



***Aedes japonicus* mosquito rRNA gene internal transcribed spacer 2 (ITS2) unanimity alignment & molecular taxonomy primer map**
 Laboratorio de Genómica Viral y Humana, Facultad de Medicina, Universidad Autónoma de San Luis Potosí, México (08/Apr/2022, v4.0)

1 | Mosq-F | 130 |
TGTGAACTGCAGGACACAT
 Consensus *****AACACCGACAAGTTGAACGCATATTGCACATCGTACATCAGTACGATGTACACATTTTTGAGTGCCTATATTTATCCATTCAACTATACGTGTGCGTGCGCGTTTCACTT
 MG232625 *****-----
 FJ403047 *****-----
 MK412709 *****-----
 MK412713 *****-----
 MK412716 *****-----

131 | Mosq-RAE2 | 260 |
 Consensus CGGGTGGACGGGCGCACGGCCTCTCGGCAGCGTAGTATAGTATCGCTCTATATCTATATCTGCCGGGCA**CGTATGCRKVG TGAYGTTTTTC**CTAGCGCCCGAGCGCGCCGGTAAAACATTGAAGATAGTC
 MG232625 -----
 FJ403047 -----
 MK412709 -----
 MK412713 -----
 MK412716 -----

261 | 390 |
 Consensus AGGGCGCGTCTGACCGCTTCCACGGTTGGCGCGAGTTGATGAATACATCCCATCATCCCATCATGGTGTGTTGCCATTGTATTCCATCACAACAGCCACATATATAAACTCCAGTAGGCCTCAAAT
 MG232625 -----G---G---
 FJ403047 -----G---
 MK412709 -----CA--G
 MK412713 -----
 MK412716 -----A-----



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          400
          |
391      | Mosq-R2
          | ATGTGTGACTACCCCTAAA
Consensus A ATGTGTGAC
MG232625 *****
FJ403047 -----
MK412709 -----
MK412713 -----
MK412716 *****
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Alignments prepared using ElimDupes (www.hiv.lanl.gov/content/sequence/elimdupesv2/elimdupes.html), CLUSTAL O (www.ebi.ac.uk/Tools/msa/clustalo/), EMBOSS Seqret (www.ebi.ac.uk/Tools/sfc/emboss_seqret/) and SURE v1.0 Sequence Unanimity Reformatting tool (<http://midasmap.uaslp.mx/suretool/>).