

CLUSTAL O(1.2.4) multiple sequence alignment

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A4XQS5|MURC_PSEMY      MAKSPAAVKAEVRRMRRIIRIHFVGI GGVMCGIAEVLLNLGYEVSGSDLKASAVTERLE      60
Q9HW02|MURC_PSEAE      MVKEPNG---VTRTMRRIRRIHFVGI GGAGMCGIAEVLLNLGYEVSGSDLKASAVTERLE      57
A6VB84|MURC_PSEA7      MVKEPNG---VTRTMRRIRRIHFVGI GGAGMCGIAEVLLNLGYEVSGSDLKASAVTERLE      57
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A4XQS5|MURC_PSEMY      SFGAKIFIGHAAENAEQADVLVSSAVNTSNPEVATALERRIPVVPRAEMLAELMRYRHG      120
Q9HW02|MURC_PSEAE      KFGAQIFIGHQAEENADGADVLVSSAINRANPEVASALERRIPVVPRAEMLAELMRYRHG      117
A6VB84|MURC_PSEA7      KFGAQIFIGHQAEENADGADVLVSSAINRANPEVASALERRIPVVPRAEMLAELMRYRHG      117
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A4XQS5|MURC_PSEMY      IAVAGTHGKTTTTSLLASVFAAGGLDPTFVIGGRLNAAGTNAQLGSSRFLIAEADESDAS      180
Q9HW02|MURC_PSEAE      IAVAGTHGKTTTTSLLIASVFAAGGLDPTFVIGGRLNAAGTNAQLGASRYLVAEADESDAS      177
A6VB84|MURC_PSEA7      IAVAGTHGKTTTTSLLIASVFAAGGLDPTFVIGGRLNAAGTNAQLGASRYLVAEADESDAS      177
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A4XQS5|MURC_PSEMY      FLHLQPMVSVVTDIDADHMSTYGGDFNRLKKTFFIEFLHNLFPFYGLAVLCVDDPVVRELLP      240
Q9HW02|MURC_PSEAE      FLHLQPMVAVVTDIDADHMATYGGDFNKLKKTFFVEFLHNLFPFYGLAVMCVDDPVVREILP      237
A6VB84|MURC_PSEA7      FLHLQPMVAVVTDIDADHMATYGGDFNKLKKTFFVEFLHNLFPFYGLAVMCVDDPVVREILP      237
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A4XQS5|MURC_PSEMY      QVGRPTVITYGFAEDADVRAINVRQEGMRTYFTVLRPDCPEPLDVSVMMPGNHNVLNALATI      300
Q9HW02|MURC_PSEAE      QIARPTVITYGLSEDADVRAINIRQEGMRTWFTVLRPEREPLDVSVMMPGLHNVLNSLATI      297
A6VB84|MURC_PSEA7      QIARPTVITYGLSEDADVRAINIRQEGMRTWFTVLRPEREPLDVSVMMPGLHNVLNSLATI      297
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A4XQS5|MURC_PSEMY      AIATDEGIDDAIVAGLSGFQGVGRRFQVYGE LQVVEGGSVMLVDDYGHHPREVAAVIKAV      360
Q9HW02|MURC_PSEAE      VIATDEGISDEAIVQGLSGFQGVGRRFQVYGE LQVEGGSVMLVDDYGHHPREVAAVIKAI      357
A6VB84|MURC_PSEA7      VIATDEGISDEAIVQGLSGFQGVGRRFQVYGE LQVEGGSVMLVDDYGHHPREVAAVIKAI      357
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A4XQS5|MURC_PSEMY      RGGWPERRLMVYQPHRYRTRDLYEDFVQVLGEANVLLLVEVYPAGEEPIPGADSRQMC      420
Q9HW02|MURC_PSEAE      RGGWPERRLMVYQPHRYRTRDLYEDFVQVLGEANVLLLMEVYPAGEEPIPGADSRQLC      417
A6VB84|MURC_PSEA7      RGGWPERRLMVYQPHRYRTRDLYEDFVQVLGEANVLLLMEVYPAGEEPIPGADSRQLC      417
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A4XQS5|MURC_PSEMY      HSIRQRGQLDPIYVERGVDLAPLLKPLL RAGDILLCQGAGDIGAVAPQLIKHPLFVGESK      480
Q9HW02|MURC_PSEAE      HSIRQRGQLDPIYFERDADLAPLVKPLL RAGDILLCQGAGDVGLAPQLIKNPLFAGKGG      477
A6VB84|MURC_PSEA7      HSIRQRGQLDPIYFERDADLAPLVKPLL RAGDILLCQGAGDVGLAPQLIRNPLFAGKGG      477
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A4XQS5|MURC_PSEMY      ---          480
Q9HW02|MURC_PSEAE      KGA          480
A6VB84|MURC_PSEA7      KGA          480

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