

logo

NTDB id 1366 NTHI RS01950 WP 011271972.1
NTDB id 254830 CSW12 RS20820 WP 001013187.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

MTSYALLHTQRVTAQNGEIFTISPDLWERNQQQQSLLRYFALPLKEENNRLWLGVDLSNLSACETIAFITGKPVPEPIL
MTSYALLHTQRVTAQNGEIFTISPDLWERNQQQQSLLRYFALPLKEENNRLWLGVDLSNLSACETIAFITGKPVPEPIL
.....
.....

80
0
0

logo

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NTDB id 254830 CSW12 RS20820 WP 001013187.1
NTDB id 96 BSU 24730 NP 390353.1
consensus

LESSQLKELLQQLTPHQMVVEEQVKFYQHETHFEQEDD
LESSQLKELLQQLTPHQMVVEEQVKFYQHETHFEQEDD
.....
.....
MNSIERVSNTEEA YRVO ASDI HIVPRRORVYVROERVDKYL
EPGVTIFAKNLFKSLCLKKI LILLETADQAAIHLRIGGA
EPVIRLLNQIFESALQKNASDIHLETADQFQVRFRIIDGVL
MNGIEIFANTILKEACRVQASDLHIVPRQKDVAVQLRVGKDL
MDSIEKVSKNLIEEAYLTKASDIHIVPRERDAITHFRVDHAL

160
42
42

logo

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consensus

QTRRLI SKEE GYVRLI SHEKELASMDIGERRKPNQNGSLYLKTTG QNVY RLSTLPT YYQ ESLVIR VCCQYSVQ SLSKLS
MPQPD KME TEAEKTVRLI SALI SKLIL DRFQFQDESDELDFM HNE KTL LAHLNANITELPFAELG
LKKHCEI
QPQPLISKIFANRIISRLKLLAKLDISENRLPQDGRFQKTTFSIDLDFRLSTLPTHWGEKIVLRAQQNKPVELSFAELG
MTRHCIEKEFGKLVSHFKFLASMDIGERRKPNQNGSLYLQIDG.QEVYLRSLSTLPTVYQESLVIRLHLQASVQ.PLSHLS
LKKRD MKKEECVRLISHFKFLSAMDIGERRKPNQNGSLTLKLE.GNVHLRMSTLPTINEESLVIRVMPQYNIP.SIDKLS

240
120
120

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LFPSTQATLLSFLSYSQGLLYFTGPTGSGKTTTLYTLLQYLRKPTTRV TLEDPEERDDVLQVQINEKAGLTYSGL
MTEKQAQAFQRS KPHPMITV SISM SA AAVEVAKTHFDKHM ALI TEDEGIT SVV PQI VDFEAL
MTENQQQAFQRSLSQPQGLLIVTGTGSGKSI SLYTALQWLNT.PDKHIMTAEDPIEIELDGIISQINPQIGLDFSRLL
LFPSTA AAKLLSFLRYSQGLLIVTGTGSGKTTTMYALLEVIRKKTTRRIITLEDPEEKRSDDVLQIQINEKAGLTYESGL
LFPKTGATLLSFLKSHGMLIFTGPTGSGKTTTLYSLVQYAKKHFNRNIVTLEDPEVETREDVLQVQVNEKAGVTYSAGL

319
200
200

logo

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KAILRHDPDMLLGEIRDEETARAYRAASGHLVLTHTNDAKGAIYRLCOYGLTRQNEIEQSLLAVAAQRLVRLKCPF
RIFLQDM TV ASIE TSL MSS R TISS YFLDF NMH NTVLTITIT BKA K
RAFLRQDPDIIMLGEIRDEESARIALRAAQGTGHLVLTHTNDADSAISRLQQLGIQHEIENSLLLVIQRLVLRKICPK
KAILRHDPDIILVGEIRDEETAKIARASLTGHLVMTLHTNDAKGAIIRFMDYGITRQIEQSLLAVAAQRLVRLKCPF
KAILRHDPDMIILGEIRDAETAETAVRAAMTGHVLTSLHTRDAKGAIYRLLFEFGINMNEIEQTVIATAAQRLVDLACPF

399
280
280

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CGNCSYVYRSTRRASVYELLYGYNLQCLQEAQYQYQYETRSIRKGYALGYLTTNVYVDPVYKNS
ENGLINSCDHSYNYRQIGIQFHWKELKATKID ECANTDFQN EEI GLEKYSQFDBDE FVVLGHEKD
CGGNLINSCHQGY.RGRIGVYQFLHWQQ.....NGYQ..TDFENLRESGLEKVSQGITDEKEIERVIGKNS.
CRGKCSI..LCKSMRQVRQASVYELLYGYELKQALKEADGECVYKHELTLESSIRKGYALGFLEDVYV.....
CENGCSVYCRQSRNTRRASVYELLYGKNLQCCIQAEGNHNANYQYQTLRQIIRKGIALGYLTTNNYDRWVYHEKD

464
347
356

X non conserved
X similar
X ≥ 50% conserved