

Jun Xie

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3087129/publications.pdf>

Version: 2024-02-01

24
papers

950
citations

933447

10
h-index

610901

24
g-index

25
all docs

25
docs citations

25
times ranked

1993
citing authors

#	ARTICLE	IF	CITATIONS
1	Adjusted Kaplan-Meier estimator and log-rank test with inverse probability of treatment weighting for survival data. <i>Statistics in Medicine</i> , 2005, 24, 3089-3110.	1.6	373
2	Cauchy Combination Test: A Powerful Test With Analytic p -Value Calculation Under Arbitrary Dependency Structures. <i>Journal of the American Statistical Association</i> , 2020, 115, 393-402.	3.1	216
3	Down-regulation of RE-1 silencing transcription factor (REST) in advanced prostate cancer by hypoxia-induced miR-106b-25. <i>Experimental Cell Research</i> , 2014, 320, 188-199.	2.6	60
4	A Proteomic Strategy for Global Analysis of Plant Protein Complexes. <i>Plant Cell</i> , 2014, 26, 3867-3882.	6.6	55
5	Analysis of protein complexes in Arabidopsis leaves using size exclusion chromatography and label-free protein correlation profiling. <i>Journal of Proteomics</i> , 2017, 166, 8-18.	2.4	48
6	Group variable selection via SCAD- L_2 . <i>Statistics</i> , 2014, 48, 49-66.	0.6	32
7	Global Analysis of Membrane-associated Protein Oligomerization Using Protein Correlation Profiling. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1972-1989.	3.8	32
8	Ultradeep sequencing differentiates patterns of skin clonal mutations associated with sun-exposure status and skin cancer burden. <i>Science Advances</i> , 2021, 7, .	10.3	29
9	A Label-free Mass Spectrometry Method to Predict Endogenous Protein Complex Composition*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1588-1606.	3.8	28
10	Accurate and Efficient p -value Calculation Via Gaussian Approximation: A Novel Monte-Carlo Method. <i>Journal of the American Statistical Association</i> , 2019, 114, 384-392.	3.1	12
11	A Bayesian Insertion/Deletion Algorithm for Distant Protein Motif Searching via Entropy Filtering. <i>Journal of the American Statistical Association</i> , 2004, 99, 409-420.	3.1	11
12	Group variable selection for data with dependent structures. <i>Journal of Statistical Computation and Simulation</i> , 2012, 82, 95-106.	1.2	10
13	Large scale two sample multinomial inferences and its applications in genome-wide association studies. <i>International Journal of Approximate Reasoning</i> , 2014, 55, 330-340.	3.3	7
14	Furosemide-induced systemic dehydration alters the proteome of rabbit vocal folds. <i>Journal of Proteomics</i> , 2022, 252, 104431.	2.4	5
15	Recurring exposure to low humidity induces transcriptional and protein level changes in the vocal folds of rabbits. <i>Scientific Reports</i> , 2021, 11, 24180.	3.3	5
16	Bayesian Models and Markov Chain Monte Carlo Methods for Protein Motifs with the Secondary Characteristics. <i>Journal of Computational Biology</i> , 2005, 12, 952-970.	1.6	4
17	Protein Multiple Alignment Incorporating Primary and Secondary Structure Information. <i>Journal of Computational Biology</i> , 2006, 13, 1615-1629.	1.6	4
18	Probabilistic inference for multiple testing. <i>International Journal of Approximate Reasoning</i> , 2014, 55, 654-665.	3.3	4

#	ARTICLE	IF	CITATIONS
19	Multi-locus Test and Correction for Confounding Effects in Genome-Wide Association Studies. International Journal of Biostatistics, 2016, 12, .	0.7	4
20	Group feature screening via the F statistic. Communications in Statistics Part B: Simulation and Computation, 2022, 51, 1921-1931.	1.2	4
21	Blinded assessment of treatment effects for survival endpoint in an ongoing trial. Pharmaceutical Statistics, 2012, 11, 204-213.	1.3	2
22	Nonparametric Variable Selection for Predictive Models and Subpopulations in Clinical Trials. Journal of Biopharmaceutical Statistics, 2015, 25, 781-794.	0.8	2
23	Powerful test based on conditional effects for genome-wide screening. Annals of Applied Statistics, 2018, 12, 567-585.	1.1	2
24	An adaptive method of defining negative mutation status for multi-sample comparison using next-generation sequencing. BMC Medical Genomics, 2021, 14, 32.	1.5	0