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CLUSTAL O(1.2.4) multiple sequence alignment


Q836E5|MURA1_ENTFA      -MKKIVINGNRPLKGEVTISGAKNSVVALIPAAILADSPV-TLDGVPDIQDVHSLIEILE    58
Q831A8|MURA2_ENTFA      MEQIIVHGGNTKLEGTVKIEGAKNAVLPILAATLLAEEGVTTLKNVPILSDVFTMNQVIK    60
                          : ** .**  *:* *.*.****:*: :: *::**:. * **..** :.**.:: ::::

Q836E5|MURA1_ENTFA      IMGAKITFEN--NTLIIDPTEVVSVPMPKGKINSLRASYYFMGSLLGRFGEGVVGLPGGC    116
Q831A8|MURA2_ENTFA      HLNVAIDFDEDANEVTIDATQPLGIEANYEYVSKMRASIVVMGPLLARNGHAKVAMPGGC    120
                         :.. * *::  * : ** *: :.:      :..:***  .** **.* *.. *.:****

Q836E5|MURA1_ENTFA      YLGPRPIDLHIKGFEALGAHVTNEHGAMYLRTDEAGLQGTRIFMDMVSIGATINVMLAAV    176
Q831A8|MURA2_ENTFA      AIGKRPIDLHLKGFQALGAKIIQKNGY--IEAIADELIGNTIYLDFPSVGATQNIMMAAV    178
                         :* ******:***:****:: :::*   ::    * *. *::*: *:*** *:*:***

Q836E5|MURA1_ENTFA      KAKGKTIIENAAREPEIIDIATLLNNMGAKVRGAGTDVIRIEGVEELHGCRHSIIPDRIE    236
Q831A8|MURA2_ENTFA      RAKGTTIIENVAREPEIVDLANILNKMGANVIGAGTETMRIEGVDKLHAVEHSIVQDRIE    238
                        :***.*****.******:*:*.:**:***:* ****:.:*****::**. .***: ****

Q836E5|MURA1_ENTFA      AGTYLAMAAAMGEGIKVRNVIYEHLESFIAKLQEMGVKMTIEEDMIEVHPSHDLKMTTVK    296
Q831A8|MURA2_ENTFA      AGTFMVAAAMTEGNVLIEEAISEHNRPLISKLTEMGAIIEEEENGIRVIGPKHLKPTDVK    298
                        ***::. **    .: :.:.* **  . :*:** ***. :  **: *.*   :.** * **

Q836E5|MURA1_ENTFA      TYPYPGFATDLQQPLTPLLLKAQGTGEIIDTIYAQRNKHIPELVRMGADASVEGNMIILN    356
Q831A8|MURA2_ENTFA      TMPHPGFPTDMQAQMTAIQMFAEGTSIVTETVFENRYQHLEEMRRMNADLKIDGNIAVIN    358
                        * *:*** **:*  :* : : *:**. : :*:: :* :*: *: **.** .::**: ::*

Q836E5|MURA1_ENTFA      GPNQLHGAEVVASDLRAGACLVTAGLMAEGTTTIYNVEYILRGYDHIIEKLTALGADIQM    416
Q831A8|MURA2_ENTFA      GGNELQGAAVEATDLRAAAALILVGLRANGITRVSNLKYLDRGYYEFHKKLQKLGANVER    418
                        * *:*:** * *:****.*.*: .** *:* * : *::*: *** .: :**  ***:::

Q836E5|MURA1_ENTFA      LETEEQEGPFEVDQ- 430
Q831A8|MURA2_ENTFA      VNDEKIEEKQATTVI 433
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