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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 610 V4T04 RS10165 WP 012897346.1        MKFENIKYTPTLDRILEKAEEYAHQYQYGTIESAHLLAAMATTSGSIAYSLLAGMNVDSSDLLI........DLEDLSSH  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 297 STER RS00545 WP 011680614.1         ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLS  76
NTDB id 1130807 H0502 RS07805 WP 179970783.1    ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSVAYLTLTDFEDRIHSEEIETAAVLAMEKRPKDLS  76
NTDB id 329 STU RS10020 WP 011225298.1          ....MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLS  76
consensus                                              ****** **  ***** **   ************  * **** ** **  **  **     *****    * *

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NTDB id 378 SMU RS02690 WP 002263569.1          ......MLCQNCKLNEATIHL...YANVNGQQKQIDLCQNCYQIMKTDPENGPLNHLSQ.....QNSSSINPFFDDFFGD  66
NTDB id 85 BSU 00860 NP 387967.1                GQEMSQTIHYTPRAK.KVIELSMDEARKLGH.SYVGTEHILLGLIRE.G.EGVAARVLNNLGVSLNKARQQVLQL.....  141
NTDB id 610 V4T04 RS10165 WP 012897346.1        VKVKRSTLRFSPRAE.EVMTAASFLAIHNNS.EAVGTEHLLYALLQV.E.DGFGLQLLKL.........QKINIVSLRKE  139
NTDB id 287 SP RS11210 WP 001109712.1           QDETFTELPFSRRLQ.VLFDEAEYVASVVHA.KVLGTEHVLYAILHD.S.NALATRILERAGFSYEDKKDQVKIAALRRN  146
NTDB id 290 KZH43 RS10025 WP 001109677.1        QDETFTELPFSRRLQ.ILFDEAEYVASVVHA.KVLGTEHVLYAILHD.G.NALATRILERAGFSYEDKKDQVKIAALRRN  146
NTDB id 289 SPD RS10700 WP 001109677.1          QDETFTELPFSRRLQ.ILFDEAEYVASVVHA.KVLGTEHVLYAILHD.G.NALATRILERAGFSYEDKKDQVKIAALRRN  146
NTDB id 377 SMU RS09275 WP 002262344.1          N..DIMLLEQSHALK.RTLAEAAAISQVTHA.KEVGTEHVLFAMLLN.P.NLLATRILELVGFHAKDDGESIRLLDLRKV  150
NTDB id 297 STER RS00545 WP 011680614.1         ESDIIDLRAQSPALE.AMLQEAQEIASVTGA.VEVGSEHVLMAFLLH.K.DLMVCRLLEVAGFQYKDDSDKPRIIDLRRS  152
NTDB id 1130807 H0502 RS07805 WP 179970783.1    ESDIIDLRAQSPALE.AMLQEAQGIASVTGA.VEVGSEHVLMAFLLH.K.DLMVCRLLEVAGFQYKDDSDKPRIIDLRRS  152
NTDB id 329 STU RS10020 WP 011225298.1          ESDIIDLRAQSPALE.AMLQEAQGIASVTGA.VEVGSEHVLMAFLLH.K.DLMVCRLLEVAGFQYKDDSDKPRIIDLRRS  152
consensus                                         *   ** *****   ** **  **** ** * ***********     **** ******** * *  ***********

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NTDB id 378 SMU RS02690 WP 002263569.1          LNNFRAFNNQDLPN.....TPPTQAGGGNGNGGNNRRPGGPQQQASQKPNGLLEEFGINLTDIARKGEIDPVIGRDEEIT  141
NTDB id 85 BSU 00860 NP 387967.1                ....LGSNET.....................G........SSAAGTNSNANTPTLDSLARDLTAIAKEDSLDPVIGRSKEIQ  190
NTDB id 610 V4T04 RS10165 WP 012897346.1        LEKRTGLKVPESKKAVTPMSKRKMAKG................VAENSTTPTLDSVSSDLTEEARLGKLDPMIGREAEID  203
NTDB id 287 SP RS11210 WP 001109712.1           LEERAGWTREDLKA.LRQRHRTV.ADKQNS........MANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEIS  216
NTDB id 290 KZH43 RS10025 WP 001109677.1        LEERAGWTREDLKA.LRQRHRTV.ADKQNS........MANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEIS  216
NTDB id 289 SPD RS10700 WP 001109677.1          LEERAGWTREDLKA.LRQRHRTV.ADKQNS........MANMMGMPQTPSGGLEDYTHDLTEQARSGKLEPVIGRDKEIS  216
NTDB id 377 SMU RS09275 WP 002262344.1          IERYAGFSKEDIKA.IFEMRKPKKVKNSSS........FSDLMKPP.SVTGELADFTRDLTELARQGRLEPVIGREQEIS  220
NTDB id 297 STER RS00545 WP 011680614.1         LERNAGLSKQDLKA.IHDLRKPKKSKASAN........FANMMQPPQSSTGELADYTKDLTALAESGNLDPVIGRDEEIS  223
NTDB id 1130807 H0502 RS07805 WP 179970783.1    LERNAGLSKQDLKA.IHDLRKPKKSKASAN........FANMMQPPQSSTGELADYTKDLTALAESGNLDPVIGRDEEIS  223
NTDB id 329 STU RS10020 WP 011225298.1          LERNAGLSKQDLKA.IHDLRKPKKSKASAN........FANMMQPPQSSTGELADYTKDLTALAESGNLDPIIGRDEEIS  223
consensus                                       *** ***** **** *  * ***  ***             ****  *** ** !*****!!**!******!*!!!* !!*
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NTDB id 378 SMU RS02690 WP 002263569.1          RVIEILNRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGDVPQKLHGKNVIRLDVVSLVQGTGIRGQFEERMQKLMEEIRQ   221
NTDB id 85 BSU 00860 NP 387967.1                RVIEVLSRRTKNNPVLIGEPGVGKTAIAEGLAQQIINNEVPEILRDKRVMTLDMGTVVAGTKYRGEFEDRLKKVMDEIRQ   270
NTDB id 610 V4T04 RS10165 WP 012897346.1        RLIHILSRRTKNNPVLVGEPGVGKSAIIEGLAQRIVNGQVPIGLMNSRIMALNMATVVAGTKFRGEFEDRLTAIVEEVSS   283
NTDB id 287 SP RS11210 WP 001109712.1           RMIQILSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEE   296
NTDB id 290 KZH43 RS10025 WP 001109677.1        RMIQILSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEE   296
NTDB id 289 SPD RS10700 WP 001109677.1          RMIQILSRKTKNNPVLVGDAGVGKTALALGLAQRIASGDVPAEMAKMRVLELDLMNVVAGTRFRGDFEERMNNIIKDIEE   296
NTDB id 377 SMU RS09275 WP 002262344.1          RMVQILSRKTKNNPVLVGDAGVGKTALAYGLAQRIVDSAVPFELADMKVLELDMMSVVAGTRFRGDFEERMNQIIADIEA   300
NTDB id 297 STER RS00545 WP 011680614.1         RMIQVLSRKTKNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEA   303
NTDB id 1130807 H0502 RS07805 WP 179970783.1    RMIQILSRKTKNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEA   303
NTDB id 329 STU RS10020 WP 011225298.1          RMIQVLSRKTKNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRILELDMMSVVAGTRFRGDFEERMNQIIDEIEA   303
consensus                                       !****!*!*!!!!!!!*!**!!!!*!***!!!!*!****!! *********!*****!*!!**!!*!!*!*********
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NTDB id 378 SMU RS02690 WP 002263569.1          RQDVILFIDEIHEIVGAGSAGDGNMDAGNILKPALARGELQLVGATTLNEYR.IIEKDAALERRMQPVKVDEPSVAETIT   300
NTDB id 85 BSU 00860 NP 387967.1                AGNIILFIDELHTLIGAGG.AEGAIDASNILKPSLARGELQCIGATTLDEYRKYIEKDAALERRFQPIQVDQPSVDESIQ   349
NTDB id 610 V4T04 RS10165 WP 012897346.1        DPDVIIFIDELHTIIGAGGGMDSVNDAANILKPALARGDFQMVGATTYHEYQKYIEKDEALERRLARINVDEPSPDEAIA   363
NTDB id 287 SP RS11210 WP 001109712.1           DGQVILFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMT   376
NTDB id 290 KZH43 RS10025 WP 001109677.1        DGQVILFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMT   376
NTDB id 289 SPD RS10700 WP 001109677.1          DGQVILFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMT   376
NTDB id 377 SMU RS09275 WP 002262344.1          DGHIVLFIDELHTIMGSGSGIDSTLDAANILKPALARGSLRTIGATTQEEYQKHIEKDAALSRRFAKVTIEEPSEEEAYQ   380
NTDB id 297 STER RS00545 WP 011680614.1         DGKIILFIDELHTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAID   383
NTDB id 1130807 H0502 RS07805 WP 179970783.1    DGKIILFIDELHTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAID   383
NTDB id 329 STU RS10020 WP 011225298.1          DGKIILFIDELHTIIGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFAKITIEEPSVSEAID   383
consensus                                       ** ***!!!!*!***!*!*******!!*!!!!!*!!!!** **!!!!**!!***!!!!*!!*!!********!!* ***
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NTDB id 378 SMU RS02690 WP 002263569.1          ILKGIQPKYEDYHHVKYTDEAIEAAANLSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFVD..PKEIDHRLIEAENLKAQ   378
NTDB id 85 BSU 00860 NP 387967.1                ILQGLRDRYEAHHRVSITDDAIEAAVKLSDRYISDRFLPDKAIDLIDEAGSKVRLRSFTTPPNLKELEQKLDEVRKEKDA   429
NTDB id 610 V4T04 RS10165 WP 012897346.1        ILQGLREKFEDYHQVKFTDQAIKSAVMLSVRYMTSRKLPDKAIDLLDEAAAAVKISVKNQQTKRLDLEKELAEAQEELSE   443
NTDB id 287 SP RS11210 WP 001109712.1           ILQGLKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL....S....PADK   448
NTDB id 290 KZH43 RS10025 WP 001109677.1        ILQGLKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL....S....PADK   448
NTDB id 289 SPD RS10700 WP 001109677.1          ILQGLKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKADDSDL....S....PADK   448
NTDB id 377 SMU RS09275 WP 002262344.1          ILLGLKKSYETYHHVIISDAAVMAAVKGAHRYLSGKNLPDSAIDLLDEASATVQGLVKK..KAPAYL....T....DLDH   450
NTDB id 297 STER RS00545 WP 011680614.1         ILNGLRSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EDKREI....T....PLDE   453
NTDB id 1130807 H0502 RS07805 WP 179970783.1    ILNGLRSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EAKREI....T....PLDE   453
NTDB id 329 STU RS10020 WP 011225298.1          ILNGLRSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSAIDLLDEASATVQVRIKK..EAKREI....T....PLDE   453
consensus                                       !!*!** **!**!*! **!*!***!******!!**** !!!*!!!!*!!!********* *** * ***
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logo
NTDB id 378 SMU RS02690 WP 002263569.1          ATRDEDYEKAAYFRDQIAKYKEMQS......AKLDKENTPVITEKNIEVIVEQKTNIPVGELKEKEQSQLIHLADDLKTR   452
NTDB id 85 BSU 00860 NP 387967.1                AVQSQEFEKAASLRDTEQRLREQVEDTKKSWKEKQGQENSEVTVDDIAMVVSSWTGVPVSKIAQTETDKLLNMENILHSR   509
NTDB id 610 V4T04 RS10165 WP 012897346.1        AVIKLDIKASRTKEKAVEKIADKIYKF.....SVKEDKRQEVTDQAVVAVASTLTGVPITQMTKSESDRLINLEKELHKR   518
NTDB id 287 SP RS11210 WP 001109712.1           ALMDGKWKQAAQLIAKE.........E.....EVP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKR   513
NTDB id 290 KZH43 RS10025 WP 001109677.1        ALMDGKWKQAAQLIAKE.........E.....EVP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKR   513
NTDB id 289 SPD RS10700 WP 001109677.1          ALMDGKWKQAAQLIAKE.........E.....EVP.VYKDLVTESDILTTLSRLSGIPVQKLTQTDAKKYLNLEAELHKR   513
NTDB id 377 SMU RS09275 WP 002262344.1          ALITNDYQLAKRLLKKE.........K.....KPLLKKRAEVKEEDILATLSKLSGIPVKKLTQADSKKYLNLERELHKR   516
NTDB id 297 STER RS00545 WP 011680614.1         ALISGDIGAAVKQYKAN.........Q.....KAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKR   519
NTDB id 1130807 H0502 RS07805 WP 179970783.1    ALISGDIGAAVKQYKAN.........Q.....KAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKR   519
NTDB id 329 STU RS10020 WP 011225298.1          ALISGDIGAAVKQYKAN.........Q.....KAKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKR   519
consensus                                       !******  ** * * *                **   ** ******** ********!* ************** *!**!
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logo
NTDB id 378 SMU RS02690 WP 002263569.1          VIGQDAAVDKIAKAIRRNRVGLGTPNRPIGSFLFVGPTGVGKTELSKQLAIELFGSEDSMIRFDMSEYMEKHAVAKLVGA   532
NTDB id 85 BSU 00860 NP 387967.1                VIGQDEAVVAVAKAVRRARAGLKDPKRPIGSFIFLGPTGVGKTELARALAESIFGDEESMIRIDMSEYMEKHSTSRLVGS   589
NTDB id 610 V4T04 RS10165 WP 012897346.1        VVGQEEAISAVSRAIRRARSGVADSRRPMGSFMFLGPTGVGKTELAKALADSVFGSEDNMIRVDMSEFMEKHSTSRLIGA   598
NTDB id 287 SP RS11210 WP 001109712.1           VIGQDQAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGA   593
NTDB id 290 KZH43 RS10025 WP 001109677.1        VIGQDQAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGA   593
NTDB id 289 SPD RS10700 WP 001109677.1          VIGQDQAVSSISRAIRRNQSGIRSHKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGA   593
NTDB id 377 SMU RS09275 WP 002262344.1          VIGQDDAVSSISRAIRRNQSGIRVGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALIRFDMSEYMEKFAASRLNGA   596
NTDB id 297 STER RS00545 WP 011680614.1         VIGQDEAVSAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGA   599
NTDB id 1130807 H0502 RS07805 WP 179970783.1    VIGQDEAVSAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGA   599
NTDB id 329 STU RS10020 WP 011225298.1          VIGQDEAVSAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKALAEVLFDDESALLRFDMSEYMEKFAASRLNGA   599
consensus                                       !*!!**!******!*!!***!***  *!!*!!!*!*!!!!!!!!!!***!!***!**!****!*!!!!*!!!*****!*!*
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logo
NTDB id 378 SMU RS02690 WP 002263569.1          PPGYVGYEEAGQLTEKVRRNRPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGK..SEA   610
NTDB id 85 BSU 00860 NP 387967.1                PPGYVGYDEGGQLTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNK   669
NTDB id 610 V4T04 RS10165 WP 012897346.1        PPGYVGYDEGGQLTERVRNKPYSVVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDK   678
NTDB id 287 SP RS11210 WP 001109712.1           PPGYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDK   673
NTDB id 290 KZH43 RS10025 WP 001109677.1        PPGYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDK   673
NTDB id 289 SPD RS10700 WP 001109677.1          PPGYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDK   673
NTDB id 377 SMU RS09275 WP 002262344.1          PPGYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDK   676
NTDB id 297 STER RS00545 WP 011680614.1         PPGYVGYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDK   679
NTDB id 1130807 H0502 RS07805 WP 179970783.1    PPGYVGYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDK   679
NTDB id 329 STU RS10020 WP 011225298.1          PPGYVGYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDK   679
consensus                                       !!!!!!!*!*!*!!!*!!**!!!**!*!!*!!!!!!*****!!*!*!!**!!**!!*!*!**!!*!!!!!*!********
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NTDB id 378 SMU RS02690 WP 002263569.1          NVGFGASREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFQALSKDNLLQIVSLMLDDVNQRLAVNAIHLDVTDKVKE   685
NTDB id 85 BSU 00860 NP 387967.1                YVGFNVQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKA   749
NTDB id 610 V4T04 RS10165 WP 012897346.1        TVGFGAKNITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLIKRLAEQDIHVKLTPSAVK   758
NTDB id 287 SP RS11210 WP 001109712.1           TVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLTEKGIDLKLQASALK   753
NTDB id 290 KZH43 RS10025 WP 001109677.1        TVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALK   753
NTDB id 289 SPD RS10700 WP 001109677.1          TVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALK   753
NTDB id 377 SMU RS09275 WP 002262344.1          TVGFGAKSFSQDYKAMESRILEELKKVYRPEFINRIDEKVVFHNLGQEDIRHIVKIMVAPLIAHLADQGITLKFQPSALK   756
NTDB id 297 STER RS00545 WP 011680614.1         TVGFGAQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALK   759
NTDB id 1130807 H0502 RS07805 WP 179970783.1    TVGFGAQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALK   759
NTDB id 329 STU RS10020 WP 011225298.1          TVGFGAQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALK   759
consensus                                       *!!!*** ** *  **  ****!!** **!!!*!!*!****!**!* * * **!**!*****  !***************

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NTDB id 378 SMU RS02690 WP 002263569.1          KLVDLGYDPKMGARPLRRTIQEHIEDAITDFYLEHPEQKEL.KAIMTSNGKIVIKASNKVETVTKATSD   753
NTDB id 85 BSU 00860 NP 387967.1                KVAEEGVDLEYGARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN........   810
NTDB id 610 V4T04 RS10165 WP 012897346.1        LIAEVGFDPEYGARPLRKALQKEVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV...........   816
NTDB id 287 SP RS11210 WP 001109712.1           LLANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIGVKAGQLKFDIA............   810
NTDB id 290 KZH43 RS10025 WP 001109677.1        LLANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA............   810
NTDB id 289 SPD RS10700 WP 001109677.1          LLANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA............   810
NTDB id 377 SMU RS09275 WP 002262344.1          HLALAGYDAEMGARPLRRTLQTEVEDKLAELILSGKLASGQTLKIGIQKEKLKFDIV............   813
NTDB id 297 STER RS00545 WP 011680614.1         HLAKDGYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV............   816
NTDB id 1130807 H0502 RS07805 WP 179970783.1    HLAKDGYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV............   816
NTDB id 329 STU RS10020 WP 011225298.1          HLAKDGYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV............   816
consensus                                        **  !*!***!!!!!!***!***!!******! * ** ********* ***** **
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X non conserved

X similar

X ≥ 50% conserved