

logo

NTDB id 1088304 ACLII2 RS09010 WP 003230267.1
NTDB id 352 BSU 24240 NP 390304.2
consensus

MLAELSIKNFAIIEELTVSFERGLTVLTGETGAGKSIIDAISLLVGGGRGSSEFVRYGEAKAELEGLFLLLESHPVLGVC
MLAELSIKNFAIIEELTVSFERGLTVLTGETGAGKSIIDAISLLVGGGRGSSEFVRYGEAKAELEGLFLLLESHPVLGVC
MLAELSIKNFAIIEELTVSFERGLTVLTGETGAGKSIIDAISLLVGGGRGSSEFVRYGEAKAELEGLFLLLESHPVLGVC
!!

80
80

logo

NTDB id 1088304 ACLII2 RS09010 WP 003230267.1
NTDB id 352 BSU 24240 NP 390304.2
consensus

AEQGI DVSD EMI V MRRDI STSGKSVCRVNGKLVTIASLREIGRLLLDIHGQHDNQLLMEDENHLQLLDKDFAGAEVESALK
AEQGIDVSD EMI V MRRDISTSGKSVCRVNGKLVTIASLREIGRLLLDIHGQHDNQLLMEDENHLQLLDKDFAGAEVESALK
AEQGIDVSD EMI V MRRDISTSGKSVCRVNGKLVTIASLREIGRLLLDIHGQHDNQLLMEDENHLQLLDKDFAGAEVESALK
!!

160
160

logo

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consensus

TYQEGYQRYVKLLKLLKQLSESEQEMAHRLDLIQFQLEEIESAKLELNEDEQLQEERQQISNFEKIYESLQNAVNALRSE
TYQEGYQRYVKLLKLLKQLSESEQEMAHRLDLIQFQLEEIESAKLELNEDEQLQEERQQISNFEKIYESLQNAVNALRSE
TYQEGYQRYVKLLKLLKQLSESEQEMAHRLDLIQFQLEEIESAKLELNEDEQLQEERQQISNFEKIYESLQNAVNALRSE
!!

240
240

logo

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consensus

QGGLDIVGMSAQL EDI SDINEPLK KMSESVSNSYLL EDATFQMRNMLDELEFDPERLNYIETRLNEIKQLKRKYGATV
QGGLDIVGMSAQL EDI SDINEPLK KMSESVSNSYLL EDATFQMRNMLDELEFDPERLNYIETRLNEIKQLKRKYGATV
QGGLDIVGMSAQL EDI SDINEPLK KMSESVSNSYLL EDATFQMRNMLDELEFDPERLNYIETRLNEIKQLKRKYGATV
!!

320
320

logo

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consensus

EDILEYASKIEEEEIDQIENRDSHLQSLKKELDVSGKDVAVEAANVSQIRKTWAKKLAD EIHRELKSLYMEKSTFDTEFKV
EDILEYASKIEEEEIDQIENRDSHLQSLKKELDVSGKDVAVEAANVSQIRKTWAKKLAD EIHRELKSLYMEKSTFDTEFKV
EDILEYASKIEEEEIDQIENRDSHLQSLKKELDVSGKDVAVEAANVSQIRKTWAKKLAD EIHRELKSLYMEKSTFDTEFKV
!!

400
400

logo

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consensus

RTASRNEEAPLVNGQPVLTEQGI DLVKFLISTNTGEPLKSLSKVASGGELSRVMLAIKSI FSSQQDVTSIIFDEVDTGV
RTASRNEEAPLVNGQPVLTEQGI DLVKFLISTNTGEPLKSLSKVASGGELSRVMLAIKSI FSSQQDVTSIIFDEVDTGV
RTASRNEEAPLVNGQPVLTEQGI DLVKFLISTNTGEPLKSLSKVASGGELSRVMLAIKSI FSSQQDVTSIIFDEVDTGV
!!

480
480

logo

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NTDB id 352 BSU 24240 NP 390304.2
consensus

SGRVAQAIAEKIHKVSI GSQVLCITHLPQVAAMADTHLYIAKELKDGRITTTTRVKPLSKQEKVAEIGRMIAGVEVTDLTKR
SGRVAQAIAEKIHKVSI GSQVLCITHLPQVAAMADTHLYIAKELKDGRITTTTRVKPLSKQEKVAEIGRMIAGVEVTDLTKR
SGRVAQAIAEKIHKVSI GSQVLCITHLPQVAAMADTHLYIAKELKDGRITTTTRVKPLSKQEKVAEIGRMIAGVEVTDLTKR
!!

560
560

logo

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consensus

HAKE~~LL~~KQADQVKTG
HAKE~~LL~~KQADQVKTG
HAKE~~LL~~KQADQVKTG
!!!!!!!!!!!!!!!!!!!!

576
576

non conserved
 similar
 $\geq 50\%$ conserved