Highly evolvable malaria vectors: The genomes of 16 <i>

Science

347, 1258522

DOI: 10.1126/science.1258522

Citation Report

#	Article	IF	Citations
1	Non-coding RNA gene families in the genomes of anopheline mosquitoes. BMC Genomics, 2014, 15, 1038.	1.2	9
2	Global maximum-parsimony based ancestral reconstruction with non-universal genes. , 2015, , .		0
3	Research highlights for issue 2: recent applications in molecular evolution. Evolutionary Applications, 2015, 8, 119-120.	1.5	0
4	Gene flow between Drosophila yakuba and Drosophila santomea in subunit V of cytochrome c oxidase: A potential case of cytonuclear cointrogression. Evolution; International Journal of Organic Evolution, 2015, 69, 1973-1986.	1.1	45
5	Insect phylogenomics. Insect Molecular Biology, 2015, 24, 403-411.	1.0	17
6	In vitro and in vivo host range of Anopheles gambiae densovirus (AgDNV). Scientific Reports, 2015, 5, 12701.	1.6	25
7	Transposons, Genome Size, and Evolutionary Insights in Animals. Cytogenetic and Genome Research, 2015, 147, 217-239.	0.6	119
8	Molecular tools for studying the major malaria vector Anopheles funestus: improving the utility of the genome using a comparative poly(A) and Ribo-Zero RNAseq analysis. BMC Genomics, 2015, 16, 931.	1.2	9
9	Does extreme asymmetric dominance promote hybridization between Anopheles coluzzii and Anopheles gambiae s.s. in seasonal malaria mosquito communities of West Africa?. Parasites and Vectors, 2015, 8, 586.	1.0	16
10	A standard photomap of ovarian nurse cell chromosomes in the <scp>E</scp>uropean malaria vector <scp>A</scp>nopheles atroparvus. Medical and Veterinary Entomology, 2015, 29, 230-237.	0.7	17
11	The narrowing olfactory landscape of insect odorant receptors. Frontiers in Ecology and Evolution, 2015, 3, .	1.1	47
12	Developmental neurogenetics of sexual dimorphism in Aedes aegypti. Frontiers in Ecology and Evolution, 2015, 3, .	1.1	9
13	Unravelling the Evolution of the Allatostatin-Type A, KISS and Galanin Peptide-Receptor Gene Families in Bilaterians: Insights from Anopheles Mosquitoes. PLoS ONE, 2015, 10, e0130347.	1.1	29
14	Diversification of the Genus Anopheles and a Neotropical Clade from the Late Cretaceous. PLoS ONE, 2015, 10, e0134462.	1.1	29
15	Hybridization in Parasites: Consequences for Adaptive Evolution, Pathogenesis, and Public Health in a Changing World. PLoS Pathogens, 2015, 11, e1005098.	2.1	108
16	Recent Advances in Antimalarial Drug Discovery â€" Challenges and Opportunities. , 0, , .		2
17	Evolution of an Epigenetic Gene Ensemble within the Genus Anopheles. Genome Biology and Evolution, 2015, 7, 901-915.	1.1	8
18	Heterochromatin, histone modifications, and nuclear architecture in disease vectors. Current Opinion in Insect Science, 2015, 10, 110-117.	2.2	24

#	Article	IF	Citations
19	Fighting Arbovirus Transmission: Natural and Engineered Control of Vector Competence in Aedes Mosquitoes. Insects, 2015, 6, 236-278.	1.0	65
20	Codon and Amino Acid Usage Are Shaped by Selection Across Divergent Model Organisms of the Pancrustacea. G3: Genes, Genomes, Genetics, 2015, 5, 2307-2321.	0.8	20
21	Genome of Rhodnius prolixus , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941.	3.3	329
22	A Genome-Scale Investigation of Incongruence in Culicidae Mosquitoes. Genome Biology and Evolution, 2015, 7, 3463-3471.	1.1	8
23	A draft genome sequence of an invasive mosquito: an ItalianAedes albopictus. Pathogens and Global Health, 2015, 109, 207-220.	1.0	35
24	â€œSalivary gland cellular architecture in the Asian malaria vector mosquito Anopheles stephensiâ€• Parasites and Vectors, 2015, 8, 617.	1.0	14
25	Advances in genetics and genomics: use and limitations in achieving malaria elimination goals. Pathogens and Global Health, 2015, 109, 123-141.	1.0	5
26	Conundrum of jumbled mosquito genomes. Science, 2015, 347, 27-28.	6.0	29
27	Wholeâ€genome sequencing reveals absence of recent gene flow and separate demographic histories for Anopheles punctulatus mosquitoes in Papua New Guinea. Molecular Ecology, 2015, 24, 1263-1274.	2.0	13
28	Evolving the world's most dangerous animal. Trends in Parasitology, 2015, 31, 39-40.	1.5	5
29	Evolution of sexual traits influencing vectorial capacity in anopheline mosquitoes. Science, 2015, 347, 985-988.	6.0	68
30	An unexpected cost of sex. Science, 2015, 347, 948-949.	6.0	0
31	A comparative analysis of reproductive biology of insect vectors of human disease. Current Opinion in Insect Science, 2015, 10, 142-148.	2.2	19
32	Connecting genotypes to medically relevant phenotypes in major vector mosquitoes. Current Opinion in Insect Science, 2015, 10, 59-64.	2.2	0
33	The CPCFC cuticular protein family: Anatomical and cuticular locations in Anopheles gambiae and distribution throughout Pancrustacea. Insect Biochemistry and Molecular Biology, 2015, 65, 57-67.	1.2	28
34	A maturing understanding of the composition of the insect gene repertoire. Current Opinion in Insect Science, 2015, 7, 15-23.	2.2	24
35	Complete Dosage Compensation inAnopheles stephensiand the Evolution of Sex-Biased Genes in Mosquitoes. Genome Biology and Evolution, 2015, 7, 1914-1924.	1.1	40
36	Chemical ecology and olfaction in arthropod vectors of diseases. Current Opinion in Insect Science, 2015, 10, 83-89.	2.2	43

#	Article	IF	Citations
37	Vector-transmitted disease vaccines: targeting salivary proteins in transmission (SPIT). Trends in Parasitology, 2015, 31, 363-372.	1.5	12
38	Long non-coding RNA discovery across the genus anopheles reveals conserved secondary structures within and beyond the Gambiae complex. BMC Genomics, 2015, 16, 337.	1.2	85
39	Beyond fruit-flies: population genomic advances in non-Drosophila arthropods. Briefings in Functional Genomics, 2015, 14, 424-431.	1.3	14
40	Genome sequence of the Asian Tiger mosquito, Aedes albopictus , reveals insights into its biology, genetics, and evolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5907-15.	3.3	251
41	Artemisinin-resistant Plasmodium falciparum clinical isolates can infect diverse mosquito vectors of Southeast Asia and Africa. Nature Communications, 2015, 6, 8614.	5.8	55
42	Chemoreceptor Evolution in Hymenoptera and Its Implications for the Evolution of Eusociality. Genome Biology and Evolution, 2015, 7, 2407-2416.	1.1	141
43	Plasmodium evasion of mosquito immunity and global malaria transmission: The lock-and-key theory. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15178-15183.	3.3	106
44	Extensive introgression in a malaria vector species complex revealed by phylogenomics. Science, 2015, 347, 1258524.	6.0	527
45	A Genome-Scale Investigation of How Sequence, Function, and Tree-Based Gene Properties Influence Phylogenetic Inference. Genome Biology and Evolution, 2016, 8, 2565-2580.	1.1	70
46	Daily Rhythms in Mosquitoes and Their Consequences for Malaria Transmission. Insects, 2016, 7, 14.	1.0	84
47	Genome-wide identification and characterization of odorant-binding protein (OBP) genes in the malaria vectorAnopheles sinensis(Diptera: Culicidae). Insect Science, 2016, 23, 366-376.	1.5	30
48	Powerful methods for detecting introgressed regions from population genomic data. Molecular Ecology, 2016, 25, 2387-2397.	2.0	78
49	Connecting Evolutionary Genomics to Cell Biology. , 2016, , 153-159.		1
50	CAMSA: A tool for comparative analysis and merging of scaffold assemblies. , 2016, , .		0
51	Structural divergence of chromosomes between malaria vectors Anopheles lesteri and Anopheles sinensis. Parasites and Vectors, 2016, 9, 608.	1.0	6
52	1.45â€…Ã… resolution structure of SRPN18 from the malaria vectorAnopheles gambiae. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 853-862.	0.4	3
53	Molecular classification based on apomorphic amino acids (Arthropoda, Hexapoda): Integrative taxonomy in the era of phylogenomics. Scientific Reports, 2016, 6, 28308.	1.6	4
54	Expression-Linked Patterns of Codon Usage, Amino Acid Frequency, and Protein Length in the Basally Branching ArthropodParasteatoda tepidariorum. Genome Biology and Evolution, 2016, 8, 2722-2736.	1.1	19

#	Article	IF	Citations
55	Radical remodeling of the Y chromosome in a recent radiation of malaria mosquitoes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2114-23.	3.3	92
57	Chromosome evolution in malaria mosquitoes inferred from physically mapped genome assemblies. Journal of Bioinformatics and Computational Biology, 2016, 14, 1630003.	0.3	8
58	Dosage compensation in the African malaria mosquitoAnopheles gambiae. Genome Biology and Evolution, 2016, 8, evw004.	1.1	35
59	High-throughput cis-regulatory element discovery in the vector mosquito Aedes aegypti. BMC Genomics, 2016, 17, 341.	1.2	25
60	Recent advances in malaria genomics and epigenomics. Genome Medicine, 2016, 8, 92.	3.6	37
61	Sexual Selection and the Evolution of Mating Systems in Mosquitoes. Advances in Insect Physiology, 2016, 51, 67-92.	1.1	7
62	Mosquito Sensory Systems. Advances in Insect Physiology, 2016, , 293-328.	1.1	53
63	The phylogeny of Anophelinae revisited: inferences about the origin and classification of Anopheles (Diptera: Culicidae). Zoologica Scripta, 2016, 45, 34-47.	0.7	36
64	A mosquito sperm's journey from male ejaculate to egg: Mechanisms, molecules, and methods for exploration. Molecular Reproduction and Development, 2016, 83, 897-911.	1.0	52
65	Insect science â€“ a vulnerable discipline?. Entomologia Experimentalis Et Applicata, 2016, 159, 121-134.	0.7	6
66	Sex-related effects of sleep deprivation on depressive- and anxiety-like behaviors in mice. Experimental Animals, 2016, 65, 97-107.	0.7	27
67	Chemosterilants for Control of Insects and Insect Vectors of Disease. Chimia, 2016, 70, 715.	0.3	10
68	Evolutionary Dynamics of Abundant Stop Codon Readthrough. Molecular Biology and Evolution, 2016, 33, 3108-3132.	3.5	53
69	Aquaglyceroporin function in the malaria mosquito Anopheles gambiae. Biology of the Cell, 2016, 108, 294-305.	0.7	23
70	Historical environmental change in Africa drives divergence and admixture of Aedes aegypti mosquitoes: a precursor to successful worldwide colonization?. Molecular Ecology, 2016, 25, 4337-4354.	2.0	52
71	Mosquito Vectors and the Globalization ofPlasmodium falciparumMalaria. Annual Review of Genetics, 2016, 50, 447-465.	3.2	51
72	Mosquito Peptide Hormones. Advances in Insect Physiology, 2016, 51, 145-188.	1.1	34
73	Genome-Wide Divergence in the West-African Malaria Vector Anopheles melas. G3: Genes, Genomes, Genetics, 2016, 6, 2867-2879.	0.8	10

#	Article	IF	Citations
74	Chromosomal inversions and ecotypic differentiation in Anopheles gambiae: the perspective from wholeâ€genome sequencing. Molecular Ecology, 2016, 25, 5889-5906.	2.0	35
75	Evaluation of DISCOVAR de novo using a mosquito sample for cost-effective short-read genome assembly. BMC Genomics, 2016, 17, 187.	1.2	60
76	Comparative pharmacological characterization of D1-like dopamine receptors from Anopheles gambiae, Aedes aegypti and Culex quinquefasciatus suggests pleiotropic signaling in mosquito vector lineages. Parasites and Vectors, 2016, 9, 192.	1.0	15
77	An Inhibitor of the Alternative Pathway of Complement in Saliva of New World Anopheline Mosquitoes. Journal of Immunology, 2016, 197, 599-610.	0.4	18
78	Disease vectors in the era of next generation sequencing. Genome Biology, 2016, 17, 95.	3.8	25
79	The mitochondrial genomes of twelve Anopheles mosquitoes (Diptera: Culicidae) and their phylogenetic implications. Conservation Genetics Resources, 2016, 8, 387-390.	0.4	8
80	Plant-Herbivore Interactions in the Era of Big Data. , 2016, , 3-48.		2
81	More than one rabbit out of the hat: Radiation, transgenic and symbiont-based approaches for sustainable management of mosquito and tsetse fly populations. Acta Tropica, 2016, 157, 115-130.	0.9	141
82	The Genetic Basis of Pheromone Evolution in Moths. Annual Review of Entomology, 2016, 61, 99-117.	5.7	90
83	Insect genome content phylogeny and functional annotation of core insect genomes. Molecular Phylogenetics and Evolution, 2016, 97, 224-232.	1.2	11
84	Mosquito Defense Strategies against Viral Infection. Trends in Parasitology, 2016, 32, 177-186.	1.5	154
85	pHEMA hydrogels with pendant triazinyl-Î²-cyclodextrin as an efficient and recyclable reservoir for loading and release of plant-based mosquito repellents: a new aqueous mosquito repellent formulation. RSC Advances, 2016, 6, 27301-27312.	1.7	8
86	CLIPB8 is part of the prophenoloxidase activation system in Anopheles gambiae mosquitoes. Insect Biochemistry and Molecular Biology, 2016, 71, 106-115.	1.2	33
87	GNBP domain of Anopheles darlingi: are polymorphic inversions and gene variation related to adaptive evolution?. Genetica, 2016, 144, 99-106.	0.5	6
88	Proteomics reveals major components of oogenesis in the reproductive tract of sugar-fed Anopheles aquasalis. Parasitology Research, 2016, 115, 1977-1989.	0.6	7
89	Identification, Validation, and Application of Molecular Diagnostics for Insecticide Resistance in Malaria Vectors. Trends in Parasitology, 2016, 32, 197-206.	1.5	87
90	Genomics at the evolving species boundary. Current Opinion in Insect Science, 2016, 13, 7-15.	2.2	9
91	Biogeography of the Anthropocene. Progress in Physical Geography, 2016, 40, 161-174.	1.4	15

#	Article	IF	Citations
92	Arthropod Innate Immune Systems and Vector-Borne Diseases. Biochemistry, 2017, 56, 907-918.	1.2	79
93	Discovery of flavivirus-derived endogenous viral elements inAnophelesmosquito genomes supports the existence ofAnopheles-associated insect-specific flaviviruses. Virus Evolution, 2017, 3, vew035.	2.2	43
94	Chromosome inversions and ecological plasticity in the main African malaria mosquitoes. Evolution; International Journal of Organic Evolution, 2017, 71, 686-701.	1.1	51
95	Identifying conserved genomic elements and designing universal bait sets to enrich them. Methods in Ecology and Evolution, 2017, 8, 1103-1112.	2.2	133
96	Anopheline salivary protein genes and gene families: an evolutionary overview after the whole genome sequence of sixteen Anopheles species. BMC Genomics, 2017, 18, 153.	1.2	59
97	The Physical Genome Mapping ofAnopheles albimanusCorrected Scaffold Misassemblies and Identified Interarm Rearrangements in GenusAnopheles. G3: Genes, Genomes, Genetics, 2017, 7, 155-164.	0.8	29
98	Genome-wide analysis of transposable elements in the coffee berry borer Hypothenemus hampei (Coleoptera: Curculionidae): description of novel families. Molecular Genetics and Genomics, 2017, 292, 565-583.	1.0	14
99	The neurobiology of gustation in insect disease vectors: progress and potential. Current Opinion in Insect Science, 2017, 20, 19-27.	2.2	14
100	Genome content analysis yields new insights into the relationship between the human malaria parasite Plasmodium falciparum and its anopheline vectors. BMC Genomics, 2017, 18, 205.	1.2	2
101	Comparative Transcriptomics of Malaria Mosquito Testes: Function, Evolution, and Linkage. G3: Genes, Genomes, Genetics, 2017, 7, 1127-1136.	0.8	9
102	Anopheline Reproductive Biology: Impacts on Vectorial Capacity and Potential Avenues for Malaria Control. Cold Spring Harbor Perspectives in Medicine, 2017, 7, a025593.	2.9	27
103	Homology-aware Phylogenomics at Gigabase Scales. Systematic Biology, 2017, 66, syw104.	2.7	34
104	DeCoSTAR: Reconstructing the Ancestral Organization of Genes or Genomes Using Reconciled Phylogenies. Genome Biology and Evolution, 2017, 9, 1312-1319.	1.1	32
105	Transposable elements in the Anopheles funestus transcriptome. Genetica, 2017, 145, 275-293.	0.5	6
106	Preferential suppression of Anopheles gambiae host sequences allows detection of the mosquito eukaryotic microbiome. Scientific Reports, 2017, 7, 3241.	1.6	38
107	Functional analyses yield detailed insight into the mechanism of thrombin inhibition by the antihemostatic salivary protein cE5 from Anopheles gambiae. Journal of Biological Chemistry, 2017, 292, 12632-12642.	1.6	20
108	The Evolutionary Origin of Diversity in Chagas Disease Vectors. Trends in Parasitology, 2017, 33, 42-52.	1.5	121
109	Differential expression of putative sodium-dependent cation-chloride cotransporters in Aedes aegypti. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2017, 214, 40-49.	0.8	13

#	Article	IF	Citations
110	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. Scientific Reports, 2017, 7, 13528.	1.6	27
111	Chromosome armâ€specific patterns of polymorphism associated with chromosomal inversions in the major African malaria vector, Anopheles funestus. Molecular Ecology, 2017, 26, 5552-5566.	2.0	9
112	Profiles of soluble proteins in chemosensory organs of three members of the afro-tropical Anopheles gambiae complex. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 24, 41-50.	0.4	12
113	Insights Into Onchocerca volvulus Population Biology Through Multilocus Immunophenotyping. Journal of Infectious Diseases, 2017, 216, 736-743.	1.9	2
114	Complete mitochondrial genomes of Anopheles stephensi and An. dirus and comparative evolutionary mitochondriomics of 50 mosquitoes. Scientific Reports, 2017, 7, 7666.	1.6	47
115	Cross-Species Y Chromosome Function Between Malaria Vectors of the Anopheles gambiae Species Complex. Genetics, 2017, 207, 729-740.	1.2	18
116	Response to Blood Meal in the Fat Body of Anopheles stephensi Using Quantitative Proteomics: Toward New Vector Control Strategies Against Malaria. OMICS A Journal of Integrative Biology, 2017, 21, 520-530.	1.0	8
117	Mosquito-Borne Diseases and Omics: Tissue-Restricted Expression and Alternative Splicing Revealed by Transcriptome Profiling of Anopheles stephensi. OMICS A Journal of Integrative Biology, 2017, 21, 488-497.	1.0	23
118	Rapid evolution of female-biased genes among four species of Anopheles malaria mosquitoes. Genome Research, 2017, 27, 1536-1548.	2.4	60
119	Preliminary characterization of putative structural cuticular proteins in the malaria vector Anopheles sinensis. Pest Management Science, 2017, 73, 2519-2528.	1.7	19
120	The Nuclear and Mitochondrial Genomes of the Facultatively Eusocial Orchid BeeEuglossa dilemma. G3: Genes, Genomes, Genetics, 2017, 7, 2891-2898.	0.8	35
121	Comparative physical genome mapping of malaria vectors Anopheles sinensis and Anopheles gambiae. Malaria Journal, 2017, 16, 235.	0.8	9
122	Prospects for malaria control through manipulation of mosquito larval habitats and olfactory-mediated behavioural responses using plant-derived compounds. Parasites and Vectors, 2017, 10, 184.	1.0	32
123	Serological measures to assess the efficacy of malaria control programme on Ambae Island, Vanuatu. Parasites and Vectors, 2017, 10, 204.	1.0	26
124	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. Genome Research, 2017, 27, 133-144.	2.4	60
125	A whole genome gene content phylogenetic analysis of anopheline mosquitoes. Molecular Phylogenetics and Evolution, 2017, 107, 266-269.	1.2	6
126	The evolutionary divergence of STAT transcription factor in different Anopheles species. Gene, 2017, 596, 89-97.	1.0	6
127	Comprehensive variation discovery and recovery of missing sequence in the pig genome using multiple de novo assemblies. Genome Research, 2017, 27, 865-874.	2.4	116

#	Article	IF	Citations
128	The Evolutionary Dynamics of the Odorant Receptor Gene Family in Corbiculate Bees. Genome Biology and Evolution, 2017, 9, 2023-2036.	1.1	44
129	Environmental Plasticity in the Intersexual Correlation and Sex Bias of Gene Expression. Journal of Heredity, 2017, 108, 754-758.	1.0	3
130	Phagocytosis in Insect Immunity. Advances in Insect Physiology, 2017, , 35-82.	1.1	32
131	Insect Antimicrobial Defences. Advances in Insect Physiology, 2017, , 1-33.	1.1	30
132	Implicating Cryptic and Novel Anophelines as Malaria Vectors in Africa. Insects, 2017, 8, 1.	1.0	99
133	Infectious Disease Genomics. , 2017, , 211-225.		2
134	Comparative genomics shows that viral integrations are abundant and express piRNAs in the arboviral vectors Aedes aegypti and Aedes albopictus. BMC Genomics, 2017, 18, 512.	1.2	138
135	How driving endonuclease genes can be used to combat pests and disease vectors. BMC Biology, 2017, 15, 81.	1.7	66
136	CAMSA: a tool for comparative analysis and merging of scaffold assemblies. BMC Bioinformatics, 2017, 18, 496.	1.2	11
137	Deciphering the olfactory repertoire of the tiger mosquito Aedes albopictus. BMC Genomics, 2017, 18, 770.	1.2	30
138	Basic and Translational Research on Sand Fly Saliva. , 2017, , 65-89.		3
139	Modulation of Mosquito Immune Defenses as a Control Strategy. , 2017, , 59-89.		1
140	Whole metagenome sequencing reveals links between mosquito microbiota and insecticide resistance in malaria vectors. Scientific Reports, 2018, 8, 2084.	1.6	101
141	Genomes of Diptera. Current Opinion in Insect Science, 2018, 25, 116-124.	2.2	26
142	Genomeâ€wide and expressionâ€profiling analyses suggest the main cytochrome P450 genes related to pyrethroid resistance in the malaria vector, Anopheles sinensis (Diptera Culicidae). Pest Management Science, 2018, 74, 1810-1820.	1.7	27
143	Pyrimidine-chloroquinoline hybrids: Synthesis and antiplasmodial activity. European Journal of Medicinal Chemistry, 2018, 148, 39-53.	2.6	44
144	Comparative Methods for Reconstructing Ancient Genome Organization. Methods in Molecular Biology, 2018, 1704, 343-362.	0.4	7
145	Mosquito Immunobiology: The Intersection of Vector Health and Vector Competence. Annual Review of Entomology, 2018, 63, 145-167.	5.7	88

#	Article	IF	Citations
146	The Evolution and Metamorphosis of Arthropod Proteomics and Genomics. Annual Review of Entomology, 2018, 63, 1-13.	5.7	10
147	Antiviral systems in vector mosquitoes. Developmental and Comparative Immunology, 2018, 83, 34-43.	1.0	13
148	Adaptations in energy metabolism and gene family expansions revealed by comparative transcriptomics of three Chagas disease triatomine vectors. BMC Genomics, 2018, 19, 296.	1.2	12
149	A standard photomap of ovarian nurse cell chromosomes and inversion polymorphism in Anopheles beklemishevi. Parasites and Vectors, 2018, 11, 211.	1.0	7
150	Partial-arm translocations in evolution of malaria mosquitoes revealed by high-coverage physical mapping of the Anopheles atroparvus genome. BMC Genomics, 2018, 19, 278.	1.2	18
151	Comparative phylogeography of Aedes mosquitoes and the role of past climatic change for evolution within Africa. Ecology and Evolution, 2018, 8, 3019-3036.	0.8	3
152	Mosquito-Derived Anophelin Sulfoproteins Are Potent Antithrombotics. ACS Central Science, 2018, 4, 468-476.	5.3	37
153	Modern Vector Control. Cold Spring Harbor Perspectives in Medicine, 2018, 8, a025643.	2.9	16
154	Genomeâ€wide identification, characterization and evolution of cuticular protein genes in the malaria vector Anopheles sinensis (Diptera: Culicidae). Insect Science, 2018, 25, 739-750.	1.5	13
155	Accurate identification of Anopheles gambiae Giles trophic preferences by MALDI-TOF MS. Infection, Genetics and Evolution, 2018, 63, 410-419.	1.0	14
156	A Divergent Strain of Culex pipiens-Associated Tunisia Virus in the Malaria Vector Anopheles epiroticus. Microbiology Resource Announcements, 2018, 7, .	0.3	2
157	Malaria Transmission in South Americaâ€"Present Status and Prospects for Elimination. , 2018, , .		16
158	A transgenic tool to assess Anopheles mating competitiveness in the field. Parasites and Vectors, 2018, 11, 651.	1.0	6
159	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	13.7	426
160	Molecular tools and genetic markers for the generation of transgenic sexing strains in Anopheline mosquitoes. Parasites and Vectors, 2018, 11, 660.	1.0	10
161	Pure early zygotic genes in the Asian malaria mosquito Anopheles stephensi. Parasites and Vectors, 2018, 11, 652.	1.0	4
162	FastNet: Fast and Accurate Statistical Inference of Phylogenetic Networks Using Large-Scale Genomic Sequence Data. Lecture Notes in Computer Science, 2018, , 242-259.	1.0	10
163	Complete mitogenome of Anopheles sinensis and mitochondrial insertion segments in the nuclear genomes of 19 mosquito species. PLoS ONE, 2018, 13, e0204667.	1.1	10

#	Article	IF	Citations
164	The Development of Cytogenetic Maps for Malaria Mosquitoes. Insects, 2018, 9, 121.	1.0	9
165	A CRISPRâ€“Cas9 gene drive targeting doublesex causes complete population suppression in caged Anopheles gambiae mosquitoes. Nature Biotechnology, 2018, 36, 1062-1066.	9.4	648
166	Odorant Receptors and Odorant-Binding Proteins as Insect Pest Control Targets: A Comparative Analysis. Frontiers in Physiology, 2018, 9, 1163.	1.3	156
167	Microevolutionary selection dynamics acting on immune genes of the greenâ€veined white butterfly, Pieris napi. Molecular Ecology, 2018, 27, 2807-2822.	2.0	9
168	The Domestication of a Large DNA Virus by the Wasp Venturia canescens Involves Targeted Genome Reduction through Pseudogenization. Genome Biology and Evolution, 2018, 10, 1745-1764.	1.1	28
169	Saliva of hematophagous insects: a multifaceted toolkit. Current Opinion in Insect Science, 2018, 29, 102-109.	2.2	52
170	An Anopheles by Any Other Name â€¦?. Journal of Medical Entomology, 2018, 55, 1069-1070.	0.9	18
171	microRNA profiles and functions in mosquitoes. PLoS Neglected Tropical Diseases, 2018, 12, e0006463.	1.3	36
172	Phylogenetic signal from rearrangements in 18 Anopheles species by joint scaffolding extant and ancestral genomes. BMC Genomics, 2018, 19, 96.	1.2	10
173	A Multi-Gene Analysis and Potential Spatial Distribution of Species of the Strodei Subgroup of the Genus Nyssorhynchus (Diptera: Culicidae). Journal of Medical Entomology, 2018, 55, 1486-1495.	0.9	4
174	A standard photomap of the ovarian nurse cell chromosomes for the dominant malaria vector in Europe and Middle East Anopheles sacharovi. Malaria Journal, 2018, 17, 276.	0.8	6
175	Reduced-representation sequencing identifies small effective population sizes of Anopheles gambiae in the north-western Lake Victoria basin, Uganda. Malaria Journal, 2018, 17, 285.	0.8	7
176	Local adaptation and the evolution of inversions on sex chromosomes and autosomes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170423.	1.8	39
177	The Effect of Hybridization on Dosage Compensation in Member Species of the Anopheles gambiae Species Complex. Genome Biology and Evolution, 2018, 10, 1663-1672.	1.1	8
178	Comparative genomics of chemosensory protein genes (CSPs) in twenty-two mosquito species (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 1	1.1	25
179	Recurrent Amplification of the Heterochromatin Protein 1 (HP1) Gene Family across Diptera. Molecular Biology and Evolution, 2018, 35, 2375-2389.	3.5	12
180	Complete Anopheles funestus mitogenomes reveal an ancient history of mitochondrial lineages and their distribution in southern and central Africa. Scientific Reports, 2018, 8, 9054.	1.6	18
181	Inversions are bigger on the X chromosome. Molecular Ecology, 2019, 28, 1238-1245.	2.0	13

#	Article	IF	Citations
182	Identification, Molecular Characterization, and In Silico Structural Analysis of Carboxypeptidase B2 ofAnopheles stephensi. Journal of Medical Entomology, 2019, 56, 72-85.	0.9	4
183	Meeting the challenge of tick-borne disease control: A proposal for 1000 Ixodes genomes. Ticks and Tick-borne Diseases, 2019, 10, 213-218.	1.1	11
184	Vector biology meets disease control: using basic research to fight vector-borne diseases. Nature Microbiology, 2019, 4, 20-34.	5.9	189
185	Transcriptomic analysis of insecticide resistance in the lymphatic filariasis vector Culex quinquefasciatus. Scientific Reports, 2019, 9, 11406.	1.6	11
186	Genome annotation improvements from cross-phyla proteogenomics and time-of-day differences in malaria mosquito proteins using untargeted quantitative proteomics. PLoS ONE, 2019, 14, e0220225.	1.1	2
187	Mosquito-fungus interactions and antifungal immunity. Insect Biochemistry and Molecular Biology, 2019, 111, 103182.	1.2	42
188	A new species in the major malaria vector complex sheds light on reticulated species evolution. Scientific Reports, 2019, 9, 14753.	1.6	56
189	Sequence-Based Prediction of Olfactory Receptor Responses. Chemical Senses, 2019, 44, 693-703.	1.1	9
190	Genomic content of chemosensory genes correlates with host range in wood-boring beetles (Dendroctonus ponderosae, Agrilus planipennis, and Anoplophora glabripennis). BMC Genomics, 2019, 20, 690.	1.2	69
191	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	3.8	71
192	Characterization of the complete mitogenome of Anopheles aquasalis, and phylogenetic divergences among Anopheles from diverse geographic zones. PLoS ONE, 2019, 14, e0219523.	1.1	20
193	Molecular Tools Used in Medical and Veterinary Entomology. , 2019, , 673-694.		2
194	A High-Quality De novo Genome Assembly from a Single Mosquito Using PacBio Sequencing. Genes, 2019, 10, 62.	1.0	121
195	Diversity and evolution of the transposable element repertoire in arthropods with particular reference to insects. Bmc Ecology and Evolution, 2019, 19, 11.	0.7	129
196	Natural Wolbachia infections are common in the major malaria vectors in Central Africa. Evolutionary Applications, 2019, 12, 1583-1594.	1.5	36
197	A chromosome-scale assembly of the major African malaria vector Anopheles funestus. GigaScience, 2019, 8, .	3.3	56
198	Gene Family Evolution in the Pea Aphid Based on Chromosome-Level Genome Assembly. Molecular Biology and Evolution, 2019, 36, 2143-2156.	3.5	84
199	The perils of intralocus recombination for inferences of molecular convergence. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180244.	1.8	33

#	Article	IF	Citations
200	Editorial overview: Revisiting Dobzhansky and the â€˜modern synthesisâ€™ in light of insect evolutionary genomics. Current Opinion in Insect Science, 2019, 31, iii-vi.	2.2	1
201	Insect genomes: progress and challenges. Insect Molecular Biology, 2019, 28, 739-758.	1.0	115
202	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. Genome Biology, 2019, 20, 98.	3.8	27
203	Birth-and-Death Evolution of the Fatty Acyl-CoA Reductase (FAR) Gene Family and Diversification of Cuticular Hydrocarbon Synthesis in Drosophila. Genome Biology and Evolution, 2019, 11, 1541-1551.	1.1	44
204	Gene Selection and Evolutionary Modeling Affect Phylogenomic Inference of Neuropterida Based on Transcriptome Data. International Journal of Molecular Sciences, 2019, 20, 1072.	1.8	8
205	Contrasting patterns of gene expression indicate differing pyrethroid resistance mechanisms across the range of the New World malaria vector Anopheles albimanus. PLoS ONE, 2019, 14, e0210586.	1.1	21
206	A re-annotation of the Anopheles darlingi mobilome. Genetics and Molecular Biology, 2019, 42, 125-131.	0.6	5
207	An insight into the sialotranscriptome and virome of Amazonian anophelines. BMC Genomics, 2019, 20, 166.	1.2	22
208	UDP-glycosyltransferase genes and their association and mutations associated with pyrethroid resistance in Anopheles sinensis (Diptera: Culicidae). Malaria Journal, 2019, 18, 62.	0.8	46
209	Evolution of sexually-transferred steroids and mating-induced phenotypes in Anopheles mosquitoes. Scientific Reports, 2019, 9, 4669.	1.6	7
210	Behavioural adaptations of mosquito vectors to insecticide control. Current Opinion in Insect Science, 2019, 34, 48-54.	2.2	89
211	Nanobiotechnology as an emerging approach to combat malaria: A systematic review. Nanomedicine: Nanotechnology, Biology, and Medicine, 2019, 18, 221-233.	1.7	64
212	Mosquitoes (Culicidae). , 2019, , 261-325.		42
213	MicroRNAs from saliva of anopheline mosquitoes mimic human endogenous miRNAs and may contribute to vector-host-pathogen interactions. Scientific Reports, 2019, 9, 2955.	1.6	25
214	Genomeâ€wide gene expression profiling reveals that cuticle alterations and P450 detoxification are associated with deltamethrin and DDT resistance in Anopheles arabiensis populations from Ethiopia. Pest Management Science, 2019, 75, 1808-1818.	1.7	42
215	Mosquitoes, Infectious Diseases, and Cancer: A Connection to Study?. International Journal of Environmental Research and Public Health, 2019, 16, 4859.	1.2	7
216	Establishment of computational biology in Greece and Cyprus: Past, present, and future. PLoS Computational Biology, 2019, 15, e1007532.	1.5	3
217	An odorant receptor from Anopheles gambiae that demonstrates enantioselectivity to the plant volatile, linalool. PLoS ONE, 2019, 14, e0225637.	1.1	16

#	Article	IF	Citations
218	K-mer-Based Motif Analysis in Insect Species across Anopheles, Drosophila, and Glossina Genera and Its Application to Species Classification. Computational and Mathematical Methods in Medicine, 2019, 2019, 1-16.	0.7	7
219	Microevolution of medically important mosquitoes â€“ A review. Acta Tropica, 2019, 191, 162-171.	0.9	25
220	How chromosomal rearrangements shape adaptation and speciation: Case studies in Drosophila pseudoobscura and its sibling species Drosophila persimilis. Molecular Ecology, 2019, 28, 1283-1301.	2.0	67
221	Physical Genome Mapping Using Fluorescence In Situ Hybridization with Mosquito Chromosomes. Methods in Molecular Biology, 2019, 1858, 177-194.	0.4	12
222	Using BUSCO to Assess Insect Genomic Resources. Methods in Molecular Biology, 2019, 1858, 59-74.	0.4	27
223	Population genetics of Anopheles funestus, the African malaria vector, Kenya. Parasites and Vectors, 2019, 12, 15.	1.0	12
224	Identification, characterization and expression analysis of Anopheles stephensi double peroxidase. Acta Tropica, 2019, 190, 210-219.	0.9	5
225	Of Genes and Genomes: Mosquito Evolution and Diversity. Trends in Parasitology, 2019, 35, 32-51.	1.5	35
226	Molecular Evolution of the Major Arthropod Chemoreceptor Gene Families. Annual Review of Entomology, 2019, 64, 227-242.	5.7	156
227	Excess of retrogene traffic in pig X chromosome. Genetica, 2019, 147, 23-32.	0.5	5
228	Proteomics reveals localization of cuticular proteins in Anopheles gambiae. Insect Biochemistry and Molecular Biology, 2019, 104, 91-105.	1.2	15
229	The Origin of a New Sex Chromosome by Introgression between Two Stickleback Fishes. Molecular Biology and Evolution, 2019, 36, 28-38.	3.5	57
230	Comparative analyses of simple sequence repeats (SSRs) in 23 mosquito species genomes: Identification, characterization and distribution (Diptera: Culicidae). Insect Science, 2019, 26, 607-619.	1.5	26
231	The SCJ Small Parsimony Problem for Weighted Gene Adjacencies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1364-1373.	1.9	6
232	Priscoculex burmanicus n. gen. et sp. (Diptera: Culicidae: Anophelinae) from mid-Cretaceous Myanmar amber. Historical Biology, 2020, 32, 1157-1162.	0.7	6
233	Building a sequence map of the pig pan-genome from multiple de novo assemblies and Hi-C data. Science China Life Sciences, 2020, 63, 750-763.	2.3	47
234	Malaria-carrying mosquitoes get a leg up on insecticides. Nature, 2020, 577, 319-320.	13.7	3
235	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	1.7	177

#	Article	IF	Citations
236	Genomic data reveal a protracted window of introgression during the diversification of a neotropical woodcreeper radiation*. Evolution; International Journal of Organic Evolution, 2020, 74, 842-858.	1.1	32
237	Expansions and contractions in gene families of independently-evolved blood-feeding insects. BMC Evolutionary Biology, 2020, 20, 87.	3.2	9
238	Culicidae evolutionary history focusing on the Culicinae subfamily based on mitochondrial phylogenomics. Scientific Reports, 2020, 10, 18823.	1.6	37
239	Chromatin Structure and Function in Mosquitoes. Frontiers in Genetics, 2020, 11, 602949.	1.1	9
240	Ultraconserved Non-coding DNA Within Diptera and Hymenoptera. G3: Genes, Genomes, Genetics, 2020, 10, 3015-3024.	0.8	3
241	TickSialoFam (TSFam): A Database That Helps to Classify Tick Salivary Proteins, a Review on Tick Salivary Protein Function and Evolution, With Considerations on the Tick Sialome Switching Phenomenon. Frontiers in Cellular and Infection Microbiology, 2020, 10, 374.	1.8	41
242	New vectors in northern Sarawak, Malaysian Borneo, for the zoonotic malaria parasite, Plasmodium knowlesi. Parasites and Vectors, 2020, 13, 472.	1.0	26
243	High-Throughput Genotyping of Common Chromosomal Inversions in the Afrotropical Malaria Mosquito Anopheles Funestus. Insects, 2020, 11, 693.	1.0	7
244	Diversity and evolution of the P450 family in arthropods. Insect Biochemistry and Molecular Biology, 2020, 127, 103490.	1.2	109
245	Regulatory gene function handoff allows essential gene loss in mosquitoes. Communications Biology, 2020, 3, 540.	2.0	6
246	Evolutionary rearrangements of X chromosomes in voles (Arvicolinae, Rodentia). Scientific Reports, 2020, 10, 13235.	1.6	5
247	Diversity, dynamics, direction, and magnitude of high-altitude migrating insects in the Sahel. Scientific Reports, 2020, 10, 20523.	1.6	21
248	The distance and median problems in the single-cut-or-join model with single-gene duplications. Algorithms for Molecular Biology, 2020, 15, 8.	0.3	5
249	Recent advances and future perspectives in vector-omics. Current Opinion in Insect Science, 2020, 40, 94-103.	2.2	6
250	Evolution of the Insecticide Target Rdl in African Anopheles Is Driven by Interspecific and Interkaryotypic Introgression. Molecular Biology and Evolution, 2020, 37, 2900-2917.	3.5	31
251	Maximum Likelihood Estimation of Species Trees from Gene Trees in the Presence of Ancestral Population Structure. Genome Biology and Evolution, 2020, 12, 3977-3995.	1.1	5
252	Structural Variation of the X Chromosome Heterochromatin in the Anopheles gambiae Complex. Genes, 2020, 11, 327.	1.0	14
253	Ancient Coretention of Paralogs of Cid Centromeric Histones and Cal1 Chaperones in Mosquito Species. Molecular Biology and Evolution, 2020, 37, 1949-1963.	3.5	11

#	Article	IF	Citations
254	Linked-read sequencing identifies abundant microinversions and introgression in the arboviral vector Aedes aegypti. BMC Biology, 2020, 18, 26.	1.7	16
255	Characterization of an adulticidal and larvicidal interfering RNA pesticide that targets a conserved sequence in mosquito G protein-coupled dopamine 1 receptor genes. Insect Biochemistry and Molecular Biology, 2020, 120, 103359.	1.2	19
256	Humbug Zooniverse: A Crowd-Sourced Acoustic Mosquito Dataset. , 2020, , .		12
257	Chromosome and Genome Divergence between the Cryptic Eurasian Malaria Vector-Species Anopheles messeae and Anopheles daciae. Genes, 2020, 11, 165.	1.0	17
258	Hemocyte-targeted gene expression in the female malaria mosquito using the hemolectin promoter from Drosophila. Insect Biochemistry and Molecular Biology, 2020, 120, 103339.	1.2	9
259	Characterization of Insect Immune Systems from Genomic Data. Springer Protocols, 2020, , 3-34.	0.1	4
260	Plasmodium falciparum evades immunity of anopheline mosquitoes by interacting with a Pfs47 midgut receptor. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2597-2605.	3.3	52
261	Taking Insect Immunity to the Single-Cell Level. Trends in Immunology, 2020, 41, 190-199.	2.9	10
262	Gene copy number and function of the APL1 immune factor changed during Anopheles evolution. Parasites and Vectors, 2020, 13, 18.	1.0	10
263	Three-dimensional Organization of Polytene Chromosomes in Somatic and Germline Tissues of Malaria Mosquitoes. Cells, 2020, 9, 339.	1.8	11
264	Elevated rates of positive selection drive the evolution of pestiferousness in the Colorado potato beetle (Leptinotarsa decemlineata, Say). Molecular Ecology, 2021, 30, 237-254.	2.0	16
265	Identification and expression of chemosensory receptor genes in the egg parasitoid Trissolcus basalis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 37, 100758.	0.4	6
266	The Legacy of Recurrent Introgression during the Radiation of Hares. Systematic Biology, 2021, 70, 593-607.	2.7	47
267	Lysozyme c-1 gene is overexpressed in Anopheles albimanus pericardial cells after an immune challenge. Developmental and Comparative Immunology, 2021, 114, 103830.	1.0	3
268	Potential role of Anopheles subpictus as a malaria vector in Ghaziabad District, Uttar Pradesh, India. International Journal of Tropical Insect Science, 2021, 41, 1107-1117.	0.4	3
269	Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. Molecular Biology and Evolution, 2021, 38, 486-501.	3.5	58
270	Transposable Elements and the Evolution of Insects. Annual Review of Entomology, 2021, 66, 355-372.	5.7	64
271	Olfactory systems across mosquito species. Cell and Tissue Research, 2021, 383, 75-90.	1.5	41

#	Article	IF	Citations
272	Biological computation and computational biology: survey, challenges, and discussion. Artificial Intelligence Review, 2021, 54, 4169-4235.	9.7	7
273	Prediction of neuropeptide precursors and differential expression of adipokinetic hormone/corazonin-related peptide, hugin and corazonin in the brain of malaria vector Nyssorhynchus albimanus during a Plasmodium berghei infection. Current Research in Insect Science, 2021, 1, 100014.	0.8	0
275	Hidden genomic features of an invasive malaria vector, Anopheles stephensi, revealed by a chromosome-level genome assembly. BMC Biology, 2021, 19, 28.	1.7	77
278	Decoding the Reproductive System of the Olive Fruit Fly, Bactrocera oleae. Genes, 2021, 12, 355.	1.0	7
279	Profile of Nora J. Besansky. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2101734118.	3.3	0
280	Total Ortholog Median Matrix as an alternative unsupervised approach for phylogenomics based on evolutionary distance between protein coding genes. Scientific Reports, 2021, 11, 3791.	1.6	2
281	Systematic identification of plausible pathways to potential harm via problem formulation for investigational releases of a population suppression gene drive to control the human malaria vector Anopheles gambiae in West Africa. Malaria Journal, 2021, 20, 170.	0.8	26
282	Transcriptional heterogeneity and tightly regulated changes in gene expression during Plasmodium berghei sporozoite development. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	32
283	Ultra-conserved sequences in the genomes of highly diverse Anopheles mosquitoes, with implications for malaria vector control. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3
284	Chromosome-level genome assemblies of the malaria vectors Anopheles coluzzii and Anopheles arabiensis. GigaScience, 2021, 10, .	3.3	12
285	femaleless Controls Sex Determination and Dosage Compensation Pathways in Females of Anopheles Mosquitoes. Current Biology, 2021, 31, 1084-1091.e4.	1.8	30
286	Summary Visualizations of Gene Ontology Terms With GO-Figure!. Frontiers in Bioinformatics, 2021, 1, .	1.0	51
287	Advances and opportunities in malaria population genomics. Nature Reviews Genetics, 2021, 22, 502-517.	7.7	61
288	Molecular evolution and the decline of purifying selection with age. Nature Communications, 2021, 12, 2657.	5.8	16
289	Characterization of Anopheles stephensi Odorant Receptor 8, an Abundant Component of the Mouthpart Chemosensory Transcriptome. Insects, 2021, 12, 593.	1.0	3
290	Utility of Complete Mitochondrial Genomes in Phylogenetic Classification of the Species of Anopheles (Culicidae: Anophelinae). Iranian Journal of Arthropod-borne Diseases, 2021, 15, 1-20.	0.8	3
291	A targeted amplicon sequencing panel to simultaneously identify mosquito species and Plasmodium presence across the entire Anopheles genus. Molecular Ecology Resources, 2022, 22, 28-44.	2.2	18
294	Phylogenomics of Opsin Genes in Diptera Reveals Lineage-Specific Events and Contrasting Evolutionary Dynamics in Anopheles and Drosophila. Genome Biology and Evolution, 2021, 13, .	1.1	16

#	Article	IF	Citations
295	Eight soybean reference genome resources from varying latitudes and agronomic traits. Scientific Data, 2021, 8, 164.	2.4	13
297	Intraspecific Transcriptome Variation and Sex-Biased Expression in Anopheles arabiensis. Genome Biology and Evolution, 2021, 13, .	1.1	3
299	Hemocyte RNA-Seq analysis of Indian malarial vectors Anopheles stephensi and Anopheles culicifacies: From similarities to differences. Gene, 2021, 798, 145810.	1.0	7
300	Complete mitogenomes of Anopheles peditaeniatus and Anopheles nitidus and phylogenetic relationships within the genus Anopheles inferred from mitogenomes. Parasites and Vectors, 2021, 14, 452.	1.0	8
302	Plasmodium development in Anopheles: a tale of shared resources. Trends in Parasitology, 2022, 38, 124-135.	1.5	27
303	Improving mosquito control strategies with population genomics. Trends in Parasitology, 2021, 37, 907-921.	1.5	11
304	Anopheles gambiae Genome Conservation as a Resource for Rational Gene Drive Target Site Selection. Insects, 2021, 12, 97.	1.0	8
305	Perspectives in Triatomine Biology Studies: â€œOMICSâ€•Based Approaches. True Bugs (Heteroptera) of the Neotropics, 2021, , 557-592.	1.2	2
306	The Rooted SCJ Median with Single Gene Duplications. Lecture Notes in Computer Science, 2018, , 28-48.	1.0	1
308	Control of malaria-transmitting mosquitoes using gene drives. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20190803.	1.8	35
334	Phylosymbiosis: Relationships and Functional Effects of Microbial Communities across Host Evolutionary History. PLoS Biology, 2016, 14, e2000225.	2.6	475
335	The creation and selection of mutations resistant to a gene drive over multiple generations in the malaria mosquito. PLoS Genetics, 2017, 13, e1007039.	1.5	243
336	Mosquito genomes are frequently invaded by transposable elements through horizontal transfer. PLoS Genetics, 2020, 16, e1008946.	1.5	31
337	malERA: An updated research agenda for basic science and enabling technologies in malaria elimination and eradication. PLoS Medicine, 2017, 14, e1002451.	3.9	29
338	Eliminating the Neglected Tropical Diseases: Translational Science and New Technologies. PLoS Neglected Tropical Diseases, 2016, 10, e0003895.	1.3	116
339	Genomic Analysis of Detoxification Supergene Families in the Mosquito Anopheles sinensis. PLoS ONE, 2015, 10, e0143387.	1.1	30
340	Draft Genomes of Anopheles cracens and Anopheles maculatus: Comparison of Simian Malaria and Human Malaria Vectors in Peninsular Malaysia. PLoS ONE, 2016, 11, e0157893.	1.1	8
341	Green tea proanthocyanidins cause impairment of hormone-regulated larval development and reproductive fitness via repression of juvenile hormone acid methyltransferase, insulin-like peptide and cytochrome P450 genes in Anopheles gambiae sensu stricto. PLoS ONE, 2017, 12, e0173564.	1.1	3

#	Article	IF	Citations
342	The antenna transcriptome changes in mosquito Anopheles sinensis, pre- and post- blood meal. PLoS ONE, 2017, 12, e0181399.	1.1	17
343	A mating-induced reproductive gene promotes Anopheles tolerance to Plasmodium falciparum infection. PLoS Pathogens, 2020, 16, e1008908.	2.1	12
344	The Beginning of the End: A Chromosomal Assembly of the New World Malaria Mosquito Ends with a Novel Telomere. G3: Genes, Genomes, Genetics, 2020, 10, 3811-3819.	0.8	17
345	Survey for positively selected coding regions in the genome of the hematophagous tsetse fly Glossina morsitans identifies candidate genes associated with feeding habits and embryonic development. Genetics and Molecular Biology, 2020, 43, e20180311.	0.6	1
347	Evolution of gene expression levels in the male reproductive organs of Anopheles mosquitoes. Life Science Alliance, 2019, 2, e201800191.	1.3	10
348	A Near-Chromosome Level Genome Assembly of Anopheles stephensi. Frontiers in Genetics, 2020, 11, 565626.	1.1	14
349	Diverse Defenses: A Perspective Comparing Dipteran Piwi-piRNA Pathways. Cells, 2020, 9, 2180.	1.8	10
350	Anthropogenic forest loss and malaria prevalence: a comparative examination of the causes and disease consequences of deforestation in developing nations. AIMS Environmental Science, 2017, 4, 217-231.	0.7	21
351	The origin of the odorant receptor gene family in insects. ELife, 2018, 7, .	2.8	103
352	Lipid hijacking: A unifying theme in vector-borne diseases. ELife, 2020, 9, .	2.8	41
353	Human attractive cues and mosquito host-seeking behavior. Trends in Parasitology, 2022, 38, 246-264.	1.5	29
354	Resistance to a CRISPR-based gene drive at an evolutionarily conserved site is revealed by mimicking genotype fixation. PLoS Genetics, 2021, 17, e1009740.	1.5	21
355	Small parsimony for natural genomes in the DCJ-indel model. Journal of Bioinformatics and Computational Biology, 2021, 19, 2140009.	0.3	3
361	Differential expression of trypsin-3 and phosrestin II genes in the main malaria vector, Anopheles darlingi, from the Brazilian Amazon region. Genetics and Molecular Research, 2017, 16, .	0.3	0
366	Quantitative real-time PCR analysis of Anopheles dirus TEP1 and NOS during Plasmodium berghei infection, using three reference genes. PeerJ, 2017, 5, e3577.	0.9	2
373	Genetik neu denken. , 2019, , 267-294.		0
374	Non-model organism research in the changing genomic landscape. Parasitologists United Journal, 2019, 12, 0-0.	0.1	0
377	Felling trees, furthering malaria: links between deforestation and disease in developing nations. The Journal of Population and Sustainability, 2019, 3, .	0.2	0

#	Article	IF	Citations
387	RNA editing: an overlooked source of fine-scale adaptation in insect vectors?. Current Opinion in Insect Science, 2020, 40, 48-55.	2.2	1
388	Comparative genomic and transcriptomic analyses of transposable elements in polychaetous annelids highlight LTR retrotransposon diversity and evolution. Mobile DNA, 2021, 12, 24.	1.3	1
389	Endogenous viral elements in mosquito genomes: current knowledge and outstanding questions. Current Opinion in Insect Science, 2022, 49, 22-30.	2.2	11
391	Transposable Elements in Anopheles Species: Refining Annotation Strategies Towards Population Genomics Analyses. Population Genomics, 2020, , 1.	0.2	1
393	High-resolution in situ analysis of Cas9 germline transcript distributions in gene-drive Anopheles mosquitoes. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	14
394	Unconventional conservation reveals structure-function relationships in the synaptonemal complex. ELife, 2021, 10, .	2.8	10
395	Rethinking Genetics. , 2022, , 237-261.		0
396	Artificial Light as a Modulator of Mosquito-Borne Disease Risk. Frontiers in Ecology and Evolution, 2022, 9, .	1.1	13
397	Multiscale analysis of the randomization limits of the chromosomal gene organization between Lepidoptera and Diptera. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20212183.	1.2	2
398	Species delimitation and mitonuclear discordance within a species complex of biting midges. Scientific Reports, 2022, 12, 1730.	1.6	14
399	Screening of olfactory genes related to blood-feeding behaviors in Culex pipiens quinquefasciatus and Culex pipiens molestus by transcriptome analysis. PLoS Neglected Tropical Diseases, 2022, 16, e0010204.	1.3	7
400	The Peptide Hormone CNMa Influences Egg Production in the Mosquito Aedes aegypti. Insects, 2022, 13, 230.	1.0	3
401	The genome trilogy of Anopheles stephensi, an urban malaria vector, reveals structure of a locus associated with adaptation to environmental heterogeneity. Scientific Reports, 2022, 12, 3610.	1.6	13
402	Positively selected genes in the hoary bat (Lasiurus cinereus) lineage: prominence of thymus expression, immune and metabolic function, and regions of ancient synteny. PeerJ, 2022, 10, e13130.	0.9	0
404	Satellitome Analysis and Transposable Elements Comparison in Geographically Distant Populations of Spodoptera frugiperda. Life, 2022, 12, 521.	1.1	5
405	Positive selection in multiple salivary gland proteins of Anophelinae reveals potential targets for vector control. Infection, Genetics and Evolution, 2022, 100, 105271.	1.0	3
406	Functional Constraints on Insect Immune System Components Govern Their Evolutionary Trajectories. Molecular Biology and Evolution, 2022, 39, .	3.5	3
407	Transposable element variants and their potential adaptive impact in urban populations of the malaria vector Anopheles coluzzii. Genome Research, 2022, 32, 189-202.	2.4	5

#	Article	IF	Citations
408	Expanding the Menu: Are Polyphagy and Gene Family Expansions Linked across Lepidoptera?. Genome Biology and Evolution, 2022, 14, .	1.1	10
409	Anopheles mosquitoes reveal new principles of 3D genome organization in insects. Nature Communications, 2022, 13, 1960.	5.8	19
410	Novel salivary anti-hemostatic activities of long-form D7 proteins from the malaria vector Anopheles gambiae facilitate hematophagy. Journal of Biological Chemistry, 2022, , 101971.	1.6	7
416	Epigenetic studies in insects and the valproic acid perspective. Brazilian Journal of Biology, 2022, 84, e256045.	0.4	2
417	Evolutionary history of Plasmodium vivax and Plasmodium simium in the Americas. Malaria Journal, 2022, 21, 141.	0.8	2
418	Functional aspects of evolution in a cluster of salivary protein genes from mosquitoes. Insect Biochemistry and Molecular Biology, 2022, 146, 103785.	1.2	4
419	Retrogene Duplication and Expression Patterns Shaped by the Evolution of Sex Chromosomes in Malaria Mosquitoes. Genes, 2022, 13, 968.	1.0	7
420	Comparisons of chemosensory gene repertoires in human and non-human feeding Anopheles mosquitoes link olfactory genes to anthropophily. IScience, 2022, 25, 104521.	1.9	2
422	Gene Conversion Explains Elevated Diversity in the Immunity Modulating APL1 Gene of the Malaria Vector Anopheles funestus. Genes, 2022, 13, 1102.	1.0	2
423	Essential functions of mosquito ecdysone importers in development and reproduction. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
424	MicroRNAs and other small RNAs in Aedes aegypti saliva and salivary glands following chikungunya virus infection. Scientific Reports, 2022, 12, .	1.6	3
425	Synthesis and Characterization of ZnO@SiO2 Nanocomposite using Gum Arabic and its Larvicidal Activity on Malaria Vectors. Oriental Journal of Chemistry, 2022, 38, 638-645.	0.1	0
426	Modeling Mosquitoes and their Potential Odonate Predators Under Different Land Uses. EcoHealth, 0, , .	0.9	0
427	Identification of a rapidlyâ€spreading triple mutant for highâ€level metabolic insecticide resistance in Anopheles gambiae provides a realâ€time molecular diagnostic for antimalarial intervention deployment. Molecular Ecology, 2022, 31, 4307-4318.	2.0	14
428	Gene drive in species complexes: defining target organisms. Trends in Biotechnology, 2022, , .	4.9	8
429	Comprehensive characterization of a transgene insertion in a highly repetitive, centromeric region of Anopheles mosquitoes. Pathogens and Global Health, 2023, 117, 273-283.	1.0	1
432	Isobaric tags for relative and absolute quantification-based proteomic analysis of host-pathogen protein interactions in the midgut of Aedes albopictus during dengue virus infection. Frontiers in Microbiology, 0, 13, .	1.5	0
433	Chromosomeâ€level assembly of Culex pipiens molestus and improved reference genome of Culex pipiens pallens (Culicidae, Diptera). Molecular Ecology Resources, 2023, 23, 486-498.	2.2	2

#	Article	IF	Citations
437	Phylogenetic relationships of the supercontig of sodium channel subunit I (NaV) in 17 species of Anopheles (Diptera: Culicidae). Revista Da Sociedade Brasileira De Medicina Tropical, 0, 55, .	0.4	0
438	High-resolution species assignment of Anopheles mosquitoes using k-mer distances on targeted sequences. ELife, 0, 11, .	2.8	1
439	A perspective on the expansion of the genetic technologies to support the control of neglected vector-borne diseases and conservation. Frontiers in Tropical Diseases, 0, 3, .	0.5	3
441	Novel genome sequences and evolutionary dynamics of the North American anopheline species Anopheles freeborni, Anopheles crucians, Anopheles quadrimaculatus, and Anopheles albimanus. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	0
442	Connecting Evolutionary Genomics to Cell Biology. , 2016, , 356-362.		0
443	Functional conservation of Anopheline linalool receptors through 100 million years of evolution. Chemical Senses, 2022, 47, .	1.1	1
444	Recurrent co-domestication of PIF/Harbinger transposable element proteins in insects. Mobile DNA, 2022, 13, .	1.3	2
445	The genome sequence of the malaria mosquito, Anopheles funestus, Giles, 1900. Wellcome Open Research, 0, 7, 287.	0.9	0
447	CLIPA7 Exhibits Pleiotropic Roles in the <i>Anopheles gambiae</i> Immune Response. Journal of Innate Immunity, 2023, 15, 317-332.	1.8	1
448	Chapter 9: Odour-mediated host selection and discrimination in mosquitoes. , 2022, , 253-276.		8
449	Chapter 32: Chronobiology of blood-feeding arthropods: influences on their role as disease vectors. , 2022, , 815-849.		8
450	Chapter 10: Olfactory-driven behaviours in kissing bugs. , 2022, , 277-296.		5
451	Chapter 6: Molecular basis of olfaction in kissing bugs. , 2022, , 153-170.		3
452	Safety and immunogenicity of AGS-v PLUS, a mosquito saliva peptide vaccine against arboviral diseases: A randomized, double-blind, placebo-controlled Phase 1 trial. EBioMedicine, 2022, 86, 104375.	2.7	7
454	An Overview of D7 Protein Structure and Physiological Roles in Blood-Feeding Nematocera. Biology, 2023, 12, 39.	1.3	2
455	Role of Pfs47 in the dispersal of ancestral Plasmodium falciparum malaria through adaptation to different anopheline vectors. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	1
456	RNAâ€Seqâ€Pop: Exploiting the sequence in <scp>RNA</scp> sequencingâ€”A Snakemake workflow reveals patterns of insecticide resistance in the malaria vector Anopheles gambiae. Molecular Ecology Resources, 2023, 23, 946-961.	2.2	4
457	Determinants of Chikungunya and Oâ€™nyong-Nyong Virus Specificity for Infection of Aedes and Anopheles Mosquito Vectors. Viruses, 2023, 15, 589.	1.5	3

#	Article	IF	Citations
458	Synteny Identifies Reliable Orthologs for Phylogenomics and Comparative Genomics of the Brassicaceae. Genome Biology and Evolution, 2023, 15, .	1.1	3
459	Standing genetic variation and chromosome differences drove rapid ecotype formation in a major malaria mosquito. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	1
460	The genome sequence of the malaria mosquito, Anopheles funestus, Giles, 1900. Wellcome Open Research, 0, 7, 287.	0.9	2
461	Population Genomic Evidence of Adaptive Response during the Invasion History ofPlasmodium falciparumin the Americas. Molecular Biology and Evolution, 2023, 40, .	3.5	2
462	Phylogenomics revealed migration routes and adaptive radiation timing of Holarctic malaria mosquito species of the Maculipennis Group. BMC Biology, 2023, 21, .	1.7	0
463	Genomic analysis of two phlebotomine sand fly vectors of Leishmania from the New and Old World. PLoS Neglected Tropical Diseases, 2023, 17, e0010862.	1.3	4
470	Physical Mapping of Two Nested Fixed Inversions in the X Chromosome of the Malaria Mosquito Anopheles messeae. Lecture Notes in Computer Science, 2023, , 84-99.	1.0	0