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List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

46,739
citations

46918

47
h-index

62479

80
g-index

98
all docs

98
docs citations

98
times ranked

55802
citing authors

#	ARTICLE	IF	CITATIONS
1	Using AnnoTree to Get More Assignments, Faster, in DIAMOND+MEGAN Microbiome Analysis. <i>MSystems</i> , 2022, 7, e0140821.	1.7	11
2	Interactive analysis of biosurfactants in fruit-waste fermentation samples using BioSurfDB and MEGAN. <i>Scientific Reports</i> , 2022, 12, 7769.	1.6	3
3	On the Application of Advanced Machine Learning Methods to Analyze Enhanced, Multimodal Data from Persons Infected with COVID-19. <i>Computation</i> , 2021, 9, 4.	1.0	10
4	Recovery of complete genomes and non-chromosomal replicons from activated sludge enrichment microbial communities with long read metagenome sequencing. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 23.	2.9	29
5	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. <i>Current Protocols</i> , 2021, 1, e59.	1.3	55
6	Interplay of Various Evolutionary Modes in Genome Diversification and Adaptive Evolution of the Family Sulfolobaceae. <i>Frontiers in Microbiology</i> , 2021, 12, 639995.	1.5	2
7	Microbial Phylogenetic Context Using Phylogenetic Outlines. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
8	Tegula “exploring a galaxy of two-dimensional periodic tilings. <i>Computer Aided Geometric Design</i> , 2021, 90, 102027.	0.5	2
9	Normalising phylogenetic networks. <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107215.	1.2	6
10	MAIRA- real-time taxonomic and functional analysis of long reads on a laptop. <i>BMC Bioinformatics</i> , 2020, 21, 390.	1.2	2
11	The Isolate <i>Caproiciproducens</i> sp. 7D4C2 Produces n-Caproate at Mildly Acidic Conditions From Hexoses: Genome and rBOX Comparison With Related Strains and Chain-Elongating Bacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 594524.	1.5	33
12	Phage tail-like particles are versatile bacterial nanomachines “ A mini-review. <i>Journal of Advanced Research</i> , 2019, 19, 75-84.	4.4	42
13	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. <i>Methods in Molecular Biology</i> , 2019, 1910, 591-604.	0.4	23
14	Enriched Environmental Conditions Modify the Gut Microbiome Composition and Fecal Markers of Inflammation in Parkinson’s Disease. <i>Frontiers in Neuroscience</i> , 2019, 13, 1032.	1.4	17
15	Annotated bacterial chromosomes from frame-shift-corrected long-read metagenomic data. <i>Microbiome</i> , 2019, 7, 61.	4.9	69
16	Autumn Algorithm”Computation of Hybridization Networks for Realistic Phylogenetic Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 398-410.	1.9	11
17	Genome Sequence of <i>Galleria mellonella</i> (Greater Wax Moth). <i>Genome Announcements</i> , 2018, 6, .	0.8	76
18	<i>Salmonella enterica</i> genomes from victims of a major sixteenth-century epidemic in Mexico. <i>Nature Ecology and Evolution</i> , 2018, 2, 520-528.	3.4	218

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19	MEGAN-LR: new algorithms allow accurate binning and easy interactive exploration of metagenomic long reads and contigs. <i>Biology Direct</i> , 2018, 13, 6.	1.9	141
20	Intestinal Dysbiosis, Barrier Dysfunction, and Bacterial Translocation Account for CKD-Related Systemic Inflammation. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 76-83.	3.0	196
21	A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. <i>Journal of Biotechnology</i> , 2017, 250, 45-50.	1.9	1
22	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. <i>Microbiome</i> , 2017, 5, 11.	4.9	31
23	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. <i>Nature</i> , 2017, 544, 357-361.	13.7	398
24	The Antibiotic Resistant Target Seeker (ARTS), an exploration engine for antibiotic cluster prioritization and novel drug target discovery. <i>Nucleic Acids Research</i> , 2017, 45, W42-W48.	6.5	142
25	SILVA, RDP, Greengenes, NCBI and OTT – how do these taxonomies compare?. <i>BMC Genomics</i> , 2017, 18, 114.	1.2	327
26	Functional Analysis in Metagenomics Using MEGAN 6. , 2017, , 65-74.		12
27	Soil biochar amendment affects the diversity of nosZ transcripts: Implications for N ₂ O formation. <i>Scientific Reports</i> , 2017, 7, 3338.	1.6	55
28	Characterization of the Gut Microbial Community of Obese Patients Following a Weight-Loss Intervention Using Whole Metagenome Shotgun Sequencing. <i>PLoS ONE</i> , 2016, 11, e0149564.	1.1	229
29	Soil biochar amendment shapes the composition of N ₂ O-reducing microbial communities. <i>Science of the Total Environment</i> , 2016, 562, 379-390.	3.9	117
30	A metagenomic-based survey of microbial (de)halogenation potential in a German forest soil. <i>Scientific Reports</i> , 2016, 6, 28958.	1.6	51
31	RiboTagger: fast and unbiased 16S/18S profiling using whole community shotgun metagenomic or metatranscriptome surveys. <i>BMC Bioinformatics</i> , 2016, 17, 508.	1.2	22
32	Extensive Mobilome-Driven Genome Diversification in Mouse Gut-Associated <i>Bacteroides vulgatus</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1197-1207.	1.1	37
33	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004957.	1.5	1,500
34	Analysis of Domain Architecture and Phylogenetics of Family 2 Glycoside Hydrolases (GH2). <i>PLoS ONE</i> , 2016, 11, e0168035.	1.1	46
35	Effects of Surgical and Dietary Weight Loss Therapy for Obesity on Gut Microbiota Composition and Nutrient Absorption. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	252
36	Antibiotic Selection Pressure Determination through Sequence-Based Metagenomics. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7335-7345.	1.4	61

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37	Fast and sensitive protein alignment using DIAMOND. <i>Nature Methods</i> , 2015, 12, 59-60.	9.0	8,761
38	A poor man's BLASTX high-throughput metagenomic protein database search using PAUDA. <i>Bioinformatics</i> , 2014, 30, 38-39.	1.8	50
39	Endotoxicity of Lipopolysaccharide as a Determinant of T-Cell Mediated Colitis Induction in Mice. <i>Gastroenterology</i> , 2014, 146, 765-775.	0.6	86
40	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.	13.7	506
41	Microbial Community Analysis Using MEGAN. <i>Methods in Enzymology</i> , 2013, 531, 465-485.	0.4	178
42	Identifying a species tree subject to random lateral gene transfer. <i>Journal of Theoretical Biology</i> , 2013, 322, 81-93.	0.8	16
43	Fast computation of minimum hybridization networks. <i>Bioinformatics</i> , 2012, 28, 191-197.	1.8	56
44	Dendroscope 3: An Interactive Tool for Rooted Phylogenetic Trees and Networks. <i>Systematic Biology</i> , 2012, 61, 1061-1067.	2.7	1,438
45	CREST Classification Resources for Environmental Sequence Tags. <i>PLoS ONE</i> , 2012, 7, e49334.	1.1	255
46	Integrative analysis of environmental sequences using MEGAN4. <i>Genome Research</i> , 2011, 21, 1552-1560.	2.4	1,245
47	A Survey of Combinatorial Methods for Phylogenetic Networks. <i>Genome Biology and Evolution</i> , 2011, 3, 23-35.	1.1	165
48	Reference-guided assembly of four diverse <i>Arabidopsis thaliana</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10249-10254.	3.3	237
49	Tanglegrams for rooted phylogenetic trees and networks. <i>Bioinformatics</i> , 2011, 27, i248-i256.	1.8	86
50	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
51	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. <i>ISME Journal</i> , 2010, 4, 1236-1242.	4.4	43
52	Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. <i>Bioinformatics</i> , 2010, 26, i124-i131.	1.8	47
53	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009, 19, 213-220.	2.4	102
54	Computing galled networks from real data. <i>Bioinformatics</i> , 2009, 25, i85-i93.	1.8	56

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55	Drawing Rooted Phylogenetic Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 103-109.	1.9	12
56	MetaSim—A Sequencing Simulator for Genomics and Metagenomics. <i>PLoS ONE</i> , 2008, 3, e3373.	1.1	375
57	Improved Layout of Phylogenetic Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 472-479.	1.9	19
58	Summarizing Multiple Gene Trees Using Cluster Networks. <i>Lecture Notes in Computer Science</i> , 2008, , 296-305.	1.0	27
59	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. <i>PLoS ONE</i> , 2008, 3, e2527.	1.1	667
60	Filtered Z-Closure Supernetworks for Extracting and Visualizing Recurrent Signal from Incongruent Gene Trees. <i>Systematic Biology</i> , 2008, 57, 939-947.	2.7	24
61	Evolution of <i>Arabidopsis thaliana</i> microRNAs from random sequences. <i>Rna</i> , 2008, 14, 2455-2459.	1.6	133
62	Sequence and Expression Differences Underlie Functional Specialization of Arabidopsis MicroRNAs miR159 and miR319. <i>Developmental Cell</i> , 2007, 13, 115-125.	3.1	399
63	MEGAN analysis of metagenomic data. <i>Genome Research</i> , 2007, 17, 377-386.	2.4	2,764
64	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	6.0	689
65	Dendroscope: An interactive viewer for large phylogenetic trees. <i>BMC Bioinformatics</i> , 2007, 8, 460.	1.2	1,127
66	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. <i>Science</i> , 2006, 311, 392-394.	6.0	519
67	Application of Phylogenetic Networks in Evolutionary Studies. <i>Molecular Biology and Evolution</i> , 2006, 23, 254-267.	3.5	7,402
68	Specificity prediction of adenylation domains in nonribosomal peptide synthetases (NRPS) using transductive support vector machines (TSVMs). <i>Nucleic Acids Research</i> , 2005, 33, 5799-5808.	6.5	388
69	Whole-genome shotgun assembly and comparison of human genome assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1916-1921.	3.3	164
70	Comparative analysis of four Campylobacterales. <i>Nature Reviews Microbiology</i> , 2004, 2, 872-885.	13.6	95
71	Constructing splits graphs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004, 1, 109-115.	1.9	120
72	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. <i>Science</i> , 2002, 296, 1661-1671.	6.0	344

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73	The Orbifold Notation for Two-Dimensional Groups. <i>Structural Chemistry</i> , 2002, 13, 247-257.	1.0	41
74	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
75	How Molecules Evolve in Eubacteria. <i>Molecular Biology and Evolution</i> , 2000, 17, 835-838.	3.5	45
76	Systematic enumeration of crystalline networks. <i>Nature</i> , 1999, 400, 644-647.	13.7	284
77	Disk-Covering, a Fast-Converging Method for Phylogenetic Tree Reconstruction. <i>Journal of Computational Biology</i> , 1999, 6, 369-386.	0.8	136
78	Orbifold Triangulations and Crystallographic Groups. <i>Periodica Mathematica Hungarica</i> , 1997, 34, 29-55.	0.5	7
79	Two-dimensional groups, orbifolds and tilings. <i>Geometriae Dedicata</i> , 1996, 60, 89.	0.1	11
80	The generation and classification of tile-k-transitive tilings of the Euclidean plane, the sphere and the hyperbolic plane. <i>Geometriae Dedicata</i> , 1993, 47, 269-296.	0.1	52
81	On tilings of the plane. <i>Geometriae Dedicata</i> , 1987, 24, 295.	0.1	48