

Chen-An Tsai

List of Publications by Year in descending order

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38
papers

1,011
citations

516215

16
h-index

433756

31
g-index

39
all docs

39
docs citations

39
times ranked

1457
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Set Correlation Analysis and Visualization Using Gene Expression Data. <i>Current Bioinformatics</i> , 2021, 16, 406-421.	0.7	2
2	Development of predictive signatures for treatment selection in precision medicine with survival outcomes. <i>Pharmaceutical Statistics</i> , 2018, 17, 105-116.	0.7	7
3	An Exhaustive Scan Method for SNP Main Effects and SNP-SNP Interactions Over Highly Homozygous Genomes. <i>Journal of Computational Biology</i> , 2017, 24, 1254-1264.	0.8	3
4	Addressing Loss of Efficiency Due to Misclassification Error in Enriched Clinical Trials for the Evaluation of Targeted Therapies Based on the Cox Proportional Hazards Model. <i>PLoS ONE</i> , 2016, 11, e0153525.	1.1	0
5	Gene set analysis using sufficient dimension reduction. <i>BMC Bioinformatics</i> , 2016, 17, 74.	1.2	7
6	MAVTgsa: An R Package for Gene Set (Enrichment) Analysis. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	5
7	An approximate approach to sample size determination in bioequivalence testing with multiple pharmacokinetic responses. <i>Statistics in Medicine</i> , 2014, 33, 3300-3317.	0.8	6
8	Asymptomatic ratio for seasonal H1N1 influenza infection among schoolchildren in Taiwan. <i>BMC Infectious Diseases</i> , 2014, 14, 80.	1.3	33
9	Random forests-based differential analysis of gene sets for gene expression data. <i>Gene</i> , 2013, 518, 179-186.	1.0	21
10	Identifying Gene Set Association Enrichment Using the Coefficient of Intrinsic Dependence. <i>PLoS ONE</i> , 2013, 8, e58851.	1.1	5
11	Recursive Feature Selection with Significant Variables of Support Vectors. <i>Computational and Mathematical Methods in Medicine</i> , 2012, 2012, 1-12.	0.7	3
12	Association of response to hepatitis B vaccination and survival in dialysis patients. <i>BMC Nephrology</i> , 2012, 13, 97.	0.8	20
13	Serological response and persistence in schoolchildren with high baseline seropositive rate after receiving 2009 pandemic influenza A(H1N1) vaccine. <i>Vaccine</i> , 2011, 29, 617-623.	1.7	9
14	Comparison of hepatitis B surface antibody decay rates after vaccination between hemodialysis and peritoneal dialysis patients. <i>Vaccine</i> , 2011, 29, 3738-3741.	1.7	12
15	Factors associated with infection by 2009 pandemic H1N1 influenza virus during different phases of the epidemic. <i>International Journal of Infectious Diseases</i> , 2011, 15, e695-e701.	1.5	6
16	Sarcosine Therapy for Obsessive Compulsive Disorder. <i>Journal of Clinical Psychopharmacology</i> , 2011, 31, 369-374.	0.7	34
17	Serological Evidence of Subclinical Transmission of the 2009 Pandemic H1N1 Influenza Virus Outside of Mexico. <i>PLoS ONE</i> , 2011, 6, e14555.	1.1	16
18	Development of biomarker classifiers from high-dimensional data. <i>Briefings in Bioinformatics</i> , 2009, 10, 537-546.	3.2	54

#	ARTICLE	IF	CITATIONS
19	Multivariate analysis of variance test for gene set analysis. <i>Bioinformatics</i> , 2009, 25, 897-903.	1.8	92
20	Effect of p53 genotype on gene expression profiles in murine liver. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 640, 54-73.	0.4	3
21	Multispectra CWT-Based Algorithm (MCWT) in Mass Spectra for Peak Extraction. <i>Journal of Biopharmaceutical Statistics</i> , 2008, 18, 869-882.	0.4	2
22	Significance analysis of groups of genes in expression profiling studies. <i>Bioinformatics</i> , 2007, 23, 2104-2112.	1.8	28
23	An Integrated Tree-Based Classification Approach to Prognostic Grouping with Application to Localized Melanoma Patients. <i>Journal of Biopharmaceutical Statistics</i> , 2007, 17, 445-460.	0.4	12
24	Incorporating the number of true null hypotheses to improve power in multiple testing: application to gene microarray data. <i>Journal of Statistical Computation and Simulation</i> , 2007, 77, 757-767.	0.7	5
25	Kernel estimation for adjusted p -values in multiple testing. <i>Computational Statistics and Data Analysis</i> , 2007, 51, 3885-3897.	0.7	5
26	Reproducibility of microarray data: a further analysis of microarray quality control (MAQC) data. <i>BMC Bioinformatics</i> , 2007, 8, 412.	1.2	121
27	Gene selection with multiple ordering criteria. <i>BMC Bioinformatics</i> , 2007, 8, 74.	1.2	29
28	Database Composition Can Affect the Structure-Activity Relationship Prediction. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2006, 69, 1527-1540.	1.1	3
29	Alterations in gene expression profiles and the DNA-damage response in ionizing radiation-exposed TK6 cells. <i>Environmental and Molecular Mutagenesis</i> , 2005, 45, 188-205.	0.9	48
30	Sample size for gene expression microarray experiments. <i>Bioinformatics</i> , 2005, 21, 1502-1508.	1.8	63
31	Multi-class clustering and prediction in the analysis of microarray data. <i>Mathematical Biosciences</i> , 2005, 193, 79-100.	0.9	32
32	Gene Selection for Sample Classifications in Microarray Experiments. <i>DNA and Cell Biology</i> , 2004, 23, 607-614.	0.9	28
33	Analysis of variance components in gene expression data. <i>Bioinformatics</i> , 2004, 20, 1436-1446.	1.8	78
34	Significance Analysis of ROC Indices for Comparing Diagnostic Markers: Applications to Gene Microarray Data. <i>Journal of Biopharmaceutical Statistics</i> , 2004, 14, 985-1003.	0.4	13
35	A Generalized Additive Model For Microarray Gene Expression Data Analysis. <i>Journal of Biopharmaceutical Statistics</i> , 2004, 14, 553-573.	0.4	6
36	Estimation of False Discovery Rates in Multiple Testing: Application to Gene Microarray Data. <i>Biometrics</i> , 2003, 59, 1071-1081.	0.8	138

#	ARTICLE	IF	CITATIONS
37	Testing for differentially expressed genes with microarray data. Nucleic Acids Research, 2003, 31, 52e-52.	6.5	62
38	Quality assessment of gene expression data. , 0, , .		0