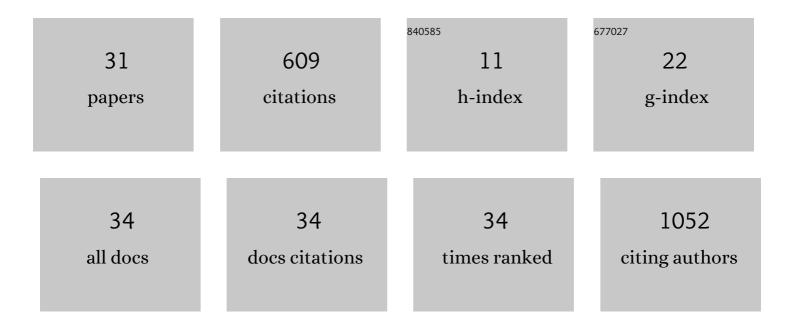
## Jiadong Ji

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8886521/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	5.8	240
2	Lung function and systemic inflammation associated with short-term air pollution exposure in chronic obstructive pulmonary disease patients in Beijing, China. Environmental Health, 2020, 19, 12.	1.7	58
3	<p>Short-term effects of ambient air pollution on chronic obstructive pulmonary disease admissions in Beijing, China (2013–2017)</p> . International Journal of COPD, 2019, Volume 14, 297-309.	0.9	40
4	JDINAC: joint density-based non-parametric differential interaction network analysis and classification using high-dimensional sparse omics data. Bioinformatics, 2017, 33, 3080-3087.	1.8	24
5	A Machine Learning Method for Identifying Critical Interactions Between Gene Pairs in Alzheimer's Disease Prediction. Frontiers in Neurology, 2019, 10, 1162.	1.1	23
6	<p>Risk Prediction of Dyslipidemia for Chinese Han Adults Using Random Forest Survival Model</p> . Clinical Epidemiology, 2019, Volume 11, 1047-1055.	1,5	21
7	Network or regression-based methods for disease discrimination: a comparison study. BMC Medical Research Methodology, 2016, 16, 100.	1.4	19
8	Dyslipidemia in rural areas of North China: prevalence, characteristics, and predictive value. Lipids in Health and Disease, 2016, 15, 154.	1.2	16
9	Prevalence of CHD-related metabolic comorbidity of diabetes mellitus in Northern Chinese adults: the REACTION study. Journal of Diabetes and Its Complications, 2016, 30, 199-205.	1.2	16
10	Molecular mechanisms involved in the side effects of fatty acid amide hydrolase inhibitors: a structural phenomics approach to proteome-wide cellular off-target deconvolution and disease association. Npj Systems Biology and Applications, 2016, 2, 16023.	1.4	14
11	A powerful score-based statistical test for group difference in weighted biological networks. BMC Bioinformatics, 2016, 17, 86.	1.2	14
12	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. Nature Communications, 2018, 9, 4418.	5.8	14
13	Detection for pathway effect contributing to disease in systems epidemiology with a case-control design. BMJ Open, 2015, 5, e006721-e006721.	0.8	13
14	A novel chiâ€square statistic for detecting group differences between pathways in systems epidemiology. Statistics in Medicine, 2016, 35, 5512-5524.	0.8	13
15	Integrated Multi-Omics Analysis Model to Identify Biomarkers Associated With Prognosis of Breast Cancer. Frontiers in Oncology, 0, 12, .	1.3	12
16	Robust feature screening for elliptical copula regression model. Journal of Multivariate Analysis, 2019, 173, 568-582.	0.5	11
17	A powerful weighted statistic for detecting group differences of directed biological networks. Scientific Reports, 2016, 6, 34159.	1.6	10
18	A powerful latent variable method for detecting and characterizing gene-based gene-gene interaction on multiple quantitative traits. BMC Genetics, 2013, 14, 89.	2.7	8

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19	The efficacy and adverse events of mTOR inhibitors in lymphangioleiomyomatosis: systematic review and meta-analysis. Orphanet Journal of Rare Diseases, 2018, 13, 134.	1.2	8
20	A new insight into underlying disease mechanism through semi-parametric latent differential network model. BMC Bioinformatics, 2018, 19, 493.	1.2	7
21	PMINR: Pointwise Mutual Information-Based Network Regression – With Application to Studies of Lung Cancer and Alzheimer's Disease. Frontiers in Genetics, 2020, 11, 556259.	1.1	6
22	Simultaneous differential network analysis and classification for matrix-variate data with application to brain connectivity. Biostatistics, 2022, 23, 967-989.	0.9	5
23	Joint estimation of multiple highâ€dimensional Gaussian copula graphical models. Australian and New Zealand Journal of Statistics, 2017, 59, 289-310.	0.4	4
24	Brain connectivity alteration detection via matrixâ€variate differential network model. Biometrics, 2021, 77, 1409-1421.	0.8	3
25	MCC-SP: a powerful integration method for identification of causal pathways from genetic variants to complex disease. BMC Genetics, 2020, 21, 90.	2.7	3
26	A novel Markov Blanket-based repeated-fishing strategy for capturing phenotype-related biomarkers in big omics data. BMC Genetics, 2016, 17, 51.	2.7	2
27	Highâ€dimensional integrative copula discriminant analysis for multiomics data. Statistics in Medicine, 2020, 39, 4869-4884.	0.8	2
28	A powerful score-based test statistic for detecting gene-gene co-association. BMC Genetics, 2016, 17, 31.	2.7	1
29	Bidirectional association between serum carcinoembryonic antigen and metabolic syndrome among the Chinese male population: two cohort studies. Lipids in Health and Disease, 2020, 19, 233.	1.2	1
30	The sparse group lasso for high-dimensional integrative linear discriminant analysis with application to alzheimer's disease prediction. Journal of Statistical Computation and Simulation, 2020, 90, 3218-3231.	0.7	1
31	Robust feature screening for multi-response trans-elliptical regression model with ultrahigh-dimensional covariates. Random Matrices: Theory and Application, 2020, 09, 2150001.	0.5	0