Grace S Shieh

List of Publications by Year
in descending order

26 papers	444 citations	759233 12 h-index	713466 21 g-index
26 all docs	26 docs citations	26 times ranked	592 citing authors

#	Article	IF	Citations
1	A weighted Kendall's tau statistic. Statistics and Probability Letters, 1998, 39, 17-24.	0.7	88
2	Identification of the common regulators for hepatocellular carcinoma induced by hepatitis B virus X antigen in a mouse model. Carcinogenesis, 2012, 33, 209-219.	2.8	51
3	A pattern recognition approach to infer time-lagged genetic interactions. Bioinformatics, 2008, 24, 1183-1190.	4.1	34
4	Optimization of fed-batch fermentation using mixture of sugars to produce ethanol. Journal of the Taiwan Institute of Chemical Engineers, 2012, 43, 1-8.	5.3	31
5	The Overexpression of FEN1 and RAD54B May Act as Independent Prognostic Factors of Lung Adenocarcinoma. PLoS ONE, 2015, 10, e0139435.	2.5	28
6	H2B ubiquitylation is part of chromatin architecture that marks exon-intron structure in budding yeast. BMC Genomics, 2011, 12, 627.	2.8	27
7	CSNK1E/CTNNB1 Are Synthetic Lethal To TP53 in Colorectal Cancer and Are Markers for Prognosis. Neoplasia, 2014, 16, 441-450.	5.3	23
8	Inferences based on a bivariate distribution with von Mises marginals. Annals of the Institute of Statistical Mathematics, 2005, 57, 789-802.	0.8	22
9	Inferring genetic interactions via a nonlinear model and an optimization algorithm. BMC Systems Biology, 2010, 4, 16.	3.0	21
10	Inferring transcriptional compensation interactions in yeast via stepwise structure equation modeling. BMC Bioinformatics, 2008, 9, 134.	2.6	19
11	Uncovering synthetic lethal interactions for therapeutic targets and predictive markers in lung adenocarcinoma. Oncotarget, 2016, 7, 73664-73680.	1.8	14
12	Uncovering transcriptional interactions via an adaptive fuzzy logic approach. BMC Bioinformatics, 2009, 10, 400.	2.6	13
13	Detection of Somatic Mutations in Exome Sequencing of Tumor-only Samples. Scientific Reports, 2017, 7, 15959.	3.3	13
14	Modeling and comparing the organization of circular genomes. Bioinformatics, 2011, 27, 912-918.	4.1	12
15	WebPARE: web-computing for inferring genetic or transcriptional interactions. Bioinformatics, 2010, 26, 582-584.	4.1	11
16	Comparison of Support Vector Machines to Other Classifiers Using Gene Expression Data. Communications in Statistics Part B: Simulation and Computation, 2006, 35, 241-256.	1.2	8
17	Immunohistochemical Expression of Five Protein Combinations Revealed as Prognostic Markers in Asian Oral Cancer. Frontiers in Genetics, 2021, 12, 643461.	2.3	6
18	Harnessing Synthetic Lethal Interactions for Personalized Medicine. Journal of Personalized Medicine, 2022, 12, 98.	2.5	6

#	Article	IF	Citations
19	Inferring coregulation of transcription factors and microRNAs in breast cancer. Gene, 2013, 518, 139-144.	2.2	5
20	GENECFE-ANFIS: A NEURO-FUZZY INFERENCE SYSTEM TO INFER GENE-GENE INTERACTIONS BASED ON RECOGNITION OF MICROARRAY GENE EXPRESSION PATTERNS. Biomedical Engineering - Applications, Basis and Communications, 2007, 19, 71-78.	0.6	4
21	Inferring Genetic Interactions via a Data-Driven Second Order Model. Frontiers in Genetics, 2012, 3, 71.	2.3	3
22	On tests of independence for spherical data-invariance and centering. Statistics and Probability Letters, 2002, 57, 327-335.	0.7	2
23	A special issue on Bioinformatics: Introduction. Statistical Methodology, 2006, 3, vii-viii.	0.5	1
24	A Bayesian approach to assessing differential expression of microarray data. Journal of Statistical Computation and Simulation, 2008, 78, 179-191.	1.2	1
25	A nonlinear correlation measure with applications to gene expression data. PLoS ONE, 2022, 17, e0270270.	2.5	1
26	Two-stage U-statistics for Hypothesis Testing. Scandinavian Journal of Statistics, 2006, 33, 861-873.	1.4	0