

# Sean M Gibbons

## List of Publications by Year in descending order

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Version: 2024-02-01

71  
papers

21,559  
citations

81743

39  
h-index

76769

74  
g-index

94  
all docs

94  
docs citations

94  
times ranked

26475  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
3	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	6.0	751
4	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. <i>Nature Communications</i> , 2017, 8, 1784.	5.8	714
5	Effects of Diurnal Variation of Gut Microbes and High-Fat Feeding on Host Circadian Clock Function and Metabolism. <i>Cell Host and Microbe</i> , 2015, 17, 681-689.	5.1	634
6	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014, 2, e545.	0.9	535
7	Health and disease markers correlate with gut microbiome composition across thousands of people. <i>Nature Communications</i> , 2020, 11, 5206.	5.8	378
8	Adaptive Evolution within Gut Microbiomes of Healthy People. <i>Cell Host and Microbe</i> , 2019, 25, 656-667.e8.	5.1	289
9	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. <i>Nature Metabolism</i> , 2021, 3, 274-286.	5.1	278
10	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. <i>Nature Medicine</i> , 2019, 25, 1442-1452.	15.2	255
11	Whole-grain wheat consumption reduces inflammation in a randomized controlled trial on overweight and obese subjects with unhealthy dietary and lifestyle behaviors: role of polyphenols bound to cereal dietary fiber. <i>American Journal of Clinical Nutrition</i> , 2015, 101, 251-261.	2.2	246
12	Blood metabolome predicts gut microbiome $\alpha$ -diversity in humans. <i>Nature Biotechnology</i> , 2019, 37, 1217-1228.	9.4	213
13	Evidence for a persistent microbial seed bank throughout the global ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4651-4655.	3.3	200
14	Spatial scale drives patterns in soil bacterial diversity. <i>Environmental Microbiology</i> , 2016, 18, 2039-2051.	1.8	194
15	Use and abuse of correlation analyses in microbial ecology. <i>ISME Journal</i> , 2019, 13, 2647-2655.	4.4	193
16	Severe plant invasions can increase mycorrhizal fungal abundance and diversity. <i>ISME Journal</i> , 2013, 7, 1424-1433.	4.4	180
17	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021, 184, 2053-2067.e18.	13.5	167
18	Characterization of the salivary microbiome in patients with pancreatic cancer. <i>PeerJ</i> , 2015, 3, e1373.	0.9	150

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19	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015, 3, 21.	4.9	140
20	454â€sequencing reveals stochastic local reassembly and high disturbance tolerance within arbuscular mycorrhizal fungal communities. <i>Journal of Ecology</i> , 2012, 100, 151-160.	1.9	131
21	The Microbiome Stress Project: Toward a Global Meta-Analysis of Environmental Stressors and Their Effects on Microbial Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 3272.	1.5	126
22	MICOM: Metagenome-Scale Modeling To Infer Metabolic Interactions in the Gut Microbiota. <i>MSystems</i> , 2020, 5, .	1.7	126
23	Human and Environmental Impacts on River Sediment Microbial Communities. <i>PLoS ONE</i> , 2014, 9, e97435.	1.1	115
24	Correcting for batch effects in case-control microbiome studies. <i>PLoS Computational Biology</i> , 2018, 14, e1006102.	1.5	108
25	Investigating the Impact of Storage Conditions on Microbial Community Composition in Soil Samples. <i>PLoS ONE</i> , 2013, 8, e70460.	1.1	108
26	Characterizing changes in soil bacterial community structure in response to short-term warming. <i>FEMS Microbiology Ecology</i> , 2014, 89, 281-292.	1.3	107
27	Microbial diversity â€” exploration of natural ecosystems and microbiomes. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 66-72.	1.5	105
28	Two dynamic regimes in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017, 13, e1005364.	1.5	101
29	Invasive Plants Rapidly Reshape Soil Properties in a Grassland Ecosystem. <i>MSystems</i> , 2017, 2, .	1.7	91
30	Ecological Succession and Viability of Human-Associated Microbiota on Restroom Surfaces. <i>Applied and Environmental Microbiology</i> , 2015, 81, 765-773.	1.4	89
31	Understanding Cultivar-Specificity and Soil Determinants of the Cannabis Microbiome. <i>PLoS ONE</i> , 2014, 9, e99641.	1.1	73
32	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. <i>Cell Reports</i> , 2018, 24, 1842-1851.	2.9	72
33	Ocean acidification shows negligible impacts on high-latitude bacterial community structure in coastal pelagic mesocosms. <i>Biogeosciences</i> , 2013, 10, 555-566.	1.3	60
34	Will different <sc>OTU</sc> delineation methods change interpretation of arbuscular mycorrhizal fungal community patterns?. <i>New Phytologist</i> , 2014, 202, 1101-1104.	3.5	58
35	The short-chain fatty acid receptor, FFA2, contributes to gestational glucose homeostasis. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 309, E840-E851.	1.8	57
36	Hyporheic Microbial Community Development Is a Sensitive Indicator of Metal Contamination. <i>Environmental Science &amp; Technology</i> , 2009, 43, 6158-6163.	4.6	51

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37	Disturbance Regimes Predictably Alter Diversity in an Ecologically Complex Bacterial System. MBio, 2016, 7, .	1.8	47
38	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. MSystems, 2017, 2, .	1.7	47
39	Longitudinal analysis reveals transition barriers between dominant ecological states in the gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13839-13845.	3.3	47
40	Genomic and functional characterization of a mucosal symbiont involved in early-stage colorectal cancer. Cell Host and Microbe, 2021, 29, 1589-1598.e6.	5.1	44
41	Microbial community ecology: Function over phylogeny. Nature Ecology and Evolution, 2017, 1, 32.	3.4	43
42	Endospores and other lysis-resistant bacteria comprise a widely shared core community within the human microbiota. ISME Journal, 2018, 12, 2403-2416.	4.4	40
43	Modeling microbial community structure and functional diversity across time and space. FEMS Microbiology Letters, 2012, 332, 91-98.	0.7	38
44	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. Scientific Reports, 2018, 8, 12699.	1.6	37
45	Athletic equipment microbiota are shaped by interactions with human skin. Microbiome, 2015, 3, 25.	4.9	36
46	Identifying predictive features of Clostridium difficile infection recurrence before, during, and after primary antibiotic treatment. Microbiome, 2017, 5, 148.	4.9	36
47	Aquarium microbiome response to ninety-percent system water change: Clues to microbiome management. Zoo Biology, 2015, 34, 360-367.	0.5	35
48	Keystone taxa indispensable for microbiome recovery. Nature Microbiology, 2020, 5, 1067-1068.	5.9	35
49	Arbuscular mycorrhizal fungal communities show low resistance and high resilience to wildfire disturbance. Plant and Soil, 2015, 397, 347-356.	1.8	33
50	The Built Environment Is a Microbial Wasteland. MSystems, 2016, 1, .	1.7	33
51	Shrub encroachment is associated with changes in soil bacterial community composition in a temperate grassland ecosystem. Plant and Soil, 2018, 425, 539-551.	1.8	30
52	Designing synbiotics for improved human health. Microbial Biotechnology, 2018, 11, 141-144.	2.0	29
53	Rapid response of arbuscular mycorrhizal fungal communities to short-term fertilization in an alpine grassland on the Qinghai-Tibet Plateau. PeerJ, 2016, 4, e2226.	0.9	29
54	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. MSystems, 2021, 6, .	1.7	28

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55	Use of Microcalorimetry To Determine the Costs and Benefits to <i>Pseudomonas putida</i> Strain KT2440 of Harboring Cadmium Efflux Genes. <i>Applied and Environmental Microbiology</i> , 2011, 77, 108-113.	1.4	24
56	Heterogeneity in statin responses explained by variation in the human gut microbiome. <i>Med</i> , 2022, 3, 388-405.e6.	2.2	21
57	Perspective: Leveraging the Gut Microbiota to Predict Personalized Responses to Dietary, Prebiotic, and Probiotic Interventions. <i>Advances in Nutrition</i> , 2022, 13, 1450-1461.	2.9	21
58	Systems biology approaches towards predictive microbial ecology. <i>Environmental Microbiology</i> , 2018, 20, 4197-4209.	1.8	19
59	From taxonomy to metabolic output: what factors define gut microbiome health?. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	19
60	The geometry of clinical labs and wellness states from deeply phenotyped humans. <i>Nature Communications</i> , 2021, 12, 3578.	5.8	19
61	Baseline Gut Metagenomic Functional Gene Signature Associated with Variable Weight Loss Responses following a Healthy Lifestyle Intervention in Humans. <i>MSystems</i> , 2021, 6, e0096421.	1.7	19
62	The role of macrobiota in structuring microbial communities along rocky shores. <i>PeerJ</i> , 2014, 2, e631.	0.9	19
63	Lettuce ( <i>Lactuca sativa</i> ) productivity influenced by microbial inocula under nitrogen-limited conditions in aquaponics. <i>PLoS ONE</i> , 2021, 16, e0247534.	1.1	14
64	Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. <i>MSystems</i> , 2021, 6, .	1.7	10
65	Defining Microbiome Health through a Host Lens. <i>MSystems</i> , 2019, 4, .	1.7	8
66	Proximate grassland and shrub-encroached sites show dramatic restructuring of soil bacterial communities. <i>PeerJ</i> , 2019, 7, e7304.	0.9	7
67	Metapopulation theory provides new insight into microbial biogeography. <i>Environmental Microbiology</i> , 2017, 19, 849-850.	1.8	5
68	Heavy metal tolerance genes alter cellular thermodynamics in <i>Pseudomonas putida</i> and river <i>Pseudomonas spp</i> . and influence amoeba predation. <i>FEMS Microbiology Letters</i> , 2013, 347, n/a-n/a.	0.7	4
69	Relative strengths of relationships between plant, microbial, and environmental parameters in heavy-metal contaminated floodplain soil. <i>Pedobiologia</i> , 2012, 55, 15-23.	0.5	2
70	Non-responder phenotype reveals apparent microbiome-wide antibiotic tolerance in the murine gut. <i>Communications Biology</i> , 2021, 4, 316.	2.0	2
71	Statistical Tools for Data Analysis. <i>Springer Protocols</i> , 2015, , 41-57.	0.1	0