

Sean M Gibbons

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

21,559
citations

81839

39
h-index

76872

74
g-index

94
all docs

94
docs citations

94
times ranked

26475
citing authors

#	ARTICLE	IF	CITATIONS
1	Heterogeneity in statin responses explained by variation in the human gut microbiome. <i>Med</i> , 2022, 3, 388-405.e6.	2.2	21
2	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
3	From taxonomy to metabolic output: what factors define gut microbiome health?. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	19
4	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
5	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. <i>MSystems</i> , 2021, 6, .	1.7	28
6	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. <i>Nature Metabolism</i> , 2021, 3, 274-286.	5.1	278
7	Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. <i>MSystems</i> , 2021, 6, .	1.7	10
8	Non-responder phenotype reveals apparent microbiome-wide antibiotic tolerance in the murine gut. <i>Communications Biology</i> , 2021, 4, 316.	2.0	2
9	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021, 184, 2053-2067.e18.	13.5	167
10	The geometry of clinical labs and wellness states from deeply phenotyped humans. <i>Nature Communications</i> , 2021, 12, 3578.	5.8	19
11	Genomic and functional characterization of a mucosal symbiont involved in early-stage colorectal cancer. <i>Cell Host and Microbe</i> , 2021, 29, 1589-1598.e6.	5.1	44
12	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
13	Health and disease markers correlate with gut microbiome composition across thousands of people. <i>Nature Communications</i> , 2020, 11, 5206.	5.8	378
14	Keystone taxa indispensable for microbiome recovery. <i>Nature Microbiology</i> , 2020, 5, 1067-1068.	5.9	35
15	Longitudinal analysis reveals transition barriers between dominant ecological states in the gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13839-13845.	3.3	47
16	MICOM: Metagenome-Scale Modeling To Infer Metabolic Interactions in the Gut Microbiota. <i>MSystems</i> , 2020, 5, .	1.7	126
17	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
18	Use and abuse of correlation analyses in microbial ecology. <i>ISME Journal</i> , 2019, 13, 2647-2655.	4.4	193

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19	Blood metabolome predicts gut microbiome α -diversity in humans. <i>Nature Biotechnology</i> , 2019, 37, 1217-1228.	9.4	213
20	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
21	Defining Microbiome Health through a Host Lens. <i>MSystems</i> , 2019, 4, .	1.7	8
22	Adaptive Evolution within Gut Microbiomes of Healthy People. <i>Cell Host and Microbe</i> , 2019, 25, 656-667.e8.	5.1	289
23	Proximate grassland and shrub-encroached sites show dramatic restructuring of soil bacterial communities. <i>PeerJ</i> , 2019, 7, e7304.	0.9	7
24	Shrub encroachment is associated with changes in soil bacterial community composition in a temperate grassland ecosystem. <i>Plant and Soil</i> , 2018, 425, 539-551.	1.8	30
25	Designing synbiotics for improved human health. <i>Microbial Biotechnology</i> , 2018, 11, 141-144.	2.0	29
26	Correcting for batch effects in case-control microbiome studies. <i>PLoS Computational Biology</i> , 2018, 14, e1006102.	1.5	108
27	Systems biology approaches towards predictive microbial ecology. <i>Environmental Microbiology</i> , 2018, 20, 4197-4209.	1.8	19
28	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. <i>Scientific Reports</i> , 2018, 8, 12699.	1.6	37
29	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. <i>Cell Reports</i> , 2018, 24, 1842-1851.	2.9	72
30	Endospores and other lysis-resistant bacteria comprise a widely shared core community within the human microbiota. <i>ISME Journal</i> , 2018, 12, 2403-2416.	4.4	40
31	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
32	Microbial community ecology: Function over phylogeny. <i>Nature Ecology and Evolution</i> , 2017, 1, 32.	3.4	43
33	Metapopulation theory provides new insight into microbial biogeography. <i>Environmental Microbiology</i> , 2017, 19, 849-850.	1.8	5
34	Invasive Plants Rapidly Reshape Soil Properties in a Grassland Ecosystem. <i>MSystems</i> , 2017, 2, .	1.7	91
35	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
36	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <i>MSystems</i> , 2017, 2, .	1.7	47

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37	Two dynamic regimes in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017, 13, e1005364.	1.5	101
38	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. <i>Nature Communications</i> , 2017, 8, 1784.	5.8	714
39	Identifying predictive features of <i>Clostridium difficile</i> infection recurrence before, during, and after primary antibiotic treatment. <i>Microbiome</i> , 2017, 5, 148.	4.9	36
40	Spatial scale drives patterns in soil bacterial diversity. <i>Environmental Microbiology</i> , 2016, 18, 2039-2051.	1.8	194
41	The Built Environment Is a Microbial Wasteland. <i>MSystems</i> , 2016, 1, .	1.7	33
42	Disturbance Regimes Predictably Alter Diversity in an Ecologically Complex Bacterial System. <i>MBio</i> , 2016, 7, .	1.8	47
43	Rapid response of arbuscular mycorrhizal fungal communities to short-term fertilization in an alpine grassland on the Qinghai-Tibet Plateau. <i>PeerJ</i> , 2016, 4, e2226.	0.9	29
44	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
45	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
46	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015, 3, 21.	4.9	140
47	Statistical Tools for Data Analysis. <i>Springer Protocols</i> , 2015, , 41-57.	0.1	0
48	Athletic equipment microbiota are shaped by interactions with human skin. <i>Microbiome</i> , 2015, 3, 25.	4.9	36
49	Aquarium microbiome response to ninety-percent system water change: Clues to microbiome management. <i>Zoo Biology</i> , 2015, 34, 360-367.	0.5	35
50	Arbuscular mycorrhizal fungal communities show low resistance and high resilience to wildfire disturbance. <i>Plant and Soil</i> , 2015, 397, 347-356.	1.8	33
51	Microbial diversity – exploration of natural ecosystems and microbiomes. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 66-72.	1.5	105
52	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
53	Ecological Succession and Viability of Human-Associated Microbiota on Restroom Surfaces. <i>Applied and Environmental Microbiology</i> , 2015, 81, 765-773.	1.4	89
54	Characterization of the salivary microbiome in patients with pancreatic cancer. <i>PeerJ</i> , 2015, 3, e1373.	0.9	150

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55	Understanding Cultivar-Specificity and Soil Determinants of the Cannabis Microbiome. <i>PLoS ONE</i> , 2014, 9, e99641.	1.1	73
56	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014, 2, e545.	0.9	535
57	Human and Environmental Impacts on River Sediment Microbial Communities. <i>PLoS ONE</i> , 2014, 9, e97435.	1.1	115
58	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
59	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	6.0	751
60	Will different <scp>OTU</scp> delineation methods change interpretation of arbuscular mycorrhizal fungal community patterns?. <i>New Phytologist</i> , 2014, 202, 1101-1104.	3.5	58
61	The role of macrobiota in structuring microbial communities along rocky shores. <i>PeerJ</i> , 2014, 2, e631.	0.9	19
62	Severe plant invasions can increase mycorrhizal fungal abundance and diversity. <i>ISME Journal</i> , 2013, 7, 1424-1433.	4.4	180
63	Heavy metal tolerance genes alter cellular thermodynamics in <i>Pseudomonas putida</i> and river <i>Pseudomonas spp</i> . and influence amebal predation. <i>FEMS Microbiology Letters</i> , 2013, 347, n/a-n/a.	0.7	4
64	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
65	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
66	Investigating the Impact of Storage Conditions on Microbial Community Composition in Soil Samples. <i>PLoS ONE</i> , 2013, 8, e70460.	1.1	108
67	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
68	454â€œsequencing 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
69	Modeling microbial community structure and functional diversity across time and space. <i>FEMS Microbiology Letters</i> , 2012, 332, 91-98.	0.7	38
70	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
71	Hyporheic Microbial Community Development Is a Sensitive Indicator of Metal Contamination. <i>Environmental Science & Technology</i> , 2009, 43, 6158-6163.	4.6	51