Russell B Corbett-Detig

List of Publications by Year
in descending order

53	3,601	236925	223800
53	**3,601**	**25**	**46**
papers	citations	h-index	g-index
76	76	76	4355
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Horizontal transmission enables flexible associations with locally adapted symbiont strains in deep-sea hydrothermal vent symbioses. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115608119.	7.1	20
2	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
3	phastSim: Efficient simulation of sequence evolution for pandemic-scale datasets. PLoS Computational Biology, 2022, 18, e1010056.	3.2	13
4	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
5	Glacial ice supports a distinct and undocumented polar bear subpopulation persisting in late 21st-century sea-ice conditions. Science, 2022, 376, 1333-1338.	12.6	18
6	Identifying SARS-CoV-2 regional introductions and transmission clusters in real time. Virus Evolution, 2022, 8, .	4.9	12
7	matOptimize: a parallel tree optimization method enables online phylogenetics for SARS-CoV-2. Bioinformatics, 2022, 38, 3734-3740.	4.1	14
8	Mutation Rates and Selection on Synonymous Mutations in SARS-CoV-2. Genome Biology and Evolution, 2021, 13, .	2.5	83
9	Shortcomings of SARS-CoV-2 genomic metadata. BMC Research Notes, 2021, 14, 189.	1.4	17
10	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. Molecular Ecology, 2021, 30, 6144-6161.	3.9	30
11	Ultrafast Sample placement on Existing tRees (UShER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. Nature Genetics, 2021, 53, 809-816.	21.4	264
12	Outbreak Associated with SARS-CoV-2 B.1.617.2 (Delta) Variant in an Elementary School — Marin County, California, May–June 2021. Morbidity and Mortality Weekly Report, 2021, 70, 1214-1219.	15.1	101
13	A Daily-Updated Database and Tools for Comprehensive SARS-CoV-2 Mutation-Annotated Trees. Molecular Biology and Evolution, 2021, 38, 5819-5824.	8.9	69
14	Inferring Adaptive Introgression Using Hidden Markov Models. Molecular Biology and Evolution, 2021, 38, 2152-2165.	8.9	21
15	ShUShER: private browser-based placement of sensitive genome samples on phylogenetic trees. Journal of Open Source Software, 2021, 6, 3677.	4.6	0
16	Predicting transfer RNA gene activity from sequence and genome context. Genome Research, 2020, 30, 85-94.	5.5	22
17	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. PLoS Genetics, 2020, 16, e1008935.	3.5	87
18	One fly—one genome: chromosome-scale genome assembly of a single outbred Drosophila melanogaster. Nucleic Acids Research, 2020, 48, e75.	14.5	20

#	ARTICLE	IF	CITATIONS
19	Phenotypic Convergence Is Not Mirrored at the Protein Level in a Lizard Adaptive Radiation. Molecular Biology and Evolution, 2020, 37, 1604-1614.	8.9	19
20	Fine-Scale Position Effects Shape the Distribution of Inversion Breakpoints in Drosophila melanogaster. Genome Biology and Evolution, 2020, 12, 1378-1391.	2.5	13
21	Stability of SARS-CoV-2 phylogenies. PLoS Genetics, 2020, 16, e1009175.	3.5	92
22	On the Distribution of Tract Lengths During Adaptive Introgression. G3: Genes, Genomes, Genetics, 2020, 10, 3663-3673.	1.8	23
23	Conserved novel ORFs in the mitochondrial genome of the ctenophore <i>Beroe forskalii</i>. PeerJ, 2020, 8, e8356.	2.0	16
24	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
25	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
26	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
27	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
28	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
29	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. , 2020, 16, e1008935.		0
30	The genome of <i>Peromyscus leucopus</i>, natural host for Lyme disease and other emerging infections. Science Advances, 2019, 5, eaaw6441.	10.3	41
31	Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. Nature Communications, 2019, 10, 4769.	12.8	55
32	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
33	Fine-Mapping Complex Inversion Breakpoints and Investigating Somatic Pairing in the<i>Anopheles gambiae</i>Species Complex Using Proximity-Ligation Sequencing. Genetics, 2019, 213, 1495-1511.	2.9	27
34	Bulk pollen sequencing reveals rapid evolution of segregation distortion in the male germline of Arabidopsis hybrids. , 2019, 3, 93.		1
35	Estimating the Timing of Multiple Admixture Pulses During Local Ancestry Inference. Genetics, 2018, 210, 1089-1107.	2.9	37
36	Linked genetic variation and not genome structure causes widespread differential expression associated with chromosomal inversions. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5492-5497.	7.1	44

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37	Transfer RNA genes experience exceptionally elevated mutation rates. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8996-9001.	7.1	40
38	Mixed transmission modes and dynamic genome evolution in an obligate animal–bacterial symbiosis. ISME Journal, 2017, 11, 1359-1371.	9.8	35
39	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. Science, 2017, 358, 951-954.	12.6	105
40	A Hidden Markov Model Approach for Simultaneously Estimating Local Ancestry and Admixture Time Using Next Generation Sequence Data in Samples of Arbitrary Ploidy. PLoS Genetics, 2017, 13, e1006529.	3.5	117
41	Selection on Coding and Regulatory Variation Maintains Individuality in Major Urinary Protein Scent Marks in Wild Mice. PLoS Genetics, 2016, 12, e1005891.	3.5	46
42	A Thousand Fly Genomes: An Expanded *Drosophila* Genome Nexus. Molecular Biology and Evolution, 2016, 33, 3308-3313.	8.9	160
43	Selection on Inversion Breakpoints Favors Proximity to Pairing Sensitive Sites in *Drosophila melanogaster*. Genetics, 2016, 204, 259-265.	2.9	27
44	SELAM: simulation of epistasis and local adaptation during admixture with mate choice. Bioinformatics, 2016, 32, 3035-3037.	4.1	29
45	Direct Gamete Sequencing Reveals No Evidence for Segregation Distortion in House Mouse Hybrids. PLoS ONE, 2015, 10, e0131933.	2.5	10
46	Natural Selection Constrains Neutral Diversity across A Wide Range of Species. PLoS Biology, 2015, 13, e1002112.	5.6	285
47	The *Drosophila* Genome Nexus: A Population Genomic Resource of 623 *Drosophila melanogaster* Genomes, Including 197 from a Single Ancestral Range Population. Genetics, 2015, 199, 1229-1241.	2.9	273
48	Genetic incompatibilities are widespread within species. Nature, 2013, 504, 135-137.	27.8	200
49	Population Genomics of Inversion Polymorphisms in Drosophila melanogaster. PLoS Genetics, 2012, 8, e1003056.	3.5	172
50	Population Genomics of Sub-Saharan Drosophila melanogaster: African Diversity and Non-African Admixture. PLoS Genetics, 2012, 8, e1003080.	3.5	318
51	Sequence-Based Detection and Breakpoint Assembly of Polymorphic Inversions. Genetics, 2012, 192, 131-137.	2.9	68
52	Genomic Variation in Natural Populations of *Drosophila melanogaster*. Genetics, 2012, 192, 533-598.	2.9	325
53	Circumventing Heterozygosity: Sequencing the Amplified Genome of a Single Haploid *Drosophila melanogaster* Embryo. Genetics, 2011, 188, 239-246.	2.9	51