Ni Zhao

List of Publications by Year
in descending order

46 papers	8,264 citations	218677 26 h-index	214800 47 g-index
49 all docs	49 docs citations	49 times ranked	14857 citing authors

#	Article	IF	Citations
1	Oral Human Papillomavirus Associated With Differences in Oral Microbiota Beta Diversity and Microbiota Abundance. Journal of Infectious Diseases, 2022, 226, 1098-1108.	4.0	15
2	MiRKAT-MC: A Distance-Based Microbiome Kernel Association Test With Multi-Categorical Outcomes. Frontiers in Genetics, 2022, 13, 841764.	2.3	4
3	MiRKAT: kernel machine regression-based global association tests for the microbiome. Bioinformatics, 2021, 37, 1595-1597.	4.1	18
4	Metaâ€analysis methods for multiple related markers: Applications to microbiome studies with the results on multiple Î± â€diversity indices. Statistics in Medicine, 2021, 40, 2859-2876.	1.6	3
5	Effects of processed meat and drinking water nitrate on oral and fecal microbial populations in a controlled feeding study. Environmental Research, 2021, 197, 111084.	7.5	16
6	Powerful and robust non-parametric association testing for microbiome data via a zero-inflated quantile approach (ZINQ). Microbiome, 2021, 9, 181.	11.1	8
7	Low Diversity in Nasal Microbiome Associated With *Staphylococcus aureus* Colonization and Bloodstream Infections in Hospitalized Neonates. Open Forum Infectious Diseases, 2021, 8, ofab475.	0.9	6
8	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
9	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota Î±-Diversity: An Individual-level Meta-analysis. Clinical Infectious Diseases, 2020, 70, 615-627.	5.8	65
10	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
11	A powerful microbial group association test based on the higher criticism analysis for sparse microbial association signals. Microbiome, 2020, 8, 63.	11.1	9
12	Composite Kernel Association Test (CKAT) for SNP-set joint assessment of genotype and genotype-by-treatment interaction in Pharmacogenetics studies. Bioinformatics, 2020, 36, 3162-3168.	4.1	3
13	Compartmental Analysis of T-cell Clonal Dynamics as a Function of Pathologic Response to Neoadjuvant PD-1 Blockade in Resectable Nonâ€"Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 1327-1337.	7.0	90
14	An Adaptive Multivariate Two-Sample Test With Application to Microbiome Differential Abundance Analysis. Frontiers in Genetics, 2019, 10, 350.	2.3	10
15	Colonic mucosal and exfoliome transcriptomic profiling and fecal microbiome response to a flaxseed lignan extract intervention in humans. American Journal of Clinical Nutrition, 2019, 110, 377-390.	4.7	29
16	A Distance-Based Kernel Association Test Based on the Generalized Linear Mixed Model for Correlated Microbiome Studies. Frontiers in Genetics, 2019, 10, 458.	2.3	31
17	Composite Kernel Machine Regression Based on Likelihood Ratio Test for Joint Testing of Genetic and Geneâ€"Environment Interaction Effect. Biometrics, 2019, 75, 625-637.	1.4	7
18	Kernel machine methods for integrative analysis of genomeâ€wide methylation and genotyping studies. Genetic Epidemiology, 2018, 42, 156-167.	1.3	8

#	Article	IF	Citations
19	A small‐sample kernel association test for correlated data with application to microbiome association studies. Genetic Epidemiology, 2018, 42, 772-782.	1.3	30
20	Generalized Hotelling's test for paired compositional data with application to human microbiome studies. Genetic Epidemiology, 2018, 42, 459-469.	1.3	20
21	MiRKAT-S: a community-level test of association between the microbiota and survival times. Microbiome, 2017, 5, 17.	11.1	50
22	A Fast Small-Sample Kernel Independence Test for Microbiome Community-Level Association Analysis. Biometrics, 2017, 73, 1453-1463.	1.4	36
23	A small-sample multivariate kernel machine test for microbiome association studies. Genetic Epidemiology, 2017, 41, 210-220.	1.3	37
24	Powerful Genetic Association Analysis for Common or Rare Variants with High-Dimensional Structured Traits. Genetics, 2017, 206, 1779-1790.	2.9	36
25	Small Sample Kernel Association Tests for Human Genetic and Microbiome Association Studies. Genetic Epidemiology, 2016, 40, 5-19.	1.3	45
26	A novel copy number variants kernel association test with application to autism spectrum disorders studies. Bioinformatics, 2016, 32, 3603-3610.	4.1	17
27	Prioritizing individual genetic variants after kernel machine testing using variable selection. Genetic Epidemiology, 2016, 40, 722-731.	1.3	15
28	Global Analysis of Methylation Profiles From High Resolution CpG Data. Genetic Epidemiology, 2015, 39, 53-64.	1.3	19
29	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
30	Elderly Patients With Squamous Cell Carcinoma of the Head and Neck and the Benefit of Multimodality Therapy. Oncologist, 2015, 20, 159-165.	3.7	39
31	Testing in Microbiome-Profiling Studies with MiRKAT, the Microbiome Regression-Based Kernel Association Test. American Journal of Human Genetics, 2015, 96, 797-807.	6.2	248
32	Rare variant testing across methods and thresholds using the multi-kernel sequence kernel association test (MK-SKAT). Statistics and Its Interface, 2015, 8, 495-505.	0.3	11
33	Alterations of LKB1 and KRAS and risk of brain metastasis: Comprehensive characterization by mutation analysis, copy number, and gene expression in non-small-cell lung carcinoma. Lung Cancer, 2014, 86, 255-261.	2.0	64
34	SigFuge: single gene clustering of RNA-seq reveals differential isoform usage among cancer samples. Nucleic Acids Research, 2014, 42, e113-e113.	14.5	17
35	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
36	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317

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37	ERCC1 Protein Expression Is Associated with Differential Survival in Oropharyngeal Head and Neck Squamous Cell Carcinoma. Otolaryngology - Head and Neck Surgery, 2013, 149, 587-595.	1.9	12
38	The LKB1 Tumor Suppressor as a Biomarker in Mouse and Human Tissues. PLoS ONE, 2013, 8, e73449.	2.5	14
39	Molecular Subtypes in Head and Neck Cancer Exhibit Distinct Patterns of Chromosomal Gain and Loss of Canonical Cancer Genes. PLoS ONE, 2013, 8, e56823.	2.5	263
40	Phase II Efficacy and Pharmacogenomic Study of Selumetinib (AZD6244; ARRY-142886) in Iodine-131 Refractory Papillary Thyroid Carcinoma with or without Follicular Elements. Clinical Cancer Research, 2012, 18, 2056-2065.	7.0	141
41	Different cellular p16INK4a localisation may signal different survival outcomes in head and neck cancer. British Journal of Cancer, 2012, 107, 482-490.	6.4	39
42	Differential Pathogenesis of Lung Adenocarcinoma Subtypes Involving Sequence Mutations, Copy Number, Chromosomal Instability, and Methylation. PLoS ONE, 2012, 7, e36530.	2.5	225
43	High XRCC1 Protein Expression Is Associated with Poorer Survival in Patients with Head and Neck Squamous Cell Carcinoma. Clinical Cancer Research, 2011, 17, 6542-6552.	7.0	49
44	Sex-specific gene expression in the BXD mouse liver. Physiological Genomics, 2010, 42, 456-468.	2.3	30
45	Visibility, air quality and daily mortality in Shanghai, China. Science of the Total Environment, 2009, 407, 3295-3300.	8.0	142
46	Diurnal Temperature Range is a Risk Factor for Coronary Heart Disease Death. Journal of Epidemiology, 2009, 19, 328-332.	2.4	54