

# Daniel H Huson

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/3813693/daniel-h-huson-publications-by-year.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

89  
papers

33,928  
citations

45  
h-index

98  
g-index

98  
ext. papers

42,077  
ext. citations

9.4  
avg. IF

7.45  
L-index

#	Paper	IF	Citations
89	Using AnnoTree to Get More Assignments, Faster, in DIAMOND+MEGAN Microbiome Analysis.. <i>MSystems</i> , <b>2022</b> , 7, e0140821	7.6	2
88	Interactive analysis of biosurfactants in fruit-waste fermentation samples using BioSurfDB and MEGAN.. <i>Scientific Reports</i> , <b>2022</b> , 12, 7769	4.9	0
87	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> , <b>2021</b> , 7, 23	8.2	10
86	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. <i>Current Protocols</i> , <b>2021</b> , 1, e59		9
85	Interplay of Various Evolutionary Modes in Genome Diversification and Adaptive Evolution of the Family. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 639995	5.7	0
84	On the Application of Advanced Machine Learning Methods to Analyze Enhanced, Multimodal Data from Persons Infected with COVID-19. <i>Computation</i> , <b>2021</b> , 9, 4	2.2	5
83	Tegula Exploring a galaxy of two-dimensional periodic tilings. <i>Computer Aided Geometric Design</i> , <b>2021</b> , 90, 102027	1.2	1
82	Normalising phylogenetic networks. <i>Molecular Phylogenetics and Evolution</i> , <b>2021</b> , 163, 107215	4.1	2
81	MAIRA- real-time taxonomic and functional analysis of long reads on a laptop. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 390	3.6	1
80	The Isolate sp. 7D4C2 Produces -Caproate at Mildly Acidic Conditions From Hexoses: Genome and rBOX Comparison With Related Strains and Chain-Elongating Bacteria. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 594524	5.7	9
79	Enriched Environmental Conditions Modify the Gut Microbiome Composition and Fecal Markers of Inflammation in Parkinson's Disease. <i>Frontiers in Neuroscience</i> , <b>2019</b> , 13, 1032	5.1	5
78	Annotated bacterial chromosomes from frame-shift-corrected long-read metagenomic data. <i>Microbiome</i> , <b>2019</b> , 7, 61	16.6	31
77	Phage tail-like particles are versatile bacterial nanomachines - A mini-review. <i>Journal of Advanced Research</i> , <b>2019</b> , 19, 75-84	13	15
76	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1910, 591-604	1.4	8
75	Autumn Algorithm-Computation of Hybridization Networks for Realistic Phylogenetic Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2018</b> , 15, 398-410	3	9
74	Genome Sequence of (Greater Wax Moth). <i>Genome Announcements</i> , <b>2018</b> , 6,		53
73	Salmonella enterica genomes from victims of a major sixteenth-century epidemic in Mexico. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 520-528	12.3	124

72	MEGAN-LR: new algorithms allow accurate binning and easy interactive exploration of metagenomic long reads and contigs. <i>Biology Direct</i> , <b>2018</b> , 13, 6	7.2	83
71	Intestinal Dysbiosis, Barrier Dysfunction, and Bacterial Translocation Account for CKD-Related Systemic Inflammation. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2017</b> , 28, 76-83	12.7	127
70	A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. <i>Journal of Biotechnology</i> , <b>2017</b> , 250, 45-50	3.7	1
69	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. <i>Microbiome</i> , <b>2017</b> , 5, 11	16.6	23
68	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. <i>Nature</i> , <b>2017</b> , 544, 357-361	50.4	263
67	The Antibiotic Resistant Target Seeker (ARTS), an exploration engine for antibiotic cluster prioritization and novel drug target discovery. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W42-W48	20.1	96
66	SILVA, RDP, Greengenes, NCBI and OTT - how do these taxonomies compare?. <i>BMC Genomics</i> , <b>2017</b> , 18, 114	4.5	201
65	Functional Analysis in Metagenomics Using MEGAN 6 <b>2017</b> , 65-74		4
64	Soil biochar amendment affects the diversity of nosZ transcripts: Implications for NO formation. <i>Scientific Reports</i> , <b>2017</b> , 7, 3338	4.9	36
63	A metagenomic-based survey of microbial (de)halogenation potential in a German forest soil. <i>Scientific Reports</i> , <b>2016</b> , 6, 28958	4.9	29
62	RiboTagger: fast and unbiased 16S/18S profiling using whole community shotgun metagenomic or metatranscriptome surveys. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 508	3.6	18
61	Extensive Mobilome-Driven Genome Diversification in Mouse Gut-Associated <i>Bacteroides vulgatus</i> mpk. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 1197-207	3.9	17
60	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004957	5	836
59	Analysis of Domain Architecture and Phylogenetics of Family 2 Glycoside Hydrolases (GH2). <i>PLoS ONE</i> , <b>2016</b> , 11, e0168035	3.7	18
58	Characterization of the Gut Microbial Community of Obese Patients Following a Weight-Loss Intervention Using Whole Metagenome Shotgun Sequencing. <i>PLoS ONE</i> , <b>2016</b> , 11, e0149564	3.7	146
57	Soil biochar amendment shapes the composition of N2O-reducing microbial communities. <i>Science of the Total Environment</i> , <b>2016</b> , 562, 379-390	10.2	86
56	Antibiotic Selection Pressure Determination through Sequence-Based Metagenomics. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2015</b> , 59, 7335-45	5.9	47
55	Fast and sensitive protein alignment using DIAMOND. <i>Nature Methods</i> , <b>2015</b> , 12, 59-60	21.6	4165

54	Effects of surgical and dietary weight loss therapy for obesity on gut microbiota composition and nutrient absorption. <i>BioMed Research International</i> , <b>2015</b> , 2015, 806248	3	190
53	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , <b>2014</b> , 514, 494-7	50.4	358
52	A poor man's BLASTX--high-throughput metagenomic protein database search using PAUDA. <i>Bioinformatics</i> , <b>2014</b> , 30, 38-9	7.2	43
51	Endotoxicity of lipopolysaccharide as a determinant of T-cell-mediated colitis induction in mice. <i>Gastroenterology</i> , <b>2014</b> , 146, 765-75	13.3	51
50	Microbial community analysis using MEGAN. <i>Methods in Enzymology</i> , <b>2013</b> , 531, 465-85	1.7	144
49	Identifying a species tree subject to random lateral gene transfer. <i>Journal of Theoretical Biology</i> , <b>2013</b> , 322, 81-93	2.3	13
48	Fast computation of minimum hybridization networks. <i>Bioinformatics</i> , <b>2012</b> , 28, 191-7	7.2	36
47	Dendroscope 3: an interactive tool for rooted phylogenetic trees and networks. <i>Systematic Biology</i> , <b>2012</b> , 61, 1061-7	8.4	1033
46	CREST--classification resources for environmental sequence tags. <i>PLoS ONE</i> , <b>2012</b> , 7, e49334	3.7	167
45	Integrative analysis of environmental sequences using MEGAN4. <i>Genome Research</i> , <b>2011</b> , 21, 1552-60	9.7	1019
44	A survey of combinatorial methods for phylogenetic networks. <i>Genome Biology and Evolution</i> , <b>2011</b> , 3, 23-35	3.9	138
43	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> , <b>2011</b> , 108, 10249-54	11.5	190
42	Tanglegrams for rooted phylogenetic trees and networks. <i>Bioinformatics</i> , <b>2011</b> , 27, i248-56	7.2	66
41	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. <i>ISME Journal</i> , <b>2010</b> , 4, 1236-42	11.9	39
40	Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. <i>Bioinformatics</i> , <b>2010</b> , 26, i124-31	7.2	40
39	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 243-8		187
38	Phylogenetic Networks: Concepts, Algorithms and Applications <b>2010</b> ,		223
37	Computing galled networks from real data. <i>Bioinformatics</i> , <b>2009</b> , 25, i85-93	7.2	49

36	Drawing rooted phylogenetic networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2009</b> , 6, 103-9	3	12
35	The mitochondrial genome sequence of the Tasmanian tiger ( <i>Thylacinus cynocephalus</i> ). <i>Genome Research</i> , <b>2009</b> , 19, 213-20	9.7	83
34	MetaSim: a sequencing simulator for genomics and metagenomics. <i>PLoS ONE</i> , <b>2008</b> , 3, e3373	3.7	305
33	Improved layout of phylogenetic networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2008</b> , 5, 472-479	3	13
32	Summarizing Multiple Gene Trees Using Cluster Networks. <i>Lecture Notes in Computer Science</i> , <b>2008</b> , 296-305	3.9	20
31	Simultaneous assessment of soil microbial community structure and function through analysis of the meta-transcriptome. <i>PLoS ONE</i> , <b>2008</b> , 3, e2527	3.7	558
30	Filtered Z-closure supernetworks for extracting and visualizing recurrent signal from incongruent gene trees. <i>Systematic Biology</i> , <b>2008</b> , 57, 939-47	8.4	22
29	Evolution of <i>Arabidopsis thaliana</i> microRNAs from random sequences. <i>Rna</i> , <b>2008</b> , 14, 2455-9	5.8	110
28	MEGAN analysis of metagenomic data. <i>Genome Research</i> , <b>2007</b> , 17, 377-86	9.7	2078
27	Common sequence polymorphisms shaping genetic diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , <b>2007</b> , 317, 338-42	33.3	596
26	Dendroscope: An interactive viewer for large phylogenetic trees. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 460	3.6	952
25	Sequence and expression differences underlie functional specialization of <i>Arabidopsis</i> microRNAs miR159 and miR319. <i>Developmental Cell</i> , <b>2007</b> , 13, 115-25	10.2	306
24	Metagenomics to paleogenomics: large-scale sequencing of mammoth DNA. <i>Science</i> , <b>2006</b> , 311, 392-4	33.3	435
23	Application of phylogenetic networks in evolutionary studies. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 254-67	8.3	5807
22	Specificity prediction of adenylation domains in nonribosomal peptide synthetases (NRPS) using transductive support vector machines (TSVMs). <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 5799-808	20.1	352
21	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> , <b>2004</b> , 101, 1916-21	11.5	142
20	Comparative analysis of four Campylobacterales. <i>Nature Reviews Microbiology</i> , <b>2004</b> , 2, 872-85	22.2	80
19	Constructing splits graphs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2004</b> , 1, 109-15	3	82

18	The Orbifold Notation for Two-Dimensional Groups. <i>Structural Chemistry</i> , <b>2002</b> , 13, 247-257	1.8	34
17	A comparison of whole-genome shotgun-derived mouse chromosome 16 and the human genome. <i>Science</i> , <b>2002</b> , 296, 1661-71	33.3	305
16	The sequence of the human genome. <i>Science</i> , <b>2001</b> , 291, 1304-51	33.3	10609
15	How molecules evolve in eubacteria. <i>Molecular Biology and Evolution</i> , <b>2000</b> , 17, 835-8	8.3	42
14	Systematic enumeration of crystalline networks. <i>Nature</i> , <b>1999</b> , 400, 644-647	50.4	249
13	Disk-covering, a fast-converging method for phylogenetic tree reconstruction. <i>Journal of Computational Biology</i> , <b>1999</b> , 6, 369-86	1.7	109
12	Orbifold Triangulations and Crystallographic Groups. <i>Periodica Mathematica Hungarica</i> , <b>1997</b> , 34, 29-55	0.4	4
11	Two-dimensional groups, orbifolds and tilings. <i>Geometriae Dedicata</i> , <b>1996</b> , 60, 89	0.5	7
10	The generation and classification of tile-k-transitive tilings of the Euclidean plane, the sphere and the hyperbolic plane. <i>Geometriae Dedicata</i> , <b>1993</b> , 47, 269-296	0.5	45
9	On tilings of the plane. <i>Geometriae Dedicata</i> , <b>1987</b> , 24, 295	0.5	32
8	Improving recovery of member genomes from enrichment reactor microbial communities using MinION-based long read metagenomics		2
7	MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman		51
6	Salmonella entericagenomes recovered from victims of a major 16th century epidemic in Mexico		11
5	Analysis procedures for assessing recovery of high quality, complete, closed genomes from Nanopore long read metagenome sequencing		4
4	Enhanced COVID-19 data for improved prediction of survival		1
3	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		2
2	Annotated bacterial chromosomes from frame-shift-corrected long read metagenomic data		1
1	Enriched environmental conditions modify the gut microbiome composition and fecal markers of inflammation in Parkinson's disease		1

