

# Robert M Waterhouse

## List of Publications by Citations

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102  
papers

15,234  
citations

42  
h-index

123  
g-index

130  
ext. papers

20,924  
ext. citations

11.3  
avg, IF

6.51  
L-index

#	Paper	IF	Citations
102	BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. <i>Bioinformatics</i> , <b>2015</b> , 31, 3210-2	7.2	5097
101	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , <b>2008</b> , 452, 949-55	50.4	1043
100	BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 543-548	8.3	1027
99	Functional and evolutionary insights from the genomes of three parasitoid <i>Nasonia</i> species. <i>Science</i> , <b>2010</b> , 327, 343-8	33.3	682
98	Evolutionary dynamics of immune-related genes and pathways in disease-vector mosquitoes. <i>Science</i> , <b>2007</b> , 316, 1738-43	33.3	461
97	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> , <b>2010</b> , 107, 12168-73	11.5	383
96	Mosquito genomics. Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , <b>2015</b> , 347, 1258524	33.3	378
95	Mosquito genomics. Highly evolvable malaria vectors: the genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , <b>2015</b> , 347, 1258522	33.3	372
94	Sequencing of <i>Culex quinquefasciatus</i> establishes a platform for mosquito comparative genomics. <i>Science</i> , <b>2010</b> , 330, 86-8	33.3	352
93	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , <b>2016</b> , 7, 10507	17.4	303
92	OrthoDB v9.1: cataloging evolutionary and functional annotations for animal, fungal, plant, archaeal, bacterial and viral orthologs. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D744-D749	20.1	289
91	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , <b>2014</b> , 15, 86	4.5	284
90	OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D358-65	20.1	277
89	Social evolution. Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , <b>2015</b> , 348, 1139-43	33.3	256
88	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , <b>2015</b> , 16, 76	18.3	229
87	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> , <b>2015</b> , 112, 14936-41	11.5	220
86	OrthoDB v8: update of the hierarchical catalog of orthologs and the underlying free software. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D250-6	20.1	217

85	Leucine-rich repeat protein complex activates mosquito complement in defense against Plasmodium parasites. <i>Science</i> , <b>2009</b> , 324, 258-61	33.3	191
84	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> , <b>2015</b> , 112, E5907-15	11.5	172
83	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , <b>2013</b> , 23, 1235-47	9.7	166
82	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> , <b>2016</b> , 17, 227	18.3	161
81	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. <i>Nature Communications</i> , <b>2014</b> , 5, 4737	17.4	151
80	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. <i>Nature Communications</i> , <b>2016</b> , 7, 10165	17.4	137
79	A massive expansion of effector genes underlies gall-formation in the wheat pest <i>Mayetiola destructor</i> . <i>Current Biology</i> , <b>2015</b> , 25, 613-20	6.3	126
78	Phylogenomics and the evolution of hemipteroid insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 12775-12780	11.5	121
77	Pathogenomics of <i>Culex quinquefasciatus</i> and meta-analysis of infection responses to diverse pathogens. <i>Science</i> , <b>2010</b> , 330, 88-90	33.3	120
76	OrthoDB: the hierarchical catalog of eukaryotic orthologs in 2011. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D2833-8.1	38.1	119
75	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , <b>2016</b> , 76, 118-147	4.5	112
74	A depauperate immune repertoire precedes evolution of sociality in bees. <i>Genome Biology</i> , <b>2015</b> , 16, 83	18.3	103
73	Genome analysis of a major urban malaria vector mosquito, <i>Anopheles stephensi</i> . <i>Genome Biology</i> , <b>2014</b> , 15, 459	18.3	80
72	Genome Sequencing of the Phytoseiid Predatory Mite <i>Metaseiulus occidentalis</i> Reveals Completely Atomized Hox Genes and Superdynamic Intron Evolution. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 1762-73.9	73.9	80
71	Discovery of Plasmodium 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> , <b>2009</b> , 106, 21270-5	11.5	75
70	Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , <b>2013</b> , 14, 749	4.5	73
69	Gene content evolution in the arthropods. <i>Genome Biology</i> , <b>2020</b> , 21, 15	18.3	63
68	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. <i>Genome Biology</i> , <b>2019</b> , 20, 64	18.3	60

67	Correlating traits of gene retention, sequence divergence, duplicability and essentiality in vertebrates, arthropods, and fungi. <i>Genome Biology and Evolution</i> , <b>2011</b> , 3, 75-86	3.9	57
66	Long non-coding RNA discovery across the genus anopheles reveals conserved secondary structures within and beyond the Gambiae complex. <i>BMC Genomics</i> , <b>2015</b> , 16, 337	4.5	56
65	Mosquito biology. Evolution of sexual traits influencing vectorial capacity in anopheline mosquitoes. <i>Science</i> , <b>2015</b> , 347, 985-8	33.3	54
64	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , <b>2015</b> , 6, 7344	17.4	51
63	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. <i>BMC Biology</i> , <b>2020</b> , 18, 1	7.3	51
62	Sequence-structure-function relations of the mosquito leucine-rich repeat immune proteins. <i>BMC Genomics</i> , <b>2010</b> , 11, 531	4.5	49
61	The SIB Swiss Institute of Bioinformatics resources: focus on curated databases. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D27-37	20.1	41
60	Genomic Features of the Damselfly <i>Calopteryx splendens</i> Representing a Sister Clade to Most Insect Orders. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 415-430	3.9	39
59	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , <b>2019</b> , 20, 187	18.3	39
58	The evolution of the Anopheles 16 genomes project. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 1191-4	3.2	38
57	Rapid evolution of female-biased genes among four species of malaria mosquitoes. <i>Genome Research</i> , <b>2017</b> , 27, 1536-1548	9.7	36
56	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , <b>2020</b> , 21, 47	4.5	35
55	Evolutionary Dynamics of Abundant Stop Codon Readthrough. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 3108-3132	8.3	32
54	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adephaga) with an evaluation of phylogenetic conflict and systematic error. <i>Molecular Phylogenetics and Evolution</i> , <b>2019</b> , 135, 270-285	4.1	28
53	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> , <b>2020</b> , 21, 227	4.5	28
52	The Novel Evolution of the Sperm Whale Genome. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 3260-3264	3.9	27
51	Tick Genome Assembled: New Opportunities for Research on Tick-Host-Pathogen Interactions. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2016</b> , 6, 103	5.9	27
50	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , <b>2019</b> , 29, 2073-2087	9.7	26

49	Phylogenetic analysis of the oriental-Palaearctic-Afrotropical members of Anopheles (Culicidae: Diptera) based on nuclear rDNA and mitochondrial DNA characteristics. <i>Japanese Journal of Infectious Diseases</i> , <b>2014</b> , 67, 361-7	2.7	25
48	BUSCO applications from quality assessments to gene prediction and phylogenomics		25
47	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , <b>2018</b> , 34, 323-329	2.9	25
46	The <i>Aedes aegypti</i> genome: a comparative perspective. <i>Insect Molecular Biology</i> , <b>2008</b> , 17, 1-8	3.4	24
45	Of Genes and Genomes: Mosquito Evolution and Diversity. <i>Trends in Parasitology</i> , <b>2019</b> , 35, 32-51	6.4	19
44	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. <i>Genome Biology</i> , <b>2019</b> , 20, 98	18.3	18
43	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> , <b>2010</b> , 40, 516-23	4.5	18
42	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> , <b>2018</b> , 10, 2997-3011	3.9	18
41	Insights Into an Unexplored Component of the Mosquito Repeatome: Distribution and Variability of Viral Sequences Integrated Into the Genome of the Arboviral Vector. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 93	4.5	17
40	A maturing understanding of the composition of the insect gene repertoire. <i>Current Opinion in Insect Science</i> , <b>2015</b> , 7, 15-23	5.1	17
39	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , <b>2020</b> , 18, 142	7.3	17
38	Nuclear Orthologs Derived from Whole Genome Sequencing Indicate Cryptic Diversity in the <i>Bemisia tabaci</i> (Insecta: Aleyrodidae) Complex of Whiteflies. <i>Diversity</i> , <b>2019</b> , 11, 151	2.5	16
37	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> , <b>2020</b> , 117, 13615-13625	11.5	16
36	RADSex: A computational workflow to study sex determination using restriction site-associated DNA sequencing data. <i>Molecular Ecology Resources</i> , <b>2021</b> , 21, 1715-1731	8.4	16
35	A remarkably stable TipE gene cluster: evolution of insect Para sodium channel auxiliary subunits. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 337	3	13
34	Using BUSCO to Assess Insect Genomic Resources. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1858, 59-74	1.4	13
33	Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 486-501	8.3	12
32	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome		11

31	Scaffold assembly based on genome rearrangement analysis. <i>Computational Biology and Chemistry</i> , <b>2015</b> , 57, 46-53	3.6	10
30	Four myriapod relatives - but who are sisters? No end to debates on relationships among the four major myriapod subgroups. <i>BMC Evolutionary Biology</i> , <b>2020</b> , 20, 144	3	10
29	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> , <b>2021</b> , 19, 41	7.3	9
28	The era of reference genomes in conservation genomics.. <i>Trends in Ecology and Evolution</i> , <b>2022</b> ,	10.9	8
27	Anopheles mosquitoes revealed new principles of 3D genome organization in insects		8
26	Functional genomics of the stable fly, <i>Stomoxys calcitrans</i> , reveals mechanisms underlying reproduction, host interactions, and novel targets for pest control		8
25	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. <i>Genome Biology and Evolution</i> , <b>2020</b> , 12, 1099-1188	3.9	7
24	Gene Content Evolution in the Arthropods		7
23	Hemocyte-targeted gene expression in the female malaria mosquito using the hemolectin promoter from <i>Drosophila</i> . <i>Insect Biochemistry and Molecular Biology</i> , <b>2020</b> , 120, 103339	4.5	6
22	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> , <b>2011</b> , 108, 6335-6335	11.5	6
21	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> , <b>2021</b> ,	8.4	6
20	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee ( <i>Halictidae</i> : ). <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 625-634	3.2	6
19	Brain microRNAs among social and solitary bees. <i>Royal Society Open Science</i> , <b>2020</b> , 7, 200517	3.3	5
18	Horizontally acquired antibacterial genes associated with adaptive radiation of ladybird beetles. <i>BMC Biology</i> , <b>2021</b> , 19, 7	7.3	5
17	Rapid evolution of female-biased genes among four species of <i>Anopheles</i> malaria mosquitoes		3
16	Assessing species coverage and assembly quality of rapidly accumulating sequenced genomes.. <i>GigaScience</i> , <b>2022</b> , 11,	7.6	3
15	CrowdGO: machine learning and semantic similarity guided consensus Gene Ontology annotation		2
14	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> , <b>2020</b> , 12, 3534-3549	3.9	2

13	Characterization of Insect Immune Systems from Genomic Data. <i>Springer Protocols</i> , <b>2020</b> , 3-34	0.3	1
12	Genome-enabled insights into the biology of thrips as crop pests		1
11	RADSex: a computational workflow to study sex determination using Restriction Site-Associated DNA Sequencing data		1
10	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		1
9	<i>Anopheles coluzzii</i> stearyl-CoA desaturase is essential for adult female survival and reproduction upon blood feeding. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009486	7.6	1
8	Functional constraints on insect immune system components govern their evolutionary trajectories		1
7	Long-distance dispersal of pigeons and doves generated new ecological opportunities for host-switching and adaptive radiation by their parasites		1
6	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> , <b>2022</b> , 289, 20220042	4.4	1
5	<i>Anopheles</i> mosquitoes reveal new principles of 3D genome organization in insects.. <i>Nature Communications</i> , <b>2022</b> , 13, 1960	17.4	1
4	Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR. <i>F1000Research</i> , 10, 1238	3.6	0
3	CrowdGO: Machine learning and semantic similarity guided consensus Gene Ontology annotation.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1010075	5	0
2	Comparative Genome Analysis <b>2009</b> , 33-58		
1	Exploring new genomic territories with emerging model insects.. <i>Current Opinion in Insect Science</i> , <b>2022</b> , 100902	5.1	