C Titus Brown

List of Publications by Year
in descending order

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	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
2	Ribosomal Database Project: data and tools for high throughput rRNA analysis. Nucleic Acids Research, 2014, 42, D633-D642.	14.5	3,768
3	A Genomic Regulatory Network for Development. Science, 2002, 295, 1669-1678.	12.6	1,399
4	The Genome of the Sea Urchin *Strongylocentrotus purpuratus*. Science, 2006, 314, 941-952.	12.6	1,018
5	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. Nature Genetics, 2013, 45, 415-421.	21.4	588
6	FunGene: the functional gene pipeline and repository. Frontiers in Microbiology, 2013, 4, 291.	3.5	518
7	Best Practices for Scientific Computing. PLoS Biology, 2014, 12, e1001745.	5.6	427
8	The khmer software package: enabling efficient nucleotide sequence analysis. F1000Research, 2015, 4, 900.	1.6	362
9	A Provisional Regulatory Gene Network for Specification of Endomesoderm in the Sea Urchin Embryo. Developmental Biology, 2002, 246, 162-190.	2.0	319
10	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
11	Diverse syntrophic partnerships from deep-sea methane vents revealed by direct cell capture and metagenomics. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7052-7057.	7.1	261
12	sourmash: a library for MinHash sketching of DNA. Journal of Open Source Software, 2016, 1, 27.	4.6	230
13	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. Standards in Genomic Sciences, 2010, 3, 243-248.	1.5	228
14	Scaling metagenome sequence assembly with probabilistic de Bruijn graphs. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13272-13277.	7.1	219
15	Sea urchin Forkhead gene family: Phylogeny and embryonic expression. Developmental Biology, 2006, 300, 49-62.	2.0	192
16	Gene families encoding transcription factors expressed in early development of Strongylocentrotus purpuratus. Developmental Biology, 2006, 300, 90-107.	2.0	138
17	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
18	Large-scale sequence comparisons with sourmash. F1000Research, 2019, 8, 1006.	1.6	130

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19	Earthshine observations of the Earth's reflectance. Geophysical Research Letters, 2001, 28, 1671-1674.	4.0	124
20	Identification and characterization of homeobox transcription factor genes in Strongylocentrotus purpuratus, and their expression in embryonic development. Developmental Biology, 2006, 300, 74-89.	2.0	123
21	New Computational Approaches for Analysis of cis-Regulatory Networks. Developmental Biology, 2002, 246, 86-102.	2.0	103
22	Standing Genetic Variation in Contingency Loci Drives the Rapid Adaptation of Campylobacter jejuni to a Novel Host. PLoS ONE, 2011, 6, e16399.	2.5	97
23	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	1.1	97
24	Patchy Interspecific Sequence Similarities Efficiently Identify Positive cis-Regulatory Elements in the Sea Urchin. Developmental Biology, 2002, 246, 148-161.	2.0	92
25	<i>FGF4</i> retrogene on CFA12 is responsible for chondrodystrophy and intervertebral disc disease in dogs. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11476-11481.	7.1	92
26	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. Nucleic Acids Research, 2018, 46, D718-D725.	14.5	90
27	Phylogeny and phylogeography of functional genes shared among seven terrestrial subsurface metagenomes reveal N-cycling and microbial evolutionary relationships. Frontiers in Microbiology, 2014, 5, 531.	3.5	87
28	Sustainable computational science: the ReScience initiative. PeerJ Computer Science, 2017, 3, e142.	4.5	86
29	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
30	Xander: employing a novel method for efficient gene-targeted metagenomic assembly. Microbiome, 2015, 3, 32.	11.1	83
31	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. Applied and Environmental Microbiology, 2016, 82, 157-166.	3.1	73
32	Microbial metabolites in the marine carbon cycle. Nature Microbiology, 2022, 7, 508-523.	13.3	71
33	Genomic and phenotypic analyses of six offspring of a genome-edited hornless bull. Nature Biotechnology, 2020, 38, 225-232.	17.5	69
34	Divergent mechanisms regulate conserved cardiopharyngeal development and gene expression in distantly related ascidians. ELife, 2014, 3, e03728.	6.0	69
35	Advancing the Microbiome Research Community. Cell, 2014, 159, 227-230.	28.9	64
36	Anaerobic regulation by an atypical Arc system in Shewanella oneidensis. Molecular Microbiology, 2005, 56, 1347-1357.	2.5	62

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37	Whole genome variant association across 100 dogs identifies a frame shift mutation in DISHEVELLED 2 which contributes to Robinow-like syndrome in Bulldogs and related screw tail dog breeds. PLoS Genetics, 2018, 14, e1007850.	3.5	61
38	Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. GigaScience, 2019, 8, .	6.4	61
39	Centromere location in *Arabidopsis* is unaltered by extreme divergence in CENH3 protein sequence. Genome Research, 2017, 27, 471-478.	5.5	58
40	High regulatory gene use in sea urchin embryogenesis: Implications for bilaterian development and evolution. Developmental Biology, 2006, 300, 27-34.	2.0	57
41	Cephalopod genomics: A plan of strategies and organization. Standards in Genomic Sciences, 2012, 7, 175-188.	1.5	53
42	A phylogenetically novel cyanobacterium most closely related to *Gloeobacter*. ISME Journal, 2020, 14, 2142-2152.	9.8	45
43	FAIRshake: Toolkit to Evaluate the FAIRness of Research Digital Resources. Cell Systems, 2019, 9, 417-421.	6.2	33
44	Paircomp, FamilyRelationsII and Cartwheel: tools for interspecific sequence comparison. BMC Bioinformatics, 2005, 6, 70.	2.6	32
45	Genomic versatility and functional variation between two dominant heterotrophic symbionts of deep-sea *Osedax* worms. ISME Journal, 2014, 8, 908-924.	9.8	32
46	Exploring neighborhoods in large metagenome assembly graphs using spacegraphcats reveals hidden sequence diversity. Genome Biology, 2020, 21, 164.	8.8	32
47	Streamlining data-intensive biology with workflow systems. GigaScience, 2021, 10, .	6.4	32
48	Haplotype-Phased Synthetic Long Reads from Short-Read Sequencing. PLoS ONE, 2016, 11, e0147229.	2.5	29
49	Strain recovery from metagenomes. Nature Biotechnology, 2015, 33, 1041-1043.	17.5	28
50	The sea lamprey has a primordial accessory olfactory system. BMC Evolutionary Biology, 2013, 13, 172.	3.2	25
51	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, Meq. Journal of Virology, 2013, 87, 9016-9029.	3.4	24
52	Visualizing Evolutionary Activity of Genotypes. Artificial Life, 1999, 5, 17-35.	1.3	23
53	Tissue resolved, gene structure refined equine transcriptome. BMC Genomics, 2017, 18, 103.	2.8	22
54	Transcriptome of the Caribbean stony coral Porites astreoides from three developmental stages. GigaScience, 2016, 5, 33.	6.4	21

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55	Kevlar: A Mapping-Free Framework for Accurate Discovery of De Novo Variants. IScience, 2019, 18, 28-36.	4.1	20
56	A Missense Mutation in the Vacuolar Protein Sorting 11 (*VPS11*) Gene Is Associated with Neuroaxonal Dystrophy in Rottweiler Dogs. G3: Genes, Genomes, Genetics, 2018, 8, 2773-2780.	1.8	19
57	Draft genome assemblies using sequencing reads from Oxford Nanopore Technology and Illumina platforms for four species of North American Fundulus killifish. GigaScience, 2020, 9, .	6.4	15
58	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage. PLoS ONE, 2020, 15, e0239677.	2.5	13
59	Genomic Resources for the Study of Sea Urchin Development. Methods in Cell Biology, 2004, 74, 733-757.	1.1	12
60	A thermogenic secondary sexual character in male sea lamprey. Journal of Experimental Biology, 2013, 216, 2702-2712.	1.7	12
61	Differentially-Expressed Pseudogenes in HIV-1 Infection. Viruses, 2015, 7, 5191-5205.	3.3	12
62	The Earthshine Project: update on photometric and spectroscopic measurements. Advances in Space Research, 2004, 34, 288-292.	2.6	11
63	Central nervous system transcriptome of Biomphalaria alexandrina, an intermediate host for schistosomiasis. BMC Research Notes, 2017, 10, 729.	1.4	11
64	Comparative Immunogenomics of Canine Natural Killer Cells as Immunotherapy Target. Frontiers in Immunology, 2021, 12, 670309.	4.8	11
65	Chapter 18 Computational Approaches to Finding and Analyzing cis€Regulatory Elements. Methods in Cell Biology, 2008, 87, 337-365.	1.1	9
66	The earthshine spectrum. Advances in Space Research, 2004, 34, 293-296.	2.6	8
67	Changing computational research. The challenges ahead. Source Code for Biology and Medicine, 2012, 7, 2.	1.7	8
68	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. Frontiers in Genetics, 2019, 10, 957.	2.3	8
69	Draft genome of tule elk Cervus elaphus nannodes. F1000Research, 2017, 6, 1691.	1.6	8
70	Hsp90 and hepatobiliary transformation during sea lamprey metamorphosis. BMC Developmental Biology, 2015, 15, 47.	2.1	7
71	Draft genome of tule elk Cervus canadensis nannodes. F1000Research, 2017, 6, 1691.	1.6	7
72	Whole genome sequencing for mutation discovery in a single case of lysosomal storage disease (MPS) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.3	7

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73	The Degenerate Tale of Ascidian Tails. Integrative and Comparative Biology, 2021, 61, 358-369.	2.0	7
74	The principles of tomorrow's university. F1000Research, 2018, 7, 1926.	1.6	6
75	METHODS TO ENSURE THE REPRODUCIBILITY OF BIOMEDICAL RESEARCH. , 2017, 22, 117-119.		5
76	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
77	Sequencing data discovery with MetaSeek. Bioinformatics, 2019, 35, 4857-4859.	4.1	4
78	khmer release v2.1: software for biological sequence analysis. Journal of Open Source Software, 2017, 2, 272.	4.6	4
79	Channeling Community Contributions to Scientific Software: A Sprint Experience. Journal of Open Research Software, 2016, 4, .	5.9	4
80	A Missense Variant in ALDH5A1 Associated with Canine Succinic Semialdehyde Dehydrogenase Deficiency (SSADHD) in the Saluki Dog. Genes, 2020, 11, 1033.	2.4	3
81	MQF and buffered MQF: quotient filters for efficient storage of k-mers with their counts and metadata. BMC Bioinformatics, 2021, 22, 71.	2.6	3
82	Abundance-distributions in artificial life and stochastic models: â€œage and areaâ€•revisited. Lecture Notes in Computer Science, 1995, , 503-514.	1.3	3
83	MAGs achieve lineage resolution. Nature Microbiology, 2022, 7, 193-194.	13.3	3
84	Keeping it light: (re)analyzing community-wide datasets without major infrastructure. GigaScience, 2019, 8, .	6.4	2
85	Draft Genome Sequences of Two Campylobacter jejuni Clinical Isolates, NW and D2600. Journal of Bacteriology, 2012, 194, 5707-5708.	2.2	1
86	Editorial: Curriculum Applications in Microbiology: Bioinformatics in the Classroom. Frontiers in Microbiology, 2021, 12, 705233.	3.5	1
87	Charting Shifts in Saccharomyces cerevisiae Gene Expression across Asynchronous Time Trajectories with Diffusion Maps. MBio, 2021, 12, e0234521.	4.1	1
88	Workshop: Graph compression approaches in assembly. , 2012, , .		0
89	Space-efficient read indexing and retrieval based on compressed de Bruijn graphs. , 2013, , .		0
90	Lessons on doing science from my father, Gerry Brown. , 2017, , 27-31.		0

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91	Draft Genome Sequence of the Free-Living, Iridescent Bacterium Tenacibaculum mesophilum Strain ECR. Microbiology Resource Announcements, 2021, 10, .	0.6	0