

William T Sloan

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

8,898
citations

126907

33
h-index

69250

77
g-index

85
all docs

85
docs citations

85
times ranked

12126
citing authors

#	ARTICLE	IF	CITATIONS
1	Economic and environmental assessment of organic waste to biomethane conversion. <i>Bioresource Technology</i> , 2022, 345, 126500.	9.6	22
2	Biochemistry shapes growth kinetics of nitrifiers and defines their activity under specific environmental conditions. <i>Biotechnology and Bioengineering</i> , 2022, 119, 1290-1300.	3.3	3
3	Validating Flow Cytometry as a Method for Quantifying <i>Bdellovibrio</i> Predatory Bacteria and Its Prey for Microbial Ecology. <i>Microbiology Spectrum</i> , 2022, 10, e0103321.	3.0	3
4	Techno-economic feasibility of distributed waste-to-hydrogen systems to support green transport in Glasgow. <i>International Journal of Hydrogen Energy</i> , 2022, 47, 13532-13551.	7.1	11
5	The role of shear dynamics in biofilm formation. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 33.	6.4	18
6	Deploying an <i>In Vitro</i> Gut Model to Assay the Impact of the Mannan-Oligosaccharide Prebiotic Bio-Mos on the Atlantic Salmon (<i>Salmo salar</i>) Gut Microbiome. <i>Microbiology Spectrum</i> , 2022, 10, e0195321.	3.0	3
7	A comprehensive artificial neural network model for gasification process prediction. <i>Applied Energy</i> , 2022, 320, 119289.	10.1	21
8	Life cycle assessment of biodiesel production from rapeseed oil: Influence of process parameters and scale. <i>Bioresource Technology</i> , 2022, 360, 127532.	9.6	29
9	Drift dynamics in microbial communities and the effective community size. <i>Environmental Microbiology</i> , 2021, 23, 2473-2483.	3.8	10
10	SalmoSim: the development of a three-compartment in vitro simulator of the Atlantic salmon GI tract and associated microbial communities. <i>Microbiome</i> , 2021, 9, 179.	11.1	5
11	Genome erosion and evidence for an intracellular niche “exploring the biology of mycoplasmas in Atlantic salmon. <i>Aquaculture</i> , 2021, 541, 736772.	3.5	27
12	In vitro and in vivo characterisation of <i>Listeria monocytogenes</i> outbreak isolates. <i>Food Control</i> , 2020, 107, 106784.	5.5	19
13	Impact of industrial production system parameters on chicken microbiomes: mechanisms to improve performance and reduce <i>Campylobacter</i> . <i>Microbiome</i> , 2020, 8, 128.	11.1	38
14	“Solar septic tank”™: evaluation of innovative decentralized treatment of blackwater in developing countries. <i>Journal of Water Sanitation and Hygiene for Development</i> , 2020, 10, 828-840.	1.8	4
15	Impact of <i>Methylobacterium</i> in the drinking water microbiome on removal of trihalomethanes. <i>International Biodeterioration and Biodegradation</i> , 2019, 141, 10-16.	3.9	13
16	Engineering artificial thermal mountains for large-scale water management and carbon drawdown. <i>Environmental Science: Water Research and Technology</i> , 2019, 5, 296-314.	2.4	0
17	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	13.3	491
18	Bioactivities and genome insights of a thermotolerant antibiotics-producing <i>Streptomyces</i> sp. TM32 reveal its potentials for novel drug discovery. <i>MicrobiologyOpen</i> , 2019, 8, e842.	3.0	14

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19	Solar Septic Tank: Next Generation Sequencing Reveals Effluent Microbial Community Composition as a Useful Index of System Performance. <i>Water (Switzerland)</i> , 2019, 11, 2660.	2.7	11
20	Herbicide-tolerant endophytic bacteria of rice plants as the biopriming agents for fertility recovery and disease suppression of unhealthy rice seeds. <i>BMC Plant Biology</i> , 2019, 19, 580.	3.6	22
21	Coupled virus - bacteria interactions and ecosystem function in an engineered microbial system. <i>Water Research</i> , 2019, 152, 264-273.	11.3	31
22	Neutral mechanisms and niche differentiation in steady-state insular microbial communities revealed by single cell analysis. <i>Environmental Microbiology</i> , 2019, 21, 164-181.	3.8	46
23	The Role of the Motility of <i>Methylobacterium</i> in Bacterial Interactions in Drinking Water. <i>Water (Switzerland)</i> , 2018, 10, 1386.	2.7	8
24	The effect of metabolic stress on genome stability of a synthetic biology chassis <i>Escherichia coli</i> K12 strain. <i>Microbial Cell Factories</i> , 2018, 17, 8.	4.0	23
25	The active microbial community more accurately reflects the anaerobic digestion process: 16S rRNA (gene) sequencing as a predictive tool. <i>Microbiome</i> , 2018, 6, 63.	11.1	138
26	Single-Cell Microfluidics to Study the Effects of Genome Deletion on Bacterial Growth Behavior. <i>ACS Synthetic Biology</i> , 2017, 6, 2219-2227.	3.8	17
27	A Keystone <i>Methylobacterium</i> Strain in Biofilm Formation in Drinking Water. <i>Water (Switzerland)</i> , 2017, 9, 778.	2.7	12
28	Bioreactor Scalability: Laboratory-Scale Bioreactor Design Influences Performance, Ecology, and Community Physiology in Expanded Granular Sludge Bed Bioreactors. <i>Frontiers in Microbiology</i> , 2017, 8, 664.	3.5	36
29	Biofilm community succession: a neutral perspective. <i>Microbiology (United Kingdom)</i> , 2017, 163, 664-668.	1.8	25
30	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , 2016, 10, 2557-2568.	9.8	570
31	Emerging investigators series: microbial communities in full-scale drinking water distribution systems – a meta-analysis. <i>Environmental Science: Water Research and Technology</i> , 2016, 2, 631-644.	2.4	98
32	The impact of sampling, PCR, and sequencing replication on discerning changes in drinking water bacterial community over diurnal time-scales. <i>Water Research</i> , 2016, 90, 216-224.	11.3	45
33	Probabilistic Models to Describe the Dynamics of Migrating Microbial Communities. <i>PLoS ONE</i> , 2015, 10, e0117221.	2.5	13
34	Insight into biases and sequencing errors for amplicon sequencing with the Illumina MiSeq platform. <i>Nucleic Acids Research</i> , 2015, 43, e37-e37.	14.5	626
35	Influence of biofilms on heavy metal immobilization in sustainable urban drainage systems (SuDS). <i>Environmental Technology (United Kingdom)</i> , 2015, 36, 2803-2814.	2.2	10
36	Nanoparticle transport in saturated porous medium using magnetic resonance imaging. <i>Chemical Engineering Journal</i> , 2015, 266, 156-162.	12.7	14

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37	Metagenomic Sequencing Unravels Gene Fragments with Phylogenetic Signatures of O ₂ -Tolerant NiFe Membrane-Bound Hydrogenases in Lacustrine Sediment. <i>Current Microbiology</i> , 2015, 71, 296-302.	2.2	1
38	Characterization of nanoparticle transport through quartz and dolomite gravels by magnetic resonance imaging. <i>International Journal of Environmental Science and Technology</i> , 2015, 12, 3373-3384.	3.5	7
39	Response to Effect of Serum Chloride on Mortality in Hypertensive Patients. <i>Hypertension</i> , 2014, 63, e15.	2.7	1
40	Fluvial network organization imprints on microbial co-occurrence networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12799-12804.	7.1	193
41	Family history of premature cardiovascular disease: blood pressure control and long-term mortality outcomes in hypertensive patients. <i>European Heart Journal</i> , 2014, 35, 563-570.	2.2	25
42	Predicting the effects of biochar on volatile petroleum hydrocarbon biodegradation and emanation from soil: A bacterial community finger-print analysis inferred modelling approach. <i>Soil Biology and Biochemistry</i> , 2014, 68, 20-30.	8.8	33
43	Spatial-Temporal Survey and Occupancy-Abundance Modeling To Predict Bacterial Community Dynamics in the Drinking Water Microbiome. <i>MBio</i> , 2014, 5, e01135-14.	4.1	160
44	Benchmarking of viral haplotype reconstruction programmes: an overview of the capacities and limitations of currently available programmes. <i>Briefings in Bioinformatics</i> , 2014, 15, 431-442.	6.5	59
45	Magnetic Resonance Imaging of Mass Transport and Structure Inside a Phototrophic Biofilm. <i>Current Microbiology</i> , 2013, 66, 456-461.	2.2	12
46	Serum Chloride Is an Independent Predictor of Mortality in Hypertensive Patients. <i>Hypertension</i> , 2013, 62, 836-843.	2.7	67
47	Blood Pressure Response to Patterns of Weather Fluctuations and Effect on Mortality. <i>Hypertension</i> , 2013, 62, 190-196.	2.7	47
48	Serum Uric Acid Level, Longitudinal Blood Pressure, Renal Function, and Long-Term Mortality in Treated Hypertensive Patients. <i>Hypertension</i> , 2013, 62, 105-111.	2.7	37
49	Headwaters are critical reservoirs of microbial diversity for fluvial networks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131760.	2.6	153
50	Long-Term and Ultra Long-Term Blood Pressure Variability During Follow-Up and Mortality in 14 522 Patients With Hypertension. <i>Hypertension</i> , 2013, 62, 698-705.	2.7	81
51	Modelling the effects of dispersal mechanisms and hydrodynamic regimes upon the structure of microbial communities within fluvial biofilms. <i>Environmental Microbiology</i> , 2013, 15, 1216-1225.	3.8	22
52	Erosion of biofilm-bound fluvial sediments. <i>Nature Geoscience</i> , 2013, 6, 770-774.	12.9	65
53	Microbial community assembly, theory and rare functions. <i>Frontiers in Microbiology</i> , 2013, 4, 68.	3.5	74
54	Investigation of Nanoparticle Transport Inside Coarse-Grained Geological Media Using Magnetic Resonance Imaging. <i>Environmental Science & Technology</i> , 2012, 46, 360-366.	10.0	15

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55	Quantifying the tensile strength of microbial mats grown over noncohesive sediments. <i>Biotechnology and Bioengineering</i> , 2012, 109, 1155-1164.	3.3	21
56	Long-Term Outcome following Attendance at a Transient Ischemic Attack Clinic. <i>International Journal of Stroke</i> , 2011, 6, 306-311.	5.9	11
57	Sustainable wastewater treatment: How might microbial fuel cells contribute. <i>Biotechnology Advances</i> , 2010, 28, 871-881.	11.7	289
58	Application of Paramagnetically Tagged Molecules for Magnetic Resonance Imaging of Biofilm Mass Transport Processes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4027-4036.	3.1	16
59	Combined niche and neutral effects in a microbial wastewater treatment community. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15345-15350.	7.1	504
60	Accurate determination of microbial diversity from 454 pyrosequencing data. <i>Nature Methods</i> , 2009, 6, 639-641.	19.0	895
61	The rational exploration of microbial diversity. <i>ISME Journal</i> , 2008, 2, 997-1006.	9.8	190
62	Predicting river flows for future climates using an autoregressive multinomial logit model. <i>Water Resources Research</i> , 2008, 44, .	4.2	15
63	Microbial landscapes: new paths to biofilm research. <i>Nature Reviews Microbiology</i> , 2007, 5, 76-81.	28.6	288
64	Neutral assembly of bacterial communities. <i>FEMS Microbiology Ecology</i> , 2007, 62, 171-180.	2.7	177
65	Modeling Taxa-Abundance Distributions in Microbial Communities using Environmental Sequence Data. <i>Microbial Ecology</i> , 2007, 53, 443-455.	2.8	151
66	Towards the design of diversity: stochastic models for community assembly in wastewater treatment plants. <i>Water Science and Technology</i> , 2006, 54, 227-236.	2.5	55
67	Taxa-area relationships for microbes: the unsampled and the unseen. <i>Ecology Letters</i> , 2006, 9, 805-812.	6.4	112
68	Quantifying the roles of immigration and chance in shaping prokaryote community structure. <i>Environmental Microbiology</i> , 2006, 8, 732-740.	3.8	971
69	What is the extent of prokaryotic diversity?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 2023-2037.	4.0	90
70	Exploring Microbial Diversity--A Vast Below. <i>Science</i> , 2005, 309, 1331-1333.	12.6	181
71	Estimating bacterial diversity from clone libraries with flat rank abundance distributions. <i>Environmental Microbiology</i> , 2004, 6, 1081-1085.	3.8	23
72	Incorporating topographic variability into a simple regional snowmelt model. <i>Hydrological Processes</i> , 2004, 18, 3371-3390.	2.6	3

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73	Prokaryotic diversity and its limits: microbial community structure in nature and implications for microbial ecology. <i>Current Opinion in Microbiology</i> , 2004, 7, 221-226.	5.1	275
74	Estimating prokaryotic diversity and its limits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 10494-10499.	7.1	975
75	Theory, community assembly, diversity and evolution in the microbial world. , 2001, , 59-76.		1
76	A physics-based function for modeling transient groundwater discharge at the watershed scale. <i>Water Resources Research</i> , 2000, 36, 225-241.	4.2	54
77	Modelling long-term contaminant migration in a catchment at fine spatial and temporal scales using the UP system. <i>Hydrological Processes</i> , 1999, 13, 823-846.	2.6	4
78	A GIS framework for modelling nitrogen leaching from agricultural areas in the Middle Hills, Nepal. <i>International Journal of Geographical Information Science</i> , 1998, 12, 479-490.	4.8	9
79	Stream chemistry in the middle hills and high mountains of the Himalayas, Nepal. <i>Journal of Hydrology</i> , 1995, 166, 61-79.	5.4	43
80	A simple model of stream nitrate concentrations in forested and deforested catchments in Mid-Wales. <i>Journal of Hydrology</i> , 1994, 158, 61-78.	5.4	11
81	The Uncountables. , 0, , 33-54.		0