYDEGGQLTEQVRNKPYSVILLDEVEKAHPDIFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATAIRDDKTVGFG  683
NTDB id 610 V4T04 RS10165 WP 012897346.1      GYDEGGQLTERVRNKPYSVVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDKTVGFG  683
NTDB id 287 SP RS11210 WP 001109712.1         GYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFG  678
NTDB id 290 KZH43 RS10025 WP 001109677.1      GYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFG  678
NTDB id 289 SPD RS10700 WP 001109677.1        GYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFG  678
NTDB id 377 SMU RS09275 WP 002262344.1        GYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFG  681
NTDB id 329 STU RS10020 WP 011225298.1        GYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFG  684
NTDB id 297 STER RS00545 WP 011680614.1       GYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFG  684
consensus                                     !!*!*!*!!!*!!**!!!**!*!!*!!!!!!*****!!*!*!!**!!**!!*!*!**!!*!!!!!*!*********!!!*
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logo
NTDB id 378 SMU RS02690 WP 002263569.1        ASREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFQALSKDNLLQIVSLMLDDVNQRLAVNAIHLDVTDKVKEKLVDL   690
NTDB id 85 BSU 00860 NP 387967.1              VQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKAKVAEE   754
NTDB id 399183 GIG89 RS02000 WP 029343521.1   AKSISTDYPAMKARIMEELKKQYRPEFLNRIDETIVFHSLTEKEIEQVVKIMSKSLVSRLKDQNIKVKFTPAALKVIADK   763
NTDB id 610 V4T04 RS10165 WP 012897346.1      AKNITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLIKRLAEQDIHVKLTPSAVKLIAEV   763
NTDB id 287 SP RS11210 WP 001109712.1         AKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLTEKGIDLKLQASALKLLANQ   758
NTDB id 290 KZH43 RS10025 WP 001109677.1      AKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLLANQ   758
NTDB id 289 SPD RS10700 WP 001109677.1        AKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLLANQ   758
NTDB id 377 SMU RS09275 WP 002262344.1        AKSFSQDYKAMESRILEELKKVYRPEFINRIDEKVVFHNLGQEDIRHIVKIMVAPLIAHLADQGITLKFQPSALKHLALA   761
NTDB id 329 STU RS10020 WP 011225298.1        AQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLAKD   764
NTDB id 297 STER RS00545 WP 011680614.1       AQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLAKD   764
consensus                                     ** ** *  **  ****!!** **!!!*!!*!****!**!* * * **!**!*****  !***** ************
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logo
NTDB id 378 SMU RS02690 WP 002263569.1        GYDPKMGARPLRRTIQEHIEDAITDFYLEHPEQKE.LKAIMTSNGKIVIKASNKVETVTKATSD   753
NTDB id 85 BSU 00860 NP 387967.1              GVDLEYGARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN........   810
NTDB id 399183 GIG89 RS02000 WP 029343521.1   GFDPEYGARPLRKALQREVEDTLSEQLLAGEIHPGDTISIGSSNKKIRISVID...........   816
NTDB id 610 V4T04 RS10165 WP 012897346.1      GFDPEYGARPLRKALQKEVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV...........   816
NTDB id 287 SP RS11210 WP 001109712.1         GYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIGVKAGQLKFDIA............   810
NTDB id 290 KZH43 RS10025 WP 001109677.1      GYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA............   810
NTDB id 289 SPD RS10700 WP 001109677.1        GYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA............   810
NTDB id 377 SMU RS09275 WP 002262344.1        GYDAEMGARPLRRTLQTEVEDKLAELILSGKLASGQTLKIGIQKEKLKFDIV............   813
NTDB id 329 STU RS10020 WP 011225298.1        GYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV............   816
NTDB id 297 STER RS00545 WP 011680614.1       GYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV............   816
consensus                                     !*!***!!!!!!***!***!!******! **** ******** ***** **
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X non conserved

X similar

X $\geq$ 50% conserved