Thomas J Sharpton

List of Publications by Year
in descending order

70	4,466	159585 30	123424 61
papers	citations	h-index	g-index

88	88	88	7774
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Metacoder: An R package for visualization and manipulation of community taxonomic diversity data. PLoS Computational Biology, 2017, 13, e1005404.	3.2	526
2	An introduction to the analysis of shotgun metagenomic data. Frontiers in Plant Science, 2014, 5, 209.	3.6	446
3	Comparative genomic analyses of the human fungal pathogens Coccidioides and their relatives. Genome Research, 2009, 19, 1722-1731.	5.5	295
4	A Taxonomic Signature of Obesity in the Microbiome? Getting to the Guts of the Matter. PLoS ONE, 2014, 9, e84689.	2.5	277
5	Global marine bacterial diversity peaks at high latitudes in winter. ISME Journal, 2013, 7, 1669-1677.	9.8	195
6	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
7	Population genomic sequencing of Coccidioides fungi reveals recent hybridization and transposon control. Genome Research, 2010, 20, 938-946.	5.5	166
8	The influence of ethnicity and geography on human gut microbiome composition. Nature Medicine, 2018, 24, 1495-1496.	30.7	158
9	Profile Hidden Markov Models for the Detection of Viruses within Metagenomic Sequence Data. PLoS ONE, 2014, 9, e105067.	2.5	153
10	Triclosan Exposure Is Associated with Rapid Restructuring of the Microbiome in Adult Zebrafish. PLoS ONE, 2016, 11, e0154632.	2.5	126
11	A Metagenomic Meta-analysis Reveals Functional Signatures of Health and Disease in the Human Gut Microbiome. MSystems, 2019, 4, .	3.8	112
12	Microbiome Multi-Omics Network Analysis: Statistical Considerations, Limitations, and Opportunities. Frontiers in Genetics, 2019, 10, 995.	2.3	101
13	Aging and serum MCP-1 are associated with gut microbiome composition in a murine model. PeerJ, 2016, 4, e1854.	2.0	89
14	Novel Bacterial Taxa in the Human Microbiome. PLoS ONE, 2012, 7, e35294.	2.5	86
15	Comparative Transcriptomics of the Saprobic and Parasitic Growth Phases in Coccidioides spp. PLoS ONE, 2012, 7, e41034.	2.5	79
16	Mechanisms of intron gain and loss in Cryptococcus. Genome Biology, 2008, 9, R24.	9.6	75
17	PhylOTU: A High-Throughput Procedure Quantifies Microbial Community Diversity and Resolves Novel Taxa from Metagenomic Data. PLoS Computational Biology, 2011, 7, e1001061.	3.2	73
18	A longitudinal assessment of host-microbe-parasite interactions resolves the zebrafish gut microbiomeâ€™s link to Pseudocapillaria tomentosa infection and pathology. Microbiome, 2019, 7, 10.	11.1	70

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19	Corals and Their Microbiomes Are Differentially Affected by Exposure to Elevated Nutrients and a Natural Thermal Anomaly. Frontiers in Marine Science, 0, 5, .	2.5	68
20	Ecophylogenetics Clarifies the Evolutionary Association between Mammals and Their Gut Microbiota. MBio, 2018, 9, .	4.1	67
21	Role of the Gut Microbiome in Vertebrate Evolution. MSystems, 2018, 3, .	3.8	64
22	Combined Effects of Three High-Energy Charged Particle Beams Important for Space Flight on Brain, Behavioral and Cognitive Endpoints in B6D2F1 Female and Male Mice. Frontiers in Physiology, 2019, 10, 179.	2.8	61
23	The gut microbiome correlates with conspecific aggression in a small population of rescued dogs(Canis familiaris). PeerJ, 2019, 7, e6103.	2.0	60
24	Automated and Accurate Estimation of Gene Family Abundance from Shotgun Metagenomes. PLoS Computational Biology, 2015, 11, e1004573.	3.2	55
25	Zebrafish microbiome studies make waves. Lab Animal, 2020, 49, 201-207.	0.4	50
26	Development of Inflammatory Bowel Disease Is Linked to a Longitudinal Restructuring of the Gut Metagenome in Mice. MSystems, 2017, 2, .	3.8	48
27	Backbones of evolutionary history test biodiversity theory for microbes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8356-8361.	7.1	44
28	Progressive Colonization of Bacteria and Degradation of Rice Straw in the Rumen by Illumina Sequencing. Frontiers in Microbiology, 2017, 8, 2165.	3.5	41
29	Gut Feelings Begin in Childhood: the Gut Metagenome Correlates with Early Environment, Caregiving, and Behavior. MBio, 2020, 11, .	4.1	40
30	Integrated analysis of behavioral, epigenetic, and gut microbiome analyses in AppNL-G-F, AppNL-F, and wild type mice. Scientific Reports, 2021, 11, 4678.	3.3	38
31	Metagenome sequence of <scp>E</scp>laphomyces granulatus from sporocarp tissue reveals <scp>A</scp>scomycota ectomycorrhizal fingerprints of genome expansion and a <scp>P</scp>roteobacteriaâ€rich microbiome. Environmental Microbiology, 2015, 17, 2952-2968.	3.8	34
32	Marginal Zinc Deficiency and Environmentally Relevant Concentrations of Arsenic Elicit Combined Effects on the Gut Microbiome. MSphere, 2018, 3, .	2.9	34
33	Improvements in Metabolic Syndrome by Xanthohumol Derivatives Are Linked to Altered Gut Microbiota and Bile Acid Metabolism. Molecular Nutrition and Food Research, 2020, 64, e1900789.	3.3	32
34	Diet and gut microbiome enterotype are associated at the population level in African buffalo. Nature Communications, 2021, 12, 2267.	12.8	31
35	Effects of Sub-Chronic MPTP Exposure on Behavioral and Cognitive Performance and the Microbiome of Wild-Type and mGlu8 Knockout Female and Male Mice. Frontiers in Behavioral Neuroscience, 2018, 12, 140.	2.0	30
36	Allelic Variation in a Single Genomic Region Alters the Microbiome of the Snail Biomphalaria glabrata. Journal of Heredity, 2018, 109, 604-609.	2.4	26

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37	Microbiome Variation in an Intertidal Sea Anemone Across Latitudes and Symbiotic States. Frontiers in Marine Science, 2019, 6, .	2.5	26
38	Bighorn sheep gut microbiomes associate with genetic and spatial structure across a metapopulation. Scientific Reports, 2020, 10, 6582.	3.3	26
39	Combined Genomic, Transcriptomic, Proteomic, and Physiological Characterization of the Growth of Pecoramyces sp. F1 in Monoculture and Co-culture With a Syntrophic Methanogen. Frontiers in Microbiology, 2019, 10, 435.	3.5	25
40	Phylogenetic Integration Reveals the Zebrafish Core Microbiome and Its Sensitivity to Environmental Exposures. Toxics, 2021, 9, 10.	3.7	25
41	Effects of zinc status on age-related T cell dysfunction and chronic inflammation. BioMetals, 2021, 34, 291-301.	4.1	25
42	Transmission of a common intestinal neoplasm in zebrafish by cohabitation. Journal of Fish Diseases, 2018, 41, 569-579.	1.9	24
43	Is adolescence the missing developmental link in Microbiomeâ€“Gutâ€“Brain axis communication?. Developmental Psychobiology, 2019, 61, 783-795.	1.6	24
44	Effects of Six Sequential Charged Particle Beams on Behavioral and Cognitive Performance in B6D2F1 Female and Male Mice. Frontiers in Physiology, 2020, 11, 959.	2.8	23
45	Experimental metatranscriptomics reveals the costs and benefits of dissolved organic matter photoâ€alteration for freshwater microbes. Environmental Microbiology, 2020, 22, 3505-3521.	3.8	21
46	Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. BMC Bioinformatics, 2012, 13, 264.	2.6	20
47	Increasing dietary nitrate has no effect on cancellous bone loss or fecal microbiome in ovariectomized rats. Molecular Nutrition and Food Research, 2017, 61, 1600372.	3.3	19
48	Germ-Free Swiss Webster Mice on a High-Fat Diet Develop Obesity, Hyperglycemia, and Dyslipidemia. Microorganisms, 2020, 8, 520.	3.6	17
49	A microbial signature following bariatric surgery is robustly consistent across multiple cohorts. Gut Microbes, 2021, 13, 1930872.	9.8	15
50	Fecal Implants From AppNLâ€“Gâ€“F and AppNLâ€“Gâ€“F/E4 Donor Mice Sufficient to Induce Behavioral Phenotypes in Germ-Free Mice. Frontiers in Behavioral Neuroscience, 2022, 16, 791128.	2.0	14
51	Xanthohumol Requires the Intestinal Microbiota to Improve Glucose Metabolism in Dietâ€Induced Obese Mice. Molecular Nutrition and Food Research, 2021, 65, e2100389.	3.3	13
52	Pseudocapillaria tomentosa,Mycoplasmaspp., and Intestinal Lesions in Experimentally Infected ZebrafishDanio rerio. Zebrafish, 2021, 18, 207-220.	1.1	12
53	Composition of the Gut Microbiome Influences Production of Sulforaphane-Nitrile and Iberin-Nitrile from Glucosinolates in Broccoli Sprouts. Nutrients, 2021, 13, 3013.	4.1	12
54	Harnessing the gut microbiome in the fight against anthelminthic drug resistance. Current Opinion in Microbiology, 2020, 53, 26-34.	5.1	11

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55	Tetrahydroxanthohumol, a xanthohumol derivative, attenuates high-fat diet-induced hepatic steatosis by antagonizing PPARÎ³. ELife, 2021, 10, .	6.0	9
56	Effects of Subclinical Mycobacterium chelonae Infections on Fecundity and Embryo Survival in Zebrafish. Zebrafish, 2016, 13, S-88-S-95.	1.1	8
57	Supplementation with Sea Vegetables Palmaria mollis and Undaria pinnatifida Exerts Metabolic Benefits in Diet-Induced Obesity in Mice. Current Developments in Nutrition, 2020, 4, nzaa072.	0.3	8
58	Pseudocapillaria tomentosa in laboratory zebrafish Danio rerio: patterns of infection and dose response. Diseases of Aquatic Organisms, 2018, 131, 121-131.	1.0	7
59	Further evaluation of the efficacy of emamectin benzoate for treating Pseudocapillaria tomentosa (Dujardin 1843) in zebrafish Danio rerio (Hamilton 1822). Journal of Fish Diseases, 2019, 42, 1351-1357.	1.9	6
60	Retrospective analysis of the Zebrafish International Resource Center diagnostic data links Pseudocapillaria tomentosa to intestinal neoplasms in zebrafish Danio rerio (Hamilton) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1	6
61	Microbial Interaction Network Estimation via Bias-Corrected Graphical Lasso. Statistics in Biosciences, 2021, 13, 329-350.	1.2	4
62	Leveraging the Knowledge of Our Peers: Online Communities Hold the Promise to Enhance Scientific Research. PLoS Biology, 2006, 4, e199.	5.6	3
63	Insights Into the Oral Microbiome and Barrett's Esophagus Early Detection: A Narrative Review. Clinical and Translational Gastroenterology, 2021, 12, e00390.	2.5	3
64	Revealing General Patterns of Microbiomes That Transcend Systems: Potential and Challenges of Deep Transfer Learning. MSystems, 2022, 7, e0105821.	3.8	3
65	Modeling the Context-Dependent Associations between the Gut Microbiome, Its Environment, and Host Health. MBio, 2015, 6, e01367-15.	4.1	2
66	Pan-tissue transcriptome analysis of long noncoding RNAs in the American beaver Castor canadensis. BMC Genomics, 2020, 21, 153.	2.8	2
67	Gut Microbial Composition of Pacific Salmonids Differs across Oregon River Basins and Hatchery Ancestry. Microorganisms, 2022, 10, 933.	3.6	2
68	Draft Genome Sequence of Pseudomonas sp. Strain DrBHI1 (Phylum Proteobacteria). Genome Announcements, 2017, 5, .	0.8	1
69	The fecal microbiota of Thai school-aged children associated with demographic factors and diet. PeerJ, 2022, 10, e13325.	2.0	1
70	Draft Genome Sequence of Plesiomonas shigelloides Strain zfcc0051 (Phylum Proteobacteria). Microbiology Resource Announcements, 0, , .	0.6	0