

# Michael J Wilkins

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

5,901  
citations

172207

29  
h-index

197535

49  
g-index

54  
all docs

54  
docs citations

54  
times ranked

6429  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbial colonization and persistence in deep fractured shales is guided by metabolic exchanges and viral predation. <i>Microbiome</i> , 2022, 10, 5.	4.9	9
2	Enhanced Speciation of Pyrogenic Organic Matter from Wildfires Enabled by 21 T FT-ICR Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 2973-2980.	3.2	22
3	Implications of sample treatment on characterization of riverine dissolved organic matter. <i>Environmental Sciences: Processes and Impacts</i> , 2022, 24, 773-782.	1.7	6
4	Comparative geochemistry of flowback chemistry from the Utica/Point Pleasant and Marcellus formations. <i>Chemical Geology</i> , 2021, 564, 120041.	1.4	11
5	Ice Cover Influences Redox Dynamics in Prairie Pothole Wetland Sediments. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2021JG006318.	1.3	2
6	Seasonal manganese transport in the hyporheic zone of a snowmelt-dominated river (East River, Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5	0.9	18
7	Identification of Persistent Sulfidogenic Bacteria in Shale Gas Produced Waters. <i>Frontiers in Microbiology</i> , 2020, 11, 286.	1.5	15
8	A Model Analysis of the Tidal Engine That Drives Nitrogen Cycling in Coastal Riparian Aquifers. <i>Water Resources Research</i> , 2020, 56, e2019WR025662.	1.7	15
9	Ecological Assembly Processes Are Coordinated between Bacterial and Viral Communities in Fractured Shale Ecosystems. <i>MSystems</i> , 2020, 5, .	1.7	15
10	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.	1.3	25
11	Capability for arsenic mobilization in groundwater is distributed across broad phylogenetic lineages. <i>PLoS ONE</i> , 2019, 14, e0221694.	1.1	15
12	In situ transformation of ethoxylate and glycol surfactants by shale-colonizing microorganisms during hydraulic fracturing. <i>ISME Journal</i> , 2019, 13, 2690-2700.	4.4	18
13	Deep-Subsurface Pressure Stimulates Metabolic Plasticity in Shale-Colonizing <i>Halanaerobium</i> spp. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
14	Wetland Sediments Host Diverse Microbial Taxa Capable of Cycling Alcohols. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	10
15	Genome-Resolved Metagenomics Extends the Environmental Distribution of the <i>Verrucomicrobia</i> Phylum to the Deep Terrestrial Subsurface. <i>MSphere</i> , 2019, 4, .	1.3	38
16	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.	1.3	41
17	Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. <i>Nature Microbiology</i> , 2019, 4, 352-361.	5.9	78
18	Influences of organic carbon speciation on hyporheic corridor biogeochemistry and microbial ecology. <i>Nature Communications</i> , 2018, 9, 585.	5.8	110

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19	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.	1.8	28
20	Members of <i>Marinobacter</i> and <i>Arcobacter</i> Influence System Biogeochemistry During Early Production of Hydraulically Fractured Natural Gas Wells in the Appalachian Basin. <i>Frontiers in Microbiology</i> , 2018, 9, 2646.	1.5	33
21	Characterizing the Deep Terrestrial Subsurface Microbiome. <i>Methods in Molecular Biology</i> , 2018, 1849, 1-15.	0.4	4
22	Microbial Community Cohesion Mediates Community Turnover in Unperturbed Aquifers. <i>MSystems</i> , 2018, 3, .	1.7	63
23	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.	3.3	69
24	Viral and metabolic controls on high rates of microbial sulfur and carbon cycling in wetland ecosystems. <i>Microbiome</i> , 2018, 6, 138.	4.9	63
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.	4.2	64
26	Water Table Dynamics and Biogeochemical Cycling in a Shallow, Variably-Saturated Floodplain. <i>Environmental Science &amp; Technology</i> , 2017, 51, 3307-3317.	4.6	100
27	Anoxia stimulates microbially catalyzed metal release from Animas River sediments. <i>Environmental Sciences: Processes and Impacts</i> , 2017, 19, 578-585.	1.7	14
28	Draft Genome Sequences of Multiple <i>Frackibacter</i> Strains Isolated from Hydraulically Fractured Shale Environments. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
29	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	1.3	62
30	Members of the Candidate Phyla Radiation are functionally differentiated by carbon- and nitrogen-cycling capabilities. <i>Microbiome</i> , 2017, 5, 112.	4.9	118
31	Snowmelt Induced Hydrologic Perturbations Drive Dynamic Microbiological and Geochemical Behaviors across a Shallow Riparian Aquifer. <i>Frontiers in Earth Science</i> , 2016, 4, .	0.8	24
32	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. <i>ISME Journal</i> , 2016, 10, 2702-2714.	4.4	98
33	Seasonal hyporheic dynamics control coupled microbiology and geochemistry in Colorado River sediments. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2016, 121, 2976-2987.	1.3	49
34	Groundwater-surface water mixing shifts ecological assembly processes and stimulates organic carbon turnover. <i>Nature Communications</i> , 2016, 7, 11237.	5.8	290
35	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	5.8	994
36	Microbial metabolisms in a 2.5-km-deep ecosystem created by hydraulic fracturing in shales. <i>Nature Microbiology</i> , 2016, 1, 16146.	5.9	207

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37	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. <i>Environmental Microbiology</i> , 2016, 18, 159-173.	1.8	164
38	Genomic Expansion of Domain Archaea Highlights Roles for Organisms from New Phyla in Anaerobic Carbon Cycling. <i>Current Biology</i> , 2015, 25, 690-701.	1.8	522
39	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	13.7	1,050
40	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015, 17, 622-636.	1.8	32
41	CO <sub>2</sub> 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.	1.5	31
42	Trends and future challenges in sampling the deep terrestrial biosphere. <i>Frontiers in Microbiology</i> , 2014, 5, 481.	1.5	35
43	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	4.4	170
44	Characterization and transcription of arsenic respiration and resistance genes during <i>in situ</i> uranium bioremediation. <i>ISME Journal</i> , 2013, 7, 370-383.	4.4	80
45	Molecular Analysis of the <i>In Situ</i> Growth Rates of Subsurface <i>Geobacter</i> Species. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1646-1653.	1.4	35
46	Fermentation, Hydrogen, and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. <i>Science</i> , 2012, 337, 1661-1665.	6.0	637
47	Acetate Availability and its Influence on Sustainable Bioremediation of Uranium-Contaminated Groundwater. <i>Geomicrobiology Journal</i> , 2011, 28, 519-539.	1.0	222
48	Proteogenomic Monitoring of <i>Geobacter</i> Physiology during Stimulated Uranium Bioremediation. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6591-6599.	1.4	136