Robert M Waterhouse

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A targeted amplicon sequencing panel to simultaneously identify mosquito species and <i>Plasmodium</i> presence across the entire <i>Anopheles</i> genus. Molecular Ecology Resources, 2022, 22, 28-44.	4.8	18
2	Convergent evolution of venom gland transcriptomes across Metazoa. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	15
3	The era of reference genomes in conservation genomics. Trends in Ecology and Evolution, 2022, 37, 197-202.	8.7	138
4	Assessing species coverage and assembly quality of rapidly accumulating sequenced genomes. GigaScience, 2022, 11, .	6.4	15
5	Long-distance dispersal of pigeons and doves generated new ecological opportunities for host-switching and adaptive radiation by their parasites. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20220042.	2.6	13
6	Exploring new genomic territories with emerging model insects. Current Opinion in Insect Science, 2022, 51, 100902.	4.4	0
7	Functional Constraints on Insect Immune System Components Govern Their Evolutionary Trajectories. Molecular Biology and Evolution, 2022, 39, .	8.9	3
8	Anopheles mosquitoes reveal new principles of 3D genome organization in insects. Nature Communications, 2022, 13, 1960.	12.8	19
9	CrowdGO: Machine learning and semantic similarity guided consensus Gene Ontology annotation. PLoS Computational Biology, 2022, 18, e1010075.	3.2	4
10	Mosquito saliva enhances virus infection through sialokinin-dependent vascular leakage. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	16
11	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.	8.9	58
12	Horizontally acquired antibacterial genes associated with adaptive radiation of ladybird beetles. BMC Biology, 2021, 19, 7.	3.8	11
13	The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. BMC Biology, 2021, 19, 41.	3.8	19
14	RADSex: A computational workflow to study sex determination using restriction siteâ€associated DNA sequencing data. Molecular Ecology Resources, 2021, 21, 1715-1731.	4.8	40
15	Summary Visualizations of Gene Ontology Terms With GO-Figure!. Frontiers in Bioinformatics, 2021, 1, .	2.1	51
16	Anopheles coluzzii stearoyl-CoA desaturase is essential for adult female survival and reproduction upon blood feeding. PLoS Pathogens, 2021, 17, e1009486.	4.7	7
17	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	3.8	177
18	The Genome of the Blind Soil-Dwelling and Ancestrally Wingless Dipluran Campodea augens: A Key Reference Hexapod for Studying the Emergence of Insect Innovations. Genome Biology and Evolution, 2020, 12, 3534-3549.	2.5	3

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19	Genome-enabled insights into the biology of thrips as crop pests. BMC Biology, 2020, 18, 142.	3.8	54
20	Brain microRNAs among social and solitary bees. Royal Society Open Science, 2020, 7, 200517.	2.4	13
21	Four myriapod relatives – but who are sisters? No end to debates on relationships among the four major myriapod subgroups. BMC Evolutionary Biology, 2020, 20, 144.	3.2	13
22	Developmental plasticity shapes social traits and selection in a facultatively eusocial bee. Proceedings of the United States of America, 2020, 117, 13615-13625.	7.1	37
23	Brown marmorated stink bug, Halyomorpha halys (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. BMC Genomics, 2020, 21, 227.	2.8	60
24	Hemocyte-targeted gene expression in the female malaria mosquito using the hemolectin promoter from Drosophila. Insect Biochemistry and Molecular Biology, 2020, 120, 103339.	2.7	9
25	Gene content evolution in the arthropods. Genome Biology, 2020, 21, 15.	8.8	150
26	Enhanced genome assembly and a new official gene set for Tribolium castaneum. BMC Genomics, 2020, 21, 47.	2.8	84
27	Characterization of Insect Immune Systems from Genomic Data. Springer Protocols, 2020, , 3-34.	0.3	4
28	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. Genome Biology and Evolution, 2020, 12, 1099-1188.	2.5	17
29	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	8.8	71
30	Nuclear Orthologs Derived from Whole Genome Sequencing Indicate Cryptic Diversity in the Bemisia tabaci (Insecta: Aleyrodidae) Complex of Whiteflies. Diversity, 2019, 11, 151.	1.7	39
31	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. Genome Biology, 2019, 20, 98.	8.8	27
32	Insights Into an Unexplored Component of the Mosquito Repeatome: Distribution and Variability of Viral Sequences Integrated Into the Genome of the Arboviral Vector Aedes albopictus. Frontiers in Genetics, 2019, 10, 93.	2.3	21
33	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64.	8.8	114
34	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adephaga) with an evaluation of phylogenetic conflict and systematic error. Molecular Phylogenetics and Evolution, 2019, 135, 270-285.	2.7	36
35	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. Genome Research, 2019, 29, 2073-2087.	5.5	52
36	Using BUSCO to Assess Insect Genomic Resources. Methods in Molecular Biology, 2019, 1858, 59-74.	0.9	27

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37	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (Halictidae: <i>Nomia melanderi</i>). G3: Genes, Genomes, Genetics, 2019, 9, 625-634.	1.8	19
38	Of Genes and Genomes: Mosquito Evolution and Diversity. Trends in Parasitology, 2019, 35, 32-51.	3.3	35
39	BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. Molecular Biology and Evolution, 2018, 35, 543-548.	8.9	1,844
40	Phylogenomics and the evolution of hemipteroid insects. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12775-12780.	7.1	275
41	Genome sequence of the wheat stem sawfly, Cephus cinctus, representing an early-branching lineage of the Hymenoptera, illuminates evolution of hymenopteran chemoreceptors. Genome Biology and Evolution, 2018, 10, 2997-3011.	2.5	24
42	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	4.1	36
43	Genomic features of the damselfly <i>Calopteryx splendens</i> representing a sister clade to most insect orders. Genome Biology and Evolution, 2017, 9, evx006.	2.5	53
44	Rapid evolution of female-biased genes among four species of <i>Anopheles</i> malaria mosquitoes. Genome Research, 2017, 27, 1536-1548.	5.5	60
45	The Novel Evolution of the Sperm Whale Genome. Genome Biology and Evolution, 2017, 9, 3260-3264.	2.5	33
46	OrthoDB v9.1: cataloging evolutionary and functional annotations for animal, fungal, plant, archaeal, bacterial and viral orthologs. Nucleic Acids Research, 2017, 45, D744-D749.	14.5	413
47	Tick Genome Assembled: New Opportunities for Research on Tick-Host-Pathogen Interactions. Frontiers in Cellular and Infection Microbiology, 2016, 6, 103.	3.9	38
48	Genome Sequencing of the Phytoseiid Predatory Mite <i>Metaseiulus occidentalis</i> Reveals Completely Atomized <i>Hox</i> Genes and Superdynamic Intron Evolution. Genome Biology and Evolution, 2016, 8, 1762-1775.	2.5	102
49	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, Manduca sexta. Insect Biochemistry and Molecular Biology, 2016, 76, 118-147.	2.7	154
50	Evolutionary Dynamics of Abundant Stop Codon Readthrough. Molecular Biology and Evolution, 2016, 33, 3108-3132.	8.9	53
51	Genome of the Asian longhorned beetle (Anoplophora glabripennis), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle–plant interface. Genome Biology, 2016, 17, 227.	8.8	244
52	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. Nature Communications, 2016, 7, 10165.	12.8	184
53	Genomic insights into the Ixodes scapularis tick vector of Lyme disease. Nature Communications, 2016, 7, 10507.	12.8	450
54	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64

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55	A depauperate immune repertoire precedes evolution of sociality in bees. Genome Biology, 2015, 16, 83.	8.8	130
56	Genome of <i>Rhodnius prolixus</i> , 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.	7.1	329
57	A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest Mayetiola destructor. Current Biology, 2015, 25, 613-620.	3.9	171
58	Evolution of sexual traits influencing vectorial capacity in anopheline mosquitoes. Science, 2015, 347, 985-988.	12.6	68
59	A maturing understanding of the composition of the insect gene repertoire. Current Opinion in Insect Science, 2015, 7, 15-23.	4.4	24
60	BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. Bioinformatics, 2015, 31, 3210-3212.	4.1	9,712
61	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	8.8	330
62	Scaffold assembly based on genome rearrangement analysis. Computational Biology and Chemistry, 2015, 57, 46-53.	2.3	12
63	Long non-coding RNA discovery across the genus anopheles reveals conserved secondary structures within and beyond the Gambiae complex. BMC Genomics, 2015, 16, 337.	2.8	85
64	Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143.	12.6	357
65	Lucilia cuprina genome unlocks parasitic fly biology to underpin future interventions. Nature Communications, 2015, 6, 7344.	12.8	67
66	Genome sequence of the Asian Tiger mosquito, <i>Aedes albopictus</i> , 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.	7.1	251
67	OrthoDB v8: update of the hierarchical catalog of orthologs and the underlying free software. Nucleic Acids Research, 2015, 43, D250-D256.	14.5	303
68	Extensive introgression in a malaria vector species complex revealed by phylogenomics. Science, 2015, 347, 1258524.	12.6	527
69	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522.	12.6	492
70	Phylogenetic Analysis of the Oriental-Palearctic-Afrotropical Members of Anopheles (Culicidae:) Tj ETQq0 0 0 rgBT Infectious Diseases, 2014, 67, 361-367.	/Overlock 1.2	10 Tf 50 14 31
71	Genome analysis of a major urban malaria vector mosquito, Anopheles stephensi. Genome Biology, 2014, 15, 459.	8.8	119
72	Big data and other challenges in the quest for orthologs. Bioinformatics, 2014, 30, 2993-2998.	4.1	109

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73	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737.	12.8	196
74	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	2.8	375
75	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. Genome Research, 2013, 23, 1235-1247.	5.5	205
76	The Evolution of the <i>Anopheles</i> 16 Genomes Project. G3: Genes, Genomes, Genetics, 2013, 3, 1191-1194.	1.8	49
77	OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs. Nucleic Acids Research, 2013, 41, D358-D365.	14.5	333
78	Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in Anopheles gambiae. BMC Genomics, 2013, 14, 749.	2.8	94
79	Correlating Traits of Gene Retention, Sequence Divergence, Duplicability and Essentiality in Vertebrates, Arthropods, and Fungi. Genome Biology and Evolution, 2011, 3, 75-86.	2.5	81
80	A remarkably stable TipE gene cluster: evolution of insect Para sodium channel auxiliary subunits. BMC Evolutionary Biology, 2011, 11, 337.	3.2	16
81	OrthoDB: the hierarchical catalog of eukaryotic orthologs in 2011. Nucleic Acids Research, 2011, 39, D283-D288.	14.5	128
82	Correction for Kirkness et al., Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6335-6335.	7.1	7
83	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. Science, 2010, 330, 86-88.	12.6	424
84	Sequence-structure-function relations of the mosquito leucine-rich repeat immune proteins. BMC Genomics, 2010, 11, 531.	2.8	59
85	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12168-12173.	7.1	482
86	A caspase-like decoy molecule enhances the activity of a paralogous caspase in the yellow fever mosquito, Aedes aegypti. Insect Biochemistry and Molecular Biology, 2010, 40, 516-523.	2.7	20
87	Pathogenomics of <i>Culex quinquefasciatus</i> and Meta-Analysis of Infection Responses to Diverse Pathogens. Science, 2010, 330, 88-90.	12.6	150
88	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. Science, 2010, 327, 343-348.	12.6	808
89	Discovery of <i>Plasmodium</i> modulators by genome-wide analysis of circulating hemocytes in <i>Anopheles gambiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21270-21275.	7.1	91
90	Leucine-Rich Repeat Protein Complex Activates Mosquito Complement in Defense Against <i>Plasmodium</i> Parasites. Science, 2009, 324, 258-261.	12.6	241

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91	Comparative Genome Analysis. , 2009, , 33-58.		0
92	Comparative genomics of insect immunity. , 2009, , 86-105.		1
93	The genome of the model beetle and pest Tribolium castaneum. Nature, 2008, 452, 949-955.	27.8	1,255
94	The <i>Aedes aegypti</i> genome: a comparative perspective. Insect Molecular Biology, 2008, 17, 1-8.	2.0	29
95	Evolutionary Dynamics of Immune-Related Genes and Pathways in Disease-Vector Mosquitoes. Science, 2007, 316, 1738-1743.	12.6	550
96	Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR. F1000Research, 0, 10, 1238.	1.6	3
97	"Phylogenetics in the Genomic Era―brings together experts in the field to present a comprehensive synthesis. Peer Community in Genomics, 0, , .	0.0	0