

CLUSTAL O(1.2.4) multiple sequence alignment

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Q833N6 |MURC_ENTFA      MGNQENKLYHFVGIKSGMSSLALVLHQKGYNVQGS DVEEYFFTQ R DLEKSGVPILPFNA 60
C7D2P5 |C7D2P5_ENTFL  MGNQENKLYHFVGIKSGMSSLALVLHQKGYNVQGS DVEEYFFTQ R DLEKSGVPILPFNA 60
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Q833N6 |MURC_ENTFA      DNIDKDMIVIAGNAFPDTHEE IARAIELGAEVIRYHDFIARFIEPYTSIAVTGSHGKTST 120
C7D2P5 |C7D2P5_ENTFL  DNIDKDMIVIAGNAFPDTHEE IARAIELGAEVIRYHDFIARFIEPYTSIAVTGSHGKTST 120
*****

Q833N6 |MURC_ENTFA      TGLLAHVLSGINPTS YLIGDGTGHGEPDADFFAF EACEYRRHFLAYS PDYAIMTNI DFDH 180
C7D2P5 |C7D2P5_ENTFL  TGLLAHVLSGINPTS YLIGDGTGHGEPDADFFAF EACEYRRHFLAYS PDYAIMTNI DFDH 180
*****

Q833N6 |MURC_ENTFA      PDYYKSIEDVFSAFQ TMAHQVKKGIFAYGDDK YLRQLESEVPVYYGVSEEDDIQARNIQ 240
C7D2P5 |C7D2P5_ENTFL  PDYYKSIEDVFSAFQ TMAHQVKKGIFAYGDDK YLRQLESEVPVYYGVSEEDDIQARNIQ 240
*****

Q833N6 |MURC_ENTFA      RTTEGSSFDVYHKDDF VGHFVLPAPFGHHNIMN ALGVI AVAYFEK LDMQKVAEEMLSFKGV 300
C7D2P5 |C7D2P5_ENTFL  RTTEGSSFDVYHKAD FVGHFVLPAPFGHHNIMN ALGVI AVAYFEK LDMQKVAEEMLSFKGV 300
*****

Q833N6 |MURC_ENTFA      KRRFSEKKVSDMI IVDYAHHPAEIKATIDGAR QKYPDKEIIAVFQPHTFTRTIALMDEF 360
C7D2P5 |C7D2P5_ENTFL  KRRFSEKKVSDMI IVDYAHHPAEIKATIDGAR QKYPDKEIIAVFQPHTFTRTIALMDEF 360
*****

Q833N6 |MURC_ENTFA      AEALDLADEVFLCN IFGSARETQGEVRIEDLGEKI QKGGQVITEDNVSPLLD FENAVVVF 420
C7D2P5 |C7D2P5_ENTFL  AEALDLADEVFLCN IFGSARETQGEVRIEDLGEKI QKGGQVITEDNVSPLLD FENAVVVF 420
*****

Q833N6 |MURC_ENTFA      MGAGDVQKFEQAYE TLLSNTTRNVL          445
C7D2P5 |C7D2P5_ENTFL  MGAGDVQKFEQAYE TLLSNTTRNVL          445
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