

logo

NTDB id 117026 AW03 RS05605 WP 015483058.1
NTDB id 120 BSU 10620 NP 388943.2
consensus

MGA EFLVGRSGSGKTKLIINSIQDELRRAPFGKPIIFLVPDQMTFLMEYELAKTPDMGGMIRAQVFSFSRLAWRVLQHTGGMSRP
MGA EFLVGRSGSGKTKLIINSIQDELRRAPFGKPIIFLVPDQMTFLMEYELAKTPDMGGMIRAQVFSFSRLAWRVLQHTGGMSRP
MGA EFLVGRSGSGKTKLIINSIQDELRRAPFGKPIIFLVPDQMTFLMEYELAKTPDMGGMIRAQVFSFSRLAWRVLQHTGGMSRP

85
85

logo

NTDB id 117026 AW03 RS05605 WP 015483058.1
NTDB id 120 BSU 10620 NP 388943.2
consensus

FLTSTGVQMLLRKLI EEHKQEFKVKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMASGTASEYRGERVLSEKLHDL SILYQ
FLTSTGVQMLLRKLI EEHKQEFKVKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMASGTASEYRGERVLSEKLHDL SILYQ
FLTSTGVQMLLRKLI EEHKQEFKVKASDKSGFTAQVERMLTEFKRYCLEPEDIRRMASGTASEYRGERVLSEKLHDL SILYQ

170
170

logo

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consensus

QMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKPSYEREPHELELFRMT
QMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKPSYEREPHELELFRMT
QMEKSLADQYLHSEDYLTLLAEHIPLAEDIKGAHIYVDGFYQFTPQEFRVLEQLMVHAEHITFSLTADKPSYEREPHELELFRMT

255
255

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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 Y 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 **V** 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 **V** 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
 *

340
340

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RYKDVAILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVLKGNWRYEAVFRCVKTELLFPLNEPKAKVREQ
RYKDVAILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVLKGNWRYEAVFRCVKTELLFPLNEPKAKVREQ
RYKDVAILARQPEDYKDMVKEVFADYEIPYFIDGKASMLNHPLIEFIRSSLDVLKGNWRYEAVFRCVKTELLFPLNEPKAKVREQ

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425

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VDQLENYCIAYGIKGDRWTKGDRFQYRRFVSLDDDDFAQTDQEIEEMNMLNDTRDWIVPPLFQLQKRMKKAKTVQEKAESLYRYLE
VDQLENYCIAYGIKGDRWTKGDRFQYRRFVSLDDDDFAQTDQEIEEMNMLNDTRDWIVPPLFQLQKRMKKAKTVQEKAESLYRYLE
VDQLENYCIAYGIKGDRWTKGDRFQYRRFVSLDDDDFAQTDQEIEEMNMLNDTRDWIVPPLFQLQKRMKKAKTVQEKAESLYRYLE

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510

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consensus

ETDVP LKLDQERQRAEDDGR I IEAQQHQQA WDAVIQLLEEFVEMMGDDE ISLDLFQQM IEAGAESLTFS LIPPALDQVFVGNMDL
ETDVP LKLDQERQRAEDDGR I IEAQQHQQA WDAVIQLLEEFVEMMGDDE ISLDLFQQM IEAGAESLTFS LIPPALDQVFVGNMDL
ETDVP LKLDQERQRAEDDGR I IEAQQHQQA WDAVIQLLEEFVEMMGDDE ISLDLFQQM IEAGAESLTFS LIPPALDQVFVGNMDL

595
595



 non conserved
 similar
 $\geq 50\%$ conserved