

Stephen Richards

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

19,712
citations

61945

43
h-index

74108

75
g-index

84
all docs

84
docs citations

84
times ranked

21685
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	6.0	5,566
2	The <i>Drosophila melanogaster</i> Genetic Reference Panel. <i>Nature</i> , 2012, 482, 173-178.	13.7	1,756
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	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	13.7	1,086
5	Mind the Gap: Upgrading Genomes with Pacific Biosciences RS Long-Read Sequencing Technology. <i>PLoS ONE</i> , 2012, 7, e47768.	1.1	896
6	Widespread Lateral Gene Transfer from Intracellular Bacteria to Multicellular Eukaryotes. <i>Science</i> , 2007, 317, 1753-1756.	6.0	693
7	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	3.3	652
8	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
9	Natural variation in genome architecture among 205 <i>Drosophila melanogaster</i> Genetic Reference Panel lines. <i>Genome Research</i> , 2014, 24, 1193-1208.	2.4	565
10	Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : Chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005, 15, 1-18.	2.4	453
11	Epistasis dominates the genetic architecture of <i>Drosophila</i> quantitative traits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15553-15559.	3.3	348
12	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
13	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. <i>BMC Biology</i> , 2017, 15, 62.	1.7	286
14	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
15	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. <i>BMC Biology</i> , 2017, 15, 63.	1.7	238
16	Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of Holometabolous insects. <i>Genome Research</i> , 2006, 16, 1334-1338.	2.4	233
17	Hemimetabolous genomes reveal molecular basis of termite eusociality. <i>Nature Ecology and Evolution</i> , 2018, 2, 557-566.	3.4	223
18	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , 2014, 12, e1002005.	2.6	221

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19	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015, 527, 459-465.	13.7	217
20	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018, 8, 1931.	1.6	215
21	Polytene Chromosomal Maps of 11 <i>Drosophila</i> Species: The Order of Genomic Scaffolds Inferred From Genetic and Physical Maps. <i>Genetics</i> , 2008, 179, 1601-1655.	1.2	191
22	Using Whole-Genome Sequence Data to Predict Quantitative Trait Phenotypes in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1002685.	1.5	191
23	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
24	Parallel Histories of Horizontal Gene Transfer Facilitated Extreme Reduction of Endosymbiont Genomes in Sap-Feeding Insects. <i>Molecular Biology and Evolution</i> , 2014, 31, 857-871.	3.5	180
25	Fine structure of the human FMR1 gene. <i>Human Molecular Genetics</i> , 1993, 2, 1147-1153.	1.4	171
26	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
27	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. <i>Molecular Biology and Evolution</i> , 2017, 34, 1838-1862.	3.5	157
28	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
29	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
30	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	2.4	147
31	The whole genome sequence of the Mediterranean fruit fly, <i>Ceratitidis capitata</i> (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. <i>Genome Biology</i> , 2016, 17, 192.	3.8	130
32	Diversity and evolution of the transposable element repertoire in arthropods with particular reference to insects. <i>Bmc Ecology and Evolution</i> , 2019, 19, 11.	0.7	129
33	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	124
34	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
35	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
36	Are feeding preferences and insecticide resistance associated with the size of detoxifying enzyme families in insect herbivores?. <i>Current Opinion in Insect Science</i> , 2016, 13, 70-76.	2.2	80

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37	The Toxicogenome of <i>Hyalella azteca</i> : A Model for Sediment Ecotoxicology and Evolutionary Toxicology. <i>Environmental Science & Technology</i> , 2018, 52, 6009-6022.	4.6	79
38	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , 2015, 6, 7344.	5.8	67
39	Best practices in insect genome sequencing: what works and what doesn't. <i>Current Opinion in Insect Science</i> , 2015, 7, 1-7.	2.2	65
40	Improved annotation of the insect vector of citrus greening disease: biocuration by a diverse genomics community. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	62
41	Genomics of Natural Populations: How Differentially Expressed Genes Shape the Evolution of Chromosomal Inversions in <i>Drosophila pseudoobscura</i> . <i>Genetics</i> , 2016, 204, 287-301.	1.2	61
42	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
43	House spider genome uncovers evolutionary shifts in the diversity and expression of black widow venom proteins associated with extreme toxicity. <i>BMC Genomics</i> , 2017, 18, 178.	1.2	57
44	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
45	Comparative Genomics of a Parthenogenesis-Inducing <i>Wolbachia</i> Symbiont. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2113-2123.	0.8	56
46	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , 2020, 18, 142.	1.7	54
47	Genomic Signatures of Cooperation and Conflict in the Social Amoeba. <i>Current Biology</i> , 2015, 25, 1661-1665.	1.8	51
48	The genome of the water strider <i>Gerris buenoi</i> reveals expansions of gene repertoires associated with adaptations to life on the water. <i>BMC Genomics</i> , 2018, 19, 832.	1.2	47
49	The maternal-effect, selfish genetic element <i>Medea</i> is associated with a composite <i>Tc1</i> transposon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10085-10089.	3.3	43
50	Avirulence gene mapping in the Hessian fly (<i>Mayetiola destructor</i>) reveals a protein phosphatase 2C effector gene family. <i>Journal of Insect Physiology</i> , 2016, 84, 22-31.	0.9	43
51	It's more than stamp collecting: how genome sequencing can unify biological research. <i>Trends in Genetics</i> , 2015, 31, 411-421.	2.9	37
52	Genomics of natural populations: Evolutionary forces that establish and maintain gene arrangements in <i>Drosophila pseudoobscura</i> . <i>Molecular Ecology</i> , 2017, 26, 6539-6562.	2.0	37
53	Comparative Genomics of Two Closely Related <i>Wolbachia</i> with Different Reproductive Effects on Hosts. <i>Genome Biology and Evolution</i> , 2016, 8, 1526-1542.	1.1	35
54	Comparative genomic study of arachnid immune systems indicates loss of beta-1,3-glucanase-related proteins and the immune deficiency pathway. <i>Journal of Evolutionary Biology</i> , 2016, 29, 277-291.	0.8	34

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55	Fine-Scale Mapping of the <i>Nasonia</i> Genome to Chromosomes Using a High-Density Genotyping Microarray. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 205-215.	0.8	33
56	Standards recommendations for the Earth BioGenome Project. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	33
57	Genomes of Diptera. <i>Current Opinion in Insect Science</i> , 2018, 25, 116-124.	2.2	26
58	A blow to the fly “ <i>Lucilia cuprina</i> draft genome and transcriptome to support advances in biology and biotechnology. <i>Biotechnology Advances</i> , 2016, 34, 605-620.	6.0	23
59	The value of new genome references. <i>Experimental Cell Research</i> , 2017, 358, 433-438.	1.2	19
60	Deep sequencing and genome-wide analysis reveals the expansion of MicroRNA genes in the gall midge <i>Mayetiola destructor</i> . <i>BMC Genomics</i> , 2013, 14, 187.	1.2	17
61	Evidence for Stabilizing Selection on Codon Usage in Chromosomal Rearrangements of <i>Drosophila pseudoobscura</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2433-2449.	0.8	17
62	Extensive Recombination Suppression and Epistatic Selection Causes Chromosome-Wide Differentiation of a Selfish Sex Chromosome in <i>Drosophila pseudoobscura</i> . <i>Genetics</i> , 2020, 216, 205-226.	1.2	17
63	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
64	Full disclosure: Genome assembly is still hard. <i>PLoS Biology</i> , 2018, 16, e2005894.	2.6	16
65	Expansions of key protein families in the German cockroach highlight the molecular basis of its remarkable success as a global indoor pest. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018, 330, 254-264.	0.6	15
66	Editorial overview: Insect genomics: Arthropod genomic resources for the 21st century. <i>Current Opinion in Insect Science</i> , 2018, 25, iv-vii.	2.2	9
67	Loss of the Polyketide Synthase <i>StlB</i> Results in Stalk Cell Overproduction in <i>Polysphondylium violaceum</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 674-683.	1.1	8
68	Arthropod Genome Sequencing and Assembly Strategies. <i>Methods in Molecular Biology</i> , 2019, 1858, 1-14.	0.4	7
69	The Battle Against Flystrike “ Past Research and New Prospects Through Genomics. <i>Advances in Parasitology</i> , 2017, 98, 227-281.	1.4	6
70	The mitogenome of the bed bug <i>Cimex lectularius</i> (Hemiptera: Cimicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 425-427.	0.2	5