```
logo
NTDB id 1168 A1552VC RS11070 WP 000957200.1    ........MLTNLVAILRQAELISATQEQAVVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSRYDYANL    72
NTDB id 1293 VP RS12240 WP 005479695.1         ........MHSNLSTILRQKGLLTFSQEESLIEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPFLSQYEYASL    72
NTDB id 1401 DSB67 RS12665 WP 010643259.1      ........MLINLSTVLRQAGILTFSQEESLLEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQYEYASL    72
NTDB id 1110 NGFG RS09235 WP 003689817.1       ........MSVGLLRILVQNQVVTVEQAEHYYNES.QAGKEVLPMLFSDGVISPKSLAALIARVFSYSILDLRHYPRHRV    71
NTDB id 1251 GC085 RS07725 WP 011946523.1      MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAAQNFGVPMLDINCIDVGTI    80
NTDB id 1061389 ACGB44 RS05325 WP 394375547.1 ...MSENTSLSGLARQMVAAGVLDEKTAQQAQAQAIRGKTPFVTYVVQNRLAKGRVIAELASEQFGVALLDLAALDKESL    77
NTDB id 1058 ABD1 RS01615 WP 001274986.1       MSALHTSPKFTGFFRRLVEEKHVSAATMQTALDAAKRAKQDTVAYLIEEVHLSPSLLAETISAEFAEPYFDLDVYDTSQI    80
NTDB id 1018 ACIAD RS01685 WP 004920473.1      MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEIISLEFGEPLLDLGVFDPALF    80
consensus                                                 ***  ***   ***  *    *         **  **     *   *** **  !**   **  ** * *

logo
NTDB id 1168 A1552VC RS11070 WP 000957200.1    CQQLGLRELITRYDALPIAKQGNLLLLAVSDPTLLQAEEEFRFATGLQVELALADHRALQAAIRRLYGRSIQGAANQGKE   152
NTDB id 1293 VP RS12240 WP 005479695.1         CQQLGLRELITRHNALPLHRTPSTLLLAVADPTNQQAEDDFRFATGLQVELVLADFRELSTAIRRLYGRSLSHEKSGLKE   152
NTDB id 1401 DSB67 RS12665 WP 010643259.1      CQTLGLRDLITRHNALPLNRTSSTLILAVADPTNLQAEDDFRFATGLQVELVLADFRELTAAIRRLYGRSLGQEKSGLKE   152
NTDB id 1110 NGFG RS09235 WP 003689817.1       LMGVLTEEQMVEFHCVPVFRRGDKVFFAVSDPTQMPQIQKTVSAAGIAVELVIVEDDQLAGLLDWVGSRSTSLL.QELGE   150
NTDB id 1251 GC085 RS07725 WP 011946523.1      PVNLVNEKLIKRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSEYVE   160
NTDB id 1061389 ACGB44 RS05325 WP 394375547.1 PKDLVSEKLAKQHRVLPLSKRGTKLYVAVSDPANHQSIADIQFSTGLSIEPILVEDDKLGEAIDKLYDSGATGL...EDL   154
NTDB id 1058 ABD1 RS01615 WP 001274986.1       PKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSKLLVEPVIVEHHKLEKVLGQHFAEESSFD...FND   157
NTDB id 1018 ACIAD RS01685 WP 004920473.1      LKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSKLKVEPIIVEHDKLERLLSEHFVEETHFN...FDT   157
consensus                                         **   ** **  *!* ***  ***!***!*** **** ** *** ** ****   !   *  **    *       *

logo
NTDB id 1168 A1552VC RS11070 WP 000957200.1    ISQDELAN..LVKVSDDELQSIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRLRCDGILVETQQPASHL   230
NTDB id 1293 VP RS12240 WP 005479695.1         INQEELAS..LVDVGADEIDNIEDLSQDESPVSRYINQILLDAVRKGASDIHFEPYEKMYRVRLRCDGILIETQQPPNHL   230
NTDB id 1401 DSB67 RS12665 WP 010643259.1      INQDELAG..LVDIGEDEIENIEDLSQDESPVSRYINQILLDAVRKGASDIHFEPYENMYRVRLRCDGILIEIQQPPSHL   230
NTDB id 1110 NGFG RS09235 WP 003689817.1       GQ.EE.........EESHTLYIDNEEAEDGPVPRFIHKTLSDALRSGASDIHFEFYEHNARIRFRVDGQLREVVQPPIAV   220
NTDB id 1251 GC085 RS07725 WP 011946523.1      DS.GDLEGLEISADDEDQDIDTATSVTDDAPIVKFVNKILLDAIRQGASDIHFEPYEREYRIRYRQDGILHEVATPPASL   239
NTDB id 1061389 ACGB44 RS05325 WP 394375547.1 GE.VDLDGLDVESVSDDGRADDAGEVADDAPVVRFVNKMLLDAIRGGSSDLHFEPYERAYRVRFRTDGILHEIARPPIQL   233
NTDB id 1058 ABD1 RS01615 WP 001274986.1       EE.FDLDVN.LDG.PTAQEDEEEAPQGDEAPIVKYINKLLIDAIRMGASDLHFEPYEKSYRVRYRVDGVLRQIANPPLQL   234
NTDB id 1018 ACIAD RS01685 WP 004920473.1      EE.LDLDVE.VDP.HTTDDDDEDDKLKDEAPIVKYINKLLIDAIRMSASDLHFEPYEKSYRVRYRVDGVLRLIATPPLQL   234
consensus                                         **    *    **     *    ***!* ******!*!!*! **!!*!!!*!!* *!*!*! !!*! ** *!*   *

logo
NTDB id 1168 A1552VC RS11070 WP 000957200.1    SRRLAARIKILSKLDIAERRLPQDGRIKLRLSR.DTAIDMRVSTLPTLWGEKIVLRLLDSSAANLDIDKLGYNPQQKQLY   309
NTDB id 1293 VP RS12240 WP 005479695.1         SRRLSARIKILSKLDIAERRLPQDGRIKLKLNQ.DTAIDMRVSTLPTLFGEKIVLRLLDSSSASLDIDKLGYSEQQKQLY   309
NTDB id 1401 DSB67 RS12665 WP 010643259.1      SRRLSARIKILSKLDIAERRLPQDGRIKLKLNQ.DTAIDMRVSTLPTLFGEKIVLRLLDSSSAALDINKLGYSDSQKQLY   309
NTDB id 1110 NGFG RS09235 WP 003689817.1       RGQLASRIKVMSRLDISEKRIPQDGRMQLTFQKGGKPVDFRVSTLPTLFGEKVVMRILNSDAASLNIDQLGFEPFQKKLL   300
NTDB id 1251 GC085 RS07725 WP 011946523.1      SSRITARIKVMSNLDISERRIPQDGGFKMKISK.SRAIDFRVSTCPTSAGEKVVMRVLDSGAAKLGIEALGFNPVQRTNF   318
NTDB id 1061389 ACGB44 RS05325 WP 394375547.1 APRISARLKVMAGLDISERRKPQDGRIKMKLSK.TKAIDFRVNTLPTLWGEKIVMRILDPSSAQMGIDALGYEEEQKALY   312
NTDB id 1058 ABD1 RS01615 WP 001274986.1       ANRLASRLKVMSQMDISEKRVPQDGRIKLKLSK.SKAIDFRVNSLPTLFGEKLVLRILDPSSAMLGIDALGYEEDQKALF   313
NTDB id 1018 ACIAD RS01685 WP 004920473.1      ATRLASRLKVMSQMDISEKRVPQDGRIKLKMSK.SKTIDFRVNSLPTLFGEKIVLRILDPASAMLGIDALGYEPEQKALF   313
consensus                                        ** *!*!*** *!!*!*!*!!!!******** ***!*!!***!!**!!!*!*!*!****! * !* !!*   !* **
```

```
logo
NTDB id 1168 A1552VC RS11070 WP 000957200.1     LNALKRPQGMILMTGPTGSGKTVSLYTGLRILNTSQINISTAEDPVEINLSGINQVQVQPKIGFGFAEALRSFLRQDPDV   389
NTDB id 1293 VP RS12240 WP 005479695.1          LEALRRPQGMILMTGPTGSGKTVSLYTGLNILNKPEINISTAEDPVEINLSGINQVQVQPKIGFGFAEALRSFLRQDPDV   389
NTDB id 1401 DSB67 RS12665 WP 010643259.1       LDALRRPQGMILMTGPTGSGKTVSLYTGLSILNKPEINISTAEDPVEIYLPGINQVQVQPKIGFGFAEALRSFLRQDPDV   389
NTDB id 1110 NGFG RS09235 WP 003689817.1        LEAIHRPYGMVLVTGPTGSGKTVSLYTCLNILNTESVNIATAEDPAEINLPGINQVNVNDKQGLTFAAALKSFLRQDPDI   380
NTDB id 1251 GC085 RS07725 WP 011946523.1       LKAIQRPQGMILVTGPTGSGKTVTLYTALNILNTIEVNISTAEDPVEIKVPGINQVNINPKAGLTFSGALRSFLRQDPDI   398
NTDB id 1061389 ACGB44 RS05325 WP 394375547.1   MQALQQPQGMILVTGPTGSGKTVSLYTGLNILNTVDVNISTAEDPVEINLEGINQVNVNPRQGMDFSQALRAFLRQDPDI   392
NTDB id 1058 ABD1 RS01615 WP 001274986.1        MEALDKPQGMLLITGPTGSGKTVSLYTGLNILNTESSNISTAEDPVEINLEGINQVNVNPKVGLTFAAALKSFLRQDPDI   393
NTDB id 1018 ACIAD RS01685 WP 004920473.1       MEALNKPQGMLLITGPTGSGKTVSLYTGLNILNTEHANISTAEDPVEINLEGVNQVNVNPKVGLTFAAALRSFLRQDPDI   393
consensus                                       **!* *!*!!*!*!!!!!!!!!!*!!!*!*!!!*  *!!*!!!!!*!!** !*!!!*****!* !* !!**!!!!!!!*

logo
NTDB id 1168 A1552VC RS11070 WP 000957200.1     VMVGEIRDLETAEIAVKAAQTGHLVLSTLHTNSAAETVIRLANMGVEPFNLASSLSLIIAQRLARRLCKHCKIAV.RPSA   468
NTDB id 1293 VP RS12240 WP 005479695.1          VMVGEIRDLDTAEIAIKASQTGHLVLSTLHTNSAAETIIRLSNMGVESFNLASSLSLIIAQRLARKLCPYCKQPQ.EHTV   468
NTDB id 1401 DSB67 RS12665 WP 010643259.1       VMVGEIRDLDTAEIAIKASQTGHLVLSTLHTNSAAETVIRLSNMGVESFNLASSLSLIIAQRLARKLCPYCRQPQ.EPNS   468
NTDB id 1110 NGFG RS09235 WP 003689817.1        IMVGEIRDLETADIAIKAAQTGHMVFSTLHTNNAPATLSRMLNMGVAPFNIASSVSLIMAQRLLRRLCSSCKQEVERPSA   460
NTDB id 1251 GC085 RS07725 WP 011946523.1       IMVGEIRDLETAEIAIKAAQTGHLVLSTLHTNSAAETLNRLVNMGIPTFNIASSVTLIIAQRLARKLCNQCKAVRDDFTN   478
NTDB id 1061389 ACGB44 RS05325 WP 394375547.1   IMVGEIRDLETAEIAIKAAQTGHMVMSTLHTNSAAETLTRLRNMGVAAFNIATSVNLIIAQRLARKLCNSCKKEI.DLPR   471
NTDB id 1058 ABD1 RS01615 WP 001274986.1        IMVGEIRDLETAEIAIKAAQTGHMVMSTLHTNSAPETLTRLRNMGVPSFNIATSVNLVIAQRLARRLCSQCKIPA.DIPK   472
NTDB id 1018 ACIAD RS01685 WP 004920473.1       IMVGEIRDLETAEIAIKAAQTGHLVMSTLHTNNAAETLTRLRNMGVASFNIATSVNLVIAQRLARRLCSQCKRPI.QVPE   472
consensus                                       *!!!!!!!!*!!*!!*!!*!!!!!*!*!!!!!!*!**!*  !*  !!!*  *!!*!*!**!**!!!!*!*!!   !*     *

logo
NTDB id 1168 A1552VC RS11070 WP 000957200.1     LLQSQFAFQPNEI....LYEANAAGCNECTG.GYSGRVGIYEVMAFNTELAEAIMQRASIHQIERLAKANGMQTLQESGL   543
NTDB id 1293 VP RS12240 WP 005479695.1          QL.QHLGIQTTDN....IFRANPDGCNECTH.GYSGRTGIYEVMRFDESLSEALIKGASVHELEKLAIANGMSTLQMSGI   542
NTDB id 1401 DSB67 RS12665 WP 010643259.1       QL.QHIGIANTEQ....IFQANPDGCNECTH.GYSGRTGIYEVMKFDESLSEALIKGASVHELEKLAIANGMQTLQMSGI   542
NTDB id 1110 NGFG RS09235 WP 003689817.1        SALKEVGFTDEDLA.KDWKLYRAVGCDRCRGQGYKGRAGVYEVMPISEEMQRVIMNNGTEVGILDVAYKEGMVDLRRAGI   539
NTDB id 1251 GC085 RS07725 WP 011946523.1       QGLIELGFKEADL..VNLKLYKAVGCEQCTS.GYRGRVGLFEVLPMTKELGQLIMSGGNSLDILKLAQSEGMLTIFQSGI   555
NTDB id 1061389 ACGB44 RS05325 WP 394375547.1   EALLEEGFPADKI..GAFKIYGPVGCDNCKG.GYKGRVGIYEVVKNTPALARIIMEDGNSIDISTQMRKDGFNDLRTSAL   548
NTDB id 1058 ABD1 RS01615 WP 001274986.1        QSLLEMGFTEQDLAHPDFRVFQPVGCLECRE.GYKGRVGIYEVMKVTPEISKIIMEDGNALEIAAASEKLGFNNLRRSGL   551
NTDB id 1018 ACIAD RS01685 WP 004920473.1       RSLLEMGFTPEDLAQPEFQIFEPVGCHDCRE.GYKGRVGIYEVMKITPEISKIIMEDGNALEIAATAETLGFNNLRRSGL   551
consensus                                         * ****   **       ** **!! *!    !!*!!*!**!!** * **  ***  *  ***  **   !** *  ***

logo
NTDB id 1168 A1552VC RS11070 WP 000957200.1     EKLREGITSFAELQRVLYF   562
NTDB id 1293 VP RS12240 WP 005479695.1          EKLKQGITSFSELQRVLYF   561
NTDB id 1401 DSB67 RS12665 WP 010643259.1       EKLKQGITSFRELQRVLYF   561
NTDB id 1110 NGFG RS09235 WP 003689817.1        LKIMQGITSLEEVTANTND   558
NTDB id 1251 GC085 RS07725 WP 011946523.1       EKVKEGITTIEEVNRVTVD   574
NTDB id 1061389 ACGB44 RS05325 WP 394375547.1   LKAMQGVTSLEEVNRVTKD   567
NTDB id 1058 ABD1 RS01615 WP 001274986.1        KKVMQGVTSLQEVNRVTSE   570
NTDB id 1018 ACIAD RS01685 WP 004920473.1       KKVMQGVTSLQEINRVTSE   570
consensus                                        !* *!*!** !***** *
```

X non conserved
X similar
X $\geq$50% conserved