

Nicholas Chia

List of Publications by Year in descending order

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Version: 2024-02-01

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	Composition, diversity and potential utility of intervention-naïve pancreatic cancer intratumoral microbiome signature profiling via endoscopic ultrasound. <i>Gut</i> , 2022, 71, 441-443.	12.1	11
2	Resource-allocation constraint governs structure and function of microbial communities in metabolic modeling. <i>Metabolic Engineering</i> , 2022, 70, 12-22.	7.0	7
3	“Answers in hours”: A prospective clinical study using nanopore sequencing for bile duct cultures. <i>Surgery</i> , 2022, 171, 693-702.	1.9	12
4	The breast tissue microbiome, stroma, immune cells and breast cancer. <i>Neoplasia</i> , 2022, 27, 100786.	5.3	9
5	A systemic review of the role of enterotoxigenic <i>Bacteroides fragilis</i> in colorectal cancer. <i>Neoplasia</i> , 2022, 29, 100797.	5.3	19
6	Potential Role of Inflammation-Promoting Biliary Microbiome in Primary Sclerosing Cholangitis and Cholangiocarcinoma. <i>Cancers</i> , 2022, 14, 2120.	3.7	10
7	<i>Acinetobacter baumannii</i> Genomic Sequence-Based Core Genome Multilocus Sequence Typing Using Ridom SeqSphere+ and Antimicrobial Susceptibility Prediction in ARESdb. <i>Journal of Clinical Microbiology</i> , 2022, 60, .	3.9	2
8	The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes. <i>Nucleic Acids Research</i> , 2021, 49, D575-D588.	14.5	119
9	Predominance of <i>Atopobium vaginae</i> at Midtrimester: a Potential Indicator of Preterm Birth Risk in a Nigerian Cohort. <i>MSphere</i> , 2021, 6, .	2.9	16
10	Prototyping CRISP: A Causal Relation and Inference Search Platform applied to Colorectal Cancer Data. , 2021, , .		4
11	Human kidney stones: a natural record of universal biomineralization. <i>Nature Reviews Urology</i> , 2021, 18, 404-432.	3.8	27
12	<i>Porphyromonas somerae</i> Invasion of Endometrial Cancer Cells. <i>Frontiers in Microbiology</i> , 2021, 12, 674835.	3.5	7
13	The role of microbiome in pancreatic cancer. <i>Cancer and Metastasis Reviews</i> , 2021, 40, 777-789.	5.9	27
14	Comparative Transcriptomic Analysis of <i>Staphylococcus aureus</i> Associated with Periprosthetic Joint Infection under in Vivo and in Vitro Conditions. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 986-999.	2.8	4
15	Amplification of Femtograms of Bacterial DNA Within 3 h Using a Digital Microfluidics Platform for MinION Sequencing. <i>ACS Omega</i> , 2021, 6, 25642-25651.	3.5	15
16	<i>Lactobacillus crispatus</i> thrives in pregnancy hormonal milieu in a Nigerian patient cohort. <i>Scientific Reports</i> , 2021, 11, 18152.	3.3	12
17	In Vivo Entombment of Bacteria and Fungi during Calcium Oxalate, Brushite, and Struvite Urolithiasis. <i>Kidney360</i> , 2021, 2, 298-311.	2.1	14
18	Cell-Type and Allele Specific Distribution of Multiple TET2 Mutations in Two Patients with Chronic Myelomonocytic Leukemia (CMML). <i>Blood</i> , 2021, 138, 1470-1470.	1.4	0

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19	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. <i>Blood</i> , 2021, 138, 2164-2164.	1.4	1
20	Transcriptomic analysis of <i>Streptococcus agalactiae</i> periprosthetic joint infection. <i>MicrobiologyOpen</i> , 2021, 10, e1256.	3.0	3
21	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. <i>PLoS Computational Biology</i> , 2020, 16, e1008240.	3.2	1
22	A predictive index for health status using species-level gut microbiome profiling. <i>Nature Communications</i> , 2020, 11, 4635.	12.8	129
23	Comparison of Three Commercial Tools for Metagenomic Shotgun Sequencing Analysis. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	9
24	Daily Vaginal Microbiota Fluctuations Associated with Natural Hormonal Cycle, Contraceptives, Diet, and Exercise. <i>MSphere</i> , 2020, 5, .	2.9	95
25	Core genome MLST and resistome analysis of <i>Klebsiella pneumoniae</i> using a clinically amenable workflow. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 97, 114996.	1.8	6
26	Fecal Metabolomic Signatures in Colorectal Adenoma Patients Are Associated with Gut Microbiota and Early Events of Colorectal Cancer Pathogenesis. <i>MBio</i> , 2020, 11, .	4.1	101
27	Comparison of Methods To Collect Fecal Samples for Microbiome Studies Using Whole-Genome Shotgun Metagenomic Sequencing. <i>MSphere</i> , 2020, 5, .	2.9	23
28	Minimizing the number of optimizations for efficient community dynamic flux balance analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1007786.	3.2	14
29	Confidence in the dynamic spread of epidemics under biased sampling conditions. <i>PeerJ</i> , 2020, 8, e9758.	2.0	1
30	The Unreasonable Effectiveness of Inverse Reinforcement Learning in Advancing Cancer Research. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2020, 34, 437-445.	4.9	0
31	Minimizing the number of optimizations for efficient community dynamic flux balance analysis. , 2020, 16, e1007786.		0
32	Minimizing the number of optimizations for efficient community dynamic flux balance analysis. , 2020, 16, e1007786.		0
33	Minimizing the number of optimizations for efficient community dynamic flux balance analysis. , 2020, 16, e1007786.		0
34	Minimizing the number of optimizations for efficient community dynamic flux balance analysis. , 2020, 16, e1007786.		0
35	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
36	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0

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37	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
38	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
39	Application of metagenomic shotgun sequencing to detect vector-borne pathogens in clinical blood samples. PLoS ONE, 2019, 14, e0222915.	2.5	39
40	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
41	Lack of correlation of virulence gene profiles of Staphylococcus aureus bacteremia isolates with mortality. Microbial Pathogenesis, 2019, 133, 103543.	2.9	9
42	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
43	Reproducibility, stability, and accuracy of microbial profiles by fecal sample collection method in three distinct populations. PLoS ONE, 2019, 14, e0224757.	2.5	19
44	Postmenopause as a key factor in the composition of the Endometrial Cancer Microbiome (ECbiome). Scientific Reports, 2019, 9, 19213.	3.3	52
45	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
46	Comparison of Oral Collection Methods for Studies of Microbiota. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 137-143.	2.5	28
47	Identification of Prosthetic Joint Infection Pathogens Using a Shotgun Metagenomics Approach. Clinical Infectious Diseases, 2018, 67, 1333-1338.	5.8	194
48	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. Scientific Reports, 2018, 8, 3161.	3.3	35
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	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
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	Whole-genome sequencing for methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) outbreak investigation in a neonatal intensive care unit. Infection Control and Hospital Epidemiology, 2018, 39, 1412-1418.	1.8	22
53	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. Genome Medicine, 2018, 10, 78.	8.2	107
54	<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

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55	Geobiology reveals how human kidney stones dissolve in vivo. <i>Scientific Reports</i> , 2018, 8, 13731.	3.3	50
56	Direct Detection and Identification of Prosthetic Joint Infection Pathogens in Synovial Fluid by Metagenomic Shotgun Sequencing. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	146
57	HGT-ID: an efficient and sensitive workflow to detect human-viral insertion sites using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2018, 19, 271.	2.6	14
58	Inferring modes of evolution from colorectal cancer with residual polyp of origin. <i>Oncotarget</i> , 2018, 9, 6780-6792.	1.8	3
59	Comparison of Fecal Collection Methods for Microbiota Studies in Bangladesh. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	50
60	Comparison of Whole-Genome Sequencing Methods for Analysis of Three Methicillin-Resistant <i>Staphylococcus aureus</i> Outbreaks. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1946-1953.	3.9	58
61	Mapping and comparing bacterial microbiota in the sinonasal cavity of healthy, allergic rhinitis, and chronic rhinosinusitis subjects. <i>International Forum of Allergy and Rhinology</i> , 2017, 7, 561-569.	2.8	86
62	Global metabolic interaction network of the human gut microbiota for context-specific community-scale analysis. <i>Nature Communications</i> , 2017, 8, 15393.	12.8	216
63	Impact of Contaminating DNA in Whole-Genome Amplification Kits Used for Metagenomic Shotgun Sequencing for Infection Diagnosis. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1789-1801.	3.9	95
64	Community metabolic modeling approaches to understanding the gut microbiome: Bridging biochemistry and ecology. <i>Free Radical Biology and Medicine</i> , 2017, 105, 102-109.	2.9	21
65	Draft Genome Sequence of <i>Methanobrevibacter smithii</i> Isolate WWM1085, Obtained from a Human Stool Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
66	Shifts in the Fecal Microbiota Associated with Adenomatous Polyps. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 85-94.	2.5	168
67	Microbiome at the Frontier of Personalized Medicine. <i>Mayo Clinic Proceedings</i> , 2017, 92, 1855-1864.	3.0	138
68	Molecular epidemiology of <i>Staphylococcus aureus</i> bacteremia in a single large Minnesota medical center in 2015 as assessed using MLST, core genome MLST and spa typing. <i>PLoS ONE</i> , 2017, 12, e0179003.	2.5	43
69	Nuclear Pore-Like Structures in a Compartmentalized Bacterium. <i>PLoS ONE</i> , 2017, 12, e0169432.	2.5	24
70	A comprehensive analysis of breast cancer microbiota and host gene expression. <i>PLoS ONE</i> , 2017, 12, e0188873.	2.5	111
71	MMinte: an application for predicting metabolic interactions among the microbial species in a community. <i>BMC Bioinformatics</i> , 2016, 17, 343.	2.6	67
72	Comparison of microbial DNA enrichment tools for metagenomic whole genome sequencing. <i>Journal of Microbiological Methods</i> , 2016, 127, 141-145.	1.6	141

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73	Fecal Microbiome in Epidemiologic Studiesâ€™Response. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 870-871.	2.5	4
74	Comparison of Collection Methods for Fecal Samples for Discovery Metabolomics in Epidemiologic Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1483-1490.	2.5	63
75	Altered gut microbiota in female mice with persistent low body weights following removal of post-weaning chronic dietary restriction. <i>Genome Medicine</i> , 2016, 8, 103.	8.2	20
76	Potential contribution of the uterine microbiome in the development of endometrial cancer. <i>Genome Medicine</i> , 2016, 8, 122.	8.2	246
77	The Microbiome of Aseptically Collected Human Breast Tissue in Benign and Malignant Disease. <i>Scientific Reports</i> , 2016, 6, 30751.	3.3	299
78	Metabolic modeling with Big Data and the gut microbiome. <i>Applied & Translational Genomics</i> , 2016, 10, 10-15.	2.1	28
79	Collecting Fecal Samples for Microbiome Analyses in Epidemiology Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 407-416.	2.5	154
80	Relationship Between Microbiota of the Colonic Mucosa vs Feces and Symptoms, Colonic Transit, and Methane Production in Female Patients With Chronic Constipation. <i>Gastroenterology</i> , 2016, 150, 367-379.e1.	1.3	286
81	Impact of demographics on human gut microbial diversity in a US Midwest population. <i>PeerJ</i> , 2016, 4, e1514.	2.0	61
82	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. <i>Annals of Clinical and Laboratory Science</i> , 2016, 46, 114-8.	0.2	1
83	Individualized medicine and the microbiome in reproductive tract. <i>Frontiers in Physiology</i> , 2015, 6, 97.	2.8	38
84	Draft Genome Sequences of Nine <i>Pseudomonas aeruginosa</i> Strains, Including Eight Clinical Isolates. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
85	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. <i>PLoS ONE</i> , 2014, 9, e114804.	2.5	110
86	Likelihood-Based Gene Annotations for Gap Filling and Quality Assessment in Genome-Scale Metabolic Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003882.	3.2	66
87	Prolonged use of a proton pump inhibitor reduces microbial diversity: implications for <i>Clostridium difficile</i> susceptibility. <i>Microbiome</i> , 2014, 2, 42.	11.1	128
88	Pertussis Outbreak, Southeastern Minnesota, 2012. <i>Mayo Clinic Proceedings</i> , 2014, 89, 1378-1388.	3.0	22
89	Pregnancy's Stronghold on the Vaginal Microbiome. <i>PLoS ONE</i> , 2014, 9, e98514.	2.5	146
90	Shifts in the fecal microbial community composition are associated with dietary fiber solubility. <i>FASEB Journal</i> , 2013, 27, 1056.2.	0.5	0

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91	Statistical Mechanics of Horizontal Gene Transfer in Evolutionary Ecology. Journal of Statistical Physics, 2011, 142, 1287-1301.	1.2	9
92	Dynamics of gene duplication and transposons in microbial genomes following a sudden environmental change. Mobile Genetic Elements, 2011, 1, 221-224.	1.8	2
93	Dynamics of gene duplication and transposons in microbial genomes following a sudden environmental change. Physical Review E, 2011, 83, 021906.	2.1	10
94	Evolution of DNA Replication Protein Complexes in Eukaryotes and Archaea. PLoS ONE, 2010, 5, e10866.	2.5	30
95	$\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"} \langle \text{mml:mi} \rangle \hat{\rho} \langle \text{mml:mi} \rangle \langle \text{mml:math} \rangle \text{-prophage induction modeled as a cooperative failure mode of lytic repression. Physical Review E, 2009, 80, 030901.}$	2.1	6
96	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