

CLUSTAL O(1.2.4) multiple sequence alignment

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A4XQS4|MURG_PSEMY      MRGNVLIMAGGTGGHVFPALACAREFQTRGYAVHWLGTSRGIENELVLPQAGLPLHLINVS      60
3S2U                   MKGNVLIMAGGTGGHVFPALACAREFQARGYAVHWLGTPRGIENDLVPKAGLPLHLIQVS      60
Q02H28|MURG_PSEAB     MKGNVLIMAGGTGGHVFPALACAREFQARGYAVHWLGTPRGIENDLVPKAGLPLHLIQVS      60
A6VB85|MURG_PSEA7     MKGNVLIMAGGTGGHVFPALACAREFQARGYAVHWLGTPRGIENDLVPKAGLPLHLIQVS      60
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A4XQS4|MURG_PSEMY      GLRGKGLSLLKAPFQLLRSLQARRIVRELQPVCVLGMGGYVTGPGGLAARLAGVPLVI      120
3S2U                   GLRGKGLKSLVKAPLELLKSLFQALRVIRQLRPVCVLGLGGYVTGPGGLAARLNGVPLVI      120
Q02H28|MURG_PSEAB     GLRGKGLKSLVKAPLELLKSLFQALRVIRQLRPVCVLGLGGYVTGPGGLAARLNGVPLVI      120
A6VB85|MURG_PSEA7     GLRGKGLKSLVKAPLELLKSLFQALRVIRQLRPVCVLGLGGYVTGPGGLAARLNGVPLVI      120
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A4XQS4|MURG_PSEMY      HEQNAVAGTANRLLSRIATRICEAFPNTFGASDKRRTTGNPVR EELFLET- PREPLVGRK      179
3S2U                   HEQNAVAGTANRSLAPIARRVCEAFPDTFPASDKRLTTGNPVRGELFLDAHARAPLTGRR      180
Q02H28|MURG_PSEAB     HEQNAVAGTANRSLAPIARRVCEAFPDTFPASDKRLTTGNPVRGELFLDAHARAPLTGRR      180
A6VB85|MURG_PSEA7     HEQNAVAGTANRSLAPIARRVCEAFPDTFPASDKRLTTGNPVRGELFLDAHARAPLTGRR      180
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A4XQS4|MURG_PSEMY      PKLLVLGGSLGAEPLNKLPAALAEIPTELRPVHFHQAGKQHAEVTAERYRDAAVEAEVA      239
3S2U                   VNLLVLGGSLGAEPLNKLPEALAQVPLEIRPAIRHQAGRQHAETAERYRTVAVEADVA      240
Q02H28|MURG_PSEAB     VNLLVLGGSLGAEPLNKLPEALAQVPLEIRPAIRHQAGRQHAETAERYRTVAVEADVA      240
A6VB85|MURG_PSEA7     VNLLVLGGSLGAEPLNKLPEALAQVPLEIRPAIRHQAGRQHAETAERYRTVAVEADVA      240
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A4XQS4|MURG_PSEMY      PFIKDMARAYGWADLVICRAGALTVSELAAGLPSFLVPLPHAI DDHQSRNAEYLAKEGA      299
3S2U                   PFISDMAAAYAWADLVICRAGALTVSELTAAGLPAFLVPLPHAI DDHQTRNAEFLVRSQA      300
Q02H28|MURG_PSEAB     PFISDMAAAYAWADLVICRAGALTVSELTAAGLPAFLVPLPHAI DDHQTRNAEFLVRSQA      300
A6VB85|MURG_PSEA7     PFISDMAAAYAWADLVICRAGALTVSELAAGLPAFLVPLPHAI DDHQTRNAEFLVRSQA      300
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A4XQS4|MURG_PSEMY      AVLLPQHATDAAKLAAQLTEVLMHLEKLNVMGATARRLAKPDATRTVVDICQEVMRG--      356
3S2U                   GRLLPQKSTGAAELAAQLSEVLMHPETLRSMADQARSLAKPEATRTVVDACLEVARGLE      359
Q02H28|MURG_PSEAB     GRLLPQKSTGAAELAAQLSEVLMHPETLRSMADQARSLAKPEATRTVVDACLEVARG--      357
A6VB85|MURG_PSEA7     GRLLPQKSTGAAELAAQLSEVLMHPETLRSMADQARSLAKPEATRTVVDACLEVARG--      357
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