

CLUSTAL O(1.2.4) multiple sequence alignment

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2vvt
Q836J0|MURI_ENTFA      SSSLVPRGSHMSNQEAIGLIDSGVGGLTVLKEALKQLPNERLIYLGDTARCPYGPRPAEQ      60
C7VBN9|C7VBN9_ENTFL  -----MSNQEAIGLIDSGVGGLTVLKEALKQLPNERLIYLGDTARCPYGPRPAEQ      50
C7X2Y0|C7X2Y0_ENTFL  -----MRMSNQEAIGLIDSGVGGLTVLKEALKQLPNERLIYLGDTARCPYGPRPAEQ      52
                        -----MRMSNQEAIGLIDSGVGGLTVLKEALKQLPNERLIYLGDTARCPYGPRPAEQ      52
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2vvt
Q836J0|MURI_ENTFA      VVQFTWEMADFLLKKRIKMLVIACNTATAVALEEIKAAPVIPVGVILPGARAAVKVTKN      120
C7VBN9|C7VBN9_ENTFL  VVQFTWEMADFLLKKRIKMLVIACNTATAVALEEIKAAPVIPVGVILPGARAAVKVTKN      110
C7X2Y0|C7X2Y0_ENTFL  VVQFTWEMADFLLKKRIKMLVIACNTATAVALEEIKAAPVIPVGVILPGARAAVKVTKN      112
                        VVQFTWEMADFLLKKRIKMLVIACNTATAVALEEIKAAPVIPVGVILPGARAAVKVTKN      112
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2vvt
Q836J0|MURI_ENTFA      NKIGVIGTLGTIKSASYEIAIKSKAPAEVETSLACPKFVPIVESNQYRSSVAKKIVAETL      180
C7VBN9|C7VBN9_ENTFL  NKIGVIGTLGTIKSASYEIAIKSKAPAEVETSLACPKFVPIVESNQYRSSVAKKIVAETL      170
C7X2Y0|C7X2Y0_ENTFL  NKIGVIGTLGTIKSASYEIAIKSKAPAEVETSLACPKFVPIVESNQYRSSVAKKIVAETL      172
                        NKIGVIGTLGTIKSASYEIAIKSKAPAEVETSLACPKFVPIVESNQYRSSVAKKIVAETL      172
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2vvt
Q836J0|MURI_ENTFA      QALQLKGLDTLILGCTHYPLLRPVIQNVMGSHVTLIDSGAETVGEVSMLLDYFDIAHTPE      240
C7VBN9|C7VBN9_ENTFL  QALQLKGLDTLILGCTHYPLLRPVIQNVMGSHVTLIDSGAETVGEVSMLLDYFDIAHTPE      230
C7X2Y0|C7X2Y0_ENTFL  QALQLKGLDTLILGCTHYPLLRPVIQNVMGSHVTLIDSGAETVGEVSMLLDYFDIAHTPE      232
                        QALQLKGLDTLILGCTHYPLLRPVIQNVMGSHVTLIDSGAETVGEVSMLLDYFDIAHTPE      232
                        *****

2vvt
Q836J0|MURI_ENTFA      APTQPHEFYTTGSAKMFEEIASSWLG IENLKAQQIHLGGN---      280
C7VBN9|C7VBN9_ENTFL  APTQPHEFYTTGSAKMFEEIASSWLG IENLKAQQIHLGGNEND      273
C7X2Y0|C7X2Y0_ENTFL  APTQPHEFYTTGSAKMFEEIASSWLG IENLKAQQIHLGGNEND      275
                        APTQPHEFYTTGSAKMFEEIASSWLG IENLKAQQIHLGGNEND      275
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