

Reed A Cartwright

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

2,366
citations

471509

17
h-index

395702

33
g-index

48
all docs

48
docs citations

48
times ranked

5021
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	21.4	816
2	The khmer software package: enabling efficient nucleotide sequence analysis. <i>F1000Research</i> , 2015, 4, 900.	1.6	362
3	DeNovoGear: de novo indel and point mutation discovery and phasing. <i>Nature Methods</i> , 2013, 10, 985-987.	19.0	169
4	The role of gene flow in rapid and repeated evolution of cave-related traits in Mexican tetra, <i>Astyanax mexicanus</i> . <i>Molecular Ecology</i> , 2018, 27, 4397-4416.	3.9	160
5	DNA assembly with gaps (Dawg): simulating sequence evolution. <i>Bioinformatics</i> , 2005, 21, iii31-iii38.	4.1	138
6	A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, .	6.0	112
7	Experimental evolution reveals an effective avenue to release catabolite repression via mutations in XylR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7349-7354.	7.1	61
8	Problems and Solutions for Estimating Indel Rates and Length Distributions. <i>Molecular Biology and Evolution</i> , 2009, 26, 473-480.	8.9	60
9	Whole Genome Sequencing of Field Isolates Reveals Extensive Genetic Diversity in <i>Plasmodium vivax</i> from Colombia. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004252.	3.0	49
10	Phylogenomic reconstruction supports supercontinent origins for <i>Leishmania</i> . <i>Infection, Genetics and Evolution</i> , 2016, 38, 101-109.	2.3	49
11	A phylogenomic approach reveals a low somatic mutation rate in a long-lived plant. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192364.	2.6	39
12	Low Base-Substitution Mutation Rate in the Germline Genome of the Ciliate <i>Tetrahymena thermophil</i> . <i>Genome Biology and Evolution</i> , 2016, 8, evw223.	2.5	38
13	The importance of selection in the evolution of blindness in cavefish. <i>BMC Evolutionary Biology</i> , 2017, 17, 45.	3.2	30
14	A composite genome approach to identify phylogenetically informative data from next-generation sequencing. <i>BMC Bioinformatics</i> , 2015, 16, 193.	2.6	26
15	Logarithmic gap costs decrease alignment accuracy. <i>BMC Bioinformatics</i> , 2006, 7, 527.	2.6	23
16	Neutral Evolution of Robustness in <i>Drosophila</i> microRNA Precursors. <i>Molecular Biology and Evolution</i> , 2011, 28, 2115-2123.	8.9	23
17	A Toxic Mutator and Selection Alternative to the Non-Mendelian RNA Cache Hypothesis for hothead Reversion. <i>Plant Cell</i> , 2005, 17, 2856-2858.	6.6	19
18	A Probabilistic Model for Indel Evolution: Differentiating Insertions from Deletions. <i>Molecular Biology and Evolution</i> , 2021, 38, 5769-5781.	8.9	19

#	ARTICLE	IF	CITATIONS
19	Ngila: global pairwise alignments with logarithmic and affine gap costs. Bioinformatics, 2007, 23, 1427-1428.	4.1	16
20	A Family-Based Probabilistic Method for Capturing De Novo Mutations from High-Throughput Short-Read Sequencing Data. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.6	16
21	Estimating error models for whole genome sequencing using mixtures of Dirichlet-multinomial distributions. Bioinformatics, 2017, 33, 2322-2329.	4.1	16
22	Frequency-Dependent Selection With Dominance: A Window Onto the Behavior of the Mean Fitness. Genetics, 2004, 167, 499-512.	2.9	15
23	Genomic skimming and nanopore sequencing uncover cryptic hybridization in one of world's most threatened primates. Scientific Reports, 2021, 11, 17279.	3.3	13
24	accuMulate: a mutation caller designed for mutation accumulation experiments. Bioinformatics, 2018, 34, 2659-2660.	4.1	11
25	Parallel experimental evolution reveals a novel repressive control of GalP on xylose fermentation in Escherichia coli. Biotechnology and Bioengineering, 2019, 116, 2074-2086.	3.3	11
26	The gut microbiome of exudivorous marmosets in the wild and captivity. Scientific Reports, 2022, 12, 5049.	3.3	11
27	Equations of the End: Teaching Mathematical Modeling Using the Zombie Apocalypse. Journal of Microbiology and Biology Education, 2016, 17, 137-142.	1.0	9
28	Mitogenomic phylogeny of Callithrix with special focus on human transferred taxa. BMC Genomics, 2021, 22, 239.	2.8	8
29	The effect of the dispersal kernel on isolation-by-distance in a continuous population. PeerJ, 2016, 4, e1848.	2.0	7
30	Inferring Indel Parameters using a Simulation-based Approach. Genome Biology and Evolution, 2015, 7, 3226-3238.	2.5	6
31	The first steps toward a global pandemic: Reconstructing the demographic history of parasite host switches in its native range. Molecular Ecology, 2022, 31, 1358-1374.	3.9	6
32	SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. Nucleic Acids Research, 2017, 45, W453-W457.	14.5	5
33	The impact of self-incompatibility systems on the prevention of biparental inbreeding. PeerJ, 2017, 5, e4085.	2.0	2