

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	Genome analysis of multiple pathogenic isolates of <i>Streptococcus agalactiae</i> : Implications for the microbial "pan-genome". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13950-13955.	7.1	2,161
2	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	27.8	929
3	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	12.6	621
4	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
5	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	27.8	166
6	Functional Dynamics of the Gut Microbiome in Elderly People during Probiotic Consumption. <i>MBio</i> , 2015, 6, .	4.1	126
7	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. <i>MBio</i> , 2014, 5, e01721.	4.1	112
8	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016, 7, 12218.	12.8	103
9	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
10	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
11	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
12	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
13	Sybil: Methods and Software for Multiple Genome Comparison and Visualization. <i>Methods in Molecular Biology</i> , 2007, 408, 93-108.	0.9	55
14	Using Sybil for interactive comparative genomics of microbes on the web. <i>Bioinformatics</i> , 2012, 28, 160-166.	4.1	53
15	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. <i>Bioinformatics</i> , 2014, 30, 3125-3127.	4.1	41
16	Mutagenesis of human genomes by endogenous mobile elements on a population scale. <i>Genome Research</i> , 2021, 31, 2225-2235.	5.5	15
17	HMPDACC: a Human Microbiome Project Multi-omic data resource. <i>Nucleic Acids Research</i> , 2021, 49, D734-D742.	14.5	13
18	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

#	ARTICLE	IF	CITATIONS
19	Deep and Wide: Comparative Genomics of <i>Chlamydia</i> . , 0, , 27-50.		2
20	TwinBLAST: When Two Is Better than One. Microbiology Resource Announcements, 2019, 8, .	0.6	1
21	Title is missing!. , 2020, 14, e0008781.		0
22	Title is missing!. , 2020, 14, e0008781.		0
23	Title is missing!. , 2020, 14, e0008781.		0
24	Title is missing!. , 2020, 14, e0008781.		0