```
logo
                                                  MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK
NTDB id 1028 TT RS08215 WP 011173991.1            MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK    80
NTDB id 1384 A4U84 RS08525 WP 010787006.1         ..................................................................................     0
NTDB id 373197 FOG69 RS12075 WP 013352872.1       ..................................................................................     0
NTDB id 96 BSU 24730 NP 390353.1                  ..................................................................................     0
consensus


logo
                                                  ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG
NTDB id 1028 TT RS08215 WP 011173991.1            ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG   160
NTDB id 1384 A4U84 RS08525 WP 010787006.1         ..................................................................................     0
NTDB id 373197 FOG69 RS12075 WP 013352872.1       ..................................................................................     0
NTDB id 96 BSU 24730 NP 390353.1                  ..................................................................................     0
consensus


logo
                                                  EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL
NTDB id 1028 TT RS08215 WP 011173991.1            EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL   240
NTDB id 1384 A4U84 RS08525 WP 010787006.1         ..................................................................................     0
NTDB id 373197 FOG69 RS12075 WP 013352872.1       ..................................................................................     0
NTDB id 96 BSU 24730 NP 390353.1                  ..................................................................................     0
consensus


logo
                                                  LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYLALPQAWEELFRRAYPQKNRLGEVLVQEGKLSREAL
NTDB id 1028 TT RS08215 WP 011173991.1            LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYLALPQAWEELFRRAYPQKNRLGEVLVQEGKLSREAL   320
NTDB id 1384 A4U84 RS08525 WP 010787006.1         ..................................................................................     0
NTDB id 373197 FOG69 RS12075 WP 013352872.1       ..................................................................................     0
NTDB id 96 BSU 24730 NP 390353.1                  ..................................................................................     0
consensus


logo
                                                                                                                  QSQYTYVEQQTER
                                                  KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATMLGYPYCDPEEDPI
NTDB id 1028 TT RS08215 WP 011173991.1            KEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEEDP.   399
NTDB id 1384 A4U84 RS08525 WP 010787006.1         ..............................................................MSQYTICEQQTERI    14
NTDB id 373197 FOG69 RS12075 WP 013352872.1       ..................................................................................     0
NTDB id 96 BSU 24730 NP 390353.1                  ..................................................................................     0
consensus                                                                                                          *   *   *


logo
                                                  FDISPDPGAKLCEEEDLCLRYGAFPHQEEEHKLVLAMDDENNTLACDDFAFALKHKGLNKEIAPAVAAEAATKKLTNALS
NTDB id 1028 TT RS08215 WP 011173991.1            ....PDPGAPLLLPEDLCRRYGVFPHRLEGNRLVLLMKDPRNILALDDVRLALKRKGLNYEVAPAVATEAAITKLI....   471
NTDB id 1384 A4U84 RS08525 WP 010787006.1         FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVDDENNLTACEIFAFM.TH....KQIEPVVIASDELKYLLNALS    89
NTDB id 373197 FOG69 RS12075 WP 013352872.1       ..................................................................................     0
NTDB id 96 BSU 24730 NP 390353.1                  ..................................................................................     0
consensus                                             *           *  **   *      ** * * *  ** * *              * * *     *  **
```

```
logo
NTDB id 1028 TT RS08215 WP 011173991.1        ...ERFYGKAELSEIAKEFAKKQAEEEVPSPLELDESAAQKFVKQVIREAFLQDASDIHIEPRQNDVQVRLRIDGALRPY   548
NTDB id 1384 A4U84 RS08525 WP 010787006.1     PEQQPIYEESELAFVEQ..........EQEQLNLN.DPIIQLLDNLFKFCLAQNASDIHIEPRKQKLIIRLRIDGVLHLY   158
NTDB id 373197 FOG69 RS12075 WP 013352872.1  ................................M.ENIETYSRNIINEAYMARASDIHIVPRERDAFIHFRIGHALVKK    45
NTDB id 96 BSU 24730 NP 390353.1              ................................M.DSIEKVSKNLIEEAYLTKASDIHIVPRERDAIIHFRVDHALLKK    45
consensus                                          *   **  *                * ** * *** **********!!!!!! !!******* !****!**

logo
NTDB id 1028 TT RS08215 WP 011173991.1        STLPKGALNAVISVVKIMGGLNIAEKRLPQDGRVRYREG.AIDVDLRLSTLPTVYGEKAVMRLLKKASDIPEIEDLGFAP   627
NTDB id 1384 A4U84 RS08525 WP 010787006.1     KSLSIQLASRLISRIKLLAKLDISELRQPQDGQFSFTTALADTLDFRVSSLPTIYGEKLVLRLQKNKPTSFDFLQLGFNP   238
NTDB id 373197 FOG69 RS12075 WP 013352872.1  RVLKKEECVRLISHFKFLSAMDIGERRKPQNGSLSLPLP.TETVHLRMSTLPTMNDESLVIRLLPKRQI.PPLDKLSLFP   123
NTDB id 96 BSU 24730 NP 390353.1              RDMKKEECVRLISHFKFLSAMDIGERRKPQNGSLTLKLK.EGNVHLRMSTLPTINEESLVIRVMPQYNI.PSIDKLSLFP   123
consensus                                     ***********!!**!******!*!*!*!! !******* ******!*!*!!!* *! *!*!******* *****!   *!

logo
NTDB id 1028 TT RS08215 WP 011173991.1        GVFERFKEVISKPYGIFLITGPTGSGKSFTTFSILKRIA.TPDKNTQTIEDPVEYEIPGINQTQVNPQAGLTFARALRAF   706
NTDB id 1384 A4U84 RS08525 WP 010787006.1     QQQTTLLNALKQPQGLILVTGPTGSGKSITLYSALNYLN.QMDKHILTAEDPVEIEIDGLIQTQVNRSIQLDFSQLLRTF   317
NTDB id 373197 FOG69 RS12075 WP 013352872.1  GAGAALLSFLKHSHGLLLFTGPTGSGKTTTLYSLVNYAKRHFNRRIVTLEDPVETRDEDVLQVQVNEKAGVTYSTGLKAI   203
NTDB id 96 BSU 24730 NP 390353.1              KTGATLLSFLKHSHGMLIFTGPTGSGKTTTLYSLVQYAKKHFNRNIVTLEDPVETRDEDVLQVQVNEKAGVTYSAGLKAI   203
consensus                                     * ************!****!!!!!!!!**!**!********* ****!*!!!!!*  * **! !!!******** *!**

logo
NTDB id 1028 TT RS08215 WP 011173991.1        LRQDPDIIMVGEIRDSETAKIATEAALTGHLVIATLHTNDAAQAITRLDEMGVEPFNISAALIGVLSQRLVRRVCEHCKV   786
NTDB id 1384 A4U84 RS08525 WP 010787006.1     LRQDPDIIMLGEIRDEESAKMALRASQTGHLVLSTLHTNDALSAVERLLQLGIQEYEIQNSLLLVIAQRLVRKLCKKCRG   397
NTDB id 373197 FOG69 RS12075 WP 013352872.1  LRHDPDMIILGEIRDAETAEIAVRAAMTGHLVLSSLHTRDAKGAIYRLLEFGVNMTEIEQTVIAIAAQRLVDLTCPFCKT   283
NTDB id 96 BSU 24730 NP 390353.1              LRHDPDMIILGEIRDAETAEIAVRAAMTGHLVLTSLHTRDAKGAIYRLLEFGINMNEIEQTVIAIAAQRLVDLACPFCEN   283
consensus                                     !!*!!!*!**!!!!!*!*! *!**!**!!!!!***!!! !!**!**!!***!*****!*********!!!! **!**!*

logo
NTDB id 1028 TT RS08215 WP 011173991.1        EVKPDPET....LRRLGLSEAEIQGARLYKGMGCERCGGTGYKGRYAIHELLVVDDEIRHAIVAGKSATEIKEIARRKGM   862
NTDB id 1384 A4U84 RS08525 WP 010787006.1     VGCDECYQGYRG..RIGVYQC.......LSRTAK......KFDKQTAYLDFSSLRESAKQKIEQQLTNET..........   452
NTDB id 373197 FOG69 RS12075 WP 013352872.1  DNCSVYCSLYRQTRRAGIYEL.......LYGKNLTQCFQ.EAKGEHANFQYQTLRRLIRKGIALGYVTTD..........   345
NTDB id 96 BSU 24730 NP 390353.1              GCSSVYCRQSRNTRRASVYEL.......LYGKNLQQCIQ.EAKGNHANYQYQTLRQIIRKGIALGYLTTN..........   345
consensus                                     * ****** *****!******        ****** ** * ******!**************!****  ***

logo
NTDB id 1028 TT RS08215 WP 011173991.1        KTLREDGLYKALQGITTLEEVLARTIE   889
NTDB id 1384 A4U84 RS08525 WP 010787006.1     ................EVDRVLGYE..   461
NTDB id 373197 FOG69 RS12075 WP 013352872.1  ................NYDRWVYHEAD   356
NTDB id 96 BSU 24730 NP 390353.1              ................NYDRWVYHEKD   356
consensus                                                     **** **** *
```

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