

Tim Urich

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5132897/tim-urich-publications-by-year.pdf>

Version: 2024-04-27

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.

96
papers

9,334
citations

47
h-index

96
g-index

109
ext. papers

11,941
ext. citations

8
avg, IF

5.84
L-index

#	Paper	IF	Citations
96	Down-regulation of the bacterial protein biosynthesis machinery in response to weeks, years, and decades of soil warming.. <i>Science Advances</i> , 2022 , 8, eabm3230	14.3	0
95	Influenza A H1N1 Induced Disturbance of the Respiratory and Fecal Microbiome of German Landrace Pigs - a Multi-Omics Characterization. <i>Microbiology Spectrum</i> , 2021 , 9, e0018221	8.9	1
94	Rewetting does not return drained fen peatlands to their old selves. <i>Nature Communications</i> , 2021 , 12, 5693	17.4	11
93	The soil microbial food web revisited: Predatory myxobacteria as keystone taxa?. <i>ISME Journal</i> , 2021 , 15, 2665-2675	11.9	10
92	Desiccation time and rainfall control gaseous carbon fluxes in an intermittent stream. <i>Biogeochemistry</i> , 2021 , 155, 381-400	3.8	3
91	Moniliella spathulata, an oil-degrading yeast, which promotes growth of barley in oil-polluted soil. <i>Applied Microbiology and Biotechnology</i> , 2021 , 105, 401-415	5.7	1
90	Divergent drivers of the microbial methane sink in temperate forest and grassland soils. <i>Global Change Biology</i> , 2021 , 27, 929-940	11.4	19
89	Microbiome structure and functional potential in permafrost soils of the Western Canadian Arctic. <i>FEMS Microbiology Ecology</i> , 2021 , 97,	4.3	1
88	Linking 16S rRNA Gene Classification to Gene Taxonomy Reveals Environmental Distribution of Ammonia-Oxidizing Archaeal Clades in Peatland Soils. <i>MSystems</i> , 2021 , e0054621	7.6	0
87	Eukaryotic rather than prokaryotic microbiomes change over seasons in rewetted fen peatlands. <i>FEMS Microbiology Ecology</i> , 2021 , 97,	4.3	3
86	North Sea spring bloom-associated Gammaproteobacteria fill diverse heterotrophic niches. <i>Environmental Microbiomes</i> , 2021 , 16, 15	5.6	2
85	Fungi in Permafrost-Affected Soils of the Canadian Arctic: Horizon- and Site-Specific Keystone Taxa Revealed by Co-Occurrence Network. <i>Microorganisms</i> , 2021 , 9,	4.9	1
84	Evidence for enzymatic backbone methylation of the main membrane lipids in the archaeon .. <i>Applied and Environmental Microbiology</i> , 2021 , aem0215421	4.8	1
83	Full Genome Sequence of a Representative Enriched from Peat Soil. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0044321	1.3	1
82	Topsoil removal reduced in-situ methane emissions in a temperate rewetted bog grassland by a hundredfold. <i>Science of the Total Environment</i> , 2020 , 721, 137763	10.2	6
81	From Understanding to Sustainable Use of Peatlands: The WETSCAPES Approach. <i>Soil Systems</i> , 2020 , 4, 14	3.5	24
80	Biotransformation of bisphenol A analogues by the biphenyl-degrading bacterium <i>Cupriavidus basilensis</i> a structure-biotransformation relationship. <i>Applied Microbiology and Biotechnology</i> , 2020 , 104, 3569-3583	5.7	14

79	Aquatic and terrestrial cyanobacteria produce methane. <i>Science Advances</i> , 2020 , 6, eaax5343	14.3	85
78	Long-Term Rewetting of Three Formerly Drained Peatlands Drives Congruent Compositional Changes in Pro- and Eukaryotic Soil Microbiomes through Environmental Filtering. <i>Microorganisms</i> , 2020 , 8,	4.9	13
77	A Multi-Omics Protocol for Swine Feces to Elucidate Longitudinal Dynamics in Microbiome Structure and Function. <i>Microorganisms</i> , 2020 , 8,	4.9	3
76	Disentangling carbon flow across microbial kingdoms in the rhizosphere of maize. <i>Soil Biology and Biochemistry</i> , 2019 , 134, 122-130	7.5	21
75	Diversity and degradative capabilities of bacteria and fungi isolated from oil-contaminated and hydrocarbon-polluted soils in Kazakhstan. <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 7261-7274	5.7	14
74	Methylotrophic methanogens everywhere - physiology and ecology of novel players in global methane cycling. <i>Biochemical Society Transactions</i> , 2019 , 47, 1895-1907	5.1	21
73	Tissue- and Population-Level Microbiome Analysis of the Wasp Spider Identified a Novel Dominant Bacterial Symbiont. <i>Microorganisms</i> , 2019 , 8,	4.9	13
72	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. <i>Nature Communications</i> , 2018 , 9, 1517	17.4	131
71	Light availability impacts structure and function of phototrophic stream biofilms across domains and trophic levels. <i>Molecular Ecology</i> , 2018 , 27, 2913-2925	5.7	23
70	Chronic Helminth Infection Perturbs the Gut-Brain Axis, Promotes Neuropathology, and Alters Behavior. <i>Journal of Infectious Diseases</i> , 2018 , 218, 1511-1516	7	3
69	Significance of dark CO ₂ fixation in arctic soils. <i>Soil Biology and Biochemistry</i> , 2018 , 119, 11-21	7.5	40
68	Holistic Assessment of Rumen Microbiome Dynamics through Quantitative Metatranscriptomics Reveals Multifunctional Redundancy during Key Steps of Anaerobic Feed Degradation. <i>MSystems</i> , 2018 , 3,	7.6	37
67	Fate of carbohydrates and lignin in north-east Siberian permafrost soils. <i>Soil Biology and Biochemistry</i> , 2018 , 116, 311-322	7.5	41
66	Drying and Rainfall Shape the Structure and Functioning of Nitrifying Microbial Communities in Riverbed Sediments. <i>Frontiers in Microbiology</i> , 2018 , 9, 2794	5.7	26
65	A plant-microbe interaction framework explaining nutrient effects on primary production. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1588-1596	12.3	49
64	Temperature response of permafrost soil carbon is attenuated by mineral protection. <i>Global Change Biology</i> , 2018 , 24, 3401-3415	11.4	66
63	Amino acid production exceeds plant nitrogen demand in Siberian tundra. <i>Environmental Research Letters</i> , 2018 , 13, 034002	6.2	39
62	Differential effects of monensin and a blend of essential oils on rumen microbiota composition of transition dairy cows. <i>Journal of Dairy Science</i> , 2017 , 100, 2765-2783	4	55

61	Lifestyle and Horizontal Gene Transfer-Mediated Evolution of , a Core Member of the Murine Gut Microbiota. <i>MSystems</i> , 2017 , 2,	7.6	88
60	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
59	Alterations in the Rumen Liquid-, Particle- and Epithelium-Associated Microbiota of Dairy Cows during the Transition from a Silage- and Concentrate-Based Ration to Pasture in Spring. <i>Frontiers in Microbiology</i> , 2017 , 8, 744	5.7	28
58	Altered carbon turnover processes and microbiomes in soils under long-term extremely high CO ₂ exposure. <i>Nature Microbiology</i> , 2016 , 1, 15025	26.6	27
57	Low abundance of Archaeorhizomycetes among fungi in soil metatranscriptomes. <i>Scientific Reports</i> , 2016 , 6, 38455	4.9	24
56	Draft Genome Sequence of "Candidatus Methanomethylophilus" sp. 1R26, Enriched from Bovine Rumen, a Methanogenic Archaeon Belonging to the Methanomassiliicoccales Order. <i>Genome Announcements</i> , 2016 , 4,		9
55	The soil food web revisited: Diverse and widespread mycophagous soil protists. <i>Soil Biology and Biochemistry</i> , 2016 , 94, 10-18	7.5	99
54	Phylogenetic and genomic analysis of Methanomassiliicoccales in wetlands and animal intestinal tracts reveals clade-specific habitat preferences. <i>FEMS Microbiology Ecology</i> , 2016 , 92,	4.3	78
53	Resource Partitioning between Bacteria, Fungi, and Protists in the Detritosphere of an Agricultural Soil. <i>Frontiers in Microbiology</i> , 2016 , 7, 1524	5.7	85
52	Plant-derived compounds stimulate the decomposition of organic matter in arctic permafrost soils. <i>Scientific Reports</i> , 2016 , 6, 25607	4.9	64
51	Unusual Butane- and Pentanetriol-Based Tetraether Lipids in Methanomassiliicoccus luminyensis, a Representative of the Seventh Order of Methanogens. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 4505-4516	4.8	47
50	Metabolic and trophic interactions modulate methane production by Arctic peat microbiota in response to warming. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E2507-16	11.5	142
49	Adaptation of soil microbial community structure and function to chronic metal contamination at an abandoned Pb-Zn mine. <i>FEMS Microbiology Ecology</i> , 2015 , 91, 1-11	4.3	85
48	Metatranscriptomic census of active protists in soils. <i>ISME Journal</i> , 2015 , 9, 2178-90	11.9	175
47	Intestinal Epithelial Cell Tyrosine Kinase 2 Transduces IL-22 Signals To Protect from Acute Colitis. <i>Journal of Immunology</i> , 2015 , 195, 5011-24	5.3	33
46	The effect of warming on the vulnerability of subducted organic carbon in arctic soils. <i>Soil Biology and Biochemistry</i> , 2015 , 90, 19-29	7.5	50
45	Properties and bioavailability of particulate and mineral-associated organic matter in Arctic permafrost soils, Lower Kolyma Region, Russia. <i>European Journal of Soil Science</i> , 2015 , 66, 722-734	3.4	42
44	Pack hunting by a common soil amoeba on nematodes. <i>Environmental Microbiology</i> , 2015 , 17, 4538-46	5.2	60

43	Storage and transformation of organic matter fractions in cryoturbated permafrost soils across the Siberian Arctic. <i>Biogeosciences</i> , 2015 , 12, 4525-4542	4.6	67
42	Intestinal Microbiota Signatures Associated with Inflammation History in Mice Experiencing Recurring Colitis. <i>Frontiers in Microbiology</i> , 2015 , 6, 1408	5.7	67
41	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. <i>ISME Journal</i> , 2014 , 8, 1101-14	11.9	121
40	Gene expression of lactobacilli in murine forestomach biofilms. <i>Microbial Biotechnology</i> , 2014 , 7, 347-59	6.3	24
39	Distinct microbial communities associated with buried soils in the Siberian tundra. <i>ISME Journal</i> , 2014 , 8, 841-53	11.9	111
38	Metatranscriptomic analysis of arctic peat soil microbiota. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5761-72	4.8	106
37	Input of easily available organic C and N stimulates microbial decomposition of soil organic matter in arctic permafrost soil. <i>Soil Biology and Biochemistry</i> , 2014 , 75, 143-151	7.5	165
36	Effects of soil organic matter properties and microbial community composition on enzyme activities in cryoturbated arctic soils. <i>PLoS ONE</i> , 2014 , 9, e94076	3.7	68
35	Site- and horizon-specific patterns of microbial community structure and enzyme activities in permafrost-affected soils of Greenland. <i>Frontiers in Microbiology</i> , 2014 , 5, 541	5.7	62
34	Rare but active taxa contribute to community dynamics of benthic biofilms in glacier-fed streams. <i>Environmental Microbiology</i> , 2014 , 16, 2514-24	5.2	68
33	Type I interferons have opposing effects during the emergence and recovery phases of colitis. <i>European Journal of Immunology</i> , 2014 , 44, 2749-60	6.1	23
32	Microbial community structure and functioning in marine sediments associated with diffuse hydrothermal venting assessed by integrated meta-omics. <i>Environmental Microbiology</i> , 2014 , 16, 2699-710	5.2	58
31	Biochar decelerates soil organic nitrogen cycling but stimulates soil nitrification in a temperate arable field trial. <i>PLoS ONE</i> , 2014 , 9, e86388	3.7	178
30	Nitrogen dynamics in Turbic Cryosols from Siberia and Greenland. <i>Soil Biology and Biochemistry</i> , 2013 , 67, 85-93	7.5	62
29	Responses of the terrestrial ammonia-oxidizing archaeon <i>Ca. Nitrososphaera viennensis</i> and the ammonia-oxidizing bacterium <i>Nitrososphaera multififormis</i> to nitrification inhibitors. <i>FEMS Microbiology Letters</i> , 2013 , 344, 121-9	2.9	135
28	Nitrification rates in Arctic soils are associated with functionally distinct populations of ammonia-oxidizing archaea. <i>ISME Journal</i> , 2013 , 7, 1620-31	11.9	131
27	Organic carbon transformations in high-Arctic peat soils: key functions and microorganisms. <i>ISME Journal</i> , 2013 , 7, 299-311	11.9	218
26	Methylotrophic methanogenic Thermoplasmata implicated in reduced methane emissions from bovine rumen. <i>Nature Communications</i> , 2013 , 4, 1428	17.4	215

25	Metatranscriptomics of the marine sponge <i>Geodia barretti</i> : tackling phylogeny and function of its microbial community. <i>Environmental Microbiology</i> , 2012 , 14, 1308-24	5.2	102
24	CREST--classification resources for environmental sequence tags. <i>PLoS ONE</i> , 2012 , 7, e49334	3.7	167
23	Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state in acute murine colitis. <i>ISME Journal</i> , 2012 , 6, 2091-106	11.9	208
22	Sulfur-oxidizing chemolithotrophic proteobacteria dominate the microbiota in high arctic thermal springs on Svalbard. <i>Astrobiology</i> , 2011 , 11, 665-78	3.7	28
21	Substrate pathways and mechanisms of inhibition in the sulfur oxygenase reductase of <i>acidianus ambivalens</i> . <i>Frontiers in Microbiology</i> , 2011 , 2, 37	5.7	19
20	The Double-RNA Approach to Simultaneously Assess the Structure and Function of a Soil Microbial Community 2011 , 587-596		7
19	Exploring the composition and diversity of microbial communities at the Jan Mayen hydrothermal vent field using RNA and DNA. <i>FEMS Microbiology Ecology</i> , 2011 , 77, 577-89	4.3	77
18	<i>Nitrososphaera viennensis</i> , an ammonia oxidizing archaeon from soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 8420-5	11.5	644
17	Functional analysis of metagenomes and metatranscriptomes using SEED and KEGG. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 1, S21	3.6	93
16	Nitrification in terrestrial hot springs of Iceland and Kamchatka. <i>FEMS Microbiology Ecology</i> , 2008 , 64, 167-74	4.3	138
15	Simultaneous assessment of soil microbial community structure and function through analysis of the meta-transcriptome. <i>PLoS ONE</i> , 2008 , 3, e2527	3.7	558
14	Production of recombinant and tagged proteins in the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Applied and Environmental Microbiology</i> , 2006 , 72, 102-11	4.8	108
13	A proteomic approach toward the selection of proteins with enhanced intrinsic conformational stability. <i>Journal of Proteome Research</i> , 2006 , 5, 2720-6	5.6	14
12	X-ray Structure of a self-compartmentalizing sulfur cycle metalloenzyme. <i>Science</i> , 2006 , 311, 996-1000	33.3	77
11	Archaea predominate among ammonia-oxidizing prokaryotes in soils. <i>Nature</i> , 2006 , 442, 806-9	50.4	1817
10	Identification of core active site residues of the sulfur oxygenase reductase from <i>Acidianus ambivalens</i> by site-directed mutagenesis. <i>FEMS Microbiology Letters</i> , 2005 , 248, 171-6	2.9	21
9	The sulfur oxygenase reductase from <i>Acidianus ambivalens</i> is an icosatetramer as shown by crystallization and Patterson analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005 , 1747, 267-70	4	15
8	Dissimilatory oxidation and reduction of elemental sulfur in thermophilic archaea. <i>Journal of Bioenergetics and Biomembranes</i> , 2004 , 36, 77-91	3.7	134

7	The sulphur oxygenase reductase from <i>Acidianus ambivalens</i> is a multimeric protein containing a low-potential mononuclear non-haem iron centre. <i>Biochemical Journal</i> , 2004 , 381, 137-46	3.8	49
6	Coupling of the pathway of sulphur oxidation to dioxygen reduction: characterization of a novel membrane-bound thiosulphate:quinone oxidoreductase. <i>Molecular Microbiology</i> , 2004 , 53, 1147-60	4.1	131
5	Molecular analysis of pDL10 from <i>Acidianus ambivalens</i> reveals a family of related plasmids from extremely thermophilic and acidophilic archaea. <i>Genetics</i> , 1999 , 152, 1307-14	4	37
4	Lignin preservation and microbial carbohydrate metabolism in permafrost soils. <i>Journal of Geophysical Research G: Biogeosciences</i> , e2020JG006181	3.7	0
3	Storage and transformation of organic matter fractions in cryoturbated permafrost soils across the Siberian Arctic		11
2	Tissue- and population-level microbiome analysis of the wasp spider <i>Argiope bruennichi</i> identifies a novel dominant bacterial symbiont		1
1	The soil microbial food web revisited with metatranscriptomics - predatory Myxobacteria as keystone taxon?		5