

Sean M Gibbons

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75
papers

10,097
citations

36
h-index

94
g-index

94
ext. papers

16,364
ext. citations

11.7
avg, IF

6.02
L-index

#	Paper	IF	Citations
75	Non-responder phenotype reveals apparent microbiome-wide antibiotic tolerance in the murine gut. <i>Communications Biology</i> , 2021 , 4, 316	6.7	1
74	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021 , 184, 2053-2067.e18	5.2	18
73	The geometry of clinical labs and wellness states from deeply phenotyped humans. <i>Nature Communications</i> , 2021 , 12, 3578	17.4	1
72	From taxonomy to metabolic output: what factors define gut microbiome health?. <i>Gut Microbes</i> , 2021 , 13, 1-20	8.8	3
71	Lettuce (<i>Lactuca sativa</i>) productivity influenced by microbial inocula under nitrogen-limited conditions in aquaponics. <i>PLoS ONE</i> , 2021 , 16, e0247534	3.7	3
70	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative Workshop and Follow-On Activities. <i>MSystems</i> , 2021 , 6,	7.6	7
69	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. <i>Nature Metabolism</i> , 2021 , 3, 274-286	14.6	77
68	Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. <i>MSystems</i> , 2021 , 6,	7.6	3
67	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	23.4	11
66	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	7.6	6
65	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	11.5	13
64	MICOM: Metagenome-Scale Modeling To Infer Metabolic Interactions in the Gut Microbiota. <i>MSystems</i> , 2020 , 5,	7.6	48
63	Health and disease markers correlate with gut microbiome composition across thousands of people. <i>Nature Communications</i> , 2020 , 11, 5206	17.4	115
62	Keystone taxa indispensable for microbiome recovery. <i>Nature Microbiology</i> , 2020 , 5, 1067-1068	26.6	11
61	Blood metabolome predicts gut microbiome diversity in humans. <i>Nature Biotechnology</i> , 2019 , 37, 1217-1228	14.3	95
60	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. <i>Nature Medicine</i> , 2019 , 25, 1442-1452	50.5	125
59	Defining Microbiome Health through a Host Lens. <i>MSystems</i> , 2019 , 4,	7.6	5

58	Adaptive Evolution within Gut Microbiomes of Healthy People. <i>Cell Host and Microbe</i> , 2019 , 25, 656-667. e334	133
57	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5 4050
56	Use and abuse of correlation analyses in microbial ecology. <i>ISME Journal</i> , 2019 , 13, 2647-2655	11.9 81
55	Proximate grassland and shrub-encroached sites show dramatic restructuring of soil bacterial communities. <i>PeerJ</i> , 2019 , 7, e7304	3.1 5
54	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	4.2 16
53	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. <i>Scientific Reports</i> , 2018 , 8, 12699	4.9 27
52	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. <i>Cell Reports</i> , 2018 , 24, 1842-1851	10.6 52
51	Endospores and other lysis-resistant bacteria comprise a widely shared core community within the human microbiota. <i>ISME Journal</i> , 2018 , 12, 2403-2416	11.9 22
50	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	5.7 66
49	Correcting for batch effects in case-control microbiome studies. <i>PLoS Computational Biology</i> , 2018 , 14, e1006102	5 55
48	Microbial community ecology: Function over phylogeny. <i>Nature Ecology and Evolution</i> , 2017 , 1, 32	12.3 27
47	Metapopulation theory provides new insight into microbial biogeography. <i>Environmental Microbiology</i> , 2017 , 19, 849-850	5.2 2
46	Invasive Plants Rapidly Reshape Soil Properties in a Grassland Ecosystem. <i>MSystems</i> , 2017 , 2,	7.6 53
45	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4 1076
44	Two dynamic regimes in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017 , 13, e1005364	5 56
43	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. <i>Nature Communications</i> , 2017 , 8, 1784	17.4 425
42	Identifying predictive features of <i>Clostridium difficile</i> infection recurrence before, during, and after primary antibiotic treatment. <i>Microbiome</i> , 2017 , 5, 148	16.6 20
41	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <i>MSystems</i> , 2017 , 2,	7.6 35

40	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	3.1	23
39	Spatial scale drives patterns in soil bacterial diversity. <i>Environmental Microbiology</i> , 2016 , 18, 2039-51	5.2	131
38	The Built Environment Is a Microbial Wasteland. <i>MSystems</i> , 2016 , 1,	7.6	26
37	Disturbance Regimes Predictably Alter Diversity in an Ecologically Complex Bacterial System. <i>MBio</i> , 2016 , 7,	7.8	26
36	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, 681-9	23.4	440
35	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015 , 3, 21	16.6	108
34	Statistical Tools for Data Analysis. <i>Springer Protocols</i> , 2015 , 41-57	0.3	
33	Athletic equipment microbiota are shaped by interactions with human skin. <i>Microbiome</i> , 2015 , 3, 25	16.6	31
32	Aquarium microbiome response to ninety-percent system water change: Clues to microbiome management. <i>Zoo Biology</i> , 2015 , 34, 360-7	1.6	14
31	Arbuscular mycorrhizal fungal communities show low resistance and high resilience to wildfire disturbance. <i>Plant and Soil</i> , 2015 , 397, 347-356	4.2	25
30	Microbial diversity--exploration of natural ecosystems and microbiomes. <i>Current Opinion in Genetics and Development</i> , 2015 , 35, 66-72	4.9	68
29	The short-chain fatty acid receptor, FFA2, contributes to gestational glucose homeostasis. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015 , 309, E840-51	6	42
28	Ecological succession and viability of human-associated microbiota on restroom surfaces. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 765-73	4.8	72
27	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, 251-61	7	198
26	Characterization of the salivary microbiome in patients with pancreatic cancer. <i>PeerJ</i> , 2015 , 3, e1373	3.1	97
25	Characterizing changes in soil bacterial community structure in response to short-term warming. <i>FEMS Microbiology Ecology</i> , 2014 , 89, 281-92	4.3	75
24	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014 , 345, 1048-52	33.3	543
23	Will different OTU delineation methods change interpretation of arbuscular mycorrhizal fungal community patterns?. <i>New Phytologist</i> , 2014 , 202, 1101-1104	9.8	50

22	Understanding cultivar-specificity and soil determinants of the cannabis microbiome. <i>PLoS ONE</i> , 2014 , 9, e99641	3.7	45
21	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014 , 2, e545	3.1	395
20	Human and environmental impacts on river sediment microbial communities. <i>PLoS ONE</i> , 2014 , 9, e97435	3.7	83
19	The role of macrobiota in structuring microbial communities along rocky shores. <i>PeerJ</i> , 2014 , 2, e631	3.1	15
18	Ocean acidification shows negligible impacts on high-latitude bacterial community structure in coastal pelagic mesocosms. <i>Biogeosciences</i> , 2013 , 10, 555-566	4.6	40
17	Severe plant invasions can increase mycorrhizal fungal abundance and diversity. <i>ISME Journal</i> , 2013 , 7, 1424-33	11.9	136
16	Heavy metal tolerance genes alter cellular thermodynamics in <i>Pseudomonas putida</i> and river <i>Pseudomonas</i> spp. and influence amoeba predation. <i>FEMS Microbiology Letters</i> , 2013 , 347, 97-106	2.9	3
15	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, 4651-5	11.5	158
14	Investigating the impact of storage conditions on microbial community composition in soil samples. <i>PLoS ONE</i> , 2013 , 8, e70460	3.7	86
13	Modeling microbial community structure and functional diversity across time and space. <i>FEMS Microbiology Letters</i> , 2012 , 332, 91-8	2.9	33
12	Relative strengths of relationships between plant, microbial, and environmental parameters in heavy-metal contaminated floodplain soil. <i>Pedobiologia</i> , 2012 , 55, 15-23	1.7	2
11	454-sequencing reveals stochastic local reassembly and high disturbance tolerance within arbuscular mycorrhizal fungal communities. <i>Journal of Ecology</i> , 2012 , 100, 151-160	6	110
10	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, 108-13	4.8	20
9	Hyporheic microbial community development is a sensitive indicator of metal contamination. <i>Environmental Science & Technology</i> , 2009 , 43, 6158-63	10.3	42
8	Correcting for batch effects in case-control microbiome studies		3
7	Industrialization is associated with elevated rates of horizontal gene transfer in the human microbiome		1
6	Gut Microbiome Pattern Reflects Healthy Aging and Predicts Extended Survival in Humans		3
5	Adaptive evolution within the gut microbiome of individual people		17

4	Orthogonal dietary niche enables reversible engraftment of a gut bacterial commensal	2
3	MICOM: metagenome-scale modeling to infer metabolic interactions in the gut microbiota	2
2	Blood metabolome signature predicts gut microbiome diversity in health and disease	1
1	Negative plant-microbiome feedback limits productivity in aquaponics	1