

CLUSTAL O(1.2.4) multiple sequence alignment

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Q6GEV1|MURA2_STAAR    MAQEVIKIRGGRTLNGEVNISGAKNSAVAIIPATLLAQG-HVKLEGLPQISDVKTLVSLL    59
Q6G7I6|MURA2_STAAS    MAQEVIKIRGGRTLNGEVNISGAKNSAVAIIPATLLAQG-HVKLEGLPQISDVKTLVSLL    59
P65456|MURA2_STAAM    MAQEVIKIRGGRTLNGEVNISGAKNSAVAIIPATLLAQG-HVKLEGLPQISDVKTLVSLL    59
Q931H5|MURA1_STAAM    --MDKIVIKGGNKLTGEVQVEGAKNAVLPLILTASLLASDKPSKLVNVPALSDVETINNVL    58
Q6GEX5|MURA1_STAAR    --MDKIVIKGGNKLTGEVQVEGAKNAVLPLILTASLLASDKPSKLVNVPALSDVETINNVL    58
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Q6GEV1|MURA2_STAAR    EDLNIKASLNG--TELEVDTTEIQNAALPNNKVESLRASYMMGAMLRGFKKCVIGLPGG    117
Q6G7I6|MURA2_STAAS    EDLNIKASLNG--MELEVDTTEIQNAALPNNKVESLRASYMMGAMLRGFKKCVIGLPGG    117
P65456|MURA2_STAAM    EDLNIKASLNG--TELEVDTTEIQNAALPNNKVESLRASYMMGAMLRGFKKCVIGLPGG    117
Q931H5|MURA1_STAAM    TTLNADVTYKKDENAVVVDATKTLNEEAPYEYVSKMRASILVMGPLLARLGHAIVALPGG    118
Q6GEX5|MURA1_STAAR    TTLNADVTYKKDENAVVVDATKTLNEEAPYEYVSKMRASILVMGPLLARLGHAIVALPGG    118
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Q6GEV1|MURA2_STAAR    CPLGPRPIDQHIKGFKALGAEIDESSTTSMKIEAKELKGAHIFLDMVSVGATINIMLAAV    177
Q6G7I6|MURA2_STAAS    CPLGPRPIDQHIKGFKALGAEIDESSTTSMKIEAKELKGAHIFLDMVSVGATINIMLAAV    177
P65456|MURA2_STAAM    CPLGPRPIDQHIKGFKALGAEIDESSTTSMKIEAKELKGAHIFLDMVSVGATINIMLAAV    177
Q931H5|MURA1_STAAM    CAIGSRPIEQHIKGFALGAEIHLNGNIYANAKDGLKGTSHLDFPSVGATQNIIMAAS    178
Q6GEX5|MURA1_STAAR    CAIGSRPIEQHIKGFALGAEIHLNGNIYANAKDGLKGTSHLDFPSVGATQNIIMAAS    178
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Q6GEV1|MURA2_STAAR    YATGQTVIENAAKEPEVVDVANFLTSMGANIKGAGTSTIKINGVKELHGSEYQVIPDRIE    237
Q6G7I6|MURA2_STAAS    YATGQTVIENAAKEPEVVDVANFLTSMGANIKGAGTSTIKINGVKELHGSEYQVIPDRIE    237
P65456|MURA2_STAAM    YATGQTVIENAAKEPEVVDVANFLTSMGANIKGAGTSTIKINGVKELHGSEYQVIPDRIE    237
Q931H5|MURA1_STAAM    LAKGKTLIENAAKEPEIVDLANYINEMGGRITGAGTDTITINGVESLHGVEHAIIPDRIE    238
Q6GEX5|MURA1_STAAR    LAKGKTLIENAAKEPEIVDLANYINEMGGRITGAGTDTITINGVESLHGVEHAIIPDRIE    238
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Q6GEV1|MURA2_STAAR    AGTYMCIAAACGENVILNIVPKHVETLTAKFSELGVNVDVRDERIRINNNAPYRFVDIK    297
Q6G7I6|MURA2_STAAS    AGTYMCIAAACGENVILNIVPKHVETLTAKFSELGVNVDVRDERIRINNNAPYRFVDIK    297
P65456|MURA2_STAAM    AGTYMCIAAACGENVILNIVPKHVETLTAKFSELGVNVDVRDERIRINNNAPYRFVDIK    297
Q931H5|MURA1_STAAM    AGTLLIAGAITRGDIFVVGAIKEHMASLVYKLEEMGVLELDYQEDGIRVRAEGELQPVDIK    298
Q6GEX5|MURA1_STAAR    AGTLLIAGAITRGDIFVVGAIKEHMASLVYKLEEMGVLELDYQEDGIRVRAEGDLQPVDIK    298
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Q6GEV1|MURA2_STAAR    TLVYPGFATDLQQPITPLLFMANGPSFVTDTIYPERFKHVEELKRMGANIEVDEGTATIK    357
Q6G7I6|MURA2_STAAS    TLVYPGFATDLQQPITPLLFMANGPSFVTDTIYPERFKHVEELKRMGANIEVDEGTATIK    357
P65456|MURA2_STAAM    TLVYPGFATDLQQPITPLLFMANGPSFVTDTIYPERFKHVEELKRMGANIEVDEGTATIK    357
Q931H5|MURA1_STAAM    TLPHPGFPTDMQSQMMALLLTANGHKVVTETVFNRFMHVAEFKRMNANINVEGRSAKLE    358
Q6GEX5|MURA1_STAAR    TLPHPGFPTDMQSQMMALLLTANGHKVVTETVFNRFMHVAEFKRMNANINVEGRSAKLE    358
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Q6GEV1|MURA2_STAAR    -PSTLHGAEVYASDLRAGACLIIAGLIAEGVTTIYNVKHIYRGYTDIVEHLKALGADIWT    416
Q6G7I6|MURA2_STAAS    -PSTLHGAEVYASDLRAGACLIIAGLIAEGVTTIYNVKHIYRGYTDIVEHLKALGADIWT    416
P65456|MURA2_STAAM    -PSTLHGAEVYASDLRAGACLIIAGLIAEGVTTIYNVKHIYRGYTDIVEHLKALGADIWT    416
Q931H5|MURA1_STAAM    GKSQQLQGAQVKATDLRAAALILAGLVADGKTSVTELTHLDRGYVDLHGKLLQLGADIER    418
Q6GEX5|MURA1_STAAR    GKSQQLQGAQVKATDLRAAALILAGLVADGKTSVTELTHLDRGYVDLHGKLLQLGADIER    418
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Q6GEV1|MURA2_STAAR    ETV          419
Q6G7I6|MURA2_STAAS    ETV          419
P65456|MURA2_STAAM    ETV          419
Q931H5|MURA1_STAAM    IND          421
Q6GEX5|MURA1_STAAR    IND          421

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