Jiadong Ji

List of Publications by Citations

Source: https://exaly.com/author-pdf/8886521/jiadong-ji-publications-by-citations.pdf
Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

28	322	9	17
papers	citations	h-index	g-index
34	504	4.2	3.2
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
28	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. *Nature Communications*, **2019**, 10, 2674	17.4	119
27	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	6	31
26	Short-term effects of ambient air pollution on chronic obstructive pulmonary disease admissions in Beijing, China (2013-2017). *International Journal of COPD*, **2019**, 14, 297-309	3	28
25	JDINAC: joint density-based non-parametric differential interaction network analysis and classification using high-dimensional sparse omics data. *Bioinformatics*, **2017**, 33, 3080-3087	7.2	15
24	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	3.2	12
23	Detection for pathway effect contributing to disease in systems epidemiology with a case-control design. *BMJ Open*, **2015**, 5, e006721	3	11
22	A Machine Learning Method for Identifying Critical Interactions Between Gene Pairs in Alzheimeras Disease Prediction. *Frontiers in Neurology*, **2019**, 10, 1162	4.1	11
21	Network or regression-based methods for disease discrimination: a comparison study. *BMC Medical Research Methodology*, **2016**, 16, 100	4.7	10
20	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	5	10
19	Dyslipidemia in rural areas of North China: prevalence, characteristics, and predictive value. *Lipids in Health and Disease*, **2016**, 15, 154	4.4	9
18	A novel chi-square statistic for detecting group differences between pathways in systems epidemiology. *Statistics in Medicine*, **2016**, 35, 5512-5524	2.3	9
17	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. *Nature Communications*, **2018**, 9, 4418	17.4	9
16	The efficacy and adverse events of mTOR inhibitors in lymphangioleiomyomatosis: systematic review and meta-analysis. *Orphanet Journal of Rare Diseases*, **2018**, 13, 134	4.2	8
15	A powerful score-based statistical test for group difference in weighted biological networks. *BMC Bioinformatics*, **2016**, 17, 86	3.6	6
14	Robust feature screening for elliptical copula regression model. *Journal of Multivariate Analysis*, **2019**, 173, 568-582	1.4	5
13	A powerful weighted statistic for detecting group differences of directed biological networks. *Scientific Reports*, **2016**, 6, 34159	4.9	5
12	A powerful latent variable method for detecting and characterizing gene-based gene-gene interaction on multiple quantitative traits. *BMC Genetics*, **2013**, 14, 89	2.6	5

List of Publications

11	Risk Prediction of Dyslipidemia for Chinese Han Adults Using Random Forest Survival Model. *Clinical Epidemiology*, **2019**, 11, 1047-1055	5.9	5
10	PMINR: Pointwise Mutual Information-Based Network Regression - With Application to Studies of Lung Cancer and Alzheimer's Disease. *Frontiers in Genetics*, **2020**, 11, 556259	4.5	3
9	A new insight into underlying disease mechanism through semi-parametric latent differential network model. *BMC Bioinformatics*, **2018**, 19, 493	3.6	3
8	MCC-SP: a powerful integration method for identification of causal pathways from genetic variants to complex disease. *BMC Genetics*, **2020**, 21, 90	2.6	2
7	Joint estimation of multiple high-dimensional Gaussian copula graphical models. *Australian and New Zealand Journal of Statistics*, **2017**, 59, 289-310	0.7	1
6	A powerful score-based test statistic for detecting gene-gene co-association. *BMC Genetics*, **2016**, 17, 31	2.6	1
5	A novel Markov Blanket-based repeated-fishing strategy for capturing phenotype-related biomarkers in big omics data. *BMC Genetics*, **2016**, 17, 51	2.6	1
4	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	4.4	0
3	High-dimensional integrative copula discriminant analysis for multiomics data. *Statistics in Medicine*, **2020**, 39, 4869-4884	2.3	0
2	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	0.9	0
1	Robust feature screening for multi-response trans-elliptical regression model with ultrahigh-dimensional covariates. *Random Matrices: Theory and Application*, **2020**, 09, 2150001	0.6	