

Stephen Richards

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

19,712
citations

61857

43
h-index

74018

75
g-index

84
all docs

84
docs citations

84
times ranked

21685
citing authors

#	ARTICLE	IF	CITATIONS
1	The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	124
2	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
3	Loss of the Polyketide Synthase StlB Results in Stalk Cell Overproduction in <i>Polysphondylium violaceum</i> . Genome Biology and Evolution, 2020, 12, 674-683.	1.1	8
4	Genome-enabled insights into the biology of thrips as crop pests. BMC Biology, 2020, 18, 142.	1.7	54
5	Extensive Recombination Suppression and Epistatic Selection Causes Chromosome-Wide Differentiation of a Selfish Sex Chromosome in <i>Drosophila pseudoobscura</i> . Genetics, 2020, 216, 205-226.	1.2	17
6	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
7	Gene content evolution in the arthropods. Genome Biology, 2020, 21, 15.	3.8	150
8	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. Genome Biology and Evolution, 2020, 12, 1099-1188.	1.1	17
9	Diversity and evolution of the transposable element repertoire in arthropods with particular reference to insects. BMC Ecology and Evolution, 2019, 19, 11.	0.7	129
10	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64.	3.8	114
11	Arthropod Genome Sequencing and Assembly Strategies. Methods in Molecular Biology, 2019, 1858, 1-14.	0.4	7
12	Earth BioGenome Project: Sequencing life for the future of life. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4325-4333.	3.3	652
13	Editorial overview: Insect genomics: Arthropod genomic resources for the 21st century. Current Opinion in Insect Science, 2018, 25, iv-vii.	2.2	9
14	The Toxicogenome of <i>Hyalella azteca</i> : A Model for Sediment Ecotoxicology and Evolutionary Toxicology. Environmental Science & Technology, 2018, 52, 6009-6022.	4.6	79
15	Genomes of Diptera. Current Opinion in Insect Science, 2018, 25, 116-124.	2.2	26
16	Hemimetabolous genomes reveal molecular basis of termite eusociality. Nature Ecology and Evolution, 2018, 2, 557-566.	3.4	223
17	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). Scientific Reports, 2018, 8, 1931.	1.6	215
18	The genome of the water strider <i>Gerris buenoi</i> reveals expansions of gene repertoires associated with adaptations to life on the water. BMC Genomics, 2018, 19, 832.	1.2	47

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19	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
20	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
21	Full disclosure: Genome assembly is still hard. <i>PLoS Biology</i> , 2018, 16, e2005894.	2.6	16
22	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. <i>Molecular Biology and Evolution</i> , 2017, 34, 1838-1862.	3.5	157
23	The value of new genome references. <i>Experimental Cell Research</i> , 2017, 358, 433-438.	1.2	19
24	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
25	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
26	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
27	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. <i>BMC Biology</i> , 2017, 15, 62.	1.7	286
28	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
29	The Battle Against Flystrike – Past Research and New Prospects Through Genomics. <i>Advances in Parasitology</i> , 2017, 98, 227-281.	1.4	6
30	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
31	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
32	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
33	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
34	The whole genome sequence of the Mediterranean fruit fly, <i>Ceratitis 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
35	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
36	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

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37	The mitogenome of the bed bug <i>Cimex lectularius</i> (Hemiptera: Cimicidae). Mitochondrial DNA Part B: Resources, 2016, 1, 425-427.	0.2	5
38	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
39	Comparative Genomics of a Parthenogenesis-Inducing <i>Wolbachia</i> Symbiont. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2113-2123.	0.8	56
40	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
41	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
42	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
43	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
44	Genomic Signatures of Cooperation and Conflict in the Social Amoeba. <i>Current Biology</i> , 2015, 25, 1661-1665.	1.8	51
45	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
46	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
47	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
48	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , 2015, 6, 7344.	5.8	67
49	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015, 527, 459-465.	13.7	217
50	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
51	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
52	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
53	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	2.4	147
54	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

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55	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
56	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
57	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
58	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
59	The <i>Drosophila melanogaster</i> Genetic Reference Panel. <i>Nature</i> , 2012, 482, 173-178.	13.7	1,756
60	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
61	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	13.7	1,086
62	Mind the Gap: Upgrading Genomes with Pacific Biosciences RS Long-Read Sequencing Technology. <i>PLoS ONE</i> , 2012, 7, e47768.	1.1	896
63	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	13.7	1,255
64	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
65	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
66	Widespread Lateral Gene Transfer from Intracellular Bacteria to Multicellular Eukaryotes. <i>Science</i> , 2007, 317, 1753-1756.	6.0	693
67	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
68	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
69	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	6.0	5,566
70	Fine structure of the human FMR1 gene. <i>Human Molecular Genetics</i> , 1993, 2, 1147-1153.	1.4	171