

# 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

471509  
17  
h-index

395702  
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. Scientific Reports, 2022, 12, 5049.	3.3	11
2	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
3	Mitogenomic phylogeny of Callithrix with special focus on human transferred taxa. BMC Genomics, 2021, 22, 239.	2.8	8
4	Genomic skimming and nanopore sequencing uncover cryptic hybridization in one of world's most threatened primates. Scientific Reports, 2021, 11, 17279.	3.3	13
5	A Probabilistic Model for Indel Evolution: Differentiating Insertions from Deletions. Molecular Biology and Evolution, 2021, 38, 5769-5781.	8.9	19
6	A phylogenomic approach reveals a low somatic mutation rate in a long-lived plant. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20192364.	2.6	39
7	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	6.0	112
8	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
9	accuMulate: a mutation caller designed for mutation accumulation experiments. Bioinformatics, 2018, 34, 2659-2660.	4.1	11
10	The role of gene flow in rapid and repeated evolution of cave-related traits in Mexican tetra, <i>Astyanax mexicanus</i> . Molecular Ecology, 2018, 27, 4397-4416.	3.9	160
11	The importance of selection in the evolution of blindness in cavefish. BMC Evolutionary Biology, 2017, 17, 45.	3.2	30
12	Experimental evolution reveals an effective avenue to release catabolite repression via mutations in XylR. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7349-7354.	7.1	61
13	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
14	Estimating error models for whole genome sequencing using mixtures of Dirichlet-multinomial distributions. Bioinformatics, 2017, 33, 2322-2329.	4.1	16
15	The impact of self-incompatibility systems on the prevention of biparental inbreeding. PeerJ, 2017, 5, e4085.	2.0	2
16	Equations of the End: Teaching Mathematical Modeling Using the Zombie Apocalypse. Journal of Microbiology and Biology Education, 2016, 17, 137-142.	1.0	9
17	Low Base-Substitution Mutation Rate in the Germline Genome of the Ciliate <i>Tetrahymena thermophil</i> . Genome Biology and Evolution, 2016, 8, evw223.	2.5	38
18	Phylogenomic reconstruction supports supercontinent origins for Leishmania. Infection, Genetics and Evolution, 2016, 38, 101-109.	2.3	49

#	ARTICLE	IF	CITATIONS
19	The effect of the dispersal kernel on isolation-by-distance in a continuous population. PeerJ, 2016, 4, e1848.	2.0	7
20	Whole Genome Sequencing of Field Isolates Reveals Extensive Genetic Diversity in Plasmodium vivax from Colombia. PLoS Neglected Tropical Diseases, 2015, 9, e0004252.	3.0	49
21	Inferring Indel Parameters using a Simulation-based Approach. Genome Biology and Evolution, 2015, 7, 3226-3238.	2.5	6
22	A composite genome approach to identify phylogenetically informative data from next-generation sequencing. BMC Bioinformatics, 2015, 16, 193.	2.6	26
23	The khmer software package: enabling efficient nucleotide sequence analysis. F1000Research, 2015, 4, 900.	1.6	362
24	DeNovoGear: de novo indel and point mutation discovery and phasing. Nature Methods, 2013, 10, 985-987.	19.0	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, .	0.6	16
26	Comparative population genomics of maize domestication and improvement. Nature Genetics, 2012, 44, 808-811.	21.4	816
27	Neutral Evolution of Robustness in Drosophila microRNA Precursors. Molecular Biology and Evolution, 2011, 28, 2115-2123.	8.9	23
28	Problems and Solutions for Estimating Indel Rates and Length Distributions. Molecular Biology and Evolution, 2009, 26, 473-480.	8.9	60
29	Ngila: global pairwise alignments with logarithmic and affine gap costs. Bioinformatics, 2007, 23, 1427-1428.	4.1	16
30	Logarithmic gap costs decrease alignment accuracy. BMC Bioinformatics, 2006, 7, 527.	2.6	23
31	A Toxic Mutator and Selection Alternative to the Non-Mendelian RNA Cache Hypothesis for hothead Reversion. Plant Cell, 2005, 17, 2856-2858.	6.6	19
32	DNA assembly with gaps (Dawg): simulating sequence evolution. Bioinformatics, 2005, 21, iii31-iii38.	4.1	138
33	Frequency-Dependent Selection With Dominance: A Window Onto the Behavior of the Mean Fitness. Genetics, 2004, 167, 499-512.	2.9	15