Jacob E Crawford

List of Publications by Year
in descending order

31 papers	2,281 citations	471477 17 h-index	414395 32 g-index
36 all docs	36 docs citations	36 times ranked	3915 citing authors

#	Article	IF	Citations
1	Reply to: Assessing the efficiency of Verilyâ€™s automated process for production and release of male Wolbachia-infected mosquitoes. Nature Biotechnology, 2022, 40, 1443-1446.	17.5	2
2	A Low-Powered and Highly Selective Trap for Male Aedes (Diptera: Culicidae) Surveillance: The Male Aedes Sound Trap. Journal of Medical Entomology, 2021, 58, 408-415.	1.8	13
3	Outcomes from international field trials with Male Aedes Sound Traps: Frequency-dependent effectiveness in capturing target species in relation to bycatch abundance. PLoS Neglected Tropical Diseases, 2021, 15, e0009061.	3.0	9
4	Designing Aedes (Diptera: Culicidae) Mosquito Traps: The Evolution of the Male Aedes Sound Trap by Iterative Evaluation. Insects, 2021, 12, 388.	2.2	3
5	Effect of BG-Lures on the Male Aedes (Diptera: Culicidae) Sound Trap Capture Rates. Journal of Medical Entomology, 2021, 58, 2425-2431.	1.8	3
6	Releasing incompatible males drives strong suppression across populations of wild and Wolbachia -carrying Aedes aegypti in Australia. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	71
7	Climate and Urbanization Drive Mosquito Preference for Humans. Current Biology, 2020, 30, 3570-3579.e6.	3.9	153
8	Improved reference genome of the arboviral vector Aedes albopictus. Genome Biology, 2020, 21, 215.	8.8	65
9	Environmental influences on Aedes aegypti catches in Biogents Sentinel traps during a Californian â€œrear and releaseâ€•program: Implications for designing surveillance programs. PLoS Neglected Tropical Diseases, 2020, 14, e0008367.	3.0	6
10	Efficient production of male Wolbachia-infected Aedes aegypti mosquitoes enables large-scale suppression of wild populations. Nature Biotechnology, 2020, 38, 482-492.	17.5	225
11	Polymorphism analyses and protein modelling inform on functional specialization of PiwiÂclade genes in the arboviral vector Aedes albopictus. PLoS Neglected Tropical Diseases, 2019, 13, e0007919.	3.0	16
12	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	27.8	426
13	Novel Form of Alternative Splicing of NFKB1. Its Role in Polycythemia and Adaptation to High Altitude in Andean Aymara. Blood, 2018, 132, 2316-2316.	1.4	2
14	Population genomics reveals that an anthropophilic population of Aedes aegypti mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. BMC Biology, 2017, 15, 16.	3.8	96
15	Asian wild rice is a hybrid swarm with extensive gene flow and feralization from domesticated rice. Genome Research, 2017, 27, 1029-1038.	5.5	100
16	Natural Selection on Genes Related to Cardiovascular Health in High-Altitude Adapted Andeans. American Journal of Human Genetics, 2017, 101, 752-767.	6.2	99
17	The complex effects of demographic history on the estimation of substitution rate: concatenated gene analysis results in no more than twofold overestimation. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170537.	2.6	13
18	Evolution of <scp>GOUNDRY</scp>, a cryptic subgroup of AnophelesÂgambiaeÂs.l., and its impact on susceptibility to Plasmodium infection. Molecular Ecology, 2016, 25, 1494-1510.	3.9	18

#	Article	IF	Citations
19	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	27.8	439
20	Diabolical survival in Death Valley: recent pupfish colonization, gene flow and genetic assimilation in the smallest species range on earth. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152334.	2.6	64
21	Reticulate Speciation and Barriers to Introgression in theAnopheles gambiaeSpecies Complex. Genome Biology and Evolution, 2015, 7, 3116-3131.	2.5	32
22	Population Genetics ofAnopheles coluzziiImmune Pathways and Genes. G3: Genes, Genomes, Genetics, 2015, 5, 329-339.	1.8	10
23	Uncovering the Genetic History of the Present-Day Greenlandic Population. American Journal of Human Genetics, 2015, 96, 54-69.	6.2	85
24	No evidence for positive selection at two potential targets for malaria transmission-blocking vaccines in Anopheles gambiae s.s. Infection, Genetics and Evolution, 2013, 16, 87-92.	2.3	3
25	Detecting adaptive trait loci in nonmodel systems: divergence or admixture mapping?. Molecular Ecology, 2013, 22, 6131-6148.	3.9	28
26	Evidence for Population-Specific Positive Selection on Immune Genes ofAnopheles gambiae. G3: Genes, Genomes, Genetics, 2012, 2, 1505-1519.	1.8	18
27	Assessing the Accuracy and Power of Population Genetic Inference from Low-Pass Next-Generation Sequencing Data. Frontiers in Genetics, 2012, 3, 66.	2.3	47
28	De Novo Transcriptome Sequencing in Anopheles funestus Using Illumina RNA-Seq Technology. PLoS ONE, 2010, 5, e14202.	2.5	132
29	The Demographic Histories of the M and S Molecular Forms of Anopheles gambiae s.s.. Molecular Biology and Evolution, 2010, 27, 1739-1744.	8.9	20
30	Identification of Genes Encoding Atypical Odorant-Binding Proteins inAedes albopictus(Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10	1.8	16
31	The distribution of hatching time in Anopheles gambiae. Malaria Journal, 2006, 5, 19.	2.3	47