

logo

NTDB id 136256 RP72 RS05830 WP 003244988.1
NTDB id 120 BSU 10620 NP 388943.2
consensus

MGA EFLVGRSGSGKTKLIINSIQDELRRAPFGKPIIFLVPDQMTFLMEYELAKTPDMGGMIRAQVFSFSRLAWRVLQHTGGMSRP
MGA EFLVGRSGSGKTKLIINSIQDELRRAPFGKPIIFLVPDQMTFLMEYELAKTPDMGGMIRAQVFSFSRLAWRVLQHTGGMSRP
MGA EFLVGRSGSGKTKLIINSIQDELRRAPFGKPIIFLVPDQMTFLMEYELAKTPDMGGMIRAQVFSFSRLAWRVLQHTGGMSRP

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85

logo

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consensus

FLTSTGVQMLLRKLI EEHKQEFKVKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMASGTASEYRGERVLSEKLHDL SILYQ
FLTSTGVQMLLRKLI EEHKQEFKVKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMASGTASEYRGERVLSEKLHDL SILYQ
FLTSTGVQMLLRKLI EEHKQEFKVKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMASGTASEYRGERVLSEKLHDL SILYQ

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QMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKPSYEREPHELELFRMT
QMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKPSYEREPHELELFRMT
QMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKPSYEREPHELELFRMT

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G K T Y Y R L H Q K A K E L N L D I T Y K E L S G T E R H T K T P E L A H L E A Q Y E A R P A I P Y A E K Q E A L T V M Q A A N R R A E L E G I A R E I H A L V R E K G Y
 G K T Y Y R L H Q K A K E L N L D I T Y K E L S G T E R H T K T P E L A H L E A Q Y E A R P A I P Y A E K Q E A L T V M Q A A N R R A E L E G I A R E I H A L V R E K G Y
 G K T Y Y R L H Q K A K E L N L D I T Y K E L S G T E R H T K T P E L A H L E A Q Y E A R P A I P Y A E K Q E A L T V M Q A A N R R A E L E G I A R E I H A L V R E K G Y

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RYKDVAILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVLKGNWRYEAVFRCVKTELLFPLNEPKAKVREQ
RYKDVAILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVLKGNWRYEAVFRCVKTELLFPLNEPKAKVREQ
RYKDVAILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVLKGNWRYEAVFRCVKTELLFPLNEPKAKVREQ

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VDQLENYCIAYGIKGDRWTKGDRFQYRRFVSLDDDDFAQTDQEIEEMNMLNDTRDWIVPPLFQLQKRMKKAKTVQEKA EALYRYLE
VDQLENYCIAYGIKGDRWTKGDRFQYRRFVSLDDDDFAQTDQEIEEMNMLNDTRDWIVPPLFQLQKRMKKAKTVQEKA EALYRYLE

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ETDVPLKLDQERQRAEDDGR|EAQQHQQAWDAVIQLLEEFVEMMGDDE|ISLDFQQMIEAGAESLTFS|LPPALDQVFVGNMDL
ETDVPLKLDQERQRAEDDGR|IEAQQHQQAWDAVIQLLEEFVEMMGDDE|ISLDFQQMIEAGAESLTFS|LPPALDQVFVGNMDL
ETDVPLKLDQERQRAEDDGR|IEAQQHQQAWDAVIQLLEEFVEMMGDDE|ISLDFQQMIEAGAESLTFS|LPPALDQVFVGNMDL

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SRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELSSGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTLI
SRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELSSGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTLI
SRMYGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELSSGGRERLLDEHFLIYMAFSSPSDRLYVSYPIADAEGKTLI

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PSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNSVAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSS
PSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNSVAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSS
PSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNSVAQSFTASQLRLWTREYDISDVVWSTYNVLMSEQDRLQSKKLFSS

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LFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNACPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSSLKLISDRLEQKLDWRDLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNACPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSSLKLISDRLEQKLDWRDLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNACPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSSLKLISDRLEQKLDWRDL

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LTKEQCELFSDAVERLAPKLQKEILLSSNRHYVKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGC
LTKEQCELFSDAVERLAPKLQKEILLSSNRHYVKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGC
LTKEQCELFSDAVERLAPKLQKEILLSSNRHYVKEKLQKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGC

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935

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TMELVGRIDRVDKAESSKGILLRIVDYKSSDKGLDLAEVYGLALQMLTYLDLSITHSADWLGMRA TPAGVLYFHIHDPMIQSNL
TMELVGRIDRVDKAESSKGILLRIVDYKSSDKGLDLAEVYGLALQMLTYLDLSITHSADWLGMRA TPAGVLYFHIHDPMIQSNL
TMELVGRIDRVDKAESSKGILLRIVDYKSSDKGLDLAEVYGLALQMLTYLDLSITHSADWLGMRA TPAGVLYFHIHDPMIQSNL

1020
1020

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PLGLDEIEQEIFKKFKMKGLLLGDQEWRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITD
PLGLDEIEQEIFKKFKMKGLLLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITD
PLGLDEIEQEIFKKFKMKGLLLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITD

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GRVSI E P Y K M K N K T P C T Y C A F K S V C Q F D E S L E E N E Y R P L K A E K D K T I L E W I K K E A D G N E H S
GRVSI E P Y K M K N K T P C T Y C A F K S V C Q F D E S L E E N E Y R P L K A E K D K T I L E W I K K E A D G N E H S
GRVSI E P Y K M K N K T P C T Y C A F K S V C Q F D E S L E E N E Y R P L K A E K D K T I L E W I K K E A D G N E H S

1166
1166

 non conserved
 similar
 $\geq 50\%$ conserved