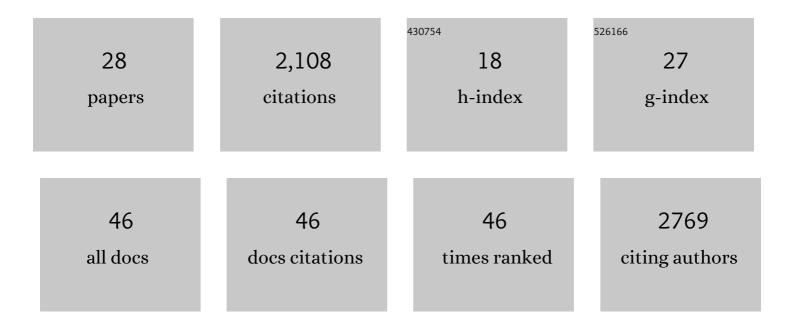
Benjamin J Tully

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
2	The reconstruction of 2,631 draft metagenome-assembled genomes from the global oceans. Scientific Data, 2018, 5, 170203.	2.4	449
3	Potential for primary productivity in a globally-distributed bacterial phototroph. ISME Journal, 2018, 12, 1861-1866.	4.4	159
4	A dynamic microbial community with high functional redundancy inhabits the cold, oxic subseafloor aquifer. ISME Journal, 2018, 12, 1-16.	4.4	148
5	BinSanity: unsupervised clustering of environmental microbial assemblies using coverage and affinity propagation. PeerJ, 2017, 5, e3035.	0.9	139
6	290 metagenome-assembled genomes from the Mediterranean Sea: a resource for marine microbiology. Peerl, 2017, 5, e3558.	0.9	71
7	Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. Nature Communications, 2019, 10, 271.	5.8	66
8	A distinct and active bacterial community in cold oxygenated fluids circulating beneath the western flank of the Mid-Atlantic ridge. Scientific Reports, 2016, 6, 22541.	1.6	62
9	Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. Environmental Microbiology, 2012, 14, 254-267.	1.8	56
10	Prospects for the study of evolution in the deep biosphere. Frontiers in Microbiology, 2011, 2, 285.	1.5	52
11	Potential Mechanisms for Microbial Energy Acquisition in Oxic Deep-Sea Sediments. Applied and Environmental Microbiology, 2016, 82, 4232-4243.	1.4	51
12	Nitrogen Cycling of Active Bacteria within Oligotrophic Sediment of the Mid-Atlantic Ridge Flank. Geomicrobiology Journal, 2018, 35, 468-483.	1.0	50
13	Microbial communities associated with ferromanganese nodules and the surrounding sediments. Frontiers in Microbiology, 2013, 4, 161.	1.5	46
14	Marine <i>Dadabacteria</i> exhibit genome streamlining and phototrophy-driven niche partitioning. ISME Journal, 2021, 15, 1248-1256.	4.4	39
15	Biases in genome reconstruction from metagenomic data. PeerJ, 2020, 8, e10119.	0.9	32
16	Petrobactin, a siderophore produced by <i>Alteromonas</i> , mediates community iron acquisition in the global ocean. ISME Journal, 2022, 16, 358-369.	4.4	30
17	Comparative genomics of planktonic Flavobacteriaceae from the Gulf of Maine using metagenomic data. Microbiome, 2014, 2, 34.	4.9	28
18	Time-series transcriptomics from cold, oxic subseafloor crustal fluids reveals a motile, mixotrophic microbial community. ISME Journal, 2021, 15, 1192-1206.	4.4	27

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#	Article	IF	CITATIONS
19	<i>De Novo</i> Sequences of <i>Haloquadratum walsbyi</i> from Lake Tyrrell, Australia, Reveal a Variable Genomic Landscape. Archaea, 2015, 2015, 1-12.	2.3	26
20	MetaSanity: an integrated microbial genome evaluation and annotation pipeline. Bioinformatics, 2020, 36, 4341-4344.	1.8	20
21	NCBl's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. Genes, 2019, 10, 714.	1.0	13
22	Genome Sequence of Geothermobacter sp. Strain EPR-M, a Deep-Sea Hydrothermal Vent Iron Reducer. Genome Announcements, 2017, 5, .	0.8	5
23	Genome Sequence of <i>Hydrogenovibrio</i> sp. Strain SC-1, a Chemolithoautotrophic Sulfur and Iron Oxidizer. Genome Announcements, 2018, 6, .	0.8	3
24	NCBI's Virus Discovery Codeathon: Building "FIVE―—The Federated Index of Viral Experiments API Inde Viruses, 2020, 12, 1424.	^{X.} 1.5	3
25	Genome Sequence of <i>Geothermobacter</i> sp. Strain HR-1, an Iron Reducer from the LÅâ€~ihi Seamount, Hawai'i. Genome Announcements, 2018, 6, .	0.8	2
26	Genome Sequence of <i>Mariprofundus</i> sp. Strain EBB-1, a Novel Marine Autotroph Isolated from an Iron-Sulfur Mineral. Microbiology Resource Announcements, 2019, 8, .	0.3	2
27	The Bioinformatics Virtual Coordination Network: An Open-Source and Interactive Learning Environment. Frontiers in Education, 2021, 6, .	1.2	2
28	Potential Phosphorus Uptake Mechanisms in the Deep Sedimentary Biosphere. Frontiers in Marine Science, 2022, 9, .	1.2	0