

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 345745 EXW27 RS21100 WP 078203155.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

MSQYTI CEQQTERI FDI SPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVD DENNL TACE I FAFMTHKQI EPVVIASDE
MSQYTI CEQQTERI FDISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVD DENNL TACE I FAFMTHKQI EPVVIASDE
.....
.....

80
0
0

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 345745 EXW27 RS21100 WP 078203155.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

LKYLLNAL SPEQQPI YEESELAFVEQEQLNLNNDPIIQLLDNLFKFC LAQNASDIHIEPRKQKLI IRLRIDGV LHLHYKS
LKYLLNAL SPEQQPI YEESELAFVEQEQLNLNNDPIIQLLDNLFKFC LAQNASDIHIEPRKQKLI IRLRIDGV LHLHYKS
.....
.....
MNSVELFANMIMKEACRVRASDLHIVPRKQDVAIQLRIGKDLITKRC
MDSIEKVSKNLIEEAYLTKASDIHIVPRERDAIIFHFRVDHALLKRRD
***** * ***** *!!!!!!* *!!!! *!!!! * *!!!!

160
47
47

logo

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NTDB id 96 BSU 24730 NP 390353.1
consensus

LSIQLASRLISR I KLLAKLDISELRQPQDQGSFTTALADT LDFRVSSLP TIYGEKLVLR LKQNKPTS FDFLQLGFNPQQ
LSIQLASRLISR I KLLAKLDISELRQPQDQGSFTTALADT LDFRVSSLP TIYGEKLVLR LKQNKPTS FDFLQLGFNPQQ
.....
.....
IEKEFGKLVSHFKFLASMDIGERRKPKQNGSLYLQIDGQEVYLRSLTPTVYQESLVIRLHLQASV.QPLSHLSLFPSS
MKKEECVRLISHFKFLSAMDIGERRKPKQNGSLTLKIK.EGNVHLRMSTLPTINEESLVIRVMPQYNI.PSIDKLSLFPKT
* *

240
125
125

logo

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consensus

QTLLSFLKSHGLLVFTGPTGSGKTTLYSLLQYARKQTRVYTL EDPVEQRKDGLLQ QMNEKAGY TYSIGL KAILR
QTLLSFLKSHGLLVFTGPTGSGKTTLYSLLQYARKQTRVYTL EDPVEQRKDGLLQ QMNEKAGY TYSIGL KAILR
.....
.....
AAKNAIQPQMTLVSI MAAVEVLKQHFDKHILTAEDPVEIEIDGLIQTQVNRSIQLD FSQLLRTFLR
AEKLLSFLKSHGLLVFTGPTGSGKTTMYALLEVARKWQTRRIITLEDPVEQRKDGLLQIQINEKAGITYKTGLKAILR
GATLLSFLKSHGMLIFTGPTGSGKTTLYSLVQYAKKHFNRNIVTLEDPVETREDVLQVQVNEKAGVTYSAGLKAILR
* *

319
205
205

logo

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consensus

HDPDIILG EIRDEETAKAVRASQ TGHVLVLTHTNDAKGAIYRLLQYGLTRY EIEQSLLAVAAQRILVRLKPCFCRGKC
HDPDIILG EIRDEETAKAVRASQ TGHVLVLTHTNDAKGAIYRLLQYGLTRY EIEQSLLAVAAQRILVRLKPCFCRGKC
.....
.....
QDPDIIMLGEIRDEESAKMALARASQTGHLVLTHTNDALS AVERLLQLGIQEYEIQNSLLLAVIAQRLVRLKCKKCRGVG
HDPDIILG EIRDEETAKAVRASLTGHVLTHTNDAKGAILRFMDYGITRQEIEQSLLAVAAQRILVRLKPCFCRGKC
HDPDIILG EIRDAETAETIAVRAAMTGHVLVLTSLHTRDAKGA IYRLLQYGLTRY EIEQSLLAVAAQRILVRLKPCFCRGKC
* *

399
285
285

logo

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consensus

STYCSYSRVRRASVYELLYGYNLQCKEASGHAHYYS TLRSYRKGIALGYLLETVYD RLVVVVYVEKD
STYCSYSRVRRASVYELLYGYNLQCKEASGHAHYYS TLRSYRKGIALGYLLETVYD RLVVVVYVEKD
.....
.....
ADVRSYGYKGIQIGIQCSRKALKAKQFKETVNLDFKSEETAKQKYEQQFTETDEVVVVLGHCKD
CD.ECYQGYRG.RIGVYQCLSRTA....KKFDKQATAYLDFSSLRSAKQKIEQQLTNETEVDRVLGYE..
AT.LCKSMRKVRQASIVYELLYGYELKQAIKEASGEHVYHYKTLESSVRKGYALGFLEEDVVV.....
SSVYCRQSRNTRRASVYELLYGKNLQCCIQAEGNHANYQYQTLRQIIRKGIALGYLTTNNYDRWVYHEKD
* *

461
347
356

[X] non conserved
[X] similar
[X] ≥ 50% conserved