

# 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  | Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.  | 13.7 | 1,050     |
| 2  | Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.  | 5.8  | 994       |
| 3  | Fermentation, Hydrogen, and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. <i>Science</i> , 2012, 337, 1661-1665.   | 6.0  | 637       |
| 4  | 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       |
| 5  | Groundwater–surface water mixing shifts ecological assembly processes and stimulates organic carbon turnover. <i>Nature Communications</i> , 2016, 7, 11237.   | 5.8  | 290       |
| 6  | Acetate Availability and its Influence on Sustainable Bioremediation of Uranium-Contaminated Groundwater. <i>Geomicrobiology Journal</i> , 2011, 28, 519-539.  | 1.0  | 222       |
| 7  | 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       |
| 8  | Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.  | 4.4  | 170       |
| 9  | 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       |
| 10 | Proteogenomic Monitoring of <i>Geobacter</i> Physiology during Stimulated Uranium Bioremediation. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6591-6599.   | 1.4  | 136       |
| 11 | Members of the Candidate Phyla Radiation are functionally differentiated by carbon- and nitrogen-cycling capabilities. <i>Microbiome</i> , 2017, 5, 112.   | 4.9  | 118       |
| 12 | Influences of organic carbon speciation on hyporheic corridor biogeochemistry and microbial ecology. <i>Nature Communications</i> , 2018, 9, 585.  | 5.8  | 110       |
| 13 | 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       |
| 14 | 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        |
| 15 | 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        |
| 16 | Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. <i>Nature Microbiology</i> , 2019, 4, 352-361.   | 5.9  | 78        |
| 17 | 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        |
| 18 | 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        |

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|----|--|-----|-----------|
| 19 | Microbial Community Cohesion Mediates Community Turnover in Unperturbed Aquifers. <i>MSystems</i> , 2018, 3, .   | 1.7 | 63        |
| 20 | 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        |
| 21 | Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .  | 1.3 | 62        |
| 22 | 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        |
| 23 | 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        |
| 24 | 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        |
| 25 | 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        |
| 26 | Trends and future challenges in sampling the deep terrestrial biosphere. <i>Frontiers in Microbiology</i> , 2014, 5, 481.  | 1.5 | 35        |
| 27 | 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        |
| 28 | Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015, 17, 622-636.   | 1.8 | 32        |
| 29 | 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        |
| 30 | 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        |
| 31 | 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        |
| 32 | 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        |
| 33 | 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        |
| 34 | Deep-Subsurface Pressure Stimulates Metabolic Plasticity in Shale-Colonizing <i>Halanaerobium</i> spp. <i>Applied and Environmental Microbiology</i> , 2019, 85, .   | 1.4 | 20        |
| 35 | 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        |
| 36 | Seasonal manganese transport in the hyporheic zone of a snowmelt-dominated river (East River,)   | 0.9 | 18        |

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|----|--|-----|-----------|
| 37 | Capability for arsenic mobilization in groundwater is distributed across broad phylogenetic lineages. PLoS ONE, 2019, 14, e0221694.                          | 1.1 | 15        |
| 38 | Identification of Persistent Sulfidogenic Bacteria in Shale Gas Produced Waters. Frontiers in Microbiology, 2020, 11, 286.                                   | 1.5 | 15        |
| 39 | A Model Analysis of the Tidal Engine That Drives Nitrogen Cycling in Coastal Riparian Aquifers. Water Resources Research, 2020, 56, e2019WR025662.           | 1.7 | 15        |
| 40 | Ecological Assembly Processes Are Coordinated between Bacterial and Viral Communities in Fractured Shale Ecosystems. MSystems, 2020, 5, .                    | 1.7 | 15        |
| 41 | Anoxia stimulates microbially catalyzed metal release from Animas River sediments. Environmental Sciences: Processes and Impacts, 2017, 19, 578-585.         | 1.7 | 14        |
| 42 | Draft Genome Sequences of Multiple Frackibacter Strains Isolated from Hydraulically Fractured Shale Environments. Genome Announcements, 2017, 5, .           | 0.8 | 11        |
| 43 | Comparative geochemistry of flowback chemistry from the Utica/Point Pleasant and Marcellus formations. Chemical Geology, 2021, 564, 120041.                  | 1.4 | 11        |
| 44 | Wetland Sediments Host Diverse Microbial Taxa Capable of Cycling Alcohols. Applied and Environmental Microbiology, 2019, 85, .                               | 1.4 | 10        |
| 45 | Microbial colonization and persistence in deep fractured shales is guided by metabolic exchanges and viral predation. Microbiome, 2022, 10, 5.               | 4.9 | 9         |
| 46 | Implications of sample treatment on characterization of riverine dissolved organic matter. Environmental Sciences: Processes and Impacts, 2022, 24, 773-782. | 1.7 | 6         |
| 47 | Characterizing the Deep Terrestrial Subsurface Microbiome. Methods in Molecular Biology, 2018, 1849, 1-15.   | 0.4 | 4         |
| 48 | Ice Cover Influences Redox Dynamics in Prairie Pothole Wetland Sediments. Journal of Geophysical Research G: Biogeosciences, 2021, 126, e2021JG006318.       | 1.3 | 2         |