

# Benjamin J Tully

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6885839/publications.pdf>

Version: 2024-02-01

28  
papers

2,108  
citations

430754

18  
h-index

526166

27  
g-index

46  
all docs

46  
docs citations

46  
times ranked

2769  
citing authors

#	ARTICLE	IF	CITATIONS
1	Petrobactin, a siderophore produced by <i>Alteromonas</i> , mediates community iron acquisition in the global ocean. <i>ISME Journal</i> , 2022, 16, 358-369.	4.4	30
2	Potential Phosphorus Uptake Mechanisms in the Deep Sedimentary Biosphere. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	0
3	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
4	Marine <i>Dadabacteria</i> exhibit genome streamlining and phototrophy-driven niche partitioning. <i>ISME Journal</i> , 2021, 15, 1248-1256.	4.4	39
5	Time-series transcriptomics from cold, oxic subseafloor crustal fluids reveals a motile, mixotrophic microbial community. <i>ISME Journal</i> , 2021, 15, 1192-1206.	4.4	27
6	The Bioinformatics Virtual Coordination Network: An Open-Source and Interactive Learning Environment. <i>Frontiers in Education</i> , 2021, 6, .	1.2	2
7	NCBI's Virus Discovery Codeathon: Building "The Federated Index of Viral Experiments API Index. <i>Viruses</i> , 2020, 12, 1424.	1.5	3
8	MetaSanity: an integrated microbial genome evaluation and annotation pipeline. <i>Bioinformatics</i> , 2020, 36, 4341-4344.	1.8	20
9	Biases in genome reconstruction from metagenomic data. <i>PeerJ</i> , 2020, 8, e10119.	0.9	32
10	NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. <i>Genes</i> , 2019, 10, 714.	1.0	13
11	Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. <i>Nature Communications</i> , 2019, 10, 271.	5.8	66
12	Genome Sequence of <i>Mariprofundus</i> sp. Strain EBB-1, a Novel Marine Autotroph Isolated from an Iron-Sulfur Mineral. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
13	Nitrogen Cycling of Active Bacteria within Oligotrophic Sediment of the Mid-Atlantic Ridge Flank. <i>Geomicrobiology Journal</i> , 2018, 35, 468-483.	1.0	50
14	The reconstruction of 2,631 draft metagenome-assembled genomes from the global oceans. <i>Scientific Data</i> , 2018, 5, 170203.	2.4	449
15	Potential for primary productivity in a globally-distributed bacterial phototroph. <i>ISME Journal</i> , 2018, 12, 1861-1866.	4.4	159
16	A dynamic microbial community with high functional redundancy inhabits the cold, oxic subseafloor aquifer. <i>ISME Journal</i> , 2018, 12, 1-16.	4.4	148
17	Genome Sequence of <i>Geothermobacter</i> sp. Strain HR-1, an Iron Reducer from the Loihi Seamount, Hawaii. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
18	Genome Sequence of <i>Hydrogenovibrio</i> sp. Strain SC-1, a Chemolithoautotrophic Sulfur and Iron Oxidizer. <i>Genome Announcements</i> , 2018, 6, .	0.8	3

#	ARTICLE	IF	CITATIONS
19	Genome Sequence of Geothermobacter sp. Strain EPR-M, a Deep-Sea Hydrothermal Vent Iron Reducer. Genome Announcements, 2017, 5, .	0.8	5
20	BinSanity: unsupervised clustering of environmental microbial assemblies using coverage and affinity propagation. PeerJ, 2017, 5, e3035.	0.9	139
21	290 metagenome-assembled genomes from the Mediterranean Sea: a resource for marine microbiology. PeerJ, 2017, 5, e3558.	0.9	71
22	Potential Mechanisms for Microbial Energy Acquisition in Oxidic Deep-Sea Sediments. Applied and Environmental Microbiology, 2016, 82, 4232-4243.	1.4	51
23	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
24	De Novo Sequences of Haloquadratum walsbyi from Lake Tyrrell, Australia, Reveal a Variable Genomic Landscape. Archaea, 2015, 2015, 1-12.	2.3	26
25	Comparative genomics of planktonic Flavobacteriaceae from the Gulf of Maine using metagenomic data. Microbiome, 2014, 2, 34.	4.9	28
26	Microbial communities associated with ferromanganese nodules and the surrounding sediments. Frontiers in Microbiology, 2013, 4, 161.	1.5	46
27	Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. Environmental Microbiology, 2012, 14, 254-267.	1.8	56
28	Prospects for the study of evolution in the deep biosphere. Frontiers in Microbiology, 2011, 2, 285.	1.5	52