

CLUSTAL O(1.2.4) multiple sequence alignment

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A4XR64|MURI_PSEMY      MNQSQAPVGVFDSGVGGLSVLREIRQLLPNESLLYVADSGHVPYGEKSAEYIRERCVLIT      60
A6VC58|MURI_PSEA7      MAAESAPVGVFDSGVGGLSVLREIRARLPAESLLYVADNAHVPYGEKSAEYIRERCERIG      60
Q9HVD0|MURI_PSEAE      MAVESAAGVGVFDSGVGGLSVLREIRARLPSESLLYVADNAHVPYGEKSAEYIRERCERIG      60
Q02G12|MURI_PSEAB      MAVESAAGVGVFDSGVGGLSVLREIRARLPSESLLYVADNAHVPYGEKSAEYIRERCERIG      60
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A4XR64|MURI_PSEMY      EHLLAQGAKALVLACNTATAAAAAELRERYPQLPIVGMETPAVKPAAAAATRSQVGVGLATT      120
A6VC58|MURI_PSEA7      DFLLEERGAKALVLACNTATAAAAAELRERYPQVPLVAMEPAVKPAAAAATRNGRVGLATT      120
Q9HVD0|MURI_PSEAE      DFLLEQGAKALVLACNTATAAAAAELRERYPQVPLVAMEPAVKPAAAAATRNGRVGLATT      120
Q02G12|MURI_PSEAB      DFLLEQGAKALVLACNTATAAAAAELRERYPQVQLVAMEPAVKPAAAAATRNGRVGLATT      120
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A4XR64|MURI_PSEMY      GTLKSARFAALLDRFASDVRVITQPCPLVECFEAGALQAPATRELLQGYVEPLLAEGCD      180
A6VC58|MURI_PSEA7      GTLKSARFAALLDRFASDVQVFTQPCPLVERIEAGDLHGARTRALLERLLGPILEQGCD      180
Q9HVD0|MURI_PSEAE      GTLKSARFAALLDRFASDVQVFTQPCPLVERIEAGDLYGPQTRALLERLLAPILEQGCD      180
Q02G12|MURI_PSEAB      GTLKSARFAALLDRFASDVQVFTQPCPLVERIEAGDLYGPQTRALLERLLAPILEQGCD      180
      *****:*****:***** ***** * . ** **: : * : *

A4XR64|MURI_PSEMY      TLILGCTHYPFVKPLLAELIPADIAVIDTGAAVARQLQRLGQHELLATQPAQATRYWSS      240
A6VC58|MURI_PSEA7      TLILGCTHYPFVKPLLAELIPADIAVIDTGAAVARQLERVLSARALLASGQAAPRFWTS      240
Q9HVD0|MURI_PSEAE      TLILGCTHYPFVKPLLAELIPAEVAVIDTGAAVARQLERVLSARALLASGQAAPRFWTS      240
Q02G12|MURI_PSEAB      TLILGCTHYPFVKPLLAELIPAEVAVIDTGAAVARQLERVLSARALLASGQAAPRFWTS      240
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A4XR64|MURI_PSEMY      GDIQRMQAVLPLLLGEQAQVHVF--      263
A6VC58|MURI_PSEA7      ALPEEMERILPILWGSQESVGLDV      265
Q9HVD0|MURI_PSEAE      ALPEEMERILPILWGSPEVGLVV      265
Q02G12|MURI_PSEAB      ALPEEMERILPILWGSPEVGLVV      265
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