Nicholas Chia

List of Publications by Year
in descending order

96 papers	4,745 citations	109321 35 h-index	110387 64 g-index
102 all docs	102 docs citations	102 times ranked	7328 citing authors

#	Article	IF	Citations
1	The Microbiome of Aseptically Collected Human Breast Tissue in Benign and Malignant Disease. Scientific Reports, 2016, 6, 30751.	3.3	299
2	Relationship Between Microbiota of the Colonic Mucosa vs Feces and Symptoms, Colonic Transit, and Methane Production in Female Patients With Chronic Constipation. Gastroenterology, 2016, 150, 367-379.e1.	1.3	286
3	Potential contribution of the uterine microbiome in the development of endometrial cancer. Genome Medicine, 2016, 8, 122.	8.2	246
4	Global metabolic interaction network of the human gut microbiota for context-specific community-scale analysis. Nature Communications, 2017, 8, 15393.	12.8	216
5	Identification of Prosthetic Joint Infection Pathogens Using a Shotgun Metagenomics Approach. Clinical Infectious Diseases, 2018, 67, 1333-1338.	5.8	194
6	Shifts in the Fecal Microbiota Associated with Adenomatous Polyps. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 85-94.	2.5	168
7	Collecting Fecal Samples for Microbiome Analyses in Epidemiology Studies. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 407-416.	2.5	154
8	Direct Detection and Identification of Prosthetic Joint Infection Pathogens in Synovial Fluid by Metagenomic Shotgun Sequencing. Journal of Clinical Microbiology, 2018, 56, .	3.9	146
9	Pregnancy's Stronghold on the Vaginal Microbiome. PLoS ONE, 2014, 9, e98514.	2.5	146
10	Comparison of microbial DNA enrichment tools for metagenomic whole genome sequencing. Journal of Microbiological Methods, 2016, 127, 141-145.	1.6	141
11	Microbiome at the Frontier of Personalized Medicine. Mayo Clinic Proceedings, 2017, 92, 1855-1864.	3.0	138
12	A predictive index for health status using species-level gut microbiome profiling. Nature Communications, 2020, 11, 4635.	12.8	129
13	Prolonged use of a proton pump inhibitor reduces microbial diversity: implications for Clostridium difficile susceptibility. Microbiome, 2014, 2, 42.	11.1	128
14	<i>Clostridioides difficile</i> uses amino acids associated with gut microbial dysbiosis in a subset of patients with diarrhea. Science Translational Medicine, 2018, 10, .	12.4	128
15	The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes. Nucleic Acids Research, 2021, 49, D575-D588.	14.5	119
16	A comprehensive analysis of breast cancer microbiota and host gene expression. PLoS ONE, 2017, 12, e0188873.	2.5	111
17	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. PLoS ONE, 2014, 9, e114804.	2.5	110
18	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. Genome Medicine, 2018, 10, 78.	8.2	107

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19	Fecal Metabolomic Signatures in Colorectal Adenoma Patients Are Associated with Gut Microbiota and Early Events of Colorectal Cancer Pathogenesis. MBio, 2020, 11, .	4.1	101
20	Impact of Contaminating DNA in Whole-Genome Amplification Kits Used for Metagenomic Shotgun Sequencing for Infection Diagnosis. Journal of Clinical Microbiology, 2017, 55, 1789-1801.	3.9	95
21	Daily Vaginal Microbiota Fluctuations Associated with Natural Hormonal Cycle, Contraceptives, Diet, and Exercise. MSphere, 2020, 5, .	2.9	95
22	Mapping and comparing bacterial microbiota in the sinonasal cavity of healthy, allergic rhinitis, and chronic rhinosinusitis subjects. International Forum of Allergy and Rhinology, 2017, 7, 561-569.	2.8	86
23	MMinte: an application for predicting metabolic interactions among the microbial species in a community. BMC Bioinformatics, 2016, 17, 343.	2.6	67
24	Likelihood-Based Gene Annotations for Gap Filling and Quality Assessment in Genome-Scale Metabolic Models. PLoS Computational Biology, 2014, 10, e1003882.	3.2	66
25	Comparison of Collection Methods for Fecal Samples for Discovery Metabolomics in Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1483-1490.	2.5	63
26	Synthesis of multi-omic data and community metabolic models reveals insights into the role of hydrogen sulfide in colon cancer. Methods, 2018, 149, 59-68.	3.8	63
27	Impact of demographics on human gut microbial diversity in a US Midwest population. PeerJ, 2016, 4, e1514.	2.0	61
28	Evaluation of the CosmosID Bioinformatics Platform for Prosthetic Joint-Associated Sonicate Fluid Shotgun Metagenomic Data Analysis. Journal of Clinical Microbiology, 2019, 57, .	3.9	59
29	Comparison of Whole-Genome Sequencing Methods for Analysis of Three Methicillin-Resistant Staphylococcus aureus Outbreaks. Journal of Clinical Microbiology, 2017, 55, 1946-1953.	3.9	58
30	Postmenopause as a key factor in the composition of the Endometrial Cancer Microbiome (ECbiome). Scientific Reports, 2019, 9, 19213.	3.3	52
31	Comparison of Fecal Collection Methods for Microbiota Studies in Bangladesh. Applied and Environmental Microbiology, 2017, 83, .	3.1	50
32	Geobiology reveals how human kidney stones dissolve in vivo. Scientific Reports, 2018, 8, 13731.	3.3	50
33	Molecular epidemiology of Staphylococcus aureus bacteremia in a single large Minnesota medical center in 2015 as assessed using MLST, core genome MLST and spa typing. PLoS ONE, 2017, 12, e0179003.	2.5	43
34	Application of metagenomic shotgun sequencing to detect vector-borne pathogens in clinical blood samples. PLoS ONE, 2019, 14, e0222915.	2.5	39
35	Individualized medicine and the microbiome in reproductive tract. Frontiers in Physiology, 2015, 6, 97.	2.8	38
36	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. Scientific Reports, 2018, 8, 3161.	3.3	35

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37	A collective mechanism for phase variation in biofilms. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14597-14602.	7.1	33
38	Evolution of DNA Replication Protein Complexes in Eukaryotes and Archaea. PLoS ONE, 2010, 5, e10866.	2.5	30
39	Metabolic modeling with Big Data and the gut microbiome. Applied & Translational Genomics, 2016, 10, 10-15.	2.1	28
40	Comparison of Oral Collection Methods for Studies of Microbiota. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 137-143.	2.5	28
41	Human kidney stones: a natural record of universal biomineralization. Nature Reviews Urology, 2021, 18, 404-432.	3.8	27
42	The role of microbiome in pancreatic cancer. Cancer and Metastasis Reviews, 2021, 40, 777-789.	5.9	27
43	Nuclear Pore-Like Structures in a Compartmentalized Bacterium. PLoS ONE, 2017, 12, e0169432.	2.5	24
44	Gut microbiome meta-analysis reveals dysbiosis is independent of body mass index in predicting risk of obesity-associated CRC. BMJ Open Gastroenterology, 2019, 6, e000247.	2.7	23
45	Comparison of Methods To Collect Fecal Samples for Microbiome Studies Using Whole-Genome Shotgun Metagenomic Sequencing. MSphere, 2020, 5, .	2.9	23
46	Pertussis Outbreak, Southeastern Minnesota, 2012. Mayo Clinic Proceedings, 2014, 89, 1378-1388.	3.0	22
47	Whole-genome sequencing for methicillin-resistant *Staphylococcus aureus* (MRSA) outbreak investigation in a neonatal intensive care unit. Infection Control and Hospital Epidemiology, 2018, 39, 1412-1418.	1.8	22
48	Community metabolic modeling approaches to understanding the gut microbiome: Bridging biochemistry and ecology. Free Radical Biology and Medicine, 2017, 105, 102-109.	2.9	21
49	Hybrid-denovo: a de novo OTU-picking pipeline integrating single-end and paired-end 16S sequence tags. GigaScience, 2018, 7, 1-7.	6.4	21
50	Altered gut microbiota in female mice with persistent low body weights following removal of post-weaning chronic dietary restriction. Genome Medicine, 2016, 8, 103.	8.2	20
51	Systematic Bias Introduced by Genomic DNA Template Dilution in 16S rRNA Gene-Targeted Microbiota Profiling in Human Stool Homogenates. MSphere, 2018, 3, .	2.9	19
52	Reproducibility, stability, and accuracy of microbial profiles by fecal sample collection method in three distinct populations. PLoS ONE, 2019, 14, e0224757.	2.5	19
53	A systemic review of the role of enterotoxic Bacteroides fragilis in colorectal cancer. Neoplasia, 2022, 29, 100797.	5.3	19
54	Predominance of Atopobium vaginae at Midtrimester: a Potential Indicator of Preterm Birth Risk in a Nigerian Cohort. MSphere, 2021, 6, .	2.9	16

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55	Amplification of Femtograms of Bacterial DNA Within 3 h Using a Digital Microfluidics Platform for MinION Sequencing. ACS Omega, 2021, 6, 25642-25651.	3.5	15
56	HGT-ID: an efficient and sensitive workflow to detect human-viral insertion sites using next-generation sequencing data. BMC Bioinformatics, 2018, 19, 271.	2.6	14
57	Minimizing the number of optimizations for efficient community dynamic flux balance analysis. PLoS Computational Biology, 2020, 16, e1007786.	3.2	14
58	In Vivo Entombment of Bacteria and Fungi during Calcium Oxalate, Brushite, and Struvite Urolithiasis. Kidney360, 2021, 2, 298-311.	2.1	14
59	Lactobacillus crispatus thrives in pregnancy hormonal milieu in a Nigerian patient cohort. Scientific Reports, 2021, 11, 18152.	3.3	12
60	â€œAnswers in hoursâ€• A prospective clinical study using nanopore sequencing for bile duct cultures. Surgery, 2022, 171, 693-702.	1.9	12
61	Composition, diversity and potential utility of intervention-naÃ¯ve pancreatic cancer intratumoral microbiome signature profiling via endoscopic ultrasound. Gut, 2022, 71, 441-443.	12.1	11
62	Dynamics of gene duplication and transposons in microbial genomes following a sudden environmental change. Physical Review E, 2011, 83, 021906.	2.1	10
63	Potential Role of Inflammation-Promoting Biliary Microbiome in Primary Sclerosing Cholangitis and Cholangiocarcinoma. Cancers, 2022, 14, 2120.	3.7	10
64	Statistical Mechanics of Horizontal Gene Transfer inÂEvolutionary Ecology. Journal of Statistical Physics, 2011, 142, 1287-1301.	1.2	9
65	Lack of correlation of virulence gene profiles of Staphylococcus aureus bacteremia isolates with mortality. Microbial Pathogenesis, 2019, 133, 103543.	2.9	9
66	Comparison of Three Commercial Tools for Metagenomic Shotgun Sequencing Analysis. Journal of Clinical Microbiology, 2020, 58, .	3.9	9
67	The breast tissue microbiome, stroma, immune cells and breast cancer. Neoplasia, 2022, 27, 100786.	5.3	9
68	Porphyromonas somerae Invasion of Endometrial Cancer Cells. Frontiers in Microbiology, 2021, 12, 674835.	3.5	7
69	Resource-allocation constraint governs structure and function of microbial communities in metabolic modeling. Metabolic Engineering, 2022, 70, 12-22.	7.0	7
70	λ-prophage induction modeled as a cooperative failure mode of lytic repression. Physical Review E, 2009, 80, 030901.	2.1	6
71	Draft Genome Sequence of Methanobrevibacter smithii Isolate WWM1085, Obtained from a Human Stool Sample. Genome Announcements, 2017, 5, .	0.8	6
72	Gut Microbiome and Colon Cancer: A Plausible Explanation for Dietary Contributions to Cancer. Journal of the American College of Surgeons, 2019, 229, 231-235.	0.5	6

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73	Core genome MLST and resistome analysis of Klebsiella pneumoniae using a clinically amenable workflow. Diagnostic Microbiology and Infectious Disease, 2020, 97, 114996.	1.8	6
74	Fecal Microbiome in Epidemiologic Studies—Response. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 870-871.	2.5	4
75	Prototyping CRISP: A Causal Relation and Inference Search Platform applied to Colorectal Cancer Data. , 2021, , .		4
76	Comparative Transcriptomic Analysis of Staphylococcus aureus Associated with Periprosthetic Joint Infection under inÂVivo and inÂVitro Conditions. Journal of Molecular Diagnostics, 2021, 23, 986-999.	2.8	4
77	Inferring modes of evolution from colorectal cancer with residual polyp of origin. Oncotarget, 2018, 9, 6780-6792.	1.8	3
78	Transcriptomic analysis of <i>Streptococcus agalactiae</i> periprosthetic joint infection. MicrobiologyOpen, 2021, 10, e1256.	3.0	3
79	Dynamics of gene duplication and transposons in microbial genomes following a sudden environmental change. Mobile Genetic Elements, 2011, 1, 221-224.	1.8	2
80	Draft Genome Sequences of Nine Pseudomonas aeruginosa Strains, Including Eight Clinical Isolates. Genome Announcements, 2015, 3, .	0.8	2
81	Acinetobacter baumannii Genomic Sequence-Based Core Genome Multilocus Sequence Typing Using Ridom SeqSphere+ and Antimicrobial Susceptibility Prediction in ARESdb. Journal of Clinical Microbiology, 2022, 60, .	3.9	2
82	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. PLoS Computational Biology, 2020, 16, e1008240.	3.2	1
83	Confidence in the dynamic spread of epidemics under biased sampling conditions. PeerJ, 2020, 8, e9758.	2.0	1
84	Clonal Hematopoiesis of Indeterminate Potential Is Associated with Increased Age-Independent Morbidity and Mortality in Patients with COVID-19- the Beyond DNA COVID-19 Project. Blood, 2021, 138, 2164-2164.	1.4	1
85	Letter to the Editor: The Surge of Type 2 Diabetes Mellitus in China - an International Alert: Physical Exercise and Low-Caloric Diet May Reduce the Risks of Type 2 Diabetes Mellitus and Dementia. Annals of Clinical and Laboratory Science, 2016, 46, 114-8.	0.2	1
86	Shifts in the fecal microbial community composition are associated with dietary fiber solubility. FASEB Journal, 2013, 27, 1056.2.	0.5	0
87	The Unreasonable Effectiveness of Inverse Reinforcement Learning in Advancing Cancer Research. Proceedings of the AAAI Conference on Artificial Intelligence, 2020, 34, 437-445.	4.9	0
88	Cell-Type and Allele Specific Distribution of Multiple TET2 Mutations in Two Patients with Chronic Myelomonocytic Leukemia (CMML). Blood, 2021, 138, 1470-1470.	1.4	0
89	Minimizing the number of optimizations for efficient community dynamic flux balance analysis. , 2020, 16, e1007786.		0
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91	Minimizing the number of optimizations for efficient community dynamic flux balance analysis. , 2020, 16, e1007786.		0
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93	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
94	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
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96	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0