

C Titus Brown

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

24,452
citations

66343

42
h-index

46799

89
g-index

121
all docs

121
docs citations

121
times ranked

31551
citing authors

#	ARTICLE	IF	CITATIONS
1	MAGs achieve lineage resolution. <i>Nature Microbiology</i> , 2022, 7, 193-194.	13.3	3
2	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
3	Microbial metabolites in the marine carbon cycle. <i>Nature Microbiology</i> , 2022, 7, 508-523.	13.3	71
4	Draft Genome Sequence of the Free-Living, Iridescent Bacterium <i>Tenacibaculum mesophilum</i> Strain ECR. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
5	Streamlining data-intensive biology with workflow systems. <i>GigaScience</i> , 2021, 10, .	6.4	32
6	MQF and buffered MQF: quotient filters for efficient storage of k-mers with their counts and metadata. <i>BMC Bioinformatics</i> , 2021, 22, 71.	2.6	3
7	The Degenerate Tale of Ascidian Tails. <i>Integrative and Comparative Biology</i> , 2021, 61, 358-369.	2.0	7
8	Editorial: Curriculum Applications in Microbiology: Bioinformatics in the Classroom. <i>Frontiers in Microbiology</i> , 2021, 12, 705233.	3.5	1
9	Comparative Immunogenomics of Canine Natural Killer Cells as Immunotherapy Target. <i>Frontiers in Immunology</i> , 2021, 12, 670309.	4.8	11
10	Charting Shifts in <i>Saccharomyces cerevisiae</i> Gene Expression across Asynchronous Time Trajectories with Diffusion Maps. <i>MBio</i> , 2021, 12, e0234521.	4.1	1
11	Genomic and phenotypic analyses of six offspring of a genome-edited hornless bull. <i>Nature Biotechnology</i> , 2020, 38, 225-232.	17.5	69
12	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage. <i>PLoS ONE</i> , 2020, 15, e0239677.	2.5	13
13	A Missense Variant in <i>ALDH5A1</i> Associated with Canine Succinic Semialdehyde Dehydrogenase Deficiency (SSADHD) in the Saluki Dog. <i>Genes</i> , 2020, 11, 1033.	2.4	3
14	A phylogenetically novel cyanobacterium most closely related to <i>Gloeobacter</i> . <i>ISME Journal</i> , 2020, 14, 2142-2152.	9.8	45
15	Draft genome assemblies using sequencing reads from Oxford Nanopore Technology and Illumina platforms for four species of North American <i>Fundulus</i> killifish. <i>GigaScience</i> , 2020, 9, .	6.4	15
16	Exploring neighborhoods in large metagenome assembly graphs using spacegraphcats reveals hidden sequence diversity. <i>Genome Biology</i> , 2020, 21, 164.	8.8	32
17	Whole genome sequencing for mutation discovery in a single case of lysosomal storage disease (MPS) Tj ETQq1 1 0,784314 rgBT /Overl 3.3	3.3	7
18	Kevlar: A Mapping-Free Framework for Accurate Discovery of De Novo Variants. <i>IScience</i> , 2019, 18, 28-36.	4.1	20

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19	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
20	Sequencing data discovery with MetaSeek. <i>Bioinformatics</i> , 2019, 35, 4857-4859.	4.1	4
21	Keeping it light: (re)analyzing community-wide datasets without major infrastructure. <i>GigaScience</i> , 2019, 8, .	6.4	2
22	FAIRshake: Toolkit to Evaluate the FAIRness of Research Digital Resources. <i>Cell Systems</i> , 2019, 9, 417-421.	6.2	33
23	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. <i>Frontiers in Genetics</i> , 2019, 10, 957.	2.3	8
24	Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. <i>GigaScience</i> , 2019, 8, .	6.4	61
25	Large-scale sequence comparisons with sourmash. <i>F1000Research</i> , 2019, 8, 1006.	1.6	130
26	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. <i>Nucleic Acids Research</i> , 2018, 46, D718-D725.	14.5	90
27	Whole genome variant association across 100 dogs identifies a frame shift mutation in <i>DISHEVELLED 2</i> which contributes to Robinow-like syndrome in Bulldogs and related screw tail dog breeds. <i>PLoS Genetics</i> , 2018, 14, e1007850.	3.5	61
28	A Missense Mutation in the Vacuolar Protein Sorting 11 (<i>VPS11</i>) Gene Is Associated with Neuroaxonal Dystrophy in Rottweiler Dogs. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2773-2780.	1.8	19
29	The principles of tomorrow's university. <i>F1000Research</i> , 2018, 7, 1926.	1.6	6
30	Centromere location in <i>Arabidopsis</i> is unaltered by extreme divergence in CENH3 protein sequence. <i>Genome Research</i> , 2017, 27, 471-478.	5.5	58
31	METHODS TO ENSURE THE REPRODUCIBILITY OF BIOMEDICAL RESEARCH. , 2017, 22, 117-119.		5
32	<i>FGF4</i> retrogene on CFA12 is responsible for chondrodystrophy and intervertebral disc disease in dogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11476-11481.	7.1	92
33	Lessons on doing science from my father, Gerry Brown. , 2017, , 27-31.		0
34	Tissue resolved, gene structure refined equine transcriptome. <i>BMC Genomics</i> , 2017, 18, 103.	2.8	22
35	Central nervous system transcriptome of <i>Biomphalaria alexandrina</i> , an intermediate host for schistosomiasis. <i>BMC Research Notes</i> , 2017, 10, 729.	1.4	11
36	Draft genome of tule elk <i>Cervus canadensis</i> nannodes. <i>F1000Research</i> , 2017, 6, 1691.	1.6	7

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37	Draft genome of tule elk <i>Cervus elaphus nannodes</i> . F1000Research, 2017, 6, 1691.	1.6	8
38	khmer release v2.1: software for biological sequence analysis. Journal of Open Source Software, 2017, 2, 272.	4.6	4
39	Sustainable computational science: the ReScience initiative. PeerJ Computer Science, 2017, 3, e142.	4.5	86
40	Transcriptome of the Caribbean stony coral <i>Porites astreoides</i> from three developmental stages. GigaScience, 2016, 5, 33.	6.4	21
41	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. Applied and Environmental Microbiology, 2016, 82, 157-166.	3.1	73
42	Haplotype-Phased Synthetic Long Reads from Short-Read Sequencing. PLoS ONE, 2016, 11, e0147229.	2.5	29
43	sourmash: a library for MinHash sketching of DNA. Journal of Open Source Software, 2016, 1, 27.	4.6	230
44	Walking the Talk: Adopting and Adapting Sustainable Scientific Software Development processes in a Small Biology Lab. Journal of Open Research Software, 2016, 4, .	5.9	5
45	Channeling Community Contributions to Scientific Software: A Sprint Experience. Journal of Open Research Software, 2016, 4, .	5.9	4
46	Hsp90 and hepatobiliary transformation during sea lamprey metamorphosis. BMC Developmental Biology, 2015, 15, 47.	2.1	7
47	Xander: employing a novel method for efficient gene-targeted metagenomic assembly. Microbiome, 2015, 3, 32.	11.1	83
48	Differentially-Expressed Pseudogenes in HIV-1 Infection. Viruses, 2015, 7, 5191-5205.	3.3	12
49	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	1.1	97
50	Strain recovery from metagenomes. Nature Biotechnology, 2015, 33, 1041-1043.	17.5	28
51	The khmer software package: enabling efficient nucleotide sequence analysis. F1000Research, 2015, 4, 900.	1.6	362
52	These Are Not the K-mers You Are Looking For: Efficient Online K-mer Counting Using a Probabilistic Data Structure. PLoS ONE, 2014, 9, e101271.	2.5	85
53	Tackling soil diversity with the assembly of large, complex metagenomes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4904-4909.	7.1	305
54	Genomic versatility and functional variation between two dominant heterotrophic symbionts of deep-sea <i>Osedax</i> worms. ISME Journal, 2014, 8, 908-924.	9.8	32

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55	Phylogeny and phylogeography of functional genes shared among seven terrestrial subsurface metagenomes reveal N-cycling and microbial evolutionary relationships. <i>Frontiers in Microbiology</i> , 2014, 5, 531.	3.5	87
56	Ribosomal Database Project: data and tools for high throughput rRNA analysis. <i>Nucleic Acids Research</i> , 2014, 42, D633-D642.	14.5	3,768
57	Best Practices for Scientific Computing. <i>PLoS Biology</i> , 2014, 12, e1001745.	5.6	427
58	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	28.9	64
59	Divergent mechanisms regulate conserved cardiopharyngeal development and gene expression in distantly related ascidians. <i>ELife</i> , 2014, 3, e03728.	6.0	69
60	The sea lamprey has a primordial accessory olfactory system. <i>BMC Evolutionary Biology</i> , 2013, 13, 172.	3.2	25
61	Sequencing of the sea lamprey (<i>Petromyzon marinus</i>) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013, 45, 415-421.	21.4	588
62	Integrated Analyses of Genome-Wide DNA Occupancy and Expression Profiling Identify Key Genes and Pathways Involved in Cellular Transformation by a Marek's Disease Virus Oncoprotein. <i>Meq. Journal of Virology</i> , 2013, 87, 9016-9029.	3.4	24
63	FunGene: the functional gene pipeline and repository. <i>Frontiers in Microbiology</i> , 2013, 4, 291.	3.5	518
64	A thermogenic secondary sexual character in male sea lamprey. <i>Journal of Experimental Biology</i> , 2013, 216, 2702-2712.	1.7	12
65	Space-efficient read indexing and retrieval based on compressed de Bruijn graphs. , 2013, , .		0
66	Workshop: Graph compression approaches in assembly. , 2012, , .		0
67	Draft Genome Sequences of Two <i>Campylobacter jejuni</i> Clinical Isolates, NW and D2600. <i>Journal of Bacteriology</i> , 2012, 194, 5707-5708.	2.2	1
68	Cephalopod genomics: A plan of strategies and organization. <i>Standards in Genomic Sciences</i> , 2012, 7, 175-188.	1.5	53
69	Scaling metagenome sequence assembly with probabilistic de Bruijn graphs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13272-13277.	7.1	219
70	Changing computational research. The challenges ahead. <i>Source Code for Biology and Medicine</i> , 2012, 7, 2.	1.7	8
71	Standing Genetic Variation in Contingency Loci Drives the Rapid Adaptation of <i>Campylobacter jejuni</i> to a Novel Host. <i>PLoS ONE</i> , 2011, 6, e16399.	2.5	97
72	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. <i>Standards in Genomic Sciences</i> , 2010, 3, 243-248.	1.5	228

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73	Diverse syntrophic partnerships from deep-sea methane vents revealed by direct cell capture and metagenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7052-7057.	7.1	261
74	Chapter 18 Computational Approaches to Finding and Analyzing cis-Regulatory Elements. <i>Methods in Cell Biology</i> , 2008, 87, 337-365.	1.1	9
75	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006, 314, 941-952.	12.6	1,018
76	Gene families encoding transcription factors expressed in early development of <i>Strongylocentrotus purpuratus</i> . <i>Developmental Biology</i> , 2006, 300, 90-107.	2.0	138
77	Identification and characterization of homeobox transcription factor genes in <i>Strongylocentrotus purpuratus</i> , and their expression in embryonic development. <i>Developmental Biology</i> , 2006, 300, 74-89.	2.0	123
78	Sea urchin Forkhead gene family: Phylogeny and embryonic expression. <i>Developmental Biology</i> , 2006, 300, 49-62.	2.0	192
79	High regulatory gene use in sea urchin embryogenesis: Implications for bilaterian development and evolution. <i>Developmental Biology</i> , 2006, 300, 27-34.	2.0	57
80	Anaerobic regulation by an atypical Arc system in <i>Shewanella oneidensis</i> . <i>Molecular Microbiology</i> , 2005, 56, 1347-1357.	2.5	62
81	Paircomp, FamilyRelationsII and Cartwheel: tools for interspecific sequence comparison. <i>BMC Bioinformatics</i> , 2005, 6, 70.	2.6	32
82	The Earthshine Project: update on photometric and spectroscopic measurements. <i>Advances in Space Research</i> , 2004, 34, 288-292.	2.6	11
83	The earthshine spectrum. <i>Advances in Space Research</i> , 2004, 34, 293-296.	2.6	8
84	Genomic Resources for the Study of Sea Urchin Development. <i>Methods in Cell Biology</i> , 2004, 74, 733-757.	1.1	12
85	A Genomic Regulatory Network for Development. <i>Science</i> , 2002, 295, 1669-1678.	12.6	1,399
86	Patchy Interspecific Sequence Similarities Efficiently Identify Positive cis-Regulatory Elements in the Sea Urchin. <i>Developmental Biology</i> , 2002, 246, 148-161.	2.0	92
87	New Computational Approaches for Analysis of cis-Regulatory Networks. <i>Developmental Biology</i> , 2002, 246, 86-102.	2.0	103
88	A Provisional Regulatory Gene Network for Specification of Endomesoderm in the Sea Urchin Embryo. <i>Developmental Biology</i> , 2002, 246, 162-190.	2.0	319
89	Earthshine observations of the Earth's reflectance. <i>Geophysical Research Letters</i> , 2001, 28, 1671-1674.	4.0	124
90	Visualizing Evolutionary Activity of Genotypes. <i>Artificial Life</i> , 1999, 5, 17-35.	1.3	23

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91	Abundance-distributions in artificial life and stochastic models: "œage and area" revisited. Lecture Notes in Computer Science, 1995, , 503-514.	1.3	3