

Michael J Wilkins

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/4116995/michael-j-wilkins-publications-by-year.pdf>

Version: 2024-04-20

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.

47
papers

3,829
citations

25
h-index

54
g-index

54
ext. papers

5,307
ext. citations

9.6
avg, IF

4.94
L-index

#	Paper	IF	Citations
47	Microbial colonization and persistence in deep fractured shales is guided by metabolic exchanges and viral predation.. <i>Microbiome</i> , 2022 , 10, 5	16.6	0
46	Comparative geochemistry of flowback chemistry from the Utica/Point Pleasant and Marcellus formations. <i>Chemical Geology</i> , 2021 , 564, 120041	4.2	5
45	Ice Cover Influences Redox Dynamics in Prairie Pothole Wetland Sediments. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021 , 126, e2021JG006318	3.7	0
44	Seasonal manganese transport in the hyporheic zone of a snowmelt-dominated river (East River, Colorado, USA). <i>Hydrogeology Journal</i> , 2020 , 28, 1323-1341	3.1	7
43	Identification of Persistent Sulfidogenic Bacteria in Shale Gas Produced Waters. <i>Frontiers in Microbiology</i> , 2020 , 11, 286	5.7	5
42	A Model Analysis of the Tidal Engine That Drives Nitrogen Cycling in Coastal Riparian Aquifers. <i>Water Resources Research</i> , 2020 , 56, e2019WR025662	5.4	6
41	Ecological Assembly Processes Are Coordinated between Bacterial and Viral Communities in Fractured Shale Ecosystems. <i>MSystems</i> , 2020 , 5,	7.6	6
40	Capability for arsenic mobilization in groundwater is distributed across broad phylogenetic lineages. <i>PLoS ONE</i> , 2019 , 14, e0221694	3.7	6
39	In situ transformation of ethoxylate and glycol surfactants by shale-colonizing microorganisms during hydraulic fracturing. <i>ISME Journal</i> , 2019 , 13, 2690-2700	11.9	13
38	Deep-Subsurface Pressure Stimulates Metabolic Plasticity in Shale-Colonizing spp. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	9
37	Wetland Sediments Host Diverse Microbial Taxa Capable of Cycling Alcohols. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	7
36	Hyporheic Zone Microbiome Assembly Is Linked to Dynamic Water Mixing Patterns in Snowmelt-Dominated Headwater Catchments. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019 , 124, 3269-3280	3.7	10
35	Genome-Resolved Metagenomics Extends the Environmental Distribution of the Phylum to the Deep Terrestrial Subsurface. <i>MSphere</i> , 2019 , 4,	5	18
34	Heterogeneity in Hyporheic Flow, Pore Water Chemistry, and Microbial Community Composition in an Alpine Streambed. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019 , 124, 3465-3478	3.7	11
33	Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. <i>Nature Microbiology</i> , 2019 , 4, 352-361	26.6	49
32	Influences of organic carbon speciation on hyporheic corridor biogeochemistry and microbial ecology. <i>Nature Communications</i> , 2018 , 9, 585	17.4	56
31	Microbial Community Cohesion Mediates Community Turnover in Unperturbed Aquifers. <i>MSystems</i> , 2018 , 3,	7.6	34

30	Coupled laboratory and field investigations resolve microbial interactions that underpin persistence in hydraulically fractured shales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E6585-E6594	11.5	35
29	Viral and metabolic controls on high rates of microbial sulfur and carbon cycling in wetland ecosystems. <i>Microbiome</i> , 2018 , 6, 138	16.6	29
28	Comparative genomics and physiology of the genus <i>Methanohalophilus</i> , a prevalent methanogen in hydraulically fractured shale. <i>Environmental Microbiology</i> , 2018 , 20, 4596-4611	5.2	16
27	Members of and Influence System Biogeochemistry During Early Production of Hydraulically Fractured Natural Gas Wells in the Appalachian Basin. <i>Frontiers in Microbiology</i> , 2018 , 9, 2646	5.7	20
26	Characterizing the Deep Terrestrial Subsurface Microbiome. <i>Methods in Molecular Biology</i> , 2018 , 1849, 1-15	1.4	3
25	Abundant carbon substrates drive extremely high sulfate reduction rates and methane fluxes in Prairie Pothole Wetlands. <i>Global Change Biology</i> , 2017 , 23, 3107-3120	11.4	39
24	Water Table Dynamics and Biogeochemical Cycling in a Shallow, Variably-Saturated Floodplain. <i>Environmental Science & Technology</i> , 2017 , 51, 3307-3317	10.3	62
23	Anoxia stimulates microbially catalyzed metal release from Animas River sediments. <i>Environmental Sciences: Processes and Impacts</i> , 2017 , 19, 578-585	4.3	10
22	Draft Genome Sequences of Multiple Strains Isolated from Hydraulically Fractured Shale Environments. <i>Genome Announcements</i> , 2017 , 5,		4
21	Members of the Candidate Phyla Radiation are functionally differentiated by carbon- and nitrogen-cycling capabilities. <i>Microbiome</i> , 2017 , 5, 112	16.6	66
20	Sulfide Generation by Dominant Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017 , 2,	5	41
19	Seasonal hyporheic dynamics control coupled microbiology and geochemistry in Colorado River sediments. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2016 , 121, 2976-2987	3.7	32
18	Groundwater-surface water mixing shifts ecological assembly processes and stimulates organic carbon turnover. <i>Nature Communications</i> , 2016 , 7, 11237	17.4	171
17	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016 , 7, 13219	17.4	589
16	Microbial metabolisms in a 2.5-km-deep ecosystem created by hydraulic fracturing in shales. <i>Nature Microbiology</i> , 2016 , 1, 16146	26.6	144
15	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. <i>Environmental Microbiology</i> , 2016 , 18, 159-73	5.2	111
14	Snowmelt Induced Hydrologic Perturbations Drive Dynamic Microbiological and Geochemical Behaviors across a Shallow Riparian Aquifer. <i>Frontiers in Earth Science</i> , 2016 , 4,	3.5	15
13	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. <i>ISME Journal</i> , 2016 , 10, 2702-2714	11.9	65

12	Genomic expansion of domain archaea highlights roles for organisms from new phyla in anaerobic carbon cycling. <i>Current Biology</i> , 2015 , 25, 690-701	6.3	354
11	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015 , 523, 208-11	5.4	688
10	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015 , 17, 622-36	5.2	28
9	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014 , 8, 1452-63	11.9	131
8	CO2 exposure at pressure impacts metabolism and stress responses in the model sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> strain Hildenborough. <i>Frontiers in Microbiology</i> , 2014 , 5, 507	5.7	21
7	Trends and future challenges in sampling the deep terrestrial biosphere. <i>Frontiers in Microbiology</i> , 2014 , 5, 481	5.7	27
6	Characterization and transcription of arsenic respiration and resistance genes during in situ uranium bioremediation. <i>ISME Journal</i> , 2013 , 7, 370-83	11.9	62
5	Molecular analysis of the in situ growth rates of subsurface <i>Geobacter</i> species. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 1646-53	4.8	32
4	Fermentation, hydrogen, and sulfur metabolism in multiple uncultivated bacterial phyla. <i>Science</i> , 2012 , 337, 1661-5	33.3	464
3	Acetate Availability and its Influence on Sustainable Bioremediation of Uranium-Contaminated Groundwater. <i>Geomicrobiology Journal</i> , 2011 , 28, 519-539	2.5	201
2	Proteogenomic monitoring of <i>Geobacter</i> physiology during stimulated uranium bioremediation. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 6591-9	4.8	116
1	Borgs are giant extrachromosomal elements with the potential to augment methane oxidation		2