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logo
NTDB id 85 BSU 00860 NP 387967.1          ..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGIAAKALQALGLGSEKIQKEVESLIG........R   70
NTDB id 610 V4T04 RS10165 WP 012897346.1  MKFENIKYTPTLDRILEKAEEYAHQYQYGTIESAHLLAAMATTSGSIAYSLLAGMNVDSSDL........LIDLEDLSSH   72
NTDB id 287 SP RS11210 WP 001109712.1     .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLEE.....VALELTETDYS   70
NTDB id 290 KZH43 RS10025 WP 001109677.1  .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLEE.....VALELTETDYS   70
NTDB id 289 SPD RS10700 WP 001109677.1    .....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 406282 GPA00 RS02470 WP 157327413.1 ....MSEYSMKMQEVFSIAQFQAARFESPYLESWHVLLAMVAVHDSVAGLTFAEYQNKIAYEEYEAAAVLALGKSPLSD.   75
NTDB id 377 SMU RS09275 WP 002262344.1    ....MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSS.   75
consensus                                    *********  !** !***   *****!*!****  * **!* ** **  **  **     *****    * *

logo
NTDB id 85 BSU 00860 NP 387967.1          GQEMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNNLGVSLNKARQQVLQ..LL......   142
NTDB id 610 V4T04 RS10165 WP 012897346.1  VKVKRSTLRFSPRAEEVMTAASFLAIHNNSEAVGTEHLLYALLQVEDGFGLQLLKLQ.........KINIVSLRKELEKR   143
NTDB id 287 SP RS11210 WP 001109712.1     QDETFTELPFSRRLQVLFDEAEYVASVVHAKVLGTEHVLYAILHDSNALATRILERAGFSYEDKKDQVKIAALRRNLEER   150
NTDB id 290 KZH43 RS10025 WP 001109677.1  QDETFTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER   150
NTDB id 289 SPD RS10700 WP 001109677.1    QDETFTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER   150
NTDB id 329 STU RS10020 WP 011225298.1    ESDIIDLRAQSPALEAMLQEAQGIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSDKPRIIDLRRSLERN   156
NTDB id 297 STER RS00545 WP 011680614.1   ESDIIDLRAQSPALEAMLQEAQEIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSDKPRIIDLRRSLERN   156
NTDB id 406282 GPA00 RS02470 WP 157327413.1 .VKNVQFLEQSKALKDVLAFAESICKVTDGTEIGTEHVLYAMLLNLDLFATRLLEVAGFKNKEDGDSVRLLDLRKSLSRN   154
NTDB id 377 SMU RS09275 WP 002262344.1    .SNDIMLLEQSHALKRTLAEAAAISQVTHAKEVGTEHVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVIERY   154
consensus                                   *    * ** **  ** **  ****  *  *!*!!*!****   *******!***** * *  * **** !** ***

logo
NTDB id 85 BSU 00860 NP 387967.1          .GSNE...................TGSSAAGTNSNANTPTLDSLARDLTAIAKEDSLDPVIGRSKEIQRVIEVLSRRTKN   202
NTDB id 610 V4T04 RS10165 WP 012897346.1  TGLKVPESKKAVTPMSKRKMAKG........VAENSTTPTLDSVSSDLTEEARLGKLDPMIGREAEIDRLIHILSRRTKN   215
NTDB id 287 SP RS11210 WP 001109712.1     AGWTREDLK.ALRQRHRT.VADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQILSRKTKN   228
NTDB id 290 KZH43 RS10025 WP 001109677.1  AGWTREDLK.ALRQRHRT.VADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQILSRKTKN   228
NTDB id 289 SPD RS10700 WP 001109677.1    AGWTREDLK.ALRQRHRT.VADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQILSRKTKN   228
NTDB id 329 STU RS10020 WP 011225298.1    AGLSKQDLK.AIHDLRKPKKSKASANFANMMQPPQSSTGELADYTKDLTALAESGNLDPIIGRDEEISRMIQVLSRKTKN   235
NTDB id 297 STER RS00545 WP 011680614.1   AGLSKQDLK.AIHDLRKPKKSKASANFANMMQPPQSSTGELADYTKDLTALAESGNLDPVIGRDEEISRMIQVLSRKTKN   235
NTDB id 406282 GPA00 RS02470 WP 157327413.1 AGFTKEKIK.AIHDLRKPKKATMGGAFSEMMKPQ.STAGELSDFTRDLTELARQGKLEPVIGREKEVSRMVQVLSRKTKN   232
NTDB id 377 SMU RS09275 WP 002262344.1    AGFSKEDIK.AIFEMRKPKKVKNSSSFSDLMKPP.SVTGELADFTRDLTELARQGRLEPVIGREQEISRMVQILSRKTKN   232
consensus                                 *!******* **  * * * *      ****  *** ** !*****!!!**!****!*!*!!!**!**!****!!!*!!!

logo
NTDB id 85 BSU 00860 NP 387967.1          NPVLIGEPGVGKTAIAEGLAQQIINNEVPEILRDKRVMTLDMGTVVAGTKYRGEFEDRLKKVMDEIRQAGNIILFIDELH   282
NTDB id 610 V4T04 RS10165 WP 012897346.1  NPVLVGEPGVGKSAIIEGLAQRIVNGQVPIGLMNSRIMALNMATVVAGTKFRGEFEDRLTAIVEEVSSDPDVIIFIDELH   295
NTDB id 287 SP RS11210 WP 001109712.1     NPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDELH   308
NTDB id 290 KZH43 RS10025 WP 001109677.1  NPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDELH   308
NTDB id 289 SPD RS10700 WP 001109677.1    NPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDELH   308
NTDB id 329 STU RS10020 WP 011225298.1    NPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEADGKIILFIDELH   315
NTDB id 297 STER RS00545 WP 011680614.1   NPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEADGKIILFIDELH   315
NTDB id 406282 GPA00 RS02470 WP 157327413.1 NPVLVGEAGVGKTALAYGLAQRIVNGEIPYELQDMRVLELDMMSVVAGTRFRGDFEERMNQIISDIEADGHIILFIDEVH   312
NTDB id 377 SMU RS09275 WP 002262344.1    NPVLVGDAGVGKTALAYGLAQRIVDSAVPFELADMKVLELDMMSVVAGTRFRGDFEERMNQIIADIEADGHIVLFIDELH   312
consensus                                 !!!!*!**!!!!*!***!!!!*!*****! *********!****!!!!!**!!*!!*!***** ***  **  ***!!!!*!
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logo
NTDB id 85 BSU 00860 NP 387967.1          TLIGAGG.AEGAIDASNILKPSLARGELQCIGATTLDEYRKYIEKDAALERRFQPIQVDQPSVDESIQILQGLRDRYEAH   361
NTDB id 610 V4T04 RS10165 WP 012897346.1  TIIGAGGGMDSVNDAANILKPALARGDFQMVGATTYHEYQKYIEKDEALERRLARINVDEPSPDEAIAILQGLREKFEDY   375
NTDB id 287 SP RS11210 WP 001109712.1     TIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEKH   388
NTDB id 290 KZH43 RS10025 WP 001109677.1  TIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEKH   388
NTDB id 289 SPD RS10700 WP 001109677.1    TIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEKH   388
NTDB id 329 STU RS10020 WP 011225298.1    TIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAIDILNGLRSSYEDY   395
NTDB id 297 STER RS00545 WP 011680614.1   TIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAIDILNGLRSSYEDY   395
NTDB id 406282 GPA00 RS02470 WP 157327413.1 TIMGSGSGIDSTLDAANILKPALARGTLHMVGATTQEEYQKHIEKDAALSRRFAKITIEEPSVEDAYQILLGLKKSYETF   392
NTDB id 377 SMU RS09275 WP 002262344.1    TIMGSGSGIDSTLDAANILKPALARGSLRTIGATTQEEYQKHIEKDAALSRRFAKVTIEEPSEEEAYQILLGLKKSYETY   392
consensus                                 !**!*!*******!!*!!!!!*!!!!**  *!!!!**!!*!*!!!!*!!*!!********!!* *** !!*!!* **!  *

logo
NTDB id 85 BSU 00860 NP 387967.1          HRVSITDDAIEAAVKLSDRYISDRFLPDKAIDLIDEAGSKVRLRSFTTPPNLKELEQKLDEVRKEKDAAVQSQEFEKAAS   441
NTDB id 610 V4T04 RS10165 WP 012897346.1  HQVKFTDQAIKSAVMLSVRYMTSRKLPDKAIDLLDEAAAAVKISVKNQQTKRLDLEKELAEAQEELSEAVIKLDIKASRT   455
NTDB id 287 SP RS11210 WP 001109712.1     HRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL........SPADKALMDGKWKQAAQ   460
NTDB id 290 KZH43 RS10025 WP 001109677.1  HRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL........SPADKALMDGKWKQAAQ   460
NTDB id 289 SPD RS10700 WP 001109677.1    HRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL........SPADKALMDGKWKQAAQ   460
NTDB id 329 STU RS10020 WP 011225298.1    HRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EAKREI........TPLDEALISGDIGAAVK   465
NTDB id 297 STER RS00545 WP 011680614.1   HRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EDKREI........TPLDEALISGDIGAAVK   465
NTDB id 406282 GPA00 RS02470 WP 157327413.1 HNVIISDEAVLTVVKAAHRYLTSKNLPDSAIDLLDETSATVQGLVKK..KAPEAL........TDIDKAILEGDFKKATK   462
NTDB id 377 SMU RS09275 WP 002262344.1    HHVIISDAAVMAAVKGAHRYLSGKNLPDSAIDLLDEASATVQGLVKK..KAPAYL........TDLDHALITNDYQLAKR   462
consensus                                 !*! **!*!****!****!!**** !!!*!!!!*!!****!* ***       **       **** !** **** *

logo
NTDB id 85 BSU 00860 NP 387967.1          LRDTEQRLREQVEDTKKSWKEKQGQENSEVTVDDIAMVVSSWTGVPVSKIAQTETDKLLNMENILHSRVIGQDEAVVAVA   521
NTDB id 610 V4T04 RS10165 WP 012897346.1  KEKAVEKIADKIYKF.....SVKEDKRQEVTDQAVVAVASTLTGVPITQMTKSESDRLINLEKELHKRVVGQEEAISAVS   530
NTDB id 287 SP RS11210 WP 001109712.1     LIAKE.........E.....EVPV.YKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQDQAVSSIS   525
NTDB id 290 KZH43 RS10025 WP 001109677.1  LIAKE.........E.....EVPV.YKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQDQAVSSIS   525
NTDB id 289 SPD RS10700 WP 001109677.1    LIAKE.........E.....EVPV.YKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQDQAVSSIS   525
NTDB id 329 STU RS10020 WP 011225298.1    QYKAN.........Q.....KAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVIGQDEAVSAIS   531
NTDB id 297 STER RS00545 WP 011680614.1   QYKAN.........Q.....KAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVIGQDEAVSAIS   531
NTDB id 406282 GPA00 RS02470 WP 157327413.1 LLKKS.........R.....KVVTRKPAVVTEDDIMATLSRLSGIPVEKMTQADSKKYLTLEKELHKRVIGQDAAISAIS   528
NTDB id 377 SMU RS09275 WP 002262344.1    LLKKE.........K.....KPLLKKRAEVKEEDILATLSKLSGIPVKKLTQADSKKYLNLERELHKRVIGQDDAVSSIS   528
consensus                                 *****              *    ** *!****** **!***!*!* ************! *!!*!!*!!**!*****

logo
NTDB id 85 BSU 00860 NP 387967.1          KAVRRARAGLKDPKRPIGSFIFLGPTGVGKTELARALAESIFGDEESMIRIDMSEYMEKHSTSRLVGSPPGYVGYDEGGQ   601
NTDB id 610 V4T04 RS10165 WP 012897346.1  RAIRRARSGVADSRRPMGSFMFLGPTGVGKTELAKALADSVFGSEDNMIRVDMSEFMEKHSTSRLIGAPPGYVGYDEGGQ   610
NTDB id 287 SP RS11210 WP 001109712.1     RAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGGE   605
NTDB id 290 KZH43 RS10025 WP 001109677.1  RAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGGE   605
NTDB id 289 SPD RS10700 WP 001109677.1    RAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGGE   605
NTDB id 329 STU RS10020 WP 011225298.1    RAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGAPPGYVGYDEGGE   611
NTDB id 297 STER RS00545 WP 011680614.1   RAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGAPPGYVGYDEGGE   611
NTDB id 406282 GPA00 RS02470 WP 157327413.1 RAIRRNQAGIRTGKRPIGSFMFLGPTGVGKTELAKALAELLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGGE   608
NTDB id 377 SMU RS09275 WP 002262344.1    RAIRRNQSGIRVGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGGE   608
consensus                                 *!*!!***!*** *!!*!!!*!!!!!!!!!!!!!!*!!!***!**!****!*!!!!*!!!***!!!!*!*!!!!!!!*!!!*
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logo

NTDB id 85 BSU 00860 NP 387967.1              LTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNKYVGFNVQDETQN   681
NTDB id 610 V4T04 RS10165 WP 012897346.1      LTERVRNKPYSVVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDKTVGFGAKNITAD   690
NTDB id 287 SP RS11210 WP 001109712.1         LTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAKDIRFD   685
NTDB id 290 KZH43 RS10025 WP 001109677.1      LTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAKDIRFD   685
NTDB id 289 SPD RS10700 WP 001109677.1        LTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAKDIRFD   685
NTDB id 329 STU RS10020 WP 011225298.1        LTEKVRNKPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAQTISHN   691
NTDB id 297 STER RS00545 WP 011680614.1       LTEKVRNKPYSVLLFDEIEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAQTISHN   691
NTDB id 406282 GPA00 RS02470 WP 157327413.1  LTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFGARDMAHD   688
NTDB id 377 SMU RS09275 WP 002262344.1        LTEKVRNKPYSVLLFDEVEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAKSFSQD   688
consensus                                     !!!*!!*!!!!!*!*!!*!!!!!!*!!**!!*!*!!**!!**!!*!!!*!!!*!!!!!*!!**!***!*!!!******  *

logo

NTDB id 85 BSU 00860 NP 387967.1              HKDMKDKVMGELKRARRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKAKVAEEGVDLEYG   761
NTDB id 610 V4T04 RS10165 WP 012897346.1      YSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLIKRLAEQDIHVKLTPSAVKLIAEVGFDPEYG   770
NTDB id 287 SP RS11210 WP 001109712.1         QENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLTEKGIDLKLQASALKLLANQGYDPEMG   765
NTDB id 290 KZH43 RS10025 WP 001109677.1      QENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLLANQGYDPEMG   765
NTDB id 289 SPD RS10700 WP 001109677.1        QENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLLANQGYDPEMG   765
NTDB id 329 STU RS10020 WP 011225298.1        HQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLAKDGYDIEMG   771
NTDB id 297 STER RS00545 WP 011680614.1       HQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLAKDGYDIEMG   771
NTDB id 406282 GPA00 RS02470 WP 157327413.1  YDAMQKRIMEELKKAYRPEFINRIDEKVVFHHLTQENMRDVVKIMVKPLIATLAEKDITLKFQPSALKYLAEAGYDPEMG   768
NTDB id 377 SMU RS09275 WP 002262344.1        YKAMESRILEELKKVYRPEFINRIDEKVVFHNLGQEDIRHIVKIMVAPLIAHLADQGITLKFQPSALKHLALAGYDAEMG   768
consensus                                       *!  ****!!!***!!!!*!!!!!**!!!*!  * * **!**!***!** !*****************!** *!  !*!*!*!

logo

NTDB id 85 BSU 00860 NP 387967.1              ARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN   810
NTDB id 610 V4T04 RS10165 WP 012897346.1      ARPLRKALQKEVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV...   816
NTDB id 287 SP RS11210 WP 001109712.1         ARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIGVKAGQLKFDIA....   810
NTDB id 290 KZH43 RS10025 WP 001109677.1      ARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA....   810
NTDB id 289 SPD RS10700 WP 001109677.1        ARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA....   810
NTDB id 329 STU RS10020 WP 011225298.1        ARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV....   816
NTDB id 297 STER RS00545 WP 011680614.1       ARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV....   816
NTDB id 406282 GPA00 RS02470 WP 157327413.1  ARPLRRTIQDKVEDKLSELILSGDLASGNTLKIGVSKGQLKFDIA....   813
NTDB id 377 SMU RS09275 WP 002262344.1        ARPLRRTLQTEVEDKLAELILSGKLASGQTLKIGIQKEKLKFDIV....   813
consensus                                     !!!!!***!**!!!*!*!**! !*** !*******  * *****
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X non conserved

X similar

X $\geq$ 50% conserved