

logo

NTDB id 1401 DSB67 RS12665 WP 010643259.1
NTDB id 80257 L6484 RS21380 WP 001013200.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

MLTNLSTVLRQAGILTFSQEESLLEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQYEYASLCQTLGLRDLITRH
MLTNLSTVLRQAGILTFSQEESLLEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQYEYASLCQTLGLRDLITRH
.....
.....

85
0
0

logo

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NTDB id 96 BSU 24730 NP 390353.1
consensus

NALPLNRTSSTLILAVADPTNLQAEDDFRFATGLQVELVLADFRELTAAIRRLYGRSLGQEKSGLKEINQDELAGLVDIGEDEIE
NALPLNRTSSTLILAVADPTNLQAEDDFRFATGLQVELVLADFRELTAAIRRLYGRSLGQEKSGLKEINQDELAGLVDIGEDEIE
.....
.....

170
0
0

logo

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consensus

NIEDLSQDESPVSRYINQILLDAVRKGASDIHFEPYENMYRVRLRCDGILTEIQPPSHLSRRLSARIKILSKLDIAERRLPQDG
.....MNGIESFANMILKEACRVQASDLHIVPRQKDVVQLRTGKDLMTKYCTIEKEFGEKLVSHFKFLASMDIGERRKPQNG
.....MDSIEKVSKNLIEEAYLTKASDIHIVPRERDAIHFVRVDHALLKKRDMKKEECVRLISHFKFLSAMDIGERRKPQNG
* **** *! * !!!!!!***** ** *! ** !* * * ** *!*****! * *!*****!*

255
77
77

logo

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consensus

SLYLKLNQGVYLRSTLPTESLVRLLQYSISPSLSLFPSTKOTLSFLRSHGMLYFTGPTGSGKTTLLSY
RTKQVDEDAHMLMNGKTLLVHDSANAALDLHGYSDKQAARYDAKHPQLTLMVSMAGVEY
RIKLKLNQDTAIDMRVSTLPTLTFGEKIVLRLIDSSAALDINKLGYSDSQKQLYLDALRRPQGMILMTGPTGSGKTVSLYTGLST
SLYLQMDGQ.EVYLRSLTLPSTVYQESLVIRLHLQASI.QPLSHLSLFPSTAKKLLSFLRYSHGLLVFTGPTGSGKTTTMYALLEV
SLTLKLKEG.NVHLRMSLTPITNEESLVIRVMPQYNI.PSIDKLSLFPKTGATLLSFLKSHSGMLIFTGPTGSGKTTTLYSLVQY
** !** * *!***** *!*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!

340
160
160

logo

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consensus

LRKKPTNRNVLTEDPVEKRNPDVLRQVNEKAGYTYSAGLKAILRHPDPVIMVGEIRDLETAELAIRASQTGHLVLTHTNDAR
AKHFEIRSIATYDDGINIYIQPIIFGFAEARSFQQMVTLEADAKVKALMSSRSIA
LNK.PEINISTAEDPVEIYLPGINQVQVQPKIGFGFAEALRSFLRQDPDVVMVGEIRDLETAELAIRASQTGHLVLTHTNLSAA
IRKKKTRRIVTLEDPVEKRNDDVLQIQINEKAGITYEAGLKAILRHPDPVILVGEIRDEETAIAIRASLTGHLVMTTLHTNDAR
AKKHFNRNIVTLEDPVETRDEDLVQVQVNEKAGVTYSAGLKAILRHPDPMITLGEIRDAETAELAVRAAMTGHVLVLTSLHTRDAK
*! *!*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!

424
245
245

logo

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GAIYRLSNMFGITSEIEQSLAIAAQRLVLLCPFCRRPCTSVYRSRQVRAVWYELLYGNLQCLQEQASRTVTYQY
ETVTLFDMVEMFNLASTVTLITADKAAYENGQEPNLQKSHNTGINTTQTFQAEPDGCNEATHGYKECATIEHE
ETVIRLSNMGVESFNIASSLSLIIAQRLARKLCPYCRQPQEPNSQLQH..IGIA.NTEQIFQANPDGCNECTHGYSGRTGIYEV
GAILRFMDFGITRQIEEQSLAIAAQRLVELKCPFCRKRCST.LCKSMRQVRQASIVYELLYGYELKQ...AIKEANGECVTKHE
GAIYRLLEFGINMNEIEQTVIAIAAQRLVDLACPFCENGCSSVYCRQSRNTRRASVYELLYGKNLQQ...CIQEAQGNHANYQYQ
*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!

506
326
327

logo

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consensus



ⓧ non conserved
ⓧ similar
ⓧ ≥ 50% conserved