

CLUSTAL O(1.2.4) multiple sequence alignment

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B0V9F6|MURC_ACIBY      MSPTTAANQAKKLIKVPEMRRIKHIHFVGIGGAMCGIAEVLANQGYKISGSDIKASKTT      60
B0VNZ8|MURC_ACIBS      MSPTTAANQAKKLIKVPEMRRIKHIHFVGIGGAMCGIAEVLANQGYKISGSDINASKTT      60
*****:*****

B0V9F6|MURC_ACIBY      QQLEENGIKVYIGHEAENIKNANVLVVSTAIDPENPEVKAAIEQRIPIVRRAEMLGELMR      120
B0VNZ8|MURC_ACIBS      QQLEENGIKVYIGHEAENIKNANVLVVSTAIDPENPEVKAAIEQRIPIVRRAEMLGELMR      120
*****

B0V9F6|MURC_ACIBY      YRHGIAVAGTHGKTTTTSLLTTMLAEENLDPTYVIGGLLNSTGVNAALGESRFIVAEADE      180
B0VNZ8|MURC_ACIBS      YRHGIAVAGTHGKTTTTSLLTTMLAEENLDPTYVIGGLLNSTGVNAALGESRFIVAEADE      180
*****

B0V9F6|MURC_ACIBY      SDASFLYLQPMAAIVTNIDADHMDTYEGSFDKLKDTFVQFLHNLPFYGLAVVCGDDANIR      240
B0VNZ8|MURC_ACIBS      SDASFLYLQPMAAIVTNIDADHMDTYEGSFDKLKDTFVQFLHNLPFYGLAVVCGDDANIR      240
*****

B0V9F6|MURC_ACIBY      EILPRVGRPVITYGFNEDNDIRAIDVEQDGMRSHFTVLRKGREPLRLTINQPLHNVLNA      300
B0VNZ8|MURC_ACIBS      EILPRVGRPVITYGFNEDNDIRAIDVERDGMRSHFTVLRKGREPLRLTINQPLHNVLNA      300
*****:*****

B0V9F6|MURC_ACIBY      LAAIGVATDEGVSDEAISRALKGFSGVGRRFQVQGEFELGEGNVKLVDDYGHHPKEVEAT      360
B0VNZ8|MURC_ACIBS      LAAIGVATDEGVSDEAISRALKGFSGVGRRFQVQGEFELGEGNVKLVDDYGHHPKEVEAT      360
*****

B0V9F6|MURC_ACIBY      IKAARQSHPDRRLVMLFQPHRYSTRDCFDDFIEVLSQVDQLLLLLEVYPAGEKPIVGADS      420
B0VNZ8|MURC_ACIBS      IKAARQSHPDRRLVMLFQPHRYSTRDCFDDFIEVLSQVDQLLLLLEVYPAGEKPIVGADS      420
*****

B0V9F6|MURC_ACIBY      RTLARSIRLRGQVEPILIDPVEGNLQNIMQNVLQPNDLLLTQGAGNVGAISVELAQHHLY      480
B0VNZ8|MURC_ACIBS      RTLARSIRLRGQVEPILIDPVEGNLQNIMQNVLQPNDLLLTQGAGNVGAISVELAQHHLY      480
*****

B0V9F6|MURC_ACIBY      VK          482
B0VNZ8|MURC_ACIBS      VK          482
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