



Culex salinarius 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 | 130 |

Mosq-F

Consensus TGTGAAC TG CAGG ACAC AT | GAAC ACCG GACA AG TT GAAC GCAT ATT GCAC AT CGTACA AAC AGTAC GAT GTAC AC ATTTT GAG TGC CT AT ATT TAT CT ATT CA ACT GT GCG TGT GCAC CCCT CT CGC GGGG

U22140 -----

U22142 -----

U22141 -----

U22139 -----

U22143 -----

U22144 -----

131 | 260 |

Mosq-RCX GCTGGCAAAACATTCAAGAC

Consensus GGTATGCACGCACGCAGCATGGTGC TT GCTGCGCTT TAGGTGC GCTGGCAAAACATTCAAGAC ACTCCGGTT CGGGTT GCAGCGACC ACTGAAACACTGGTGCGGACACACGAACGTGAGAATACA

U22140 ----- T -----

U22142 ----- • ----- C -----

U22141 ----- G ----- C -----

U22139 ----- • ----- C -----

U22143 ----- • ----- C -----

U22144 ----- • ----- C -----

261 | 390 |

Consensus TACCACTGCTCCAACCTGGCTGGCGCCGATGTAAGCTCTCGCGTTGCTACGTCGCTGCGGTACCGCGGTGCTAGAACAGCCGACACCGACACTAGATAGACACCCCATGTAGGCC

U22140 ----- • ----- • -----

U22142 ----- • ----- G -----

U22141 ----- • ----- • -----

U22139 ----- • ----- G -----

U22143 ----- ----- -----

U22144 ----- ----- -----



Culex salinarius 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)

391 Mosq-R2 426

Consensus	TCAAATAATGTGTGACTACCCCCCTAAAATTAAAGCAT
U22140	-----
U22142	-----
U22141	-----
U22139	-----
U22143	-----
U22144	-----

The sequence alignment shows the consensus sequence TCAAATAATGTGTGACTACCCCCCTAAAATTAAAGCAT. Positions 391 and 426 are marked above the sequence. A primer site 'Mosq-R2' is indicated between positions 391 and 426. Below the consensus sequence, six sequences (U22140, U22142, U22141, U22139, U22143, U22144) are shown as dashed red boxes, indicating they have identical sequences to the consensus at these positions.

Alignments prepared using ElimDuplicates (www.hiv.lanl.gov/content/sequence/elimduplicatesv2/elimduplicates.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/>).