

Grace S Shieh

List of Publications by Year in descending order

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Version: 2024-02-01

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	Harnessing Synthetic Lethal Interactions for Personalized Medicine. <i>Journal of Personalized Medicine</i> , 2022, 12, 98.	2.5	6
2	A nonlinear correlation measure with applications to gene expression data. <i>PLoS ONE</i> , 2022, 17, e0270270.	2.5	1
3	Immunohistochemical Expression of Five Protein Combinations Revealed as Prognostic Markers in Asian Oral Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 643461.	2.3	6
4	Detection of Somatic Mutations in Exome Sequencing of Tumor-only Samples. <i>Scientific Reports</i> , 2017, 7, 15959.	3.3	13
5	Uncovering synthetic lethal interactions for therapeutic targets and predictive markers in lung adenocarcinoma. <i>Oncotarget</i> , 2016, 7, 73664-73680.	1.8	14
6	The Overexpression of FEN1 and RAD54B May Act as Independent Prognostic Factors of Lung Adenocarcinoma. <i>PLoS ONE</i> , 2015, 10, e0139435.	2.5	28
7	CSNK1E/CTNNB1 Are Synthetic Lethal To TP53 in Colorectal Cancer and Are Markers for Prognosis. <i>Neoplasia</i> , 2014, 16, 441-450.	5.3	23
8	Inferring coregulation of transcription factors and microRNAs in breast cancer. <i>Gene</i> , 2013, 518, 139-144.	2.2	5
9	Identification of the common regulators for hepatocellular carcinoma induced by hepatitis B virus X antigen in a mouse model. <i>Carcinogenesis</i> , 2012, 33, 209-219.	2.8	51
10	Inferring Genetic Interactions via a Data-Driven Second Order Model. <i>Frontiers in Genetics</i> , 2012, 3, 71.	2.3	3
11	Optimization of fed-batch fermentation using mixture of sugars to produce ethanol. <i>Journal of the Taiwan Institute of Chemical Engineers</i> , 2012, 43, 1-8.	5.3	31
12	H2B ubiquitylation is part of chromatin architecture that marks exon-intron structure in budding yeast. <i>BMC Genomics</i> , 2011, 12, 627.	2.8	27
13	Modeling and comparing the organization of circular genomes. <i>Bioinformatics</i> , 2011, 27, 912-918.	4.1	12
14	Inferring genetic interactions via a nonlinear model and an optimization algorithm. <i>BMC Systems Biology</i> , 2010, 4, 16.	3.0	21
15	WebPARE: web-computing for inferring genetic or transcriptional interactions. <i>Bioinformatics</i> , 2010, 26, 582-584.	4.1	11
16	Uncovering transcriptional interactions via an adaptive fuzzy logic approach. <i>BMC Bioinformatics</i> , 2009, 10, 400.	2.6	13
17	Inferring transcriptional compensation interactions in yeast via stepwise structure equation modeling. <i>BMC Bioinformatics</i> , 2008, 9, 134.	2.6	19
18	A Bayesian approach to assessing differential expression of microarray data. <i>Journal of Statistical Computation and Simulation</i> , 2008, 78, 179-191.	1.2	1

#	ARTICLE	IF	CITATIONS
19	A pattern recognition approach to infer time-lagged genetic interactions. <i>Bioinformatics</i> , 2008, 24, 1183-1190.	4.1	34
20	GENECFE-ANFIS: A NEURO-FUZZY INFERENCE SYSTEM TO INFER GENE-GENE INTERACTIONS BASED ON RECOGNITION OF MICROARRAY GENE EXPRESSION PATTERNS. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2007, 19, 71-78.	0.6	4
21	Comparison of Support Vector Machines to Other Classifiers Using Gene Expression Data. <i>Communications in Statistics Part B: Simulation and Computation</i> , 2006, 35, 241-256.	1.2	8
22	Two-stage U-statistics for Hypothesis Testing. <i>Scandinavian Journal of Statistics</i> , 2006, 33, 861-873.	1.4	0
23	A special issue on Bioinformatics: Introduction. <i>Statistical Methodology</i> , 2006, 3, vii-viii.	0.5	1
24	Inferences based on a bivariate distribution with von Mises marginals. <i>Annals of the Institute of Statistical Mathematics</i> , 2005, 57, 789-802.	0.8	22
25	On tests of independence for spherical data-invariance and centering. <i>Statistics and Probability Letters</i> , 2002, 57, 327-335.	0.7	2
26	A weighted Kendall's tau statistic. <i>Statistics and Probability Letters</i> , 1998, 39, 17-24.	0.7	88