

Jonathan Crabtree

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5882624/publications.pdf>

Version: 2024-02-01

24
papers

5,105
citations

567281

15
h-index

794594

19
g-index

25
all docs

25
docs citations

25
times ranked

9319
citing authors

#	ARTICLE	IF	CITATIONS
1	HMPDACC: a Human Microbiome Project Multi-omic data resource. <i>Nucleic Acids Research</i> , 2021, 49, D734-D742.	14.5	13
2	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	27.8	166
3	Mutagenesis of human genomes by endogenous mobile elements on a population scale. <i>Genome Research</i> , 2021, 31, 2225-2235.	5.5	15
4	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020, 12, 6.	8.2	61
5	A comprehensive non-redundant gene catalog reveals extensive within-community intraspecies diversity in the human vagina. <i>Nature Communications</i> , 2020, 11, 940.	12.8	86
6	Capture-based enrichment of <i>Theileria parva</i> DNA enables full genome assembly of first buffalo-derived strain and reveals exceptional intra-specific genetic diversity. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008781.	3.0	6
7	Title is missing!. , 2020, 14, e0008781.		0
8	Title is missing!. , 2020, 14, e0008781.		0
9	Title is missing!. , 2020, 14, e0008781.		0
10	Title is missing!. , 2020, 14, e0008781.		0
11	TwinBLAST: When Two Is Better than One. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
12	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. <i>Nature Biotechnology</i> , 2017, 35, 1077-1086.	17.5	400
13	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	27.8	929
14	Distinguishing potential bacteria-tumor associations from contamination in a secondary data analysis of public cancer genome sequence data. <i>Microbiome</i> , 2017, 5, 9.	11.1	62
15	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016, 7, 12218.	12.8	103
16	Genome-wide diversity and gene expression profiling of <i>Babesia microti</i> isolates identify polymorphic genes that mediate host-pathogen interactions. <i>Scientific Reports</i> , 2016, 6, 35284.	3.3	74
17	Functional Dynamics of the Gut Microbiome in Elderly People during Probiotic Consumption. <i>MBio</i> , 2015, 6, .	4.1	126
18	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. <i>Bioinformatics</i> , 2014, 30, 3125-3127.	4.1	41

#	ARTICLE	IF	CITATIONS
19	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. MBio, 2014, 5, e01721.	4.1	112
20	Using Sybil for interactive comparative genomics of microbes on the web. Bioinformatics, 2012, 28, 160-166.	4.1	53
21	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	12.6	621
22	Sybil: Methods and Software for Multiple Genome Comparison and Visualization. Methods in Molecular Biology, 2007, 408, 93-108.	0.9	55
23	Genome analysis of multiple pathogenic isolates of <i>Streptococcus agalactiae</i> : Implications for the microbial "pan-genome". Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13950-13955.	7.1	2,161
24	Deep and Wide: Comparative Genomics of <i>Chlamydia</i> . , 0, , 27-50.		2