

Tim Urich

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

13,455
citations

31902

53
h-index

37111

96
g-index

109
all docs

109
docs citations

109
times ranked

16095
citing authors

#	ARTICLE	IF	CITATIONS
1	Lignin Preservation and Microbial Carbohydrate Metabolism in Permafrost Soils. Journal of Geophysical Research G: Biogeosciences, 2022, 127, e2020JG006181.	1.3	5
2	Evidence for Enzymatic Backbone Methylation of the Main Membrane Lipids in the Archaeon Methanomassiliicoccus luminyensis. Applied and Environmental Microbiology, 2022, 88, aem0215421.	1.4	3
3	Down-regulation of the bacterial protein biosynthesis machinery in response to weeks, years, and decades of soil warming. Science Advances, 2022, 8, eabm3230.	4.7	18
4	Linking transcriptional dynamics of CH ₄ -cycling grassland soil microbiomes to seasonal gas fluxes. ISME Journal, 2022, 16, 1788-1797.	4.4	12
5	Moniliella spathulata, an oil-degrading yeast, which promotes growth of barley in oil-polluted soil. Applied Microbiology and Biotechnology, 2021, 105, 401-415.	1.7	5
6	Divergent drivers of the microbial methane sink in temperate forest and grassland soils. Global Change Biology, 2021, 27, 929-940.	4.2	49
7	Microbiome structure and functional potential in permafrost soils of the Western Canadian Arctic. FEMS Microbiology Ecology, 2021, 97, .	1.3	9
8	The soil microbial food web revisited: Predatory myxobacteria as keystone taxa?. ISME Journal, 2021, 15, 2665-2675.	4.4	73
9	Desiccation time and rainfall control gaseous carbon fluxes in an intermittent stream. Biogeochemistry, 2021, 155, 381-400.	1.7	12
10	Linking 16S rRNA Gene Classification to <i>amoA</i> Gene Taxonomy Reveals Environmental Distribution of Ammonia-Oxidizing Archaeal Clades in Peatland Soils. MSystems, 2021, 6, e0054621.	1.7	9
11	Eukaryotic rather than prokaryotic microbiomes change over seasons in rewetted fen peatlands. FEMS Microbiology Ecology, 2021, 97, .	1.3	8
12	North Sea spring bloom-associated Gammaproteobacteria fill diverse heterotrophic niches. Environmental Microbiomes, 2021, 16, 15.	2.2	32
13	Fungi in Permafrost-Affected Soils of the Canadian Arctic: Horizon- and Site-Specific Keystone Taxa Revealed by Co-Occurrence Network. Microorganisms, 2021, 9, 1943.	1.6	9
14	Influenza A H1N1 Induced Disturbance of the Respiratory and Fecal Microbiome of German Landrace Pigs – a Multi-Omics Characterization. Microbiology Spectrum, 2021, 9, e0018221.	1.2	14
15	Rewetting does not return drained fen peatlands to their old selves. Nature Communications, 2021, 12, 5693.	5.8	75
16	Increased microbial expression of organic nitrogen cycling genes in long-term warmed grassland soils. ISME Communications, 2021, 1, .	1.7	14
17	Full Genome Sequence of a <i>Methanomassiliicoccales</i> Representative Enriched from Peat Soil. Microbiology Resource Announcements, 2021, 10, e0044321.	0.3	4
18	Tissue- and Population-Level Microbiome Analysis of the Wasp Spider Argiope bruennichi Identified a Novel Dominant Bacterial Symbiont. Microorganisms, 2020, 8, 8.	1.6	26

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19	Temporal dynamics in the taxonomic and functional profile of the Sphagnum-associated fungi (mycobiomes) in a Sphagnum farming field site in Northwestern Germany. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	2
20	A Multi-Omics Protocol for Swine Feces to Elucidate Longitudinal Dynamics in Microbiome Structure and Function. <i>Microorganisms</i> , 2020, 8, 1887.	1.6	15
21	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.	3.9	19
22	From Understanding to Sustainable Use of Peatlands: The WETSCAPES Approach. <i>Soil Systems</i> , 2020, 4, 14.	1.0	45
23	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.	1.7	24
24	Aquatic and terrestrial cyanobacteria produce methane. <i>Science Advances</i> , 2020, 6, eaax5343.	4.7	178
25	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, 550.	1.6	25
26	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.	1.7	25
27	Disentangling carbon flow across microbial kingdoms in the rhizosphere of maize. <i>Soil Biology and Biochemistry</i> , 2019, 134, 122-130.	4.2	38
28	Methylotrophic methanogens everywhere — physiology and ecology of novel players in global methane cycling. <i>Biochemical Society Transactions</i> , 2019, 47, 1895-1907.	1.6	66
29	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. <i>Nature Communications</i> , 2018, 9, 1517.	5.8	256
30	Light availability impacts structure and function of phototrophic stream biofilms across domains and trophic levels. <i>Molecular Ecology</i> , 2018, 27, 2913-2925.	2.0	35
31	Chronic Helminth Infection Perturbs the Gut-Brain Axis, Promotes Neuropathology, and Alters Behavior. <i>Journal of Infectious Diseases</i> , 2018, 218, 1511-1516.	1.9	6
32	Significance of dark CO ₂ fixation in arctic soils. <i>Soil Biology and Biochemistry</i> , 2018, 119, 11-21.	4.2	58
33	Fate of carbohydrates and lignin in north-east Siberian permafrost soils. <i>Soil Biology and Biochemistry</i> , 2018, 116, 311-322.	4.2	59
34	Drying and Rainfall Shape the Structure and Functioning of Nitrifying Microbial Communities in Riverbed Sediments. <i>Frontiers in Microbiology</i> , 2018, 9, 2794.	1.5	37
35	A plant–microbe interaction framework explaining nutrient effects on primary production. <i>Nature Ecology and Evolution</i> , 2018, 2, 1588-1596.	3.4	100
36	Temperature response of permafrost soil carbon is attenuated by mineral protection. <i>Global Change Biology</i> , 2018, 24, 3401-3415.	4.2	107

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37	Amino acid production exceeds plant nitrogen demand in Siberian tundra. <i>Environmental Research Letters</i> , 2018, 13, 034002.	2.2	49
38	Holistic Assessment of Rumen Microbiome Dynamics through Quantitative Metatranscriptomics Reveals Multifunctional Redundancy during Key Steps of Anaerobic Feed Degradation. <i>MSystems</i> , 2018, 3, .	1.7	74
39	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.	1.4	109
40	Lifestyle and Horizontal Gene Transfer-Mediated Evolution of <i>Mucispirillum schaedleri</i> , a Core Member of the Murine Gut Microbiota. <i>MSystems</i> , 2017, 2, .	1.7	148
41	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
42	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.	1.5	78
43	Resource Partitioning between Bacteria, Fungi, and Protists in the Detritosphere of an Agricultural Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 1524.	1.5	143
44	Plant-derived compounds stimulate the decomposition of organic matter in arctic permafrost soils. <i>Scientific Reports</i> , 2016, 6, 25607.	1.6	87
45	Unusual Butane- and Pentanetriol-Based Tetraether Lipids in <i>Methanomassiliicoccus luminyensis</i> , a Representative of the Seventh Order of Methanogens. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4505-4516.	1.4	64
46	Altered carbon turnover processes and microbiomes in soils under long-term extremely high CO ₂ exposure. <i>Nature Microbiology</i> , 2016, 1, 15025.	5.9	52
47	Low abundance of Archaeorhizomycetes among fungi in soil metatranscriptomes. <i>Scientific Reports</i> , 2016, 6, 38455.	1.6	32
48	Draft Genome Sequence of <i>Candidatus</i> <i>Methanomethylophilus</i> sp. 1R26, Enriched from Bovine Rumen, a Methanogenic Archaeon Belonging to the <i>Methanomassiliicoccales</i> Order. <i>Genome Announcements</i> , 2016, 4, .	0.8	17
49	The soil food web revisited: Diverse and widespread mycophagous soil protists. <i>Soil Biology and Biochemistry</i> , 2016, 94, 10-18.	4.2	175
50	Phylogenetic and genomic analysis of <i>Methanomassiliicoccales</i> in wetlands and animal intestinal tracts reveals clade-specific habitat preferences. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv149.	1.3	110
51	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.	1.8	59
52	Pack hunting by a common soil amoeba on nematodes. <i>Environmental Microbiology</i> , 2015, 17, 4538-4546.	1.8	93
53	Storage and transformation of organic matter fractions in cryoturbated permafrost soils across the Siberian Arctic. <i>Biogeosciences</i> , 2015, 12, 4525-4542.	1.3	85
54	Intestinal Microbiota Signatures Associated with Inflammation History in Mice Experiencing Recurring Colitis. <i>Frontiers in Microbiology</i> , 2015, 6, 1408.	1.5	106

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55	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.	3.3	207
56	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.	1.3	119
57	Metatranscriptomic census of active protists in soils. <i>ISME Journal</i> , 2015, 9, 2178-2190.	4.4	274
58	Intestinal Epithelial Cell Tyrosine Kinase 2 Transduces IL-22 Signals To Protect from Acute Colitis. <i>Journal of Immunology</i> , 2015, 195, 5011-5024.	0.4	40
59	The effect of warming on the vulnerability of subducted organic carbon in arctic soils. <i>Soil Biology and Biochemistry</i> , 2015, 90, 19-29.	4.2	68
60	Effects of Soil Organic Matter Properties and Microbial Community Composition on Enzyme Activities in Cryoturbated Arctic Soils. <i>PLoS ONE</i> , 2014, 9, e94076.	1.1	90
61	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.	1.5	73
62	Rare but active taxa contribute to community dynamics of benthic biofilms in glacier-affected streams. <i>Environmental Microbiology</i> , 2014, 16, 2514-2524.	1.8	101
63	Type I interferons have opposing effects during the emergence and recovery phases of colitis. <i>European Journal of Immunology</i> , 2014, 44, 2749-2760.	1.6	39
64	Microbial community structure and functioning in marine sediments associated with diffuse hydrothermal venting assessed by integrated metabolomics. <i>Environmental Microbiology</i> , 2014, 16, 2699-2710.	1.8	109
65	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. <i>ISME Journal</i> , 2014, 8, 1101-1114.	4.4	174
66	Gene expression of lactobacilli in murine forestomach biofilms. <i>Microbial Biotechnology</i> , 2014, 7, 347-359.	2.0	31
67	Distinct microbial communities associated with buried soils in the Siberian tundra. <i>ISME Journal</i> , 2014, 8, 841-853.	4.4	137
68	Metatranscriptomic Analysis of Arctic Peat Soil Microbiota. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5761-5772.	1.4	169
69	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.	4.2	213
70	Biochar Decelerates Soil Organic Nitrogen Cycling but Stimulates Soil Nitrification in a Temperate Arable Field Trial. <i>PLoS ONE</i> , 2014, 9, e86388.	1.1	231
71	Nitrogen dynamics in Turbic Cryosols from Siberia and Greenland. <i>Soil Biology and Biochemistry</i> , 2013, 67, 85-93.	4.2	78
72	Responses of the terrestrial ammonia-oxidizing archaeon <i>Candidatus Nitrososphaera viennensis</i> and the ammonia-oxidizing bacterium <i>Nitrososphaera multiformis</i> to nitrification inhibitors. <i>FEMS Microbiology Letters</i> , 2013, 344, 121-129.	0.7	172

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73	Nitrification rates in Arctic soils are associated with functionally distinct populations of ammonia-oxidizing archaea. <i>ISME Journal</i> , 2013, 7, 1620-1631.	4.4	163
74	Organic carbon transformations in high-Arctic peat soils: key functions and microorganisms. <i>ISME Journal</i> , 2013, 7, 299-311.	4.4	292
75	Methylophilic methanogenic Thermoplasmata implicated in reduced methane emissions from bovine rumen. <i>Nature Communications</i> , 2013, 4, 1428.	5.8	328
76	CREST – Classification Resources for Environmental Sequence Tags. <i>PLoS ONE</i> , 2012, 7, e49334.	1.1	255
77	Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state in acute murine colitis. <i>ISME Journal</i> , 2012, 6, 2091-2106.	4.4	291
78	Metatranscriptomics of the marine sponge <i>Geodia barretti</i> : tackling phylogeny and function of its microbial community. <i>Environmental Microbiology</i> , 2012, 14, 1308-1324.	1.8	124
79	Sulfur-Oxidizing Chemolithotrophic Proteobacteria Dominate the Microbiota in High Arctic Thermal Springs on Svalbard. <i>Astrobiology</i> , 2011, 11, 665-678.	1.5	36
80	Substrate Pathways and Mechanisms of Inhibition in the Sulfur Oxygenase Reductase of <i>Acidianus Ambivalens</i> . <i>Frontiers in Microbiology</i> , 2011, 2, 37.	1.5	28
81	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, 577-589.	1.3	98
82	<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, 8420-8425.	3.3	810
83	Functional analysis of metagenomes and metatranscriptomes using SEED and KEGG. <i>BMC Bioinformatics</i> , 2011, 12, S21.	1.2	116
84	Nitrification in terrestrial hot springs of Iceland and Kamchatka. <i>FEMS Microbiology Ecology</i> , 2008, 64, 167-174.	1.3	173
85	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. <i>PLoS ONE</i> , 2008, 3, e2527.	1.1	667
86	A Proteomic Approach toward the Selection of Proteins with Enhanced Intrinsic Conformational Stability. <i>Journal of Proteome Research</i> , 2006, 5, 2720-2726.	1.8	14
87	X-ray Structure of a Self-Compartmentalizing Sulfur Cycle Metalloenzyme. <i>Science</i> , 2006, 311, 996-1000.	6.0	91
88	Structure of a spherical selfcompartmentalizing sulphur cycle metalloenzyme. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2006, 62, s28-s28.	0.3	0
89	Archaea predominate among ammonia-oxidizing prokaryotes in soils. <i>Nature</i> , 2006, 442, 806-809.	13.7	2,144
90	Production of Recombinant and Tagged Proteins in the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 102-111.	1.4	116

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91	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, 171-176.	0.7	26
92	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, 267-270.	1.1	17
93	The sulfur oxygenase reductase from <i>Acidianus ambivalens</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2005, 61, c265-c265.	0.3	0
94	Dissimilatory Oxidation and Reduction of Elemental Sulfur in Thermophilic Archaea. <i>Journal of Bioenergetics and Biomembranes</i> , 2004, 36, 77-91.	1.0	152
95	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, 137-146.	1.7	57
96	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, 1147-1160.	1.2	160
97	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, 1307-1314.	1.2	40