

Robert M Waterhouse

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

24,358
citations

50170

46
h-index

35952

97
g-index

130
all docs

130
docs citations

130
times ranked

28710
citing authors

#	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. <i>Molecular Ecology Resources</i> , 2022, 22, 28-44.	2.2	18
2	Convergent evolution of venom gland transcriptomes across Metazoa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	15
3	The era of reference genomes in conservation genomics. <i>Trends in Ecology and Evolution</i> , 2022, 37, 197-202.	4.2	138
4	Assessing species coverage and assembly quality of rapidly accumulating sequenced genomes. <i>GigaScience</i> , 2022, 11, .	3.3	15
5	Long-distance dispersal of pigeons and doves generated new ecological opportunities for host-switching and adaptive radiation by their parasites. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220042.	1.2	13
6	Exploring new genomic territories with emerging model insects. <i>Current Opinion in Insect Science</i> , 2022, 51, 100902.	2.2	0
7	Functional Constraints on Insect Immune System Components Govern Their Evolutionary Trajectories. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
8	<i>Anopheles</i> mosquitoes reveal new principles of 3D genome organization in insects. <i>Nature Communications</i> , 2022, 13, 1960.	5.8	19
9	CrowdGO: Machine learning and semantic similarity guided consensus Gene Ontology annotation. <i>PLoS Computational Biology</i> , 2022, 18, e1010075.	1.5	4
10	Mosquito saliva enhances virus infection through sialokinin-dependent vascular leakage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	16
11	Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. <i>Molecular Biology and Evolution</i> , 2021, 38, 486-501.	3.5	58
12	Horizontally acquired antibacterial genes associated with adaptive radiation of ladybird beetles. <i>BMC Biology</i> , 2021, 19, 7.	1.7	11
13	The genome of the stable fly, <i>Stomoxys calcitrans</i> , reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021, 19, 41.	1.7	19
14	RADSex: A computational workflow to study sex determination using restriction site-associated DNA sequencing data. <i>Molecular Ecology Resources</i> , 2021, 21, 1715-1731.	2.2	40
15	Summary Visualizations of Gene Ontology Terms With GO-Figure!. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	51
16	<i>Anopheles coluzzii</i> stearoyl-CoA desaturase is essential for adult female survival and reproduction upon blood feeding. <i>PLoS Pathogens</i> , 2021, 17, e1009486.	2.1	7
17	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	1.7	177
18	The Genome of the Blind Soil-Dwelling and Ancestrally Wingless Dipluran <i>Campodea augens</i> : A Key Reference Hexapod for Studying the Emergence of Insect Innovations. <i>Genome Biology and Evolution</i> , 2020, 12, 3534-3549.	1.1	3

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19	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , 2020, 18, 142.	1.7	54
20	Brain microRNAs among social and solitary bees. <i>Royal Society Open Science</i> , 2020, 7, 200517.	1.1	13
21	Four myriapod relatives “but who are sisters? No end to debates on relationships among the four major myriapod subgroups. <i>BMC Evolutionary Biology</i> , 2020, 20, 144.	3.2	13
22	Developmental plasticity shapes social traits and selection in a facultatively eusocial bee. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13615-13625.	3.3	37
23	Brown marmorated stink bug, <i>Halyomorpha halys</i> (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. <i>BMC Genomics</i> , 2020, 21, 227.	1.2	60
24	Hemocyte-targeted gene expression in the female malaria mosquito using the hemolectin promoter from <i>Drosophila</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 120, 103339.	1.2	9
25	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
26	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2020, 21, 47.	1.2	84
27	Characterization of Insect Immune Systems from Genomic Data. <i>Springer Protocols</i> , 2020, , 3-34.	0.1	4
28	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , 2020, 12, 1099-1188.	1.1	17
29	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019, 20, 187.	3.8	71
30	Nuclear Orthologs Derived from Whole Genome Sequencing Indicate Cryptic Diversity in the <i>Bemisia tabaci</i> (Insecta: Aleyrodidae) Complex of Whiteflies. <i>Diversity</i> , 2019, 11, 151.	0.7	39
31	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. <i>Genome Biology</i> , 2019, 20, 98.	3.8	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 <i>Aedes albopictus</i> . <i>Frontiers in Genetics</i> , 2019, 10, 93.	1.1	21
33	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. <i>Genome Biology</i> , 2019, 20, 64.	3.8	114
34	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adephaga) with an evaluation of phylogenetic conflict and systematic error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 270-285.	1.2	36
35	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , 2019, 29, 2073-2087.	2.4	52
36	Using BUSCO to Assess Insect Genomic Resources. <i>Methods in Molecular Biology</i> , 2019, 1858, 59-74.	0.4	27

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37	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (<i>Halictidae</i> : <i>Nomia melanderi</i>). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 625-634.	0.8	19
38	Of Genes and Genomes: Mosquito Evolution and Diversity. <i>Trends in Parasitology</i> , 2019, 35, 32-51.	1.5	35
39	BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. <i>Molecular Biology and Evolution</i> , 2018, 35, 543-548.	3.5	1,844
40	Phylogenomics and the evolution of hemipteroid insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12775-12780.	3.3	275
41	Genome sequence of the wheat stem sawfly, <i>Cephus cinctus</i> , representing an early-branching lineage of the Hymenoptera, illuminates evolution of hymenopteran chemoreceptors. <i>Genome Biology and Evolution</i> , 2018, 10, 2997-3011.	1.1	24
42	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
43	Genomic features of the damselfly <i>Calopteryx splendens</i> representing a sister clade to most insect orders. <i>Genome Biology and Evolution</i> , 2017, 9, evx006.	1.1	53
44	Rapid evolution of female-biased genes among four species of <i>Anopheles</i> malaria mosquitoes. <i>Genome Research</i> , 2017, 27, 1536-1548.	2.4	60
45	The Novel Evolution of the Sperm Whale Genome. <i>Genome Biology and Evolution</i> , 2017, 9, 3260-3264.	1.1	33
46	OrthoDB v9.1: cataloging evolutionary and functional annotations for animal, fungal, plant, archaeal, bacterial and viral orthologs. <i>Nucleic Acids Research</i> , 2017, 45, D744-D749.	6.5	413
47	Tick Genome Assembled: New Opportunities for Research on Tick-Host-Pathogen Interactions. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 103.	1.8	38
48	Genome Sequencing of the Phytoseiid Predatory Mite <i>Metaseiulus occidentalis</i> Reveals Completely Atomized <i>Hox</i> Genes and Superdynamic Intron Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 1762-1775.	1.1	102
49	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 118-147.	1.2	154
50	Evolutionary Dynamics of Abundant Stop Codon Readthrough. <i>Molecular Biology and Evolution</i> , 2016, 33, 3108-3132.	3.5	53
51	Genome of the Asian longhorned beetle (<i>Anoplophora glabripennis</i>), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle-plant interface. <i>Genome Biology</i> , 2016, 17, 227.	3.8	244
52	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. <i>Nature Communications</i> , 2016, 7, 10165.	5.8	184
53	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	5.8	450
54	The SIB Swiss Institute of Bioinformatics'™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64

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55	A depauperate immune repertoire precedes evolution of sociality in bees. <i>Genome Biology</i> , 2015, 16, 83.	3.8	130
56	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14936-14941.	3.3	329
57	A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest <i>Mayetiola destructor</i> . <i>Current Biology</i> , 2015, 25, 613-620.	1.8	171
58	Evolution of sexual traits influencing vectorial capacity in anopheline mosquitoes. <i>Science</i> , 2015, 347, 985-988.	6.0	68
59	A maturing understanding of the composition of the insect gene repertoire. <i>Current Opinion in Insect Science</i> , 2015, 7, 15-23.	2.2	24
60	BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. <i>Bioinformatics</i> , 2015, 31, 3210-3212.	1.8	9,712
61	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
62	Scaffold assembly based on genome rearrangement analysis. <i>Computational Biology and Chemistry</i> , 2015, 57, 46-53.	1.1	12
63	Long non-coding RNA discovery across the genus <i>Anopheles</i> reveals conserved secondary structures within and beyond the <i>Gambiae</i> complex. <i>BMC Genomics</i> , 2015, 16, 337.	1.2	85
64	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	6.0	357
65	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , 2015, 6, 7344.	5.8	67
66	Genome sequence of the Asian Tiger mosquito, <i>Aedes albopictus</i> , reveals insights into its biology, genetics, and evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5907-15.	3.3	251
67	OrthoDB v8: update of the hierarchical catalog of orthologs and the underlying free software. <i>Nucleic Acids Research</i> , 2015, 43, D250-D256.	6.5	303
68	Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , 2015, 347, 1258524.	6.0	527
69	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258522.	6.0	492
70	Phylogenetic Analysis of the Oriental-Palearctic-Afrotropical Members of <i>Anopheles</i> (Culicidae: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 14 Infectious Diseases</i> , 2014, 67, 361-367.	0.5	31
71	Genome analysis of a major urban malaria vector mosquito, <i>Anopheles stephensi</i> . <i>Genome Biology</i> , 2014, 15, 459.	3.8	119
72	Big data and other challenges in the quest for orthologs. <i>Bioinformatics</i> , 2014, 30, 2993-2998.	1.8	109

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73	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. <i>Nature Communications</i> , 2014, 5, 4737.	5.8	196
74	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
75	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , 2013, 23, 1235-1247.	2.4	205
76	The Evolution of the <i>Anopheles</i> 16 Genomes Project. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1191-1194.	0.8	49
77	OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs. <i>Nucleic Acids Research</i> , 2013, 41, D358-D365.	6.5	333
78	Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2013, 14, 749.	1.2	94
79	Correlating Traits of Gene Retention, Sequence Divergence, Duplicability and Essentiality in Vertebrates, Arthropods, and Fungi. <i>Genome Biology and Evolution</i> , 2011, 3, 75-86.	1.1	81
80	A remarkably stable TipE gene cluster: evolution of insect Para sodium channel auxiliary subunits. <i>BMC Evolutionary Biology</i> , 2011, 11, 337.	3.2	16
81	OrthoDB: the hierarchical catalog of eukaryotic orthologs in 2011. <i>Nucleic Acids Research</i> , 2011, 39, D283-D288.	6.5	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6335-6335.	3.3	7
83	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. <i>Science</i> , 2010, 330, 86-88.	6.0	424
84	Sequence-structure-function relations of the mosquito leucine-rich repeat immune proteins. <i>BMC Genomics</i> , 2010, 11, 531.	1.2	59
85	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12168-12173.	3.3	482
86	A caspase-like decoy molecule enhances the activity of a paralogous caspase in the yellow fever mosquito, <i>Aedes aegypti</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2010, 40, 516-523.	1.2	20
87	Pathogenomics of <i>Culex quinquefasciatus</i> and Meta-Analysis of Infection Responses to Diverse Pathogens. <i>Science</i> , 2010, 330, 88-90.	6.0	150
88	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
89	Discovery of <i>Plasmodium</i> modulators by genome-wide analysis of circulating hemocytes in <i>Anopheles gambiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21270-21275.	3.3	91
90	Leucine-Rich Repeat Protein Complex Activates Mosquito Complement in Defense Against <i>Plasmodium</i> Parasites. <i>Science</i> , 2009, 324, 258-261.	6.0	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 <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	13.7	1,255
94	The <i>Aedes aegypti</i> genome: a comparative perspective. <i>Insect Molecular Biology</i> , 2008, 17, 1-8.	1.0	29
95	Evolutionary Dynamics of Immune-Related Genes and Pathways in Disease-Vector Mosquitoes. <i>Science</i> , 2007, 316, 1738-1743.	6.0	550
96	Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR. <i>F1000Research</i> , 0, 10, 1238.	0.8	3
97	“Phylogenetics in the Genomic Era” brings together experts in the field to present a comprehensive synthesis. <i>Peer Community in Genomics</i> , 0, , .	0.0	0