Paul Davis

List of Publications by Year
in descending order

30	8,124	230014	511568
papers	citations	27 h-index	30 g-index

30	30	30	14761
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	6.5	141
2	WormBase in 2022â€”data, processes, and tools for analyzing Caenorhabditis elegans. Genetics, 2022, 220, .	1.2	128
3	Harmonizing model organism data in the Alliance of Genome Resources. Genetics, 2022, 220, .	1.2	52
4	WormBase: a modern Model Organism Information Resource. Nucleic Acids Research, 2020, 48, D762-D767.	6.5	213
5	Ensembl Genomes 2020â€”enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	6.5	416
6	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	6.5	153
7	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. Nucleic Acids Research, 2018, 46, D802-D808.	6.5	489
8	WormBase 2017: molting into a new stage. Nucleic Acids Research, 2018, 46, D869-D874.	6.5	172
9	Using WormBase: A Genome Biology Resource for Caenorhabditis elegans and Related Nematodes. Methods in Molecular Biology, 2018, 1757, 399-470.	0.4	28
10	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	6.5	530
11	WormBase 2016: expanding to enable helminth genomic research. Nucleic Acids Research, 2016, 44, D774-D780.	6.5	329
12	WormBase 2014: new views of curated biology. Nucleic Acids Research, 2014, 42, D789-D793.	6.5	149
13	Ensembl Genomes 2013: scaling up access to genome-wide data. Nucleic Acids Research, 2014, 42, D546-D552.	6.5	205
14	Overview of gene structure in C. elegans. WormBook, 2014, , 1-18.	5.3	21
15	A simplified counter-selection recombineering protocol for creating fluorescent protein reporter constructs directly from C. elegans fosmid genomic clones. BMC Biotechnology, 2013, 13, 1.	1.7	98
16	WormBase. Worm, 2012, 1, 15-21.	1.0	14
17	WormBase 2012: more genomes, more data, new website. Nucleic Acids Research, 2012, 40, D735-D741.	6.5	175
18	Automatic categorization of diverse experimental information in the bioscience literature. BMC Bioinformatics, 2012, 13, 16.	1.2	37

#	Article	IF	Citations
19	WormBase: a comprehensive resource for nematode research. Nucleic Acids Research, 2010, 38, D463-D467.	6.5	325
20	Insights from the complete genome sequence of Mycobacterium marinum on the evolution of Mycobacterium tuberculosis. Genome Research, 2008, 18, 729-741.	2.4	471
21	WormBase: new content and better access. Nucleic Acids Research, 2007, 35, D506-D510.	6.5	80
22	WormBase 2007. Nucleic Acids Research, 2007, 36, D612-D617.	6.5	95
23	The genome of Rhizobium leguminosarum has recognizable core and accessory components. Genome Biology, 2006, 7, R34.	13.9	489
24	The multidrug-resistant human pathogen Clostridium difficile has a highly mobile, mosaic genome. Nature Genetics, 2006, 38, 779-786.	9.4	821
25	WormBase: better software, richer content. Nucleic Acids Research, 2006, 34, D475-D478.	6.5	74
26	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. Nucleic Acids Research, 2004, 33, D383-D389.	6.5	155
27	Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14240-14245.	3.3	675
28	Genomic and Genetic Analysis of Bordetella Bacteriophages Encoding Reverse Transcriptase-Mediated Tropism-Switching Cassettes. Journal of Bacteriology, 2004, 186, 1503-1517.	1.0	81
29	WormBase: a multi-species resource for nematode biology and genomics. Nucleic Acids Research, 2004, 32, 411D-417.	6.5	610
30	Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica. Nature Genetics, 2003, 35, 32-40.	9.4	898