

CLUSTAL O(1.2.4) multiple sequence alignment

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5U4H          SNAMDKFLITGGVVKLEGEVRISGAKNAALPLLAAMILADSPITLTNVPNPKDVNTLVKLI      60
Q9HVVW7 |MURA_PSEAE    ---MDKLIITGGNRLDGEIRISGAKNSALPILAAATLLADTPVTVCNLPHLHDITTMIELF    57
Q02GZ1 |MURA_PSEAB    ---MDKLIITGGNRLDGEIRISGAKNSALPILAAATLLADTPVTVCNLPHLHDITTMIELF    57
B7UZY9 |MURA_PSEA8    ---MDKLIITGGNRLDGEIRISGAKNSALPILAAATLLADTPVTVCNLPHLHDITTMIELF    57
A6VBC3 |MURA_PSEA7    ---MDKLIITGGNRLDGEIRISGAKNSALPILAAATLLADTPVTVCNLPHLHDITTMIELF    57
                   ***** :*:**:*:*****:****:* :***:*:*: *:*:*:*: _*::**:*:

5U4H          GGLGVTISYE-NDTVKADTSTLDNQFAPYELVKTMRASILVLGPPLARYGNKVSLLPGGC     119
Q9HVVW7 |MURA_PSEAE    GRMGVQPIIDEKLNVEVDASSIKTLVAPYELVKTMRASILVLGPMLARFGAEVALPGGC     117
Q02GZ1 |MURA_PSEAB    GRMGVQPIIDEKLNVEVDASSIKTLVAPYELVKTMRASILVLGPMLARFGAEVALPGGC     117
B7UZY9 |MURA_PSEA8    GRMGVQPIIDEKLNVEVDASSIKTLVAPYELVKTMRASILVLGPMLARFGAEVALPGGC     117
A6VBC3 |MURA_PSEA7    GRMGVQPIIDEKLNVEVDASSIKTLVAPYELVKTMRASILVLGPMLARFGAEVALPGGC     117
                   *  :**          :  :  _*:*:*:.....*****:****:*:*:*:*:*:*

5U4H          AIGSRPVDQHLLKALEALGAHIEVENGYVHAT-VDGRLLKGGEVVFDVMTVGGTENILMAAA     178
Q9HVVW7 |MURA_PSEAE    AIGSRPVDLHIRGLEAMGAQIEVEGGYIKAKAPAGGLRGGHFFFDTVSVTGTENLMAAA     177
Q02GZ1 |MURA_PSEAB    AIGSRPVDLHIRGLEAMGAQIEVEGGYIKAKAPAGGLRGGHFFFDTVSVTGTENLMAAA     177
B7UZY9 |MURA_PSEA8    AIGSRPVDLHIRGLEAMGAQIEVEGGYIKAKAPAGGLRGGHFFFDTVSVTGTENLMAAA     177
A6VBC3 |MURA_PSEA7    AIGSRPVDLHIRGLEAMGAQIEVEGGYIKAKAPVGLHGGQFFFDTVSVTGTENLMAAA     177
                   ***** *::*:*:*:*:*:*:*_* *:*:*:_** *:* *****:****

5U4H          LADGVTTIRNAAREPEITDLAQMLIKMGAKIEGLDTDTLVVTGVESLHGCEYAVVADRIE     238
Q9HVVW7 |MURA_PSEAE    LANGRTVLQNAAREPEVVDLANCLNAMGANVQGAGSDTIVIEGVKRLGGARYDVLPRDIE     237
Q02GZ1 |MURA_PSEAB    LANGRTVLQNAAREPEVVDLANCLNAMGANVQGAGSDTIVIEGVKRLGGARYDVLPRDIE     237
B7UZY9 |MURA_PSEA8    LANGRTVLQNAAREPEVVDLANCLNAMGANVQGAGSDTIVIEGVKRLGGARYDVLPRDIE     237
A6VBC3 |MURA_PSEA7    LANGRTVLQNAAREPEVVDLANCLNAMGANVQGAGSDTIVIDGVKRLGGARYDVLPRDIE     237
                   **:* *_::*****:****_* *****:*_::***:* *:*_*_*: *****

5U4H          TGSYLAAAAITGGRVKTTHTDPSLLEAVLDKFEEMGAEVTRGDDWIELDMLGKRPKAVSF     298
Q9HVVW7 |MURA_PSEAE    TGTYLVAAAAATGGRVCLKDTPTILEAVLQKLEEAGAHISTGSNWIELDMKGNRPKAVNV     297
Q02GZ1 |MURA_PSEAB    TGTYLVAAAAATGGRVCLKDTPTILEAVLQKLEEAGAHISTGSNWIELDMKGNRPKAVNV     297
B7UZY9 |MURA_PSEA8    TGTYLVAAAAATGGRVCLKDTPTILEAVLQKLEEAGAHISTGSNWIELDMKGNRPKAVNV     297
A6VBC3 |MURA_PSEA7    TGTYLVAAAAATGGRVCLKDTPTILEAVLQKLEEAGAHINTGNNWIELDMKGNRPKAVNI     297
                   **:**_*** ***** _*****:*****:***_*_*_::*_*_*_*_*_*_*_*_*_*_*

5U4H          RTLPHPFPPTDMQAQIMAVNAIEGRGFATISSETIFENRFMHVPELSRGMGANIQVEGHDAVV     358
Q9HVVW7 |MURA_PSEAE    RTAPYPAPFPTDMQAQFISMNAVAEGTGAVIETVFNRFMHVYEMNRMGAQILVEGNTAIV     357
Q02GZ1 |MURA_PSEAB    RTAPYPAPFPTDMQAQFISMNAVAEGTGAVIETVFNRFMHVYEMNRMGAQILVEGNTAIV     357
B7UZY9 |MURA_PSEA8    RTAPYPAPFPTDMQAQFISMNAVAEGTGAVIETVFNRFMHVYEMNRMGAQILVEGNTAIV     357
A6VBC3 |MURA_PSEA7    RTAPYPAPFPTDMQAQFISMNAVAEGTGAVIETVFNRFMHVYEMNRMGAQILVEGNTAIV     357
                   **_*** *****:***_*_*_*_*_*_*_*_*_*_*_*_*_*_*_*_*_*_*_*_*_*_*

5U4H          TGVEKLQAAPVMATDLRASFSVLVAALVAEGDTLIDRIYHIDRGYEHVEEKLQGLGAKIK     418
Q9HVVW7 |MURA_PSEAE    TGVPKLGAPVMATDLRASASLVIAGLVAEGDTLIDRIYHIDRGYECIEEKLQLLGAKIR     417
Q02GZ1 |MURA_PSEAB    TGVPKLGAPVMATDLRASASLVIAGLVAEGDTLIDRIYHIDRGYECIEEKLQLLGAKIR     417
B7UZY9 |MURA_PSEA8    TGVPKLGAPVMATDLRASASLVIAGLVAEGDTLIDRIYHIDRGYECIEEKLQLLGAKIR     417
A6VBC3 |MURA_PSEA7    TGVPRLKGAPVMATDLRASASLVIAGLVAEGDTLIDRIYHIDRGYECIEEKLQLLGAKIR     417
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5U4H          RVS-              421
Q9HVVW7 |MURA_PSEAE    RVPG              421
Q02GZ1 |MURA_PSEAB    RVPG              421
B7UZY9 |MURA_PSEA8    RVPG              421
A6VBC3 |MURA_PSEA7    RVPG              421
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