

# Reed A Cartwright

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2795987/publications.pdf>

Version: 2024-02-01

33  
papers

2,366  
citations

471061

17  
h-index

395343

33  
g-index

48  
all docs

48  
docs citations

48  
times ranked

5021  
citing authors

#	ARTICLE	IF	CITATIONS
1	The gut microbiome of exudivorous marmosets in the wild and captivity. <i>Scientific Reports</i> , 2022, 12, 5049.	1.6	11
2	The first steps toward a global pandemic: Reconstructing the demographic history of parasite host switches in its native range. <i>Molecular Ecology</i> , 2022, 31, 1358-1374.	2.0	6
3	Mitogenomic phylogeny of <i>Callithrix</i> with special focus on human transferred taxa. <i>BMC Genomics</i> , 2021, 22, 239.	1.2	8
4	Genomic skimming and nanopore sequencing uncover cryptic hybridization in one of world's most threatened primates. <i>Scientific Reports</i> , 2021, 11, 17279.	1.6	13
5	A Probabilistic Model for Indel Evolution: Differentiating Insertions from Deletions. <i>Molecular Biology and Evolution</i> , 2021, 38, 5769-5781.	3.5	19
6	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.	1.2	39
7	A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, .	2.8	112
8	Parallel experimental evolution reveals a novel repressive control of GalP on xylose fermentation in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2019, 116, 2074-2086.	1.7	11
9	accuMulate: a mutation caller designed for mutation accumulation experiments. <i>Bioinformatics</i> , 2018, 34, 2659-2660.	1.8	11
10	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.	2.0	160
11	The importance of selection in the evolution of blindness in cavefish. <i>BMC Evolutionary Biology</i> , 2017, 17, 45.	3.2	30
12	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.	3.3	61
13	SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. <i>Nucleic Acids Research</i> , 2017, 45, W453-W457.	6.5	5
14	Estimating error models for whole genome sequencing using mixtures of Dirichlet-multinomial distributions. <i>Bioinformatics</i> , 2017, 33, 2322-2329.	1.8	16
15	The impact of self-incompatibility systems on the prevention of biparental inbreeding. <i>PeerJ</i> , 2017, 5, e4085.	0.9	2
16	Equations of the End: Teaching Mathematical Modeling Using the Zombie Apocalypse. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 137-142.	0.5	9
17	Low Base-Substitution Mutation Rate in the Germline Genome of the Ciliate <i>Tetrahymena thermophilus</i> . <i>Genome Biology and Evolution</i> , 2016, 8, eww223.	1.1	38
18	Phylogenomic reconstruction supports supercontinent origins for <i>Leishmania</i> . <i>Infection, Genetics and Evolution</i> , 2016, 38, 101-109.	1.0	49

#	ARTICLE	IF	CITATIONS
19	The effect of the dispersal kernel on isolation-by-distance in a continuous population. PeerJ, 2016, 4, e1848.	0.9	7
20	Whole Genome Sequencing of Field Isolates Reveals Extensive Genetic Diversity in Plasmodium vivax from Colombia. PLoS Neglected Tropical Diseases, 2015, 9, e0004252.	1.3	49
21	Inferring Indel Parameters using a Simulation-based Approach. Genome Biology and Evolution, 2015, 7, 3226-3238.	1.1	6
22	A composite genome approach to identify phylogenetically informative data from next-generation sequencing. BMC Bioinformatics, 2015, 16, 193.	1.2	26
23	The khmer software package: enabling efficient nucleotide sequence analysis. F1000Research, 2015, 4, 900.	0.8	362
24	DeNovoGear: de novo indel and point mutation discovery and phasing. Nature Methods, 2013, 10, 985-987.	9.0	169
25	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, .	0.2	16
26	Comparative population genomics of maize domestication and improvement. Nature Genetics, 2012, 44, 808-811.	9.4	816
27	Neutral Evolution of Robustness in Drosophila microRNA Precursors. Molecular Biology and Evolution, 2011, 28, 2115-2123.	3.5	23
28	Problems and Solutions for Estimating Indel Rates and Length Distributions. Molecular Biology and Evolution, 2009, 26, 473-480.	3.5	60
29	Ngila: global pairwise alignments with logarithmic and affine gap costs. Bioinformatics, 2007, 23, 1427-1428.	1.8	16
30	Logarithmic gap costs decrease alignment accuracy. BMC Bioinformatics, 2006, 7, 527.	1.2	23
31	A Toxic Mutator and Selection Alternative to the Non-Mendelian RNA Cache Hypothesis for hothead Reversion. Plant Cell, 2005, 17, 2856-2858.	3.1	19
32	DNA assembly with gaps (Dawg): simulating sequence evolution. Bioinformatics, 2005, 21, iii31-iii38.	1.8	138
33	Frequency-Dependent Selection With Dominance: A Window Onto the Behavior of the Mean Fitness. Genetics, 2004, 167, 499-512.	1.2	15