## Xiang Zhan

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2226997/publications.pdf

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		687363	713466
37	552	13	21
papers	citations	h-index	g-index
42	42	42	727
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Vaginal microbiota and genitourinary menopausal symptoms: a cross-sectional analysis. Menopause, 2017, 24, 1160-1166.	2.0	62
2	MiRKAT-S: a community-level test of association between the microbiota and survival times. Microbiome, 2017, 5, 17.	11.1	50
3	A small-sample multivariate kernel machine test for microbiome association studies. Genetic Epidemiology, 2017, 41, 210-220.	1.3	37
4	A Fast Small-Sample Kernel Independence Test for Microbiome Community-Level Association Analysis. Biometrics, 2017, 73, 1453-1463.	1.4	36
5	Powerful Genetic Association Analysis for Common or Rare Variants with High-Dimensional Structured Traits. Genetics, 2017, 206, 1779-1790.	2.9	36
6	Loss of Skin Microbial Diversity and Alteration of Bacterial Metabolic Function in Hidradenitis Suppurativa. Journal of Investigative Dermatology, 2020, 140, 716-720.	0.7	32
7	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
8	A smallâ€sample kernel association test for correlated data with application to microbiome association studies. Genetic Epidemiology, 2018, 42, 772-782.	1.3	30
9	Kernel approaches for differential expression analysis of mass spectrometry-based metabolomics data. BMC Bioinformatics, 2015, 16, 77.	2.6	27
10	Generalized Hotelling's test for paired compositional data with application to human microbiome studies. Genetic Epidemiology, 2018, 42, 459-469.	1.3	20
11	Trend of influenza vaccine Facebook posts in last 4 years: a content analysis. American Journal of Infection Control, 2020, 48, 361-367.	2.3	20
12	MiRKAT: kernel machine regression-based global association tests for the microbiome. Bioinformatics, 2021, 37, 1595-1597.	4.1	18
13	A novel copy number variants kernel association test with application to autism spectrum disorders studies. Bioinformatics, 2016, 32, 3603-3610.	4.1	17
14	Prioritizing genetic variants in GWAS with lasso using permutation-assisted tuning. Bioinformatics, 2020, 36, 3811-3817.	4.1	15
15	Identification of Key Signaling Pathways Orchestrating Substrate Topography Directed Osteogenic Differentiation Through High-Throughput siRNA Screening. Scientific Reports, 2019, 9, 1001.	3.3	11
16	Compositional knockoff filter for highâ€dimensional regression analysis of microbiome data. Biometrics, 2021, 77, 984-995.	1.4	11
17	Assessing Contamination of Stream Networks near Shale Gas Development Using a New Geospatial Tool. Environmental Science & Technology, 2020, 54, 8632-8639.	10.0	11
18	A behavioral model for mapping the genetic architecture of gut-microbiota networks. Gut Microbes, 2021, 13, 1820847.	9.8	11

#	Article	IF	CITATIONS
19	An Adaptive Multivariate Two-Sample Test With Application to Microbiome Differential Abundance Analysis. Frontiers in Genetics, 2019, 10, 350.	2.3	10
20	An Adaptive Genetic Association Test Using Double Kernel Machines. Statistics in Biosciences, 2015, 7, 262-281.	1.2	8
21	Kernel machine methods for integrative analysis of genomeâ€wide methylation and genotyping studies. Genetic Epidemiology, 2018, 42, 156-167.	1.3	8
22	Interrogation of Internal Workings in Microbial Community Assembly: Play a Game through a Behavioral Network?. MSystems, 2019, 4, .	3.8	7
23	Relationship Between MiRKAT and Coefficient of Determination in Similarity Matrix Regression. Processes, 2019, 7, 79.	2.8	5
24	Safety of bariatric surgery in patients with coronary artery disease. Surgery for Obesity and Related Diseases, 2020, 16, 2031-2037.	1.2	4
25	Associations between stool micro-transcriptome, gut microbiota, and infant growth. Journal of Developmental Origins of Health and Disease, 2021, 12, 876-882.	1.4	4
26	MiRKAT-MC: A Distance-Based Microbiome Kernel Association Test With Multi-Categorical Outcomes. Frontiers in Genetics, 2022, 13, 841764.	2.3	4
27	Reader Reaction: A Note on Testing and Estimation in Marker-set Association Study Using Semiparametric Quantile Regression Kernel Machine. Biometrics, 2018, 74, 764-766.	1.4	3
28	Testing microbiome association using integrated quantile regression models. Bioinformatics, 2022, 38, 419-425.	4.1	3
29	Resident Training and the Assessment of Orthopaedic Surgical Skills. JBJS Open Access, 2021, 6, .	1.5	3
30	Adaptive and powerful microbiome multivariate association analysis via feature selection. NAR Genomics and Bioinformatics, 2022, 4, Iqab120.	3.2	3
31	Incorporating auxiliary information for improved prediction using combination of kernel machines. Statistical Methodology, 2015, 22, 47-57.	0.5	2
32	Surgical Management of Vestibular Schwannoma: Practice Pattern Analysis via NSQIP. Annals of Otology, Rhinology and Laryngology, 2020, 129, 230-237.	1.1	2
33	Variantâ€set association test for generalized linear mixed model. Genetic Epidemiology, 2021, 45, 402-412.	1.3	2
34	Assessment of Patient Perspectives and Barriers to Self-Infusion of Augmentation Therapy for Alpha-1 Antitrypsin Deficiency During the COVID-19 Pandemic. Pulmonary Therapy, 2022, 8, 95.	2.2	2
35	Nonlinear predictive directions in clinical trials. Computational Statistics and Data Analysis, 2022, 174, 107476.	1.2	2
36	Response to Ring et al.: In Silico Predictive Metagenomic Analyses Highlight Key Metabolic Pathways Impacted in the Hidradenitis Suppurativa Skin Microbiome. Journal of Investigative Dermatology, 2020, 140, 1476-1479.	0.7	1

#	Article	IF	CITATIONS
37	A novel power-based approach to Gaussian kernel selection in the kernel-based association test. Statistical Methodology, 2016, 33, 180-191.	0.5	0