



## *Aedes atropalpus* mosquito rRNA gene internal transcribed spacer 2 (ITS2) unanimity alignment & molecular taxonomy primer map

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1 | 130
MG232605 | ACAAGTTGAACGCATATTGCACATCGTACAACAGTACGATGTACACATTTTTGAGTGCCTATATTTATCTATTCAACTATACGTGTATGCGCGTTTCACCTCGGGTGGACAGGCGCATGGCCCCGTAAGC |

131 Mosq-RAE2 | 260
MG232605 | CGTATGCRKVGTTGAYGTTTTTC |
| CGTATGCGTAGTGTATTTTTCCGGCCTTCGGTGGTCCGGTAAAACATTGAAGATAGTCAGGCGCGTCCCGTCCGGCGCGGCGAGCGACGCGGTTGATGAATACATCCCCTAGACCACACCACCCGGTTG |

261 | 318
MG232605 | GTTATGTTGTATTCCATCACACACTCGAACTCTCGAACTCGGATAGCATATCCAGTAG |
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Alignments prepared using ElimDupes ([www.hiv.lanl.gov/content/sequence/elimdupesv2/elimdupes.html](http://www.hiv.lanl.gov/content/sequence/elimdupesv2/elimdupes.html)), CLUSTAL O ([www.ebi.ac.uk/Tools/msa/clustalo/](http://www.ebi.ac.uk/Tools/msa/clustalo/)), EMBOSS Seqret ([www.ebi.ac.uk/Tools/sfc/emboss\\_seqret/](http://www.ebi.ac.uk/Tools/sfc/emboss_seqret/)) and SURE v1.0 Sequence Unanimity Reformatting tool (<http://midasmap.uaslp.mx/suretool/>).