

Katrine L Whiteson

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

4,972
citations

196777

29
h-index

129628

63
g-index

75
all docs

75
docs citations

75
times ranked

8101
citing authors

#	ARTICLE	IF	CITATIONS
1	Solutions in microbiome engineering: prioritizing barriers to organism establishment. ISME Journal, 2022, 16, 331-338.	4.4	58
2	Conceptual Exchanges for Understanding Free-Living and Host-Associated Microbiomes. MSystems, 2022, 7, e0137421.	1.7	3
3	Integrating Virus Monitoring Strategies for Safe Non-Potable Water Reuse. Water (Switzerland), 2022, 14, 1187.	1.2	7
4	The cure from within? a review of the microbiome and diet in melanoma. Cancer and Metastasis Reviews, 2022, 41, 261-280.	2.7	8
5	Fecal Microbial Community Composition in Myeloproliferative Neoplasm Patients Is Associated with an Inflammatory State. Microbiology Spectrum, 2022, 10, e0003222.	1.2	8
6	Phage Cocktails Constrain the Growth of <i>Enterococcus</i> . MSystems, 2022, 7, .	1.7	9
7	Liquid Chromatography Mass Spectrometry Detection of Antibiotic Agents in Sputum from Persons with Cystic Fibrosis. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	5
8	Comparing Stable Isotope Enrichment by Gas Chromatography with Time-of-Flight, Quadrupole Time-of-Flight, and Quadrupole Mass Spectrometry. Analytical Chemistry, 2021, 93, 2174-2182.	3.2	4
9	High-Fiber, Whole-Food Dietary Intervention Alters the Human Gut Microbiome but Not Fecal Short-Chain Fatty Acids. MSystems, 2021, 6, .	1.7	69
10	Design and Development of a Model to Study the Effect of Supplemental Oxygen on the Cystic Fibrosis Airway Microbiome. Journal of Visualized Experiments, 2021, , .	0.2	4
11	Model Systems to Study the Chronic, Polymicrobial Infections in Cystic Fibrosis: Current Approaches and Exploring Future Directions. MBio, 2021, 12, e0176321.	1.8	26
12	RNA Viromics of Southern California Wastewater and Detection of SARS-CoV-2 Single-Nucleotide Variants. Applied and Environmental Microbiology, 2021, 87, e0144821.	1.4	40
13	Lumacaftor/ivacaftor changes the lung microbiome and metabolome in cystic fibrosis patients. ERJ Open Research, 2021, 7, 00731-2020.	1.1	21
14	The emergence of microbiome centres. Nature Microbiology, 2020, 5, 2-3.	5.9	13
15	Fecal Microbiota Transplantation for the Treatment of Refractory Recurrent Urinary Tract Infection. Obstetrics and Gynecology, 2020, 136, 771-773.	1.2	12
16	Metagenomics of Wastewater Influent from Southern California Wastewater Treatment Facilities in the Era of COVID-19. Microbiology Resource Announcements, 2020, 9, .	0.3	11
17	Thriving Under Stress: <i>Pseudomonas aeruginosa</i> Outcompetes the Background Polymicrobial Community Under Treatment Conditions in a Novel Chronic Wound Model. Frontiers in Cellular and Infection Microbiology, 2020, 10, 569685.	1.8	8
18	Cervicovaginal Microbiome Composition Is Associated with Metabolic Profiles in Healthy Pregnancy. MBio, 2020, 11, .	1.8	30

#	ARTICLE	IF	CITATIONS
19	Fiber Force: A Fiber Diet Intervention in an Advanced Course-Based Undergraduate Research Experience (CURE) Course. <i>Journal of Microbiology and Biology Education</i> , 2020, 21, .	0.5	15
20	Longitudinal Associations of the Cystic Fibrosis Airway Microbiome and Volatile Metabolites: A Case Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 174.	1.8	19
21	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020, 6, 192-204.	3.8	162
22	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184
23	PQS Produced by the <i>Pseudomonas aeruginosa</i> Stress Response Repels Swarms Away from Bacteriophage and Antibiotics. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	49
24	Maturation of the infant rhesus macaque gut microbiome and its role in the development of diarrheal disease. <i>Genome Biology</i> , 2019, 20, 173.	3.8	40
25	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
26	Cystic Fibrosis-Associated <i>Stenotrophomonas maltophilia</i> Strain-Specific Adaptations and Responses to pH. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	11
27	Vive la Persistence: Engineering Human Microbiomes in the 21st Century. <i>MSystems</i> , 2018, 3, .	1.7	2
28	Fermentation products in the cystic fibrosis airways induce aggregation and dormancy-associated expression profiles in a CF clinical isolate of <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	27
29	Longitudinal Monitoring of Biofilm Formation via Robust Surface-Enhanced Raman Scattering Quantification of <i>Pseudomonas aeruginosa</i> -Produced Metabolites. <i>ACS Applied Materials & Interfaces</i> , 2018, 10, 12364-12373.	4.0	51
30	The Phosphate Binder Ferric Citrate Alters the Gut Microbiome in Rats with Chronic Kidney Disease. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2018, 367, 452-460.	1.3	33
31	Getting Our Fingers on the Pulse of Slow-Growing Bacteria in Hard-To-Reach Places. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	7
32	Gut microbial and metabolomic profiles after fecal microbiota transplantation in pediatric ulcerative colitis patients. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	73
33	Tracking Polymicrobial Metabolism in Cystic Fibrosis Airways: <i>Pseudomonas aeruginosa</i> Metabolism and Physiology Are Influenced by <i>Rothia mucilaginosa</i> -Derived Metabolites. <i>MSphere</i> , 2018, 3, .	1.3	34
34	The Microbiome and Metabolome of Preterm Infant Stool Are Personalized and Not Driven by Health Outcomes, Including Necrotizing Enterocolitis and Late-Onset Sepsis. <i>MSphere</i> , 2018, 3, .	1.3	107
35	Predictable Molecular Adaptation of Coevolving <i>Enterococcus faecium</i> and Lytic Phage EfV12-phi1. <i>Frontiers in Microbiology</i> , 2018, 9, 3192.	1.5	30
36	Investigating the Role of the Gut Microbiome in the Inflammatory State of Myeloproliferative Neoplasms. <i>Blood</i> , 2018, 132, 3051-3051.	0.6	2

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37	Stable isotope profiles reveal active production of VOCs from human-associated microbes. <i>Journal of Breath Research</i> , 2017, 11, 017101.	1.5	26
38	Making It Last: Storage Time and Temperature Have Differential Impacts on Metabolite Profiles of Airway Samples from Cystic Fibrosis Patients. <i>MSystems</i> , 2017, 2, .	1.7	11
39	Editorial: Virus Discovery by Metagenomics: The (Im)possibilities. <i>Frontiers in Microbiology</i> , 2017, 8, 1710.	1.5	32
40	Plasma Metabolomics in Response to an Acute Bout of Exercise in Adolescents Boys and Girls. <i>Medicine and Science in Sports and Exercise</i> , 2017, 49, 282-283.	0.2	1
41	Bacteria in the airways of patients with cystic fibrosis are genetically capable of producing VOCs in breath. <i>Journal of Breath Research</i> , 2016, 10, 047103.	1.5	30
42	Ecological networking of cystic fibrosis lung infections. <i>Npj Biofilms and Microbiomes</i> , 2016, 2, 4.	2.9	77
43	Microbial, host and xenobiotic diversity in the cystic fibrosis sputum metabolome. <i>ISME Journal</i> , 2016, 10, 1483-1498.	4.4	88
44	Metabolomics of pulmonary exacerbations reveals the personalized nature of cystic fibrosis disease. <i>PeerJ</i> , 2016, 4, e2174.	0.9	45
45	A Winogradsky-based culture system shows an association between microbial fermentation and cystic fibrosis exacerbation. <i>ISME Journal</i> , 2015, 9, 1024-1038.	4.4	59
46	Breath gas metabolites and bacterial metagenomes from cystic fibrosis airways indicate active pH neutral 2,3-butanedione fermentation. <i>ISME Journal</i> , 2014, 8, 1247-1258.	4.4	114
47	Noma Affected Children from Niger Have Distinct Oral Microbial Communities Based on High-Throughput Sequencing of 16S rRNA Gene Fragments. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3240.	1.3	14
48	Biogeochemical Forces Shape the Composition and Physiology of Polymicrobial Communities in the Cystic Fibrosis Lung. <i>MBio</i> , 2014, 5, e00956-13.	1.8	94
49	The Upper Respiratory Tract as a Microbial Source for Pulmonary Infections in Cystic Fibrosis. Parallels from Island Biogeography. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014, 189, 1309-1315.	2.5	100
50	A genomic perspective on a new bacterial genus and species from the Alcaligenaceae family, <i>Basilea pissitacipulmonis</i> . <i>BMC Genomics</i> , 2014, 15, 169.	1.2	10
51	Bacteriophage adhering to mucus provide a non-host-derived immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10771-10776.	3.3	753
52	Mechanistic Model of <i>Rothia mucilaginosa</i> Adaptation toward Persistence in the CF Lung, Based on a Genome Reconstructed from Metagenomic Data. <i>PLoS ONE</i> , 2013, 8, e64285.	1.1	51
53	Going viral: next-generation sequencing applied to phage populations in the human gut. <i>Nature Reviews Microbiology</i> , 2012, 10, 607-617.	13.6	377
54	Infant gut microbial colonization and health: recent findings from metagenomics studies. <i>Journal of Integrated OMICS</i> , 2012, 2, .	0.5	4

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55	Analysis of the salivary microbiome using culture-independent techniques. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 4.	1.2	54
56	Bacterial Diversity in Oral Samples of Children in Niger with Acute Noma, Acute Necrotizing Gingivitis, and Healthy Controls. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1556.	1.3	66
57	The salivary microbiome, assessed by a high-throughput and culture-independent approach. <i>Journal of Integrated OMICS</i> , 2011, 1, .	0.5	11
58	The CodY pleiotropic repressor controls virulence in gram-positive pathogens. <i>FEMS Immunology and Medical Microbiology</i> , 2011, 62, 123-139.	2.7	94
59	Study of inter- and intra-individual variations in the salivary microbiota. <i>BMC Genomics</i> , 2010, 11, 523.	1.2	212
60	Metagenomic study of the oral microbiota by Illumina high-throughput sequencing. <i>Journal of Microbiological Methods</i> , 2009, 79, 266-271.	0.7	289
61	Binding and Catalytic Contributions to Site Recognition by Flp Recombinase. <i>Journal of Biological Chemistry</i> , 2008, 283, 11414-11423.	1.6	12
62	Identification of a Potential General Acid/Base in the Reversible Phosphoryl Transfer Reactions Catalyzed by Tyrosine Recombinases: Flp H305. <i>Chemistry and Biology</i> , 2007, 14, 121-129.	6.2	24
63	Mechanisms of Site-Specific Recombination. <i>Annual Review of Biochemistry</i> , 2006, 75, 567-605.	5.0	708