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	Revealing General Patterns of Microbiomes That Transcend Systems: Potential and Challenges of Deep Transfer Learning. MSystems, 2022, 7, e0105821.	3.8	3
2	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
3	The fecal microbiota of Thai school-aged children associated with demographic factors and diet. PeerJ, 2022, 10, e13325.	2.0	1
4	Gut Microbial Composition of Pacific Salmonids Differs across Oregon River Basins and Hatchery Ancestry. Microorganisms, 2022, 10, 933.	3.6	2
5	Microbial Interaction Network Estimation via Bias-Corrected Graphical Lasso. Statistics in Biosciences, 2021, 13, 329-350.	1.2	4
6	Phylogenetic Integration Reveals the Zebrafish Core Microbiome and Its Sensitivity to Environmental Exposures. Toxics, 2021, 9, 10.	3.7	25
7	A microbial signature following bariatric surgery is robustly consistent across multiple cohorts. Gut Microbes, 2021, 13, 1930872.	9.8	15
8	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
9	Diet and gut microbiome enterotype are associated at the population level in African buffalo. Nature Communications, 2021, 12, 2267.	12.8	31
10	Tetrahydroxanthohumol, a xanthohumol derivative, attenuates high-fat diet-induced hepatic steatosis by antagonizing PPARÎ³. ELife, 2021, 10, .	6.0	9
11	Pseudocapillaria tomentosa,Mycoplasmaspp., and Intestinal Lesions in Experimentally Infected ZebrafishDanio rerio. Zebrafish, 2021, 18, 207-220.	1.1	12
12	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
13	Insights Into the Oral Microbiome and Barrett's Esophagus Early Detection: A Narrative Review. Clinical and Translational Gastroenterology, 2021, 12, e00390.	2.5	3
14	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
15	Effects of zinc status on age-related T cell dysfunction and chronic inflammation. BioMetals, 2021, 34, 291-301.	4.1	25
16	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
17	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
18	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	1

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19	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
20	Gut Feelings Begin in Childhood: the Gut Metagenome Correlates with Early Environment, Caregiving, and Behavior. MBio, 2020, 11, .	4.1	40
21	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
22	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
23	Zebrafish microbiome studies make waves. Lab Animal, 2020, 49, 201-207.	0.4	50
24	Harnessing the gut microbiome in the fight against anthelminthic drug resistance. Current Opinion in Microbiology, 2020, 53, 26-34.	5.1	11
25	Pan-tissue transcriptome analysis of long noncoding RNAs in the American beaver Castor canadensis. BMC Genomics, 2020, 21, 153.	2.8	2
26	Bighorn sheep gut microbiomes associate with genetic and spatial structure across a metapopulation. Scientific Reports, 2020, 10, 6582.	3.3	26
27	Germ-Free Swiss Webster Mice on a High-Fat Diet Develop Obesity, Hyperglycemia, and Dyslipidemia. Microorganisms, 2020, 8, 520.	3.6	17
28	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
29	Microbiome Multi-Omics Network Analysis: Statistical Considerations, Limitations, and Opportunities. Frontiers in Genetics, 2019, 10, 995.	2.3	101
30	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
31	Is adolescence the missing developmental link in Microbiomeâ€“Gutâ€“Brain axis communication?. Developmental Psychobiology, 2019, 61, 783-795.	1.6	24
32	Microbiome Variation in an Intertidal Sea Anemone Across Latitudes and Symbiotic States. Frontiers in Marine Science, 2019, 6, .	2.5	26
33	A Metagenomic Meta-analysis Reveals Functional Signatures of Health and Disease in the Human Gut Microbiome. MSystems, 2019, 4, .	3.8	112
34	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
35	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
36	The gut microbiome correlates with conspecific aggression in a small population of rescued dogs(Canis familiaris). PeerJ, 2019, 7, e6103.	2.0	60

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37	Role of the Gut Microbiome in Vertebrate Evolution. MSystems, 2018, 3, .	3.8	64
38	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
39	Transmission of a common intestinal neoplasm in zebrafish by cohabitation. Journal of Fish Diseases, 2018, 41, 569-579.	1.9	24
40	Marginal Zinc Deficiency and Environmentally Relevant Concentrations of Arsenic Elicit Combined Effects on the Gut Microbiome. MSphere, 2018, 3, .	2.9	34
41	The influence of ethnicity and geography on human gut microbiome composition. Nature Medicine, 2018, 24, 1495-1496.	30.7	158
42	Ecophylogenetics Clarifies the Evolutionary Association between Mammals and Their Gut Microbiota. MBio, 2018, 9, .	4.1	67
43	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
44	Pseudocapillaria tomentosa in laboratory zebrafish Danio rerio: patterns of infection and dose response. Diseases of Aquatic Organisms, 2018, 131, 121-131.	1.0	7
45	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
46	Development of Inflammatory Bowel Disease Is Linked to a Longitudinal Restructuring of the Gut Metagenome in Mice. MSystems, 2017, 2, .	3.8	48
47	Progressive Colonization of Bacteria and Degradation of Rice Straw in the Rumen by Illumina Sequencing. Frontiers in Microbiology, 2017, 8, 2165.	3.5	41
48	Draft Genome Sequence of Pseudomonas sp. Strain DrBHI1 (Phylum Proteobacteria). Genome Announcements, 2017, 5, .	0.8	1
49	Metacoder: An R package for visualization and manipulation of community taxonomic diversity data. PLoS Computational Biology, 2017, 13, e1005404.	3.2	526
50	Triclosan Exposure Is Associated with Rapid Restructuring of the Microbiome in Adult Zebrafish. PLoS ONE, 2016, 11, e0154632.	2.5	126
51	Effects of Subclinical Mycobacterium chelonae Infections on Fecundity and Embryo Survival in Zebrafish. Zebrafish, 2016, 13, S-88-S-95.	1.1	8
52	Aging and serum MCP-1 are associated with gut microbiome composition in a murine model. PeerJ, 2016, 4, e1854.	2.0	89
53	Modeling the Context-Dependent Associations between the Gut Microbiome, Its Environment, and Host Health. MBio, 2015, 6, e01367-15.	4.1	2
54	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

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55	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
56	Automated and Accurate Estimation of Gene Family Abundance from Shotgun Metagenomes. PLoS Computational Biology, 2015, 11, e1004573.	3.2	55
57	An introduction to the analysis of shotgun metagenomic data. Frontiers in Plant Science, 2014, 5, 209.	3.6	446
58	Profile Hidden Markov Models for the Detection of Viruses within Metagenomic Sequence Data. PLoS ONE, 2014, 9, e105067.	2.5	153
59	A Taxonomic Signature of Obesity in the Microbiome? Getting to the Guts of the Matter. PLoS ONE, 2014, 9, e84689.	2.5	277
60	Global marine bacterial diversity peaks at high latitudes in winter. ISME Journal, 2013, 7, 1669-1677.	9.8	195
61	Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. BMC Bioinformatics, 2012, 13, 264.	2.6	20
62	Comparative Transcriptomics of the Saprobic and Parasitic Growth Phases in Coccidioides spp. PLoS ONE, 2012, 7, e41034.	2.5	79
63	Novel Bacterial Taxa in the Human Microbiome. PLoS ONE, 2012, 7, e35294.	2.5	86
64	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
65	Population genomic sequencing of Coccidioides fungi reveals recent hybridization and transposon control. Genome Research, 2010, 20, 938-946.	5.5	166
66	Comparative genomic analyses of the human fungal pathogens Coccidioides and their relatives. Genome Research, 2009, 19, 1722-1731.	5.5	295
67	Mechanisms of intron gain and loss in Cryptococcus. Genome Biology, 2008, 9, R24.	9.6	75
68	Leveraging the Knowledge of Our Peers: Online Communities Hold the Promise to Enhance Scientific Research. PLoS Biology, 2006, 4, e199.	5.6	3
69	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
70	Draft Genome Sequence of Plesiomonas shigelloides Strain zfcc0051 (Phylum Proteobacteria). Microbiology Resource Announcements, 0, , .	0.6	0