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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Using AnnoTree to Get More Assignments, Faster, in DIAMOND+MEGAN Microbiome Analysis. MSystems, 2022, 7, e0140821.	3.8	11
2	Interactive analysis of biosurfactants in fruit-waste fermentation samples using BioSurfDB and MEGAN. Scientific Reports, 2022, 12, 7769.	3.3	3
3	On the Application of Advanced Machine Learning Methods to Analyze Enhanced, Multimodal Data from Persons Infected with COVID-19. Computation, 2021, 9, 4.	2.0	10
4	Recovery of complete genomes and non-chromosomal replicons from activated sludge enrichment microbial communities with long read metagenome sequencing. Npj Biofilms and Microbiomes, 2021, 7, 23.	6.4	29
5	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. Current Protocols, 2021, 1, e59.	2.9	55
6	Interplay of Various Evolutionary Modes in Genome Diversification and Adaptive Evolution of the Family Sulfolobaceae. Frontiers in Microbiology, 2021, 12, 639995.	3.5	2
7	Microbial Phylogenetic Context Using Phylogenetic Outlines. Genome Biology and Evolution, 2021, 13, .	2.5	6
8	Tegula – exploring a galaxy of two-dimensional periodic tilings. Computer Aided Geometric Design, 2021, 90, 102027.	1.2	2
9	Normalising phylogenetic networks. Molecular Phylogenetics and Evolution, 2021, 163, 107215.	2.7	6
10	MAIRA- real-time taxonomic and functional analysis of long reads on a laptop. BMC Bioinformatics, 2020, 21, 390.	2.6	2
11	The Isolate Caproiciproducens sp. 7D4C2 Produces n-Caproate at Mildly Acidic Conditions From Hexoses: Genome and rBOX Comparison With Related Strains and Chain-Elongating Bacteria. Frontiers in Microbiology, 2020, 11, 594524.	3.5	33
12	Phage tail-like particles are versatile bacterial nanomachines – A mini-review. Journal of Advanced Research, 2019, 19, 75-84.	9.5	42
13	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. Methods in Molecular Biology, 2019, 1910, 591-604.	0.9	23
14	Enriched Environmental Conditions Modify the Gut Microbiome Composition and Fecal Markers of Inflammation in Parkinson's Disease. Frontiers in Neuroscience, 2019, 13, 1032.	2.8	17
15	Annotated bacterial chromosomes from frame-shift-corrected long-read metagenomic data. Microbiome, 2019, 7, 61.	11.1	69
16	Autumn Algorithm—Computation of Hybridization Networks for Realistic Phylogenetic Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 398-410.	3.0	11
17	Genome Sequence of <i>Galleria mellonella</i> (Greater Wax Moth). Genome Announcements, 2018, 6, .	0.8	76
18	Salmonella enterica genomes from victims of a major sixteenth-century epidemic in Mexico. Nature Ecology and Evolution, 2018, 2, 520-528.	7.8	218

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19	MEGAN-LR: new algorithms allow accurate binning and easy interactive exploration of metagenomic long reads and contigs. Biology Direct, 2018, 13, 6.	4.6	141
20	Intestinal Dysbiosis, Barrier Dysfunction, and Bacterial Translocation Account for CKD–Related Systemic Inflammation. Journal of the American Society of Nephrology: JASN, 2017, 28, 76-83.	6.1	196
21	A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. Journal of Biotechnology, 2017, 250, 45-50.	3.8	1
22	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. Microbiome, 2017, 5, 11.	11.1	31
23	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. Nature, 2017, 544, 357-361.	27.8	398
24	The Antibiotic Resistant Target Seeker (ARTS), an exploration engine for antibiotic cluster prioritization and novel drug target discovery. Nucleic Acids Research, 2017, 45, W42-W48.	14.5	142
25	SILVA, RDP, Greengenes, NCBI and OTT — how do these taxonomies compare?. BMC Genomics, 2017, 18, 114.	2.8	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 N2O formation. Scientific Reports, 2017, 7, 3338.	3.3	55
28	Characterization of the Gut Microbial Community of Obese Patients Following a Weight-Loss Intervention Using Whole Metagenome Shotgun Sequencing. PLoS ONE, 2016, 11, e0149564.	2.5	229
29	Soil biochar amendment shapes the composition of N2O-reducing microbial communities. Science of the Total Environment, 2016, 562, 379-390.	8.0	117
30	A metagenomic-based survey of microbial (de)halogenation potential in a German forest soil. Scientific Reports, 2016, 6, 28958.	3.3	51
31	RiboTagger: fast and unbiased 16S/18S profiling using whole community shotgun metagenomic or metatranscriptome surveys. BMC Bioinformatics, 2016, 17, 508.	2.6	22
32	Extensive Mobilome-Driven Genome Diversification in Mouse Gut-Associated <i>Bacteroides vulgatus</i> mpk. Genome Biology and Evolution, 2016, 8, 1197-1207.	2.5	37
33	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. PLoS Computational Biology, 2016, 12, e1004957.	3.2	1,500
34	Analysis of Domain Architecture and Phylogenetics of Family 2 Glycoside Hydrolases (GH2). PLoS ONE, 2016, 11, e0168035.	2.5	46
35	Effects of Surgical and Dietary Weight Loss Therapy for Obesity on Gut Microbiota Composition and Nutrient Absorption. BioMed Research International, 2015, 2015, 1-12.	1.9	252
36	Antibiotic Selection Pressure Determination through Sequence-Based Metagenomics. Antimicrobial Agents and Chemotherapy, 2015, 59, 7335-7345.	3.2	61

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37	Fast and sensitive protein alignment using DIAMOND. Nature Methods, 2015, 12, 59-60.	19.0	8,761
38	A poor man's BLASTX—high-throughput metagenomic protein database search using PAUDA. Bioinformatics, 2014, 30, 38-39.	4.1	50
39	Endotoxicity of Lipopolysaccharide as a Determinant of T-Cellâ^'Mediated Colitis Induction in Mice. Gastroenterology, 2014, 146, 765-775.	1.3	86
40	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. Nature, 2014, 514, 494-497.	27.8	506
41	Microbial Community Analysis Using MEGAN. Methods in Enzymology, 2013, 531, 465-485.	1.0	178
42	Identifying a species tree subject to random lateral gene transfer. Journal of Theoretical Biology, 2013, 322, 81-93.	1.7	16
43	Fast computation of minimum hybridization networks. Bioinformatics, 2012, 28, 191-197.	4.1	56
44	Dendroscope 3: An Interactive Tool for Rooted Phylogenetic Trees and Networks. Systematic Biology, 2012, 61, 1061-1067.	5.6	1,438
45	CREST – Classification Resources for Environmental Sequence Tags. PLoS ONE, 2012, 7, e49334.	2.5	255
46	Integrative analysis of environmental sequences using MEGAN4. Genome Research, 2011, 21, 1552-1560.	5.5	1,245
47	A Survey of Combinatorial Methods for Phylogenetic Networks. Genome Biology and Evolution, 2011, 3, 23-35.	2.5	165
48	Reference-guided assembly of four diverse <i>Arabidopsis thaliana</i> genomes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10249-10254.	7.1	237
49	Tanglegrams for rooted phylogenetic trees and networks. Bioinformatics, 2011, 27, i248-i256.	4.1	86
50	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
51	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. ISME Journal, 2010, 4, 1236-1242.	9.8	43
52	Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. Bioinformatics, 2010, 26, i124-i131.	4.1	47
53	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). Genome Research, 2009, 19, 213-220.	5.5	102
54	Computing galled networks from real data. Bioinformatics, 2009, 25, i85-i93.	4.1	56

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55	Drawing Rooted Phylogenetic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 103-109.	3.0	12
56	MetaSim—A Sequencing Simulator for Genomics and Metagenomics. PLoS ONE, 2008, 3, e3373.	2.5	375
57	Improved Layout of Phylogenetic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 472-479.	3.0	19
58	Summarizing Multiple Gene Trees Using Cluster Networks. Lecture Notes in Computer Science, 2008, , 296-305.	1.3	27
59	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. PLoS ONE, 2008, 3, e2527.	2.5	667
60	Filtered Z-Closure Supernetworks for Extracting and Visualizing Recurrent Signal from Incongruent Gene Trees. Systematic Biology, 2008, 57, 939-947.	5.6	24
61	Evolution of <i>Arabidopsis thaliana</i> microRNAs from random sequences. Rna, 2008, 14, 2455-2459.	3.5	133
62	Sequence and Expression Differences Underlie Functional Specialization of Arabidopsis MicroRNAs miR159 and miR319. Developmental Cell, 2007, 13, 115-125.	7.0	399
63	MEGAN analysis of metagenomic data. Genome Research, 2007, 17, 377-386.	5.5	2,764
64	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . Science, 2007, 317, 338-342.	12.6	689
65	Dendroscope: An interactive viewer for large phylogenetic trees. BMC Bioinformatics, 2007, 8, 460.	2.6	1,127
66	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. Science, 2006, 311, 392-394.	12.6	519
67	Application of Phylogenetic Networks in Evolutionary Studies. Molecular Biology and Evolution, 2006, 23, 254-267.	8.9	7,402
68	Specificity prediction of adenylation domains in nonribosomal peptide synthetases (NRPS) using transductive support vector machines (TSVMs). Nucleic Acids Research, 2005, 33, 5799-5808.	14.5	388
69	Whole-genome shotgun assembly and comparison of human genome assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1916-1921.	7.1	164
70	Comparative analysis of four Campylobacterales. Nature Reviews Microbiology, 2004, 2, 872-885.	28.6	95
71	Constructing splits graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 109-115.	3.0	120
72	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	12.6	344

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73	The Orbifold Notation for Two-Dimensional Groups. Structural Chemistry, 2002, 13, 247-257.	2.0	41
74	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
75	How Molecules Evolve in Eubacteria. Molecular Biology and Evolution, 2000, 17, 835-838.	8.9	45
76	Systematic enumeration of crystalline networks. Nature, 1999, 400, 644-647.	27.8	284
77	Disk-Covering, a Fast-Converging Method for Phylogenetic Tree Reconstruction. Journal of Computational Biology, 1999, 6, 369-386.	1.6	136
78	Orbifold Triangulations and Crystallographic Groups. Periodica Mathematica Hungarica, 1997, 34, 29-55.	0.9	7
79	Two-dimensional groups, orbifolds and tilings. Geometriae Dedicata, 1996, 60, 89.	0.3	11
80	The generation and classification of tile-k-transitive tilings of the Euclidean plane, the sphere and the hyperbolic plane. Geometriae Dedicata, 1993, 47, 269-296.	0.3	52
81	On tilings of the plane. Geometriae Dedicata, 1987, 24, 295.	0.3	48