

Russell B Corbett-Detig

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

3,601
citations

236925

25
h-index

223800

46
g-index

76
all docs

76
docs citations

76
times ranked

4355
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Variation in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2012, 192, 533-598.	2.9	325
2	Population Genomics of Sub-Saharan <i>Drosophila melanogaster</i> : African Diversity and Non-African Admixture. <i>PLoS Genetics</i> , 2012, 8, e1003080.	3.5	318
3	Natural Selection Constrains Neutral Diversity across A Wide Range of Species. <i>PLoS Biology</i> , 2015, 13, e1002112.	5.6	285
4	The <i>Drosophila</i> Genome Nexus: A Population Genomic Resource of 623 <i>Drosophila melanogaster</i> Genomes, Including 197 from a Single Ancestral Range Population. <i>Genetics</i> , 2015, 199, 1229-1241.	2.9	273
5	Ultrafast Sample placement on Existing tRees (USHER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. <i>Nature Genetics</i> , 2021, 53, 809-816.	21.4	264
6	Genetic incompatibilities are widespread within species. <i>Nature</i> , 2013, 504, 135-137.	27.8	200
7	Population Genomics of Inversion Polymorphisms in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1003056.	3.5	172
8	A Thousand Fly Genomes: An Expanded <i>Drosophila</i> Genome Nexus. <i>Molecular Biology and Evolution</i> , 2016, 33, 3308-3313.	8.9	160
9	A Hidden Markov Model Approach for Simultaneously Estimating Local Ancestry and Admixture Time Using Next Generation Sequence Data in Samples of Arbitrary Ploidy. <i>PLoS Genetics</i> , 2017, 13, e1006529.	3.5	117
10	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. <i>Science</i> , 2017, 358, 951-954.	12.6	105
11	Outbreak Associated with SARS-CoV-2 B.1.617.2 (Delta) Variant in an Elementary School – Marin County, California, May–June 2021. <i>Morbidity and Mortality Weekly Report</i> , 2021, 70, 1214-1219.	15.1	101
12	Stability of SARS-CoV-2 phylogenies. <i>PLoS Genetics</i> , 2020, 16, e1009175.	3.5	92
13	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. <i>PLoS Genetics</i> , 2020, 16, e1008935.	3.5	87
14	Mutation Rates and Selection on Synonymous Mutations in SARS-CoV-2. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	83
15	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. <i>Molecular Biology and Evolution</i> , 2021, 38, 5819-5824.	8.9	69
16	Sequence-Based Detection and Breakpoint Assembly of Polymorphic Inversions. <i>Genetics</i> , 2012, 192, 131-137.	2.9	68
17	Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. <i>Nature Communications</i> , 2019, 10, 4769.	12.8	55
18	Circumventing Heterozygosity: Sequencing the Amplified Genome of a Single Haploid <i>Drosophila melanogaster</i> Embryo. <i>Genetics</i> , 2011, 188, 239-246.	2.9	51

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19	Selection on Coding and Regulatory Variation Maintains Individuality in Major Urinary Protein Scents in Wild Mice. <i>PLoS Genetics</i> , 2016, 12, e1005891.	3.5	46
20	Linked genetic variation and not genome structure causes widespread differential expression associated with chromosomal inversions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5492-5497.	7.1	44
21	The genome of <i>Peromyscus leucopus</i> , natural host for Lyme disease and other emerging infections. <i>Science Advances</i> , 2019, 5, eaaw6441.	10.3	41
22	Transfer RNA genes experience exceptionally elevated mutation rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8996-9001.	7.1	40
23	Estimating the Timing of Multiple Admixture Pulses During Local Ancestry Inference. <i>Genetics</i> , 2018, 210, 1089-1107.	2.9	37
24	Mixed transmission modes and dynamic genome evolution in an obligate animal-bacterial symbiosis. <i>ISME Journal</i> , 2017, 11, 1359-1371.	9.8	35
25	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. <i>Molecular Ecology</i> , 2021, 30, 6144-6161.	3.9	30
26	SELAM: simulation of epistasis and local adaptation during admixture with mate choice. <i>Bioinformatics</i> , 2016, 32, 3035-3037.	4.1	29
27	Selection on Inversion Breakpoints Favors Proximity to Pairing Sensitive Sites in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 204, 259-265.	2.9	27
28	Fine-Mapping Complex Inversion Breakpoints and Investigating Somatic Pairing in the <i>Anopheles gambiae</i> Species Complex Using Proximity-Ligation Sequencing. <i>Genetics</i> , 2019, 213, 1495-1511.	2.9	27
29	On the Distribution of Tract Lengths During Adaptive Introgression. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3663-3673.	1.8	23
30	Predicting transfer RNA gene activity from sequence and genome context. <i>Genome Research</i> , 2020, 30, 85-94.	5.5	22
31	Inferring Adaptive Introgression Using Hidden Markov Models. <i>Molecular Biology and Evolution</i> , 2021, 38, 2152-2165.	8.9	21
32	One fly-one genome: chromosome-scale genome assembly of a single outbred <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2020, 48, e75.	14.5	20
33	Horizontal transmission enables flexible associations with locally adapted symbiont strains in deep-sea hydrothermal vent symbioses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2115608119.	7.1	20
34	Phenotypic Convergence Is Not Mirrored at the Protein Level in a Lizard Adaptive Radiation. <i>Molecular Biology and Evolution</i> , 2020, 37, 1604-1614.	8.9	19
35	Glacial ice supports a distinct and undocumented polar bear subpopulation persisting in late 21st-century sea-ice conditions. <i>Science</i> , 2022, 376, 1333-1338.	12.6	18
36	Shortcomings of SARS-CoV-2 genomic metadata. <i>BMC Research Notes</i> , 2021, 14, 189.	1.4	17

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37	Conserved novel ORFs in the mitochondrial genome of the ctenophore <i>Beroë forskalii</i> . PeerJ, 2020, 8, e8356.	2.0	16
38	matOptimize: a parallel tree optimization method enables online phylogenetics for SARS-CoV-2. Bioinformatics, 2022, 38, 3734-3740.	4.1	14
39	Bulk pollen sequencing reveals rapid evolution of segregation distortion in the male germline of Arabidopsis hybrids. Evolution Letters, 2019, 3, 93-103.	3.3	13
40	Fine-Scale Position Effects Shape the Distribution of Inversion Breakpoints in <i>Drosophila melanogaster</i> . Genome Biology and Evolution, 2020, 12, 1378-1391.	2.5	13
41	phastSim: Efficient simulation of sequence evolution for pandemic-scale datasets. PLoS Computational Biology, 2022, 18, e1010056.	3.2	13
42	Identifying SARS-CoV-2 regional introductions and transmission clusters in real time. Virus Evolution, 2022, 8, .	4.9	12
43	Direct Gamete Sequencing Reveals No Evidence for Segregation Distortion in House Mouse Hybrids. PLoS ONE, 2015, 10, e0131933.	2.5	10
44	Expanding Efforts and Support to Respond to the HIV and COVID-19 Intersecting Pandemics. JAMA - Journal of the American Medical Association, 2022, 327, 1227.	7.4	8
45	Neo-sex chromosome evolution shapes sex-dependent asymmetrical introgression barrier. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2119382119.	7.1	7
46	Bulk pollen sequencing reveals rapid evolution of segregation distortion in the male germline of Arabidopsis hybrids. , 2019, 3, 93.		1
47	ShUSHER: private browser-based placement of sensitive genome samples on phylogenetic trees. Journal of Open Source Software, 2021, 6, 3677.	4.6	0
48	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
49	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
50	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
51	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
52	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
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