

Christopher Quince

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

22,921
citations

87888

38
h-index

144013

57
g-index

79
all docs

79
docs citations

79
times ranked

28599
citing authors

#	ARTICLE	IF	CITATIONS
1	O9â€¦STOP-colitis pilot: prospective, open-label, randomised study comparing nasogastric versus colonic FMT delivery in ulcerative colitis. , 2021, , .		1
2	Strainberry: automated strain separation in low-complexity metagenomes using long reads. Nature Communications, 2021, 12, 4485.	12.8	25
3	STRONG: metagenomics strain resolution on assembly graphs. Genome Biology, 2021, 22, 214.	8.8	59
4	Impact of sulfamethoxazole on a riverine microbiome. Water Research, 2021, 201, 117382.	11.3	19
5	Mobile resistome of human gut and pathogen drives anthropogenic bloom of antibiotic resistance. Microbiome, 2020, 8, 2.	11.1	80
6	Size Shapes the Active Microbiome of Methanogenic Granules, Corroborating a Biofilm Life Cycle. MSystems, 2020, 5, .	3.8	10
7	The pathophysiology of bile acid diarrhoea: differences in the colonic microbiome, metabolome and bile acids. Scientific Reports, 2020, 10, 20436.	3.3	27
8	Gene duplication drives genome expansion in a major lineage of Thaumarchaeota. Nature Communications, 2020, 11, 5494.	12.8	55
9	Growth and Break-Up of Methanogenic Granules Suggests Mechanisms for Biofilm and Community Development. Frontiers in Microbiology, 2020, 11, 1126.	3.5	17
10	Ecosystem-wide metagenomic binning enables prediction of ecological niches from genomes. Communications Biology, 2020, 3, 119.	4.4	64
11	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. Genetics, 2020, 214, 719-733.	2.9	20
12	Reply. Gastroenterology, 2019, 157, 1161-1162.	1.3	0
13	Recent mixing of <i>Vibrio parahaemolyticus</i> populations. ISME Journal, 2019, 13, 2578-2588.	9.8	41
14	Treatment of Active Crohnâ€™s Disease With an Ordinary Food-based Diet That Replicates Exclusive Enteral Nutrition. Gastroenterology, 2019, 156, 1354-1367.e6.	1.3	213
15	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. Cell, 2019, 176, 649-662.e20.	28.9	1,087
16	STOP-Colitis pilot trial protocol: a prospective, open-label, randomised pilot study to assess two possible routes of faecal microbiota transplant delivery in patients with ulcerative colitis. BMJ Open, 2019, 9, e030659.	1.9	9
17	Accurate Reconstruction of Microbial Strains from Metagenomic Sequencing Using Representative Reference Genomes. Lecture Notes in Computer Science, 2018, , 225-240.	1.3	16
18	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	13.3	717

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19	Linking Microbial Community Structure and Function During the Acidified Anaerobic Digestion of Grass. <i>Frontiers in Microbiology</i> , 2018, 9, 540.	3.5	56
20	Pan-genome Analysis of Ancient and Modern <i>Salmonella enterica</i> Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. <i>Current Biology</i> , 2018, 28, 2420-2428.e10.	3.9	65
21	Nitrogen-fixing populations of Planctomycetes and Proteobacteria are abundant in surface ocean metagenomes. <i>Nature Microbiology</i> , 2018, 3, 804-813.	13.3	436
22	Linking Statistical and Ecological Theory: Hubbell's Unified Neutral Theory of Biodiversity as a Hierarchical Dirichlet Process. <i>Proceedings of the IEEE</i> , 2017, 105, 516-529.	21.3	55
23	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	19.0	635
24	Shotgun metagenomics, from sampling to analysis. <i>Nature Biotechnology</i> , 2017, 35, 833-844.	17.5	1,196
25	The distinct features of microbial "dysbiosis" of Crohn's disease do not occur to the same extent in their unaffected, genetically-linked kindred. <i>PLoS ONE</i> , 2017, 12, e0172605.	2.5	33
26	DESMAN: a new tool for de novo extraction of strains from metagenomes. <i>Genome Biology</i> , 2017, 18, 181.	8.8	152
27	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , 2016, 10, 2557-2568.	9.8	570
28	Low-strength ultrasonication positively affects methanogenic granules toward higher AD performance: Implications from microbial community shift. <i>Ultrasonics Sonochemistry</i> , 2016, 32, 198-203.	8.2	12
29	Metabarcoding and metabolome analyses of copepod grazing reveal feeding preference and linkage to metabolite classes in dynamic microbial plankton communities. <i>Molecular Ecology</i> , 2016, 25, 5585-5602.	3.9	45
30	The effect of DNA extraction methodology on gut microbiota research applications. <i>BMC Research Notes</i> , 2016, 9, 365.	1.4	66
31	Assessment of the influence of intrinsic environmental and geographical factors on the bacterial ecology of pit latrines. <i>Microbial Biotechnology</i> , 2016, 9, 209-223.	4.2	76
32	Bioaugmentation Mitigates the Impact of Estrogen on Coliform-Grazing Protozoa in Slow Sand Filters. <i>Environmental Science & Technology</i> , 2016, 50, 3101-3110.	10.0	28
33	Illumina error profiles: resolving fine-scale variation in metagenomic sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 125.	2.6	303
34	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. <i>BMC Genomics</i> , 2016, 17, 55.	2.8	387
35	Phylogenetic congruence and ecological coherence in terrestrial Thaumarchaeota. <i>ISME Journal</i> , 2016, 10, 85-96.	9.8	94
36	PhyloPythiaS+: a self-training method for the rapid reconstruction of low-ranking taxonomic bins from metagenomes. <i>PeerJ</i> , 2016, 4, e1603.	2.0	87

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37	VSEARCH: a versatile open source tool for metagenomics. PeerJ, 2016, 4, e2584.	2.0	7,113
38	<tt>Seqenv</tt>: linking sequences to environments through text mining. PeerJ, 2016, 4, e2690.	2.0	26
39	The Relationship between Microbial Community Evenness and Function in Slow Sand Filters. MBio, 2015, 6, e00729-15.	4.1	42
40	Swarm v2: highly-scalable and high-resolution amplicon clustering. PeerJ, 2015, 3, e1420.	2.0	528
41	Insight into biases and sequencing errors for amplicon sequencing with the Illumina MiSeq platform. Nucleic Acids Research, 2015, 43, e37-e37.	14.5	626
42	Extensive Modulation of the Fecal Metagenome in Children With Crohn's Disease During Exclusive Enteral Nutrition. American Journal of Gastroenterology, 2015, 110, 1718-1729.	0.4	229
43	The skin microbiome in psoriatic arthritis: methodology development and pilot data. Lancet, The, 2015, 385, S27.	13.7	7
44	Stable-isotope probing and metagenomics reveal predation by protozoa drives <i>E. coli</i> removal in slow sand filters. ISME Journal, 2015, 9, 797-808.	9.8	36
45	Response of Archaeal and Bacterial Soil Communities to Changes Associated with Outdoor Cattle Overwintering. PLoS ONE, 2015, 10, e0135627.	2.5	11
46	Anvi'o: an advanced analysis and visualization platform for omics data. PeerJ, 2015, 3, e1319.	2.0	1,488
47	Swarm: robust and fast clustering method for amplicon-based studies. PeerJ, 2014, 2, e593.	2.0	828
48	Fluvial network organization imprints on microbial co-occurrence networks. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12799-12804.	7.1	193
49	Metagenetic analysis of patterns of distribution and diversity of marine meiobenthic eukaryotes. Global Ecology and Biogeography, 2014, 23, 1293-1302.	5.8	96
50	Binning metagenomic contigs by coverage and composition. Nature Methods, 2014, 11, 1144-1146.	19.0	1,709
51	Replicating the microbial community and water quality performance of full-scale slow sand filters in laboratory-scale filters. Water Research, 2014, 61, 141-151.	11.3	44
52	A Culture-Independent Sequence-Based Metagenomics Approach to the Investigation of an Outbreak of Shiga-Toxigenic Escherichia coli O104:H4. JAMA - Journal of the American Medical Association, 2013, 309, 1502.	7.4	290
53	Comparative metagenomic and rRNA microbial diversity characterization using archaeal and bacterial synthetic communities. Environmental Microbiology, 2013, 15, 1882-1899.	3.8	202
54	Towards standardization of the description and publication of next-generation sequencing datasets of fungal communities. New Phytologist, 2011, 191, 314-318.	7.3	85

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55	Removing Noise From Pyrosequenced Amplicons. BMC Bioinformatics, 2011, 12, 38.	2.6	1,320
56	Accurate determination of microbial diversity from 454 pyrosequencing data. Nature Methods, 2009, 6, 639-641.	19.0	895
57	The rational exploration of microbial diversity. ISME Journal, 2008, 2, 997-1006.	9.8	190
58	The Uncountables. , 0, , 33-54.		0