

# Xingjie Shi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10416513/publications.pdf>

Version: 2024-02-01

22  
papers

535  
citations

687363

13  
h-index

713466

21  
g-index

22  
all docs

22  
docs citations

22  
times ranked

640  
citing authors

#	ARTICLE	IF	CITATIONS
1	MR-Corr2: a two-sample Mendelian randomization method that accounts for correlated horizontal pleiotropy using correlated instrumental variants. <i>Bioinformatics</i> , 2022, 38, 303-310.	4.1	10
2	SC-MEB: spatial clustering with hidden Markov random field using empirical Bayes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	44
3	Joint dimension reduction and clustering analysis of single-cell RNA-seq and spatial transcriptomics data. <i>Nucleic Acids Research</i> , 2022, 50, e72-e72.	14.5	26
4	Using Collaborative Mixed Models to Account for Imputation Uncertainty in Transcriptome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2021, 2212, 93-103.	0.9	2
5	CoMM-S2: a collaborative mixed model using summary statistics in transcriptome-wide association studies. <i>Bioinformatics</i> , 2020, 36, 2009-2016.	4.1	30
6	A tissue-specific collaborative mixed model for jointly analyzing multiple tissues in transcriptome-wide association studies. <i>Nucleic Acids Research</i> , 2020, 48, e109-e109.	14.5	15
7	MR-LDP: a two-sample Mendelian randomization for GWAS summary statistics accounting for linkage disequilibrium and horizontal pleiotropy. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa028.	3.2	27
8	Promoting sign consistency in the cure model estimation and selection. <i>Statistical Methods in Medical Research</i> , 2020, 29, 15-28.	1.5	6
9	Horizontal and vertical integrative analysis methods for mental disorders omics data. <i>Scientific Reports</i> , 2019, 9, 13430.	3.3	5
10	VIMCO: variational inference for multiple correlated outcomes in genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 3693-3700.	4.1	9
11	Analysis of cancer gene expression data with an assisted robust marker identification approach. <i>Genetic Epidemiology</i> , 2017, 41, 779-789.	1.3	16
12	Analyzing Association Mapping in Pedigree-Based GWAS Using a Penalized Multitrait Mixed Model. <i>Genetic Epidemiology</i> , 2016, 40, 382-393.	1.3	11
13	Integrated analysis of multidimensional omics data on cutaneous melanoma prognosis. <i>Genomics</i> , 2016, 107, 223-230.	2.9	57
14	A penalized robust semiparametric approach for gene-environment interactions. <i>Statistics in Medicine</i> , 2015, 34, 4016-4030.	1.6	26
15	Deciphering the associations between gene expression and copy number alteration using a sparse double Laplacian shrinkage approach. <i>Bioinformatics</i> , 2015, 31, 3977-3983.	4.1	27
16	Measures for the degree of overlap of gene signatures and applications to TCGA. <i>Briefings in Bioinformatics</i> , 2015, 16, 735-744.	6.5	15
17	Integrative analysis of omics data using penalty functions. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2015, 7, 99-108.	3.9	34
18	Combining multidimensional genomic measurements for predicting cancer prognosis: observations from TCGA. <i>Briefings in Bioinformatics</i> , 2015, 16, 291-303.	6.5	122

#	ARTICLE	IF	CITATIONS
19	Integrative Analysis of High-throughput Cancer Studies With Contrasted Penalization. Genetic Epidemiology, 2014, 38, 144-151.	1.3	17
20	A Penalized Robust Method for Identifying Gene-Environment Interactions. Genetic Epidemiology, 2014, 38, 220-230.	1.3	24
21	Similarity of markers identified from cancer gene expression studies: observations from GEO. Briefings in Bioinformatics, 2014, 15, 671-684.	6.5	12
22	Penalized Integrative Analysis of High-Dimensional Omics Data. , 0, , 174-204.		0