

logo

NTDB id 969241 MHB62 RS05655 WP 032721292.1
NTDB id 120 BSU 10620 NP 388943.2
consensus

MGAEFLVGRSGSGKTKLIINSIQDELRRAPFGKPIIFLVPDQMTFLMEYELAKTPDMGGMIRAQVFSFSRLAWRVLQHTG
MGAEFLVGRSGSGKTKLIINSIQDELRRAPFGKPIIFLVPDQMTFLMEYELAKTPDMGGMIRAQVFSFSRLAWRVLQHTG
!!

80
80

logo

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consensus

GMSRPFLTSTGVQMLLRKLIIEEHKQEFKVVYQKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMESGTASEYRGERVLS
GMSRPFLTSTGVQMLLRKLIIEEHKQEFKVVYQKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMESGTASEYRGERVLS
GMSRPFLTSTGVQMLLRKLIIEEHKQEFKVVYQKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMESGTASEYRGERVLS
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160
160

logo

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consensus

KLHDLSILYQQMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKP
KLHDLSILYQQMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKP
KLHDLSILYQQMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKP
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240
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logo

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consensus

SYEREPHELELFRMTGKTYRRLHQAQKELNLDITYKELSGTERHTKTPELAHLEAQYEARPAYPYAEKQEALTMQAANR
SYEREPHELELFRMTGKTYRRLHQAQKELNLDITYKELSGTERHTKTPELAHLEAQYEARPAYPYAEKQEALTMQAANR
SYEREPHELELFRMTGKTYRRLHQAQKELNLDITYKELSGTERHTKTPELAHLEAQYEARPAYPYAEKQEALTMQAANR
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320
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logo

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RAELEGIAREIHALVREKGYRYKDVAIILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVVKGNWR
RAELEGIAREIHALVREKGYRYKDVAIILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVVKGNWR
RAELEGIAREIHALVREKGYRYKDVAIILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVVKGNWR
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400
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logo

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EAVFRCVKTELLFPLNEPKAKVREQVDQLENYCIAYGIKGRWTKGDRFYRRFVSLDDDDFAQTDQEIEEMNMLNDRDW
EAVFRCVKTELLFPLNEPKAKVREQVDQLENYCIAYGIKGRWTKGDRFYRRFVSLDDDDFAQTDQEIEEMNMLNDRDW
EAVFRCVKTELLFPLNEPKAKVREQVDQLENYCIAYGIKGRWTKGDRFYRRFVSLDDDDFAQTDQEIEEMNMLNDRDW
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480
480

logo

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IVPPLFQLQKRMKKAKTVQEKAEALRYRLEETDVPLKLDQERQRAEEDGRIIEAQQHQQAWDVAVIQLLEEFVEMMGDDEI
IVPPLFQLQKRMKKAKTVQEKAEALRYRLEETDVPLKLDQERQRAEEDGRIIEAQQHQQAWDVAVIQLLEEFVEMMGDDEI
IVPPLFQLQKRMKKAKTVQEKAEALRYRLEETDVPLKLDQERQRAEEDGRIIEAQQHQQAWDVAVIQLLEEFVEMMGDDEI
!!

560
560

logo

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consensus

SLDLFQQMIETGAESLTFSLIPPALDQVFVGNMDSLRYMGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS
SLDLFQQMIETGAESLTFSLIPPALDQVFVGNMDSLRYMGTSCTFVLGANDGVLPARPDENGVLSDDDREWLKTI GVELS
!!

640
640

logo

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SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTLPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
SGGRERLLDEHFLIYMAFSSPSDRLVSYPIADAEGKTLPSMIVKRLEELFPHHKERLLTNEPEQVSDEEQLMYVVKNS
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720
720

logo

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consensus

VAQSFTASQLRLWTREYDISDVVWSTYNVLMSE^QDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVVWSTYNVLMSE^QDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
VAQSFTASQLRLWTREYDISDVVWSTYNVLMSE^QDRLQSKKLFSSLFFRNEVKQLERSVSRQLYGERIQGSVSRMETFNA
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800
800

logo

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CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
CPFSHFASHGLHLKERQFFKLEAPDIGQLFHSSLKLISDRLREQKLDWRDLTKEQCELFSDAVERLAPKLQKEILLSSN
!!

880
880

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RHYVVEKLEKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVVEKLEKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
RHYVVEKLEKIVTRVSGILSEHAKASGFVPIGLELFGGKGPLPPLTFQLKNGCTMELVGRIDRVDKAESSKGLLLRIV
!!

960
960

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DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIEFKKFKMKGL
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIEFKKFKMKGL
DYKSSDKGLDLAEVYGLALQMLTYLDSLITHSADWLGMRATPAGVLYFHIHDPMIQSNLPLGLDEIEQEIEFKKFKMKGL
!!

1040
1040

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LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
LLGDQEVVRLMDTTLQEGRSNIINAGLKKDGSLSRSDSAAVGEKEFDLLTKHVRRTFQEAGEQITDGRVSI EPYKMKNKTP
!!

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CTYCAFKSVQCQFDESLEENEYRPLKAEKDKTILEWIKKEADGNEHS
CTYCAFKSVQCQFDESLEENEYRPLKAEKDKTILEWIKKEADGNEHS
CTYCAFKSVQCQFDESLEENEYRPLKAEKDKTILEWIKKEADGNEHS
!!

1166
1166

- non conserved
- similar
- ≥ 50% conserved