Daniel H Huson

List of Publications by Year
in descending order

81 papers	46,739 citations	47004 47 h-index	62593 80 g-index
98 all docs	98 docs citations	98 times ranked	55802 citing authors

#	Article	IF	Citations
1	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
2	Fast and sensitive protein alignment using DIAMOND. Nature Methods, 2015, 12, 59-60.	19.0	8,761
3	Application of Phylogenetic Networks in Evolutionary Studies. Molecular Biology and Evolution, 2006, 23, 254-267.	8.9	7,402
4	MEGAN analysis of metagenomic data. Genome Research, 2007, 17, 377-386.	5.5	2,764
5	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. PLoS Computational Biology, 2016, 12, e1004957.	3.2	1,500
6	Dendroscope 3: An Interactive Tool for Rooted Phylogenetic Trees and Networks. Systematic Biology, 2012, 61, 1061-1067.	5.6	1,438
7	Integrative analysis of environmental sequences using MEGAN4. Genome Research, 2011, 21, 1552-1560.	5.5	1,245
8	Dendroscope: An interactive viewer for large phylogenetic trees. BMC Bioinformatics, 2007, 8, 460.	2.6	1,127
9	Common Sequence Polymorphisms Shaping Genetic Diversity in *Arabidopsis thaliana*. Science, 2007, 317, 338-342.	12.6	689
10	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. PLoS ONE, 2008, 3, e2527.	2.5	667
11	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. Science, 2006, 311, 392-394.	12.6	519
12	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. Nature, 2014, 514, 494-497.	27.8	506
13	Sequence and Expression Differences Underlie Functional Specialization of Arabidopsis MicroRNAs miR159 and miR319. Developmental Cell, 2007, 13, 115-125.	7.0	399
14	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. Nature, 2017, 544, 357-361.	27.8	398
15	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
16	MetaSimâ€"A Sequencing Simulator for Genomics and Metagenomics. PLoS ONE, 2008, 3, e3373.	2.5	375
17	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	12.6	344
18	SILVA, RDP, Greengenes, NCBI and OTT â€" how do these taxonomies compare?. BMC Genomics, 2017, 18, 114.	2.8	327

#	ARTICLE	IF	CITATIONS
19	Systematic enumeration of crystalline networks. Nature, 1999, 400, 644-647.	27.8	284
20	CREST â€" Classification Resources for Environmental Sequence Tags. PLoS ONE, 2012, 7, e49334.	2.5	255
21	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
22	Reference-guided assembly of four diverse *Arabidopsis thaliana* genomes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10249-10254.	7.1	237
23	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
24	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
25	Salmonella enterica genomes from victims of a major sixteenth-century epidemic in Mexico. Nature Ecology and Evolution, 2018, 2, 520-528.	7.8	218
26	Intestinal Dysbiosis, Barrier Dysfunction, and Bacterial Translocation Account for CKDâ€"Related Systemic Inflammation. Journal of the American Society of Nephrology: JASN, 2017, 28, 76-83.	6.1	196
27	Microbial Community Analysis Using MEGAN. Methods in Enzymology, 2013, 531, 465-485.	1.0	178
28	A Survey of Combinatorial Methods for Phylogenetic Networks. Genome Biology and Evolution, 2011, 3, 23-35.	2.5	165
29	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
30	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
31	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
32	Disk-Covering, a Fast-Converging Method for Phylogenetic Tree Reconstruction. Journal of Computational Biology, 1999, 6, 369-386.	1.6	136
33	Evolution of *Arabidopsis thaliana* microRNAs from random sequences. Rna, 2008, 14, 2455-2459.	3.5	133
34	Constructing splits graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 109-115.	3.0	120
35	Soil biochar amendment shapes the composition of N2O-reducing microbial communities. Science of the Total Environment, 2016, 562, 379-390.	8.0	117
36	The mitochondrial genome sequence of the Tasmanian tiger (*Thylacinus cynocephalus*). Genome Research, 2009, 19, 213-220.	5.5	102

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37	Comparative analysis of four Campylobacterales. Nature Reviews Microbiology, 2004, 2, 872-885.	28.6	95
38	Tanglegrams for rooted phylogenetic trees and networks. Bioinformatics, 2011, 27, i248-i256.	4.1	86
39	Endotoxicity of Lipopolysaccharide as a Determinant of T-Cellâˆ'Mediated Colitis Induction in Mice. Gastroenterology, 2014, 146, 765-775.	1.3	86
40	Genome Sequence of <i>Galleria mellonella</i> (Greater Wax Moth). Genome Announcements, 2018, 6, .	0.8	76
41	Annotated bacterial chromosomes from frame-shift-corrected long-read metagenomic data. Microbiome, 2019, 7, 61.	11.1	69
42	Antibiotic Selection Pressure Determination through Sequence-Based Metagenomics. Antimicrobial Agents and Chemotherapy, 2015, 59, 7335-7345.	3.2	61
43	Computing galled networks from real data. Bioinformatics, 2009, 25, i85-i93.	4.1	56
44	Fast computation of minimum hybridization networks. Bioinformatics, 2012, 28, 191-197.	4.1	56
45	Soil biochar amendment affects the diversity of nosZ transcripts: Implications for N2O formation. Scientific Reports, 2017, 7, 3338.	3.3	55
46	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. Current Protocols, 2021, 1, e59.	2.9	55
47	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
48	A metagenomic-based survey of microbial (de)halogenation potential in a German forest soil. Scientific Reports, 2016, 6, 28958.	3.3	51
49	A poor manâ€™s BLASTXâ€"high-throughput metagenomic protein database search using PAUDA. Bioinformatics, 2014, 30, 38-39.	4.1	50
50	On tilings of the plane. Geometriae Dedicata, 1987, 24, 295.	0.3	48
51	Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. Bioinformatics, 2010, 26, i124-i131.	4.1	47
52	Analysis of Domain Architecture and Phylogenetics of Family 2 Glycoside Hydrolases (GH2). PLoS ONE, 2016, 11, e0168035.	2.5	46
53	How Molecules Evolve in Eubacteria. Molecular Biology and Evolution, 2000, 17, 835-838.	8.9	45
54	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. ISME Journal, 2010, 4, 1236-1242.	9.8	43

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55	Phage tail-like particles are versatile bacterial nanomachines â€" A mini-review. Journal of Advanced Research, 2019, 19, 75-84.	9.5	42
56	The Orbifold Notation for Two-Dimensional Groups. Structural Chemistry, 2002, 13, 247-257.	2.0	41
57	Extensive Mobilome-Driven Genome Diversification in Mouse Gut-Associated *Bacteroides vulgatus* mpk. Genome Biology and Evolution, 2016, 8, 1197-1207.	2.5	37
58	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
59	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. Microbiome, 2017, 5, 11.	11.1	31
60	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
61	Summarizing Multiple Gene Trees Using Cluster Networks. Lecture Notes in Computer Science, 2008, , 296-305.	1.3	27
62	Filtered Z-Closure Supernetworks for Extracting and Visualizing Recurrent Signal from Incongruent Gene Trees. Systematic Biology, 2008, 57, 939-947.	5.6	24
63	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. Methods in Molecular Biology, 2019, 1910, 591-604.	0.9	23
64	RiboTagger: fast and unbiased 16S/18S profiling using whole community shotgun metagenomic or metatranscriptome surveys. BMC Bioinformatics, 2016, 17, 508.	2.6	22
65	Improved Layout of Phylogenetic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 472-479.	3.0	19
66	Enriched Environmental Conditions Modify the Gut Microbiome Composition and Fecal Markers of Inflammation in Parkinsonâ€™s Disease. Frontiers in Neuroscience, 2019, 13, 1032.	2.8	17
67	Identifying a species tree subject to random lateral gene transfer. Journal of Theoretical Biology, 2013, 322, 81-93.	1.7	16
68	Drawing Rooted Phylogenetic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 103-109.	3.0	12
69	Functional Analysis in Metagenomics Using MEGAN 6. , 2017, , 65-74.		12
70	Two-dimensional groups, orbifolds and tilings. Geometriae Dedicata, 1996, 60, 89.	0.3	11
71	Autumn Algorithmâ€"Computation of Hybridization Networks for Realistic Phylogenetic Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 398-410.	3.0	11
72	Using AnnoTree to Get More Assignments, Faster, in DIAMOND+MEGAN Microbiome Analysis. MSystems, 2022, 7, e0140821.	3.8	11

#	ARTICLE	IF	CITATIONS
73	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
74	Orbifold Triangulations and Crystallographic Groups. Periodica Mathematica Hungarica, 1997, 34, 29-55.	0.9	7
75	Microbial Phylogenetic Context Using Phylogenetic Outlines. Genome Biology and Evolution, 2021, 13, .	2.5	6
76	Normalising phylogenetic networks. Molecular Phylogenetics and Evolution, 2021, 163, 107215.	2.7	6
77	Interactive analysis of biosurfactants in fruit-waste fermentation samples using BioSurfDB and MEGAN. Scientific Reports, 2022, 12, 7769.	3.3	3
78	MAIRA- real-time taxonomic and functional analysis of long reads on a laptop. BMC Bioinformatics, 2020, 21, 390.	2.6	2
79	Interplay of Various Evolutionary Modes in Genome Diversification and Adaptive Evolution of the Family Sulfolobaceae. Frontiers in Microbiology, 2021, 12, 639995.	3.5	2
80	Tegula â€" exploring a galaxy of two-dimensional periodic tilings. Computer Aided Geometric Design, 2021, 90, 102027.	1.2	2
81	A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. Journal of Biotechnology, 2017, 250, 45-50.	3.8	1