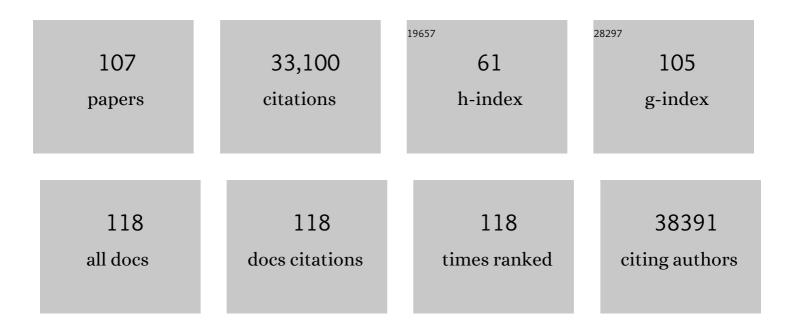
Thomas M Schmidt

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
2	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
3	The Ribosomal Database Project (RDP-II): previewing a new autoaligner that allows regular updates and the new prokaryotic taxonomy. Nucleic Acids Research, 2003, 31, 442-443.	14.5	1,219
4	Identification of the Uncultured Bacillus of Whipple's Disease. New England Journal of Medicine, 1992, 327, 293-301.	27.0	1,196
5	Fundamentals of Microbial Community Resistance and Resilience. Frontiers in Microbiology, 2012, 3, 417.	3.5	1,131
6	The Agent of Bacillary Angiomatosis. New England Journal of Medicine, 1990, 323, 1573-1580.	27.0	985
7	Decreased Diversity of the Fecal Microbiome in Recurrent <i>Clostridium difficile</i> –Associated Diarrhea. Journal of Infectious Diseases, 2008, 197, 435-438.	4.0	954
8	rRNA Operon Copy Number Reflects Ecological Strategies of Bacteria. Applied and Environmental Microbiology, 2000, 66, 1328-1333.	3.1	932
9	rrndb: the Ribosomal RNA Operon Copy Number Database. Nucleic Acids Research, 2001, 29, 181-184.	14.5	882
10	A new version of the RDP (Ribosomal Database Project). Nucleic Acids Research, 1999, 27, 171-173.	14.5	863
11	rrnDB: improved tools for interpreting rRNA gene abundance in bacteria and archaea and a new foundation for future development. Nucleic Acids Research, 2015, 43, D593-D598.	14.5	817
12	Comparison of the Respiratory Microbiome in Healthy Nonsmokers and Smokers. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1067-1075.	5.6	655
13	Analysis of the Upper Respiratory Tract Microbiotas as the Source of the Lung and Gastric Microbiotas in Healthy Individuals. MBio, 2015, 6, e00037.	4.1	601
14	Gut microbiome–derived metabolites modulate intestinal epithelial cell damage and mitigate graft-versus-host disease. Nature Immunology, 2016, 17, 505-513.	14.5	536
15	Dynamics of Human Gut Microbiota and Short-Chain Fatty Acids in Response to Dietary Interventions with Three Fermentable Fibers. MBio, 2019, 10, .	4.1	515
16	Reproducible Community Dynamics of the Gastrointestinal Microbiota following Antibiotic Perturbation. Infection and Immunity, 2009, 77, 2367-2375.	2.2	489
17	Systematic artifacts in metagenomes from complex microbial communities. ISME Journal, 2009, 3, 1314-1317.	9.8	412
18	rrnDB: documenting the number of rRNA and tRNA genes in bacteria and archaea. Nucleic Acids Research, 2009, 37, D489-D493.	14.5	398

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19	Exploiting rRNA operon copy number to investigate bacterial reproductive strategies. Nature Microbiology, 2016, 1, 16160.	13.3	371
20	New Strategies for Cultivation and Detection of Previously Uncultured Microbes. Applied and Environmental Microbiology, 2004, 70, 4748-4755.	3.1	369
21	Perennial grasslands enhance biodiversity and multiple ecosystem services in bioenergy landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1652-1657.	7.1	366
22	Land-use history has a stronger impact on soil microbial community composition than aboveground vegetation and soil properties. Soil Biology and Biochemistry, 2011, 43, 2184-2193.	8.8	362
23	Application of a Neutral Community Model To Assess Structuring of the Human Lung Microbiome. MBio, 2015, 6, .	4.1	325
24	Isolation and Characterization of Soil Bacteria That Define Terriglobus gen. nov., in the Phylum Acidobacteria. Applied and Environmental Microbiology, 2007, 73, 2708-2717.	3.1	301
25	Acetogenesis from H ₂ Plus CO ₂ by Spirochetes from Termite Guts. Science, 1999, 283, 686-689.	12.6	297
26	Antibiotic-Associated Diarrhea Accompanied by Large-Scale Alterations in the Composition of the Fecal Microbiota. Journal of Clinical Microbiology, 2004, 42, 1203-1206.	3.9	282
27	SwissFEL: The Swiss X-ray Free Electron Laser. Applied Sciences (Switzerland), 2017, 7, 720.	2.5	272
28	Variable responses of human microbiomes to dietary supplementation with resistant starch. Microbiome, 2016, 4, 33.	11.1	269
29	Diversity and dynamics of microbial communities in soils from agro-ecosystems. Environmental Microbiology, 2003, 5, 441-452.	3.8	266
30	Influence of Plant Polymers on the Distribution and Cultivation of Bacteria in the Phylum <i>Acidobacteria</i> . Applied and Environmental Microbiology, 2011, 77, 586-596.	3.1	227
31	Changes in the gut microbiome and fermentation products concurrent with enhanced longevity in acarbose-treated mice. BMC Microbiology, 2019, 19, 130.	3.3	218
32	Neonatal acquisition of <i>Clostridia</i> species protects against colonization by bacterial pathogens. Science, 2017, 356, 315-319.	12.6	199
33	Shallow breathing: bacterial life at low O2. Nature Reviews Microbiology, 2013, 11, 205-212.	28.6	188
34	Phylogenetic Analysis of Nonthermophilic Members of the Kingdom <i>Crenarchaeota</i> and Their Diversity and Abundance in Soils. Applied and Environmental Microbiology, 1998, 64, 4333-4339.	3.1	187
35	Symbiotic bacteria appear to mediate hyena social odors. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19832-19837.	7.1	184
36	Farming for Ecosystem Services: An Ecological Approach to Production Agriculture. BioScience, 2014, 64, 404-415.	4.9	184

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37	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. Trends in Cancer, 2020, 6, 192-204.	7.4	162
38	The physiology and ecological implications of efficient growth. ISME Journal, 2015, 9, 1481-1487.	9.8	155
39	Evolution of competitive fitness in experimental populations of E. coli: what makes one genotype a better competitor than another?. Antonie Van Leeuwenhoek, 1998, 73, 35-47.	1.7	154
40	Life History Implications of rRNA Gene Copy Number in Escherichia coli. Applied and Environmental Microbiology, 2004, 70, 6670-6677.	3.1	141
41	A compact and cost-effective hard X-ray free-electron laser driven by a high-brightness and low-energy electron beam. Nature Photonics, 2020, 14, 748-754.	31.4	140
42	Agriculture's impact on microbial diversity and associated fluxes of carbon dioxide and methane. ISME Journal, 2011, 5, 1683-1691.	9.8	138
43	Bacterial colonization stimulates a complex physiological response in the immature human intestinal epithelium. ELife, 2017, 6, .	6.0	132
44	A gene-targeted approach to investigate the intestinal butyrate-producing bacterialcommunity. Microbiome, 2013, 1, 8.	11.1	129
45	The daily dynamics of cystic fibrosis airway microbiota during clinical stability and at exacerbation. Microbiome, 2015, 3, 12.	11.1	122
46	Multicenter Comparison of Lung and Oral Microbiomes of HIV-infected and HIV-uninfected Individuals. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 1335-1344.	5.6	120
47	Genomic and Physiological Characterization of the Verrucomicrobia Isolate Diplosphaera colitermitum gen. nov., sp. nov., Reveals Microaerophily and Nitrogen Fixation Genes. Applied and Environmental Microbiology, 2012, 78, 1544-1555.	3.1	115
48	Phylogenetic relationships among the agent of bacillary angiomatosis, Bartonella bacilliformis, and other alpha-proteobacteria. Molecular Microbiology, 1992, 6, 1801-1807.	2.5	111
49	Environmental factors influencing the distribution of rRNA from Verrucomicrobia in soil. FEMS Microbiology Ecology, 2001, 35, 105-112.	2.7	108
50	Evidence for a bacterial mechanism for group-specific social odors among hyenas. Scientific Reports, 2012, 2, 615.	3.3	107
51	Archaeal nucleic acids in picoplankton from great lakes on three continents. Microbial Ecology, 2003, 46, 238-248.	2.8	101
52	Lung and gut microbiota are altered by hyperoxia and contribute to oxygen-induced lung injury in mice. Science Translational Medicine, 2020, 12, .	12.4	97
53	A Small, Dilute-Cytoplasm, High-Affinity, Novel Bacterium Isolated by Extinction Culture and Having Kinetic Constants Compatible with Growth at Ambient Concentrations of Dissolved Nutrients in Seawater. Applied and Environmental Microbiology, 1998, 64, 4467-4476.	3.1	92
54	Functional Gene Differences in Soil Microbial Communities from Conventional, Low-Input, and Organic Farmlands. Applied and Environmental Microbiology, 2013, 79, 1284-1292.	3.1	90

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55	Effects of Atypical Antipsychotic Treatment and Resistant Starch Supplementation on Gut Microbiome Composition in a Cohort of Patients with Bipolar Disorder or Schizophrenia. Pharmacotherapy, 2019, 39, 161-170.	2.6	81
56	Performance of the Translational Apparatus Varies with the Ecological Strategies of Bacteria. Journal of Bacteriology, 2007, 189, 3237-3245.	2.2	77
57	Bacterial Dissemination to the Brain in Sepsis. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 747-756.	5.6	74
58	Colonization of the Cecal Mucosa by Helicobacter hepaticus Impacts the Diversity of the Indigenous Microbiota. Infection and Immunity, 2005, 73, 6952-6961.	2.2	72
59	[16] Phylogenetic identification of uncultured pathogens using ribosomal RNA sequences. Methods in Enzymology, 1994, 235, 205-222.	1.0	71
60	Rates and Consequences of Recombination between rRNA Operons. Journal of Bacteriology, 2003, 185, 966-972.	2.2	71
61	Vertebrate Hosts as Islands: Dynamics of Selection, Immigration, Loss, Persistence, and Potential Function of Bacteria on Salamander Skin. Frontiers in Microbiology, 2016, 7, 333.	3.5	65
62	Biomass and biofuel crop effects on biodiversity and ecosystem services in the North Central US. Biomass and Bioenergy, 2018, 114, 18-29.	5.7	61
63	Bacterial growth efficiency varies in soils under different land management practices. Soil Biology and Biochemistry, 2014, 69, 282-290.	8.8	60
64	A synthesis of bacterial and archaeal phenotypic trait data. Scientific Data, 2020, 7, 170.	5.3	59
65	<i>Muribaculaceae</i> Genomes Assembled from Metagenomes Suggest Genetic Drivers of Differential Response to Acarbose Treatment in Mice. MSphere, 2021, 6, e0085121.	2.9	53
66	Role of Rhodobacter sp. Strain PS9, a Purple Non-Sulfur Photosynthetic Bacterium Isolated from an Anaerobic Swine Waste Lagoon, in Odor Remediation. Applied and Environmental Microbiology, 2003, 69, 1710-1720.	3.1	51
67	The SwissFEL soft X-ray free-electron laser beamline: Athos. Journal of Synchrotron Radiation, 2019, 26, 1073-1084.	2.4	51
68	The first cellular bioenergetic process: Primitive generation of a proton-motive force. Journal of Molecular Evolution, 1991, 33, 297-304.	1.8	44
69	Distribution of the tfdA Gene in Soil Bacteria That Do Not Degrade 2,4-Dichlorophenoxyacetic Acid (2,4-D). Microbial Ecology, 1997, 34, 90-96.	2.8	43
70	Nucleic acid content of Synechococcus spp. during growth in continuous light and light/dark cycles. Archives of Microbiology, 1998, 170, 201-207.	2.2	43
71	Butyrogenic bacteria after acute graft-versus-host disease (GVHD) are associated with the development of steroid-refractory GVHD. Blood Advances, 2019, 3, 2866-2869.	5.2	40
72	Multiphasic analysis of the temporal development of the distal gut microbiota in patients following ileal pouch anal anastomosis. Microbiome, 2013, 1, 9.	11.1	35

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73	Overview of the Gastrointestinal Microbiota. Advances in Experimental Medicine and Biology, 2008, 635, 29-40.	1.6	35
74	Growth Rate-Dependent Accumulation of RNA from Plasmid-Borne rRNA Operons in <i>Escherichia coli</i> . Journal of Bacteriology, 1998, 180, 1970-1972.	2.2	32
75	Spectral characterization of c-type cytochromes purified from Beggiatoa alba. Archives of Microbiology, 1990, 154, 453-458.	2.2	29
76	Targeting the Gut Microbiome to Mitigate Immunotherapy-Induced Colitis in Cancer. Trends in Cancer, 2021, 7, 583-593.	7.4	26
77	Diverse events have transferred genes for edible seaweed digestion from marine to human gut bacteria. Cell Host and Microbe, 2022, 30, 314-328.e11.	11.0	25
78	Phylogenetic Characterization and Prevalence of " <i>Spirobacillus cienkowskii</i> ,―a Red-Pigmented, Spiral-Shaped Bacterial Pathogen of Freshwater <i>Daphnia</i> Species. Applied and Environmental Microbiology, 2008, 74, 1575-1582.	3.1	24
79	The maturing of microbial ecology. International Microbiology, 2006, 9, 217-23.	2.4	24
80	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota. Nature Microbiology, 2022, 7, 556-569.	13.3	21
81	Studying the Enteric Microbiome in Inflammatory Bowel Diseases: Getting through the Growing Pains and Moving Forward. Frontiers in Microbiology, 2011, 2, 144.	3.5	20
82	Development of an ecophysiological model for <i>Diplosphaera colotermitum</i> TAV2, a termite hindgut Verrucomicrobium. ISME Journal, 2013, 7, 1803-1813.	9.8	18
83	Undulator beamline optimization with integrated chicanes for X-ray free-electron-laser facilities. Journal of Synchrotron Radiation, 2016, 23, 861-868.	2.4	18
84	Protein synthesis by Beggiatoa alba B18LD in the presence and absence of sulfide. Archives of Microbiology, 1986, 144, 158-162.	2.2	17
85	Identifying and Removing Artificial Replicates from 454 Pyrosequencing Data. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5409-pdb.prot5409.	0.3	14
86	Multiplicity of Ribosomal RNA Operons in Prokaryotic Genomes. , 1998, , 221-229.		14
87	The emergence of microbiome centres. Nature Microbiology, 2020, 5, 2-3.	13.3	13
88	A Little O2 May Go a Long Way in Structuring the GI Microbiome. Gastroenterology, 2014, 147, 956-959.	1.3	12
89	Application of Traditional and Phylogenetically Based Comparative Methods to Test for a Trade-off in Bacterial Growth Rate at Low versus High Substrate Concentration. Microbial Ecology, 1999, 38, 191.	2.8	12
90	Electron transport and respiration in Beggiatoa and Vitreoscilla. Archives of Microbiology, 1986, 145, 71-75.	2.2	11

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91	Differences in codon bias cannot explain differences in translational power among microbes. BMC Bioinformatics, 2005, 6, 3.	2.6	11
92	Bacterial Communities in Malagasy Soils with Differing Levels of Disturbance Affecting Botanical Diversity. PLoS ONE, 2014, 9, e85097.	2.5	11
93	The effect of natural selection on the performance of maximum parsimony. BMC Evolutionary Biology, 2007, 7, 94.	3.2	8
94	Analysis of the first magnetic results of the PSI APPLE X undulators in elliptical polarisation. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2021, 987, 164741.	1.6	8
95	Age-Related Variation in the Scent Pouch Bacterial Communities of Striped Hyenas (Hyaena hyaena). , 2016, , 87-103.		8
96	Physiological and Ecological Adaptations of Slow-Growing, Heterotrophic Microbes and Consequences for Cultivation. Microbiology Monographs, 2009, , 257-276.	0.6	6
97	Demonstration of a compact x-ray free-electron laser using the optical klystron effect. Applied Physics Letters, 2021, 119, .	3.3	6
98	A systems approach to model natural variation in reactive properties of bacterial ribosomes. BMC Systems Biology, 2008, 2, 62.	3.0	5
99	Microfluidic Sensors with Impregnated Fluorophores for Simultaneous Imaging of Spatial Structure and Chemical Oxygen Gradients. ACS Sensors, 2019, 4, 317-325.	7.8	5
100	Environmental factors influencing the distribution of rRNA from Verrucomicrobia in soil. FEMS Microbiology Ecology, 2001, 35, 105-112.	2.7	4
101	The Effect of Natural Selection on Phylogeny Reconstruction Algorithms. Lecture Notes in Computer Science, 2003, , 13-24.	1.3	3
102	Conceptual Exchanges for Understanding Free-Living and Host-Associated Microbiomes. MSystems, 2022, 7, e0137421.	3.8	3
103	Bacteria Battling for Survival. , 2012, , 59-64.		2
104	Changes in Synechococcus Population Size and Cellular Ribosomal RNA Content in Response to Predation and Nutrient Limitation. Microbial Ecology, 2004, 48, 1-9.	2.8	1
105	Rational Modification of Intestinal Microbiome and Metabolites after Allogeneic Hematopoietic Stem Cell Transplantation with Resistant Starch: A Pilot Study. Blood, 2019, 134, 3276-3276.	1.4	1
106	Measurement of rRNA Abundance by Hybridization with Oligodeoxynucleotide Probes. , 0, , 897-908.		0
107	Stitching together a healthy gut microbiome with fiber. Cell Host and Microbe, 2022, 30, 762-763.	11.0	0