```
logo
NTDB id 85 BSU 00860 NP 387967.1                  ..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGIAAKALQALGLGSEKIQKEVESLIGRGQ......   72
NTDB id 610 V4T04 RS10165 WP 012897346.1          MKFENIKYTPTLDRILEKAEEYAHQYQYGTIESAHLLAAMATTSGSIAYSLLAGMNVDSSDLLIDLED........LSSH   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 297 STER RS00545 WP 011680614.1           ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLS   76
NTDB id 329 STU RS10020 WP 011225298.1            ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLS   76
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1    ....MIDYSIKMQEIFKQAQYQAARFGSSHLETWHILLAMVKEEGSLAGLVFSEFNNKISEEEYEAAAILAVGKSPQDDI   76
NTDB id 377 SMU RS09275 WP 002262344.1           ....MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSSS   76
consensus                                             * *********  !** !****  *****!*!****  * **!* ** **  **  ** *   *****    * *

logo
NTDB id 85 BSU 00860 NP 387967.1                  ..EMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNNLGVSLNKARQQVLQLLGSNE....  146
NTDB id 610 V4T04 RS10165 WP 012897346.1          VKVKRSTLRFSPRAEEVMTAASFLAIHNNSEAVGTEHLLYALLQVEDGFGLQLLKLQ..........KINIVSLRKELEK  142
NTDB id 290 KZH43 RS10025 WP 001109677.1          QDETFTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKD.QVKIAALRRNLEE  149
NTDB id 289 SPD RS10700 WP 001109677.1            QDETFTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKD.QVKIAALRRNLEE  149
NTDB id 287 SP RS11210 WP 001109712.1             QDETFTELPFSRRLQVLFDEAEYVASVVHAKVLGTEHVLYAILHDSNALATRILERAGFSYEDKKD.QVKIAALRRNLEE  149
NTDB id 297 STER RS00545 WP 011680614.1           ESDIIDLRAQSPALEAMLQEAQEIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSD.KPRIIDLRRSLER  155
NTDB id 329 STU RS10020 WP 011225298.1            ESDIIDLRAQSPALEAMLQEAQGIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSD.KPRIIDLRRSLER  155
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1    K..EVHFLGQSKTLTNILKFSEMISLVTNASEVGSEHVLFAILLNPDIMAARLLEMAGFKIKDDGQGQPKLADLRKAIEI  154
NTDB id 377 SMU RS09275 WP 002262344.1           N..DIMLLEQSHALKRTLAEAAAISQVTHAKEVGTEHVLFAMLLNPNLLATRILELVGFHAKDDGESI.RLLDLRKVIER  153
consensus                                           *    * ** **  ** **  ****  *  *!*!!*!****   **** **!***** * *  *  **** *** **

logo
NTDB id 85 BSU 00860 NP 387967.1                  .TG................SSAAG........TNSNANTPTLDSLARDLTAIAKEDSLDPVIGRSKEIQRVIEVLSRRTK  201
NTDB id 610 V4T04 RS10165 WP 012897346.1          RTGLKVPESKKAVTPMSKRKMAKGVA........ENSTTPTLDSVSSDLTEEARLGKLDPMIGREAEIDRLIHILSRRTK  214
NTDB id 290 KZH43 RS10025 WP 001109677.1          RAGWTREDL.KALRQRHRT.VADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQILSRKTK  227
NTDB id 289 SPD RS10700 WP 001109677.1            RAGWTREDL.KALRQRHRT.VADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQILSRKTK  227
NTDB id 287 SP RS11210 WP 001109712.1             RAGWTREDL.KALRQRHRT.VADKQNSMANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEISRMIQILSRKTK  227
NTDB id 297 STER RS00545 WP 011680614.1           NAGLSKQDL.KAIHDLRKPKKSKASANFANMMQPPQSSTGELADYTKDLTALAESGNLDPVIGRDEEISRMIQVLSRKTK  234
NTDB id 329 STU RS10020 WP 011225298.1            NAGLSKQDL.KAIHDLRKPKKSKASANFANMMQPPQSSTGELADYTKDLTALAESGNLDPIIGRDEEISRMIQVLSRKTK  234
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1    QAAYSKETI.KAIHELRKPKKAKGAGSFSDMMKPA.STAGDLSDFTRDLTEMANQGLLEPVIGRDKEITRMIQVLSRKTK  232
NTDB id 377 SMU RS09275 WP 002262344.1           YAGFSKEDI.KAIFEMRKPKKVKNSSSFSDLMKPP.SVTGELADFTRDLTELARQGRLEPVIGREQEISRMVQILSRKTK  231
consensus                                         ******** ***  * * * ***  * ****  *** ** !*****!!!**!****!*!*!!!**!!*!****!!!*!!

logo
NTDB id 85 BSU 00860 NP 387967.1                  NNPVLIGEPGVGKTAIAEGLAQQIINNEVPEILRDKRVMTLDMGTVVAGTKYRGEFEDRLKKVMDEIRQAGNIILFIDEL  281
NTDB id 610 V4T04 RS10165 WP 012897346.1          NNPVLVGEPGVGKSAIIEGLAQRIVNGQVPIGLMNSRIMALNMATVVAGTKFRGEFEDRLTAIVEEVSSDPDVIIFIDEL  294
NTDB id 290 KZH43 RS10025 WP 001109677.1          NNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDEL  307
NTDB id 289 SPD RS10700 WP 001109677.1            NNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDEL  307
NTDB id 287 SP RS11210 WP 001109712.1             NNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEEDGQVILFIDEL  307
NTDB id 297 STER RS00545 WP 011680614.1           NNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEADGKIILFIDEL  314
NTDB id 329 STU RS10020 WP 011225298.1            NNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEADGKIILFIDEL  314
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1    NNPVLVGDAGVGKTALAYGLAQRIANGSIPYELQDMRVLELDMMSVVAGTRFRGDFEERMNQIIDDIETDGQIILFVDEL  312
NTDB id 377 SMU RS09275 WP 002262344.1           NNPVLVGDAGVGKTALAYGLAQRIVDSAVPFELADMKVLELDMMSVVAGTRFRGDFEERMNQIIADIEADGHIVLFIDEL  311
consensus                                        !!!!!*!**!!!!*!***!!!!*!*****! ********!****!!!!!**!!*!!*!********* ******!*!!!
```

```
logo

NTDB id 85 BSU 00860 NP 387967.1          HTLIGAGG.AEGAIDASNILKPSLARGELQCIGATTLDEYRKYIEKDAALERRFQPIQVDQPSVDESIQILQGLRDRYEA   360
NTDB id 610 V4T04 RS10165 WP 012897346.1  HTIIGAGGGMDSVNDAANILKPALARGDFQMVGATTYHEYQKYIEKDEALERRLARINVDEPSPDEAIAILQGLREKFED   374
NTDB id 290 KZH43 RS10025 WP 001109677.1  HTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEK   387
NTDB id 289 SPD RS10700 WP 001109677.1    HTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEK   387
NTDB id 287 SP RS11210 WP 001109712.1     HTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEK   387
NTDB id 297 STER RS00545 WP 011680614.1   HTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAIDILNGLRSSYED   394
NTDB id 329 STU RS10020 WP 011225298.1    HTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAIDILNGLRSSYED   394
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1 HTIMGSGSGIDSTLDAANILKPALSRGTLHMVGATTQEEYQKHIEKDAALSRRFAKVLIEEPNLEDAYQILLGLKGSYER   392
NTDB id 377 SMU RS09275 WP 002262344.1    HTIMGSGSGIDSTLDAANILKPALARGSLRTIGATTQEEYQKHIEKDAALSRRFAKVTIEEPSEEEAYQILLGLKKSYET   391
consensus                                 !!**!*!*******!!*!!!!!*!*!!**  *!!!!**!!*!*!!!!*!!*!!********!** *** !!*!!* **!

logo

NTDB id 85 BSU 00860 NP 387967.1          HHRVSITDDAIEAAVKLSDRYISDRFLPDKAIDLIDEAGSKVRLRSFTTPPNLKELEQKLDEVRKEKDAAVQSQEFEKAA   440
NTDB id 610 V4T04 RS10165 WP 012897346.1  YHQVKFTDQAIKSAVMLSVRYMTSRKLPDKAIDLLDEAAAAVKISVKNQQTKRLDLEKELAEAQEELSEAVIKLDIKASR   454
NTDB id 290 KZH43 RS10025 WP 001109677.1  HHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDLS........PADKALMDGKWKQAA   459
NTDB id 289 SPD RS10700 WP 001109677.1    HHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDLS........PADKALMDGKWKQAA   459
NTDB id 287 SP RS11210 WP 001109712.1     HHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDLS........PADKALMDGKWKQAA   459
NTDB id 297 STER RS00545 WP 011680614.1   YHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EDKREIT........PLDEALISGDIGAAV   464
NTDB id 329 STU RS10020 WP 011225298.1    YHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EAKREIT........PLDEALISGDIGAAV   464
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1 FHNVSISDQAVKTAVKVAHRYLTSKNLPDSAIDLLDEASATVQGLVKK..EKASILT........PIDQAILEKDFKTVS   462
NTDB id 377 SMU RS09275 WP 002262344.1    YHHVIISDAAVMAAVKGAHRYLSGKNLPDSAIDLLDEASATVQGLVKK..KAPAYLT........DLDHALITNDYQLAK   461
consensus                                 *!*!  **!  !***!!*****!**** !!!*!!!!*!!!***!* ***       ***         *** !**  **** *

logo

NTDB id 85 BSU 00860 NP 387967.1          SLRDTEQRLREQVEDTKKSWKEKQGQENSEVTVDDIAMVVSSWTGVPVSKIAQTETDKLLNMENILHSRVIGQDEAVVAV   520
NTDB id 610 V4T04 RS10165 WP 012897346.1  TKEKAVEKIADKIYK.....FSVKEDKRQEVTDQAVVAVASTLTGVPITQMTKSESDRLINLEKELHKRVVGQEEAISAV   529
NTDB id 290 KZH43 RS10025 WP 001109677.1  QLIAK.........E.....EEV.PVYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQDQAVSSI   524
NTDB id 289 SPD RS10700 WP 001109677.1    QLIAK.........E.....EEV.PVYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQDQAVSSI   524
NTDB id 287 SP RS11210 WP 001109712.1     QLIAK.........E.....EEV.PVYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKRVIGQDQAVSSI   524
NTDB id 297 STER RS00545 WP 011680614.1   KQYKA.........N.....QKAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVIGQDEAVSAI   530
NTDB id 329 STU RS10020 WP 011225298.1    KQYKA.........N.....QKAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVIGQDEAVSAI   530
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1 KLLKA.........Q.....VNNKSAKPTLVTEDNIMSTLSKLSGIPVEKLTQADSKKYLNLEKELHKRVIGQEDAVSAI   528
NTDB id 377 SMU RS09275 WP 002262344.1    RLLKK.........E.....KKPLLKKRAEVKEEDILATLSKLSGIPVKKLTQADSKKYLNLERELHKRVIGQDDAVSSI   527
consensus                                  ***          *           ** *!******  **!***!*!*  ************!*!  *!!*!!*!!**!****

logo

NTDB id 85 BSU 00860 NP 387967.1          AKAVRRARAGLKDPKRPIGSFIFLGPTGVGKTELARALAESIFGDEESMIRIDMSEYMEKHSTSRLVGSPPGYVGYDEGG   600
NTDB id 610 V4T04 RS10165 WP 012897346.1  SRAIRRARSGVADSRRPMGSFMFLGPTGVGKTELAKALADSVFGSEDNMIRVDMSEFMEKHSTSRLIGAPPGYVGYDEGG   609
NTDB id 290 KZH43 RS10025 WP 001109677.1  SRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGG   604
NTDB id 289 SPD RS10700 WP 001109677.1    SRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGG   604
NTDB id 287 SP RS11210 WP 001109712.1     SRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGG   604
NTDB id 297 STER RS00545 WP 011680614.1   SRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGAPPGYVGYDEGG   610
NTDB id 329 STU RS10020 WP 011225298.1    SRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGAPPGYVGYDEGG   610
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1 SRAIRRNQSGIRTGRRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGG   608
NTDB id 377 SMU RS09275 WP 002262344.1    SRAIRRNQSGIRVGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGAPPGYVGYEEGG   607
consensus                                 **!*!!***!*** *!!*!!!*!!!!!!!!!!!!!!*!!!***!**!****!*!!!!*!!!***!!!*!*!!!!!!!*!!!
```

```
logo

NTDB id 85 BSU 00860 NP 387967.1              QLTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNKYVGFNVQDEIQ   680
NTDB id 610 V4T04 RS10165 WP 012897346.1      QLTERVRNKPYSVVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDKTVGFGAKNITA   689
NTDB id 290 KZH43 RS10025 WP 001109677.1      ELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAKDIRF   684
NTDB id 289 SPD RS10700 WP 001109677.1        ELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAKDIRF   684
NTDB id 287 SP RS11210 WP 001109712.1         ELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAKDIRF   684
NTDB id 297 STER RS00545 WP 011680614.1       ELTEKVRNKPYSVLLFDEIEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAQTISH   690
NTDB id 329 STU RS10020 WP 011225298.1        ELTEKVRNKPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAQTISH   690
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1 ELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGMLTDSRGRRVDFSNTIIIMTSNLGATALRDDKTVGFGAKDISQ   688
NTDB id 377 SMU RS09275 WP 002262344.1        ELTEKVRNKPYSVLLFDEVEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFGAKSFSQ   687
consensus                                     *!!!*!!*!!!!!*!*!!*!!!!!!*!!**!!*!*!!**!!**!!*!!!*!!!*!!!!!*!!**!***!*!!!******

logo

NTDB id 85 BSU 00860 NP 387967.1              NHKDMKDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKAKVAEEGVDLEY   760
NTDB id 610 V4T04 RS10165 WP 012897346.1      DYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLIKRLAEQDIHVKLTPSAVKLIAEVGFDPEY   769
NTDB id 290 KZH43 RS10025 WP 001109677.1      DQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLLANQGYDPEM   764
NTDB id 289 SPD RS10700 WP 001109677.1        DQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLLANQGYDPEM   764
NTDB id 287 SP RS11210 WP 001109712.1         DQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLTEKGIDLKLQASALKLLANQGYDPEM   764
NTDB id 297 STER RS00545 WP 011680614.1       NHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLAKDGYDIEM   770
NTDB id 329 STU RS10020 WP 011225298.1        NHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLAKDGYDIEM   770
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1 DHQAMEKRILEELKKSYRPEFINRIDEKVVFHSLSQEDMKEVVMIMVKPLVTNLAEKGVSLKIQPSALNYLSEEGYDVEM   768
NTDB id 377 SMU RS09275 WP 002262344.1        DYKAMESRILEELKKVYRPEFINRIDEKVVFHNLGQEDIRHIVKIMVAPLIAHLADQGITLKFQPSALKHLALAGYDAEM   767
consensus                                     *  *!* ****!!!* *!!!!*!!!!!**!!!*!  * * **!**!***!*  !*************!** **  !*! !*

logo

NTDB id 85 BSU 00860 NP 387967.1              GARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN   810
NTDB id 610 V4T04 RS10165 WP 012897346.1      GARPLRKALQKEVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV...   816
NTDB id 290 KZH43 RS10025 WP 001109677.1      GARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA....   810
NTDB id 289 SPD RS10700 WP 001109677.1        GARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA....   810
NTDB id 287 SP RS11210 WP 001109712.1         GARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIGVKAGQLKFDIA....   810
NTDB id 297 STER RS00545 WP 011680614.1       GARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV....   816
NTDB id 329 STU RS10020 WP 011225298.1        GARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV....   816
NTDB id 1063745 ACG3JH RS08375 WP 013794487.1 GARPLRRTLQTHIEDKLSELILSGDLSSGHQLKIGMSHGKLKFDIE....   814
NTDB id 377 SMU RS09275 WP 002262344.1        GARPLRRTLQTEVEDKLAELILSGKLASGQTLKIGIQKEKLKFDIV....   813
consensus                                     !!!!!!***!***!!*!*!**! !*** !* *****  *******
```

X non conserved

X similar

X $\geq$ 50% conserved