Daniel H Huson

List of Publications by Citations

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	The sequence of the human genome. *Science*, **2001**, 291, 1304-51	33.3	10609
88	Application of phylogenetic networks in evolutionary studies. *Molecular Biology and Evolution*, **2006**, 23, 254-67	8.3	5807
87	Fast and sensitive protein alignment using DIAMOND. *Nature Methods*, **2015**, 12, 59-60	21.6	4165
86	MEGAN analysis of metagenomic data. *Genome Research*, **2007**, 17, 377-86	9.7	2078
85	Dendroscope 3: an interactive tool for rooted phylogenetic trees and networks. *Systematic Biology*, **2012**, 61, 1061-7	8.4	1033
84	Integrative analysis of environmental sequences using MEGAN4. *Genome Research*, **2011**, 21, 1552-60	9.7	1019
83	Dendroscope: An interactive viewer for large phylogenetic trees. *BMC Bioinformatics*, **2007**, 8, 460	3.6	952
82	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. *PLoS Computational Biology*, **2016**, 12, e1004957	5	836
81	Common sequence polymorphisms shaping genetic diversity in Arabidopsis thaliana. *Science*, **2007**, 317, 338-42	33.3	596
80	Simultaneous assessment of soil microbial community structure and function through analysis of the meta-transcriptome. *PLoS ONE*, **2008**, 3, e2527	3.7	558
79	Metagenomics to paleogenomics: large-scale sequencing of mammoth DNA. *Science*, **2006**, 311, 392-4	33.3	435
78	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. *Nature*, **2014**, 514, 494-7	50.4	358
77	Specificity prediction of adenylation domains in nonribosomal peptide synthetases (NRPS) using transductive support vector machines (TSVMs). *Nucleic Acids Research*, **2005**, 33, 5799-808	20.1	352
76	Sequence and expression differences underlie functional specialization of Arabidopsis microRNAs miR159 and miR319. *Developmental Cell*, **2007**, 13, 115-25	10.2	306
75	MetaSim: a sequencing simulator for genomics and metagenomics. *PLoS ONE*, **2008**, 3, e3373	3.7	305
74	A comparison of whole-genome shotgun-derived mouse chromosome 16 and the human genome. *Science*, **2002**, 296, 1661-71	33.3	305
73	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. *Nature*, **2017**, 544, 357-361	50.4	263

72	Systematic enumeration of crystalline networks. *Nature*, **1999**, 400, 644-647	50.4	249
71	Phylogenetic Networks: Concepts, Algorithms and Applications **2010**,		223
70	SILVA, RDP, Greengenes, NCBI and OTT - how do these taxonomies compare?. *BMC Genomics*, **2017**, 18, 114	4.5	201
69	Effects of surgical and dietary weight loss therapy for obesity on gut microbiota composition and nutrient absorption. *BioMed Research International*, **2015**, 2015, 806248	3	190
68	Reference-guided assembly of four diverse Arabidopsis thaliana genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 10249-54	11.5	190
67	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. *Standards in Genomic Sciences*, **2010**, 3, 243-8		187
66	CREST--classification resources for environmental sequence tags. *PLoS ONE*, **2012**, 7, e49334	3.7	167
65	Characterization of the Gut Microbial Community of Obese Patients Following a Weight-Loss Intervention Using Whole Metagenome Shotgun Sequencing. *PLoS ONE*, **2016**, 11, e0149564	3.7	146
64	Microbial community analysis using MEGAN. *Methods in Enzymology*, **2013**, 531, 465-85	1.7	144
63	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, 1916-21	11.5	142
62	A survey of combinatorial methods for phylogenetic networks. *Genome Biology and Evolution*, **2011**, 3, 23-35	3.9	138
61	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	12.7	127
60	Salmonella enterica genomes from victims of a major sixteenth-century epidemic in Mexico. *Nature Ecology and Evolution*, **2018**, 2, 520-528	12.3	124
59	Evolution of Arabidopsis thaliana microRNAs from random sequences. *Rna*, **2008**, 14, 2455-9	5.8	110
58	Disk-covering, a fast-converging method for phylogenetic tree reconstruction. *Journal of Computational Biology*, **1999**, 6, 369-86	1.7	109
57	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	20.1	96
56	Soil biochar amendment shapes the composition of N2O-reducing microbial communities. *Science of the Total Environment*, **2016**, 562, 379-390	10.2	86
55	MEGAN-LR: new algorithms allow accurate binning and easy interactive exploration of metagenomic long reads and contigs. *Biology Direct*, **2018**, 13, 6	7.2	83

54	The mitochondrial genome sequence of the Tasmanian tiger (Thylacinus cynocephalus). *Genome Research*, **2009**, 19, 213-20	9.7	83
53	Constructing splits graphs. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2004**, 1, 109-15	3	82
52	Comparative analysis of four Campylobacterales. *Nature Reviews Microbiology*, **2004**, 2, 872-85	22.2	80
51	Tanglegrams for rooted phylogenetic trees and networks. *Bioinformatics*, **2011**, 27, i248-56	7.2	66
50	Genome Sequence of (Greater Wax Moth). *Genome Announcements*, **2018**, 6,		53
49	Endotoxicity of lipopolysaccharide as a determinant of T-cell-mediated colitis induction in mice. *Gastroenterology*, **2014**, 146, 765-75	13.3	51
48	MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman		51
47	Computing galled networks from real data. *Bioinformatics*, **2009**, 25, i85-93	7.2	49
46	Antibiotic Selection Pressure Determination through Sequence-Based Metagenomics. *Antimicrobial Agents and Chemotherapy*, **2015**, 59, 7335-45	5.9	47
45	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	0.5	45
44	A poor man's BLASTX--high-throughput metagenomic protein database search using PAUDA. *Bioinformatics*, **2014**, 30, 38-9	7.2	43
43	How molecules evolve in eubacteria. *Molecular Biology and Evolution*, **2000**, 17, 835-8	8.3	42
42	Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. *Bioinformatics*, **2010**, 26, i124-31	7.2	40
41	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. *ISME Journal*, **2010**, 4, 1236-42	11.9	39
40	Soil biochar amendment affects the diversity of nosZ transcripts: Implications for NO formation. *Scientific Reports*, **2017**, 7, 3338	4.9	36
39	Fast computation of minimum hybridization networks. *Bioinformatics*, **2012**, 28, 191-7	7.2	36
38	The Orbifold Notation for Two-Dimensional Groups. *Structural Chemistry*, **2002**, 13, 247-257	1.8	34
37	On tilings of the plane. *Geometriae Dedicata*, **1987**, 24, 295	0.5	32

36	Annotated bacterial chromosomes from frame-shift-corrected long-read metagenomic data. *Microbiome*, **2019**, 7, 61	16.6	31
35	A metagenomic-based survey of microbial (de)halogenation potential in a German forest soil. *Scientific Reports*, **2016**, 6, 28958	4.9	29
34	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. *Microbiome*, **2017**, 5, 11	16.6	23
33	Filtered Z-closure supernetworks for extracting and visualizing recurrent signal from incongruent gene trees. *Systematic Biology*, **2008**, 57, 939-47	8.4	22
32	Summarizing Multiple Gene Trees Using Cluster Networks. *Lecture Notes in Computer Science*, **2008**, 296-305	3.9	20
31	RiboTagger: fast and unbiased 16S/18S profiling using whole community shotgun metagenomic or metatranscriptome surveys. *BMC Bioinformatics*, **2016**, 17, 508	3.6	18
30	Analysis of Domain Architecture and Phylogenetics of Family 2 Glycoside Hydrolases (GH2). *PLoS ONE*, **2016**, 11, e0168035	3.7	18
29	Extensive Mobilome-Driven Genome Diversification in Mouse Gut-Associated Bacteroides vulgatus mpk. *Genome Biology and Evolution*, **2016**, 8, 1197-207	3.9	17
28	Phage tail-like particles are versatile bacterial nanomachines - A mini-review. *Journal of Advanced Research*, **2019**, 19, 75-84	13	15
27	Identifying a species tree subject to random lateral gene transfer. *Journal of Theoretical Biology*, **2013**, 322, 81-93	2.3	13
26	Improved layout of phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2008**, 5, 472-479	3	13
25	Drawing rooted phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2009**, 6, 103-9	3	12
24	Salmonella entericagenomes recovered from victims of a major 16th century epidemic in Mexico		11
23	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	8.2	10
22	Autumn Algorithm-Computation of Hybridization Networks for Realistic Phylogenetic Trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2018**, 15, 398-410	3	9
21	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. *Current Protocols*, **2021**, 1, e59		9
20	The Isolate sp. 7D4C2 Produces -Caproate at Mildly Acidic Conditions From Hexoses: Genome and rBOX Comparison With Related Strains and Chain-Elongating Bacteria. *Frontiers in Microbiology*, **2020**, 11, 594524	5.7	9
19	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. *Methods in Molecular Biology*, **2019**, 1910, 591-604	1.4	8

18	Two-dimensional groups, orbifolds and tilings. *Geometriae Dedicata*, **1996**, 60, 89	0.5	7
17	Enriched Environmental Conditions Modify the Gut Microbiome Composition and Fecal Markers of Inflammation in Parkinson's Disease. *Frontiers in Neuroscience*, **2019**, 13, 1032	5.1	5
16	On the Application of Advanced Machine Learning Methods to Analyze Enhanced, Multimodal Data from Persons Infected with COVID-19. *Computation*, **2021**, 9, 4	2.2	5
15	Functional Analysis in Metagenomics Using MEGAN 6 **2017**, 65-74		4
14	Orbifold Triangulations and Crystallographic Groups. *Periodica Mathematica Hungarica*, **1997**, 34, 29-55	0.4	4
13	Analysis procedures for assessing recovery of high quality, complete, closed genomes from Nanopore long read metagenome sequencing		4
12	Improving recovery of member genomes from enrichment reactor microbial communities using MinION-based long read metagenomics		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		2
10	Normalising phylogenetic networks. *Molecular Phylogenetics and Evolution*, **2021**, 163, 107215	4.1	2
9	Using AnnoTree to Get More Assignments, Faster, in DIAMOND+MEGAN Microbiome Analysis.. *MSystems*, **2022**, 7, e0140821	7.6	2
8	A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. *Journal of Biotechnology*, **2017**, 250, 45-50	3.7	1
7	Enhanced COVID-19 data for improved prediction of survival		1
6	Annotated bacterial chromosomes from frame-shift-corrected long read metagenomic data		1
5	Enriched environmental conditions modify the gut microbiome composition and fecal markers of inflammation in Parkinson's disease		1
4	MAIRA- real-time taxonomic and functional analysis of long reads on a laptop. *BMC Bioinformatics*, **2020**, 21, 390	3.6	1
3	Tegula – exploring a galaxy of two-dimensional periodic tilings. *Computer Aided Geometric Design*, **2021**, 90, 102027	1.2	1
2	Interplay of Various Evolutionary Modes in Genome Diversification and Adaptive Evolution of the Family. *Frontiers in Microbiology*, **2021**, 12, 639995	5.7	0
1	Interactive analysis of biosurfactants in fruit-waste fermentation samples using BioSurfDB and MEGAN.. *Scientific Reports*, **2022**, 12, 7769	4.9	0