

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	BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. <i>Bioinformatics</i> , 2015, 31, 3210-3212.	1.8	9,712
2	BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. <i>Molecular Biology and Evolution</i> , 2018, 35, 543-548.	3.5	1,844
3	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	13.7	1,255
4	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
5	Evolutionary Dynamics of Immune-Related Genes and Pathways in Disease-Vector Mosquitoes. <i>Science</i> , 2007, 316, 1738-1743.	6.0	550
6	Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , 2015, 347, 1258-1264.	6.0	527
7	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258-1264.	6.0	492
8	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
9	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	5.8	450
10	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. <i>Science</i> , 2010, 330, 86-88.	6.0	424
11	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
12	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
13	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	6.0	357
14	OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs. <i>Nucleic Acids Research</i> , 2013, 41, D358-D365.	6.5	333
15	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
16	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
17	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
18	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

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19	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.	3.3	251
20	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. Genome Biology, 2016, 17, 227.	3.8	244
21	Leucine-Rich Repeat Protein Complex Activates Mosquito Complement in Defense Against <i>Plasmodium</i> Parasites. Science, 2009, 324, 258-261.	6.0	241
22	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. Genome Research, 2013, 23, 1235-1247.	2.4	205
23	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737.	5.8	196
24	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. Nature Communications, 2016, 7, 10165.	5.8	184
25	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	1.7	177
26	A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest <i>Mayetiola destructor</i> . Current Biology, 2015, 25, 613-620.	1.8	171
27	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . Insect Biochemistry and Molecular Biology, 2016, 76, 118-147.	1.2	154
28	Pathogenomics of <i>Culex quinquefasciatus</i> and Meta-Analysis of Infection Responses to Diverse Pathogens. Science, 2010, 330, 88-90.	6.0	150
29	Gene content evolution in the arthropods. Genome Biology, 2020, 21, 15.	3.8	150
30	The era of reference genomes in conservation genomics. Trends in Ecology and Evolution, 2022, 37, 197-202.	4.2	138
31	A depauperate immune repertoire precedes evolution of sociality in bees. Genome Biology, 2015, 16, 83.	3.8	130
32	OrthoDB: the hierarchical catalog of eukaryotic orthologs in 2011. Nucleic Acids Research, 2011, 39, D283-D288.	6.5	128
33	Genome analysis of a major urban malaria vector mosquito, <i>Anopheles stephensi</i> . Genome Biology, 2014, 15, 459.	3.8	119
34	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64.	3.8	114
35	Big data and other challenges in the quest for orthologs. Bioinformatics, 2014, 30, 2993-2998.	1.8	109
36	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.	1.1	102

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37	Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in <i>Anopheles gambiae</i> . BMC Genomics, 2013, 14, 749.	1.2	94
38	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.	3.3	91
39	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
40	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . BMC Genomics, 2020, 21, 47.	1.2	84
41	Correlating Traits of Gene Retention, Sequence Divergence, Duplicability and Essentiality in Vertebrates, Arthropods, and Fungi. Genome Biology and Evolution, 2011, 3, 75-86.	1.1	81
42	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	3.8	71
43	Evolution of sexual traits influencing vectorial capacity in anopheline mosquitoes. Science, 2015, 347, 985-988.	6.0	68
44	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. Nature Communications, 2015, 6, 7344.	5.8	67
45	The SIB Swiss Institute of Bioinformatics's™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
46	Rapid evolution of female-biased genes among four species of <i>Anopheles</i> malaria mosquitoes. Genome Research, 2017, 27, 1536-1548.	2.4	60
47	Brown marmorated stink bug, <i>Halyomorpha halys</i> (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. BMC Genomics, 2020, 21, 227.	1.2	60
48	Sequence-structure-function relations of the mosquito leucine-rich repeat immune proteins. BMC Genomics, 2010, 11, 531.	1.2	59
49	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
50	Genome-enabled insights into the biology of thrips as crop pests. BMC Biology, 2020, 18, 142.	1.7	54
51	Evolutionary Dynamics of Abundant Stop Codon Readthrough. Molecular Biology and Evolution, 2016, 33, 3108-3132.	3.5	53
52	Genomic features of the damselfly <i>Calopteryx splendens</i> representing a sister clade to most insect orders. Genome Biology and Evolution, 2017, 9, evx006.	1.1	53
53	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.	2.4	52
54	Summary Visualizations of Gene Ontology Terms With GO-Figure!. Frontiers in Bioinformatics, 2021, 1, .	1.0	51

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55	The Evolution of the <i>Anopheles</i> 16 Genomes Project. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1191-1194.	0.8	49
56	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
57	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
58	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
59	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
60	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
61	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
62	Of Genes and Genomes: Mosquito Evolution and Diversity. <i>Trends in Parasitology</i> , 2019, 35, 32-51.	1.5	35
63	The Novel Evolution of the Sperm Whale Genome. <i>Genome Biology and Evolution</i> , 2017, 9, 3260-3264.	1.1	33
64	Phylogenetic Analysis of the Oriental-Palearctic-Afrotropical Members of <i>Anopheles</i> (Culicidae: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38</i>) Infectious Diseases, 2014, 67, 361-367.	0.5	31
65	The <i>Aedes aegypti</i> genome: a comparative perspective. <i>Insect Molecular Biology</i> , 2008, 17, 1-8.	1.0	29
66	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. <i>Genome Biology</i> , 2019, 20, 98.	3.8	27
67	Using BUSCO to Assess Insect Genomic Resources. <i>Methods in Molecular Biology</i> , 2019, 1858, 59-74.	0.4	27
68	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
69	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
70	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
71	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
72	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (Halictidae: <i>Nomia melanderi</i>). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 625-634.	0.8	19

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73	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
74	<i>Anopheles</i> mosquitoes reveal new principles of 3D genome organization in insects. <i>Nature Communications</i> , 2022, 13, 1960.	5.8	19
75	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
76	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
77	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
78	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
79	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
80	Assessing species coverage and assembly quality of rapidly accumulating sequenced genomes. <i>GigaScience</i> , 2022, 11, .	3.3	15
81	Brain microRNAs among social and solitary bees. <i>Royal Society Open Science</i> , 2020, 7, 200517.	1.1	13
82	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
83	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
84	Scaffold assembly based on genome rearrangement analysis. <i>Computational Biology and Chemistry</i> , 2015, 57, 46-53.	1.1	12
85	Horizontally acquired antibacterial genes associated with adaptive radiation of ladybird beetles. <i>BMC Biology</i> , 2021, 19, 7.	1.7	11
86	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
87	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
88	<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
89	Characterization of Insect Immune Systems from Genomic Data. <i>Springer Protocols</i> , 2020, , 3-34.	0.1	4
90	CrowdGO: Machine learning and semantic similarity guided consensus Gene Ontology annotation. <i>PLoS Computational Biology</i> , 2022, 18, e1010075.	1.5	4

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91	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
92	Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR. <i>F1000Research</i> , 0, 10, 1238.	0.8	3
93	Functional Constraints on Insect Immune System Components Govern Their Evolutionary Trajectories. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
94	Comparative genomics of insect immunity. , 2009, , 86-105.		1
95	Comparative Genome Analysis. , 2009, , 33-58.		0
96	“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
97	Exploring new genomic territories with emerging model insects. <i>Current Opinion in Insect Science</i> , 2022, 51, 100902.	2.2	0