

CLUSTAL O(1.2.4) multiple sequence alignment

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Q9HVZ8 |MRAY_PSEAE      MLLLLAEYLQQFYKGFVGFQYLTLRGILSVLTALSLSLWLGPMIRTLQIRQIGQAVRND      60
A4XQS1 |MRAY_PSEMY      MLLLLAEYLQQFHKGFVGFQYLTLRGILGVLTAALSLWLGPMIRTLQVRQIGQAVRND      60
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Q9HVZ8 |MRAY_PSEAE      GPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV      120
A4XQS1 |MRAY_PSEMY      GPQSHLSKKGTPTMGGALILTAIAVSTLLWADLSNRYVWVVLAVTLLFGAIGWVDDYRKV      120
*****:*****_*:*****_*:*****_*:*****_*

Q9HVZ8 |MRAY_PSEAE      IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFVVLV      180
A4XQS1 |MRAY_PSEMY      IEKNSRGLPSRWKYFWQSVFGLAAIFLYMTAQSPEVETTLILPLLKDVSIPLGIGFVVLV      180
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Q9HVZ8 |MRAY_PSEAE      YFVIVGSSNAVNLTDGLDGLAIMPVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI      240
A4XQS1 |MRAY_PSEMY      YFVIVGSSNAVNLTDGLDGLAILPTVMVAGALAVFCYLSGNVNFAYLLIPYVPGAGELI      240
*****_*:*****_*:*****_*:*****_*

Q9HVZ8 |MRAY_PSEAE      VFCAALVGAGLGFLEWNTYPAQVFMGDVGALALGAALGTIAVIVRQEVVLFIMGGVFVME      300
A4XQS1 |MRAY_PSEMY      VFCAALVGAGLGFLEWNTYPAQVFMGDVGALALGAALGTIAVIVRQEVVLFIMGGVFVME      300
*****:*****_*:*****_*:*****_*

Q9HVZ8 |MRAY_PSEAE      TLSVMIQVASFKLTGRRVFRMAPIHFFELKGWPEPRVIVRFWIITVILVLIGLATLKL      360
A4XQS1 |MRAY_PSEMY      TLSVMIQVASFKLTGRRVFRMAPIHFFELKGWPEPRVIVRFWIITVILVLIGLATLKL      360
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