

Russell D Wolfinger

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

3,250
citations

471509

17
h-index

794594

19
g-index

23
all docs

23
docs citations

23
times ranked

4912
citing authors

#	ARTICLE	IF	CITATIONS
1	Forecasting with gradient boosted trees: augmentation, tuning, and cross-validation strategies. <i>International Journal of Forecasting</i> , 2022, 38, 1426-1433.	6.5	7
2	Breeding-assisted genomics: Applying meta-GWAS for milling and baking quality in CIMMYT wheat breeding program. <i>PLoS ONE</i> , 2018, 13, e0204757.	2.5	50
3	Predicting human olfactory perception from chemical features of odor molecules. <i>Science</i> , 2017, 355, 820-826.	12.6	194
4	An efficient hierarchical generalized linear mixed model for pathway analysis of genome-wide association studies. <i>Bioinformatics</i> , 2011, 27, 686-692.	4.1	50
5	Geographical genomics of human leukocyte gene expression variation in southern Morocco. <i>Nature Genetics</i> , 2010, 42, 62-67.	21.4	142
6	A Unified Mixed Effects Model for Gene Set Analysis of Time Course Microarray Experiments. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009, 8, 1-18.	0.6	30
7	Statistical Analysis of Relative Labeled Mass Spectrometry Data from Complex Samples Using ANOVA. <i>Journal of Proteome Research</i> , 2008, 7, 225-233.	3.7	185
8	An Integrated Approach for the Analysis of Biological Pathways using Mixed Models. <i>PLoS Genetics</i> , 2008, 4, e1000115.	3.5	59
9	Comparison of Gene Expression Effects in Liver Tissue and Primary Hepatocyte Cell Cultures After Exposure to Hexahydro-1, 3, 5-Trinitro-1, 3, 5-Triazine. , 2006, , .		0
10	Performance comparison of one-color and two-color platforms within the Microarray Quality Control (MAQC) project. <i>Nature Biotechnology</i> , 2006, 24, 1140-1150.	17.5	440
11	Comparison of transcriptional responses in liver tissue and primary hepatocyte cell cultures after exposure to hexahydro-1, 3, 5-trinitro-1, 3, 5-triazine. <i>BMC Bioinformatics</i> , 2006, 7, S22.	2.6	16
12	Consequences of reductive evolution for gene expression in an obligate endosymbiont. <i>Molecular Microbiology</i> , 2003, 48, 1491-1500.	2.5	126
13	Generalizable mass spectrometry mining used to identify disease state biomarkers from blood serum. <i>Proteomics</i> , 2003, 3, 1710-1715.	2.2	19
14	Carbohydrate-induced Differential Gene Expression Patterns in the Hyperthermophilic Bacterium <i>Thermotoga maritima</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 7540-7552.	3.4	117
15	Mixed-Model Reanalysis of Primate Data Suggests Tissue and Species Biases in Oligonucleotide-Based Gene Expression Profiles. <i>Genetics</i> , 2003, 165, 747-757.	2.9	133
16	The contributions of sex, genotype and age to transcriptional variance in <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2001, 29, 389-395.	21.4	595
17	Assessing Gene Significance from cDNA Microarray Expression Data via Mixed Models. <i>Journal of Computational Biology</i> , 2001, 8, 625-637.	1.6	987
18	Nonconjugate Bayesian Analysis of Variance Component Models. <i>Biometrics</i> , 2000, 56, 768-774.	1.4	31

#	ARTICLE	IF	CITATIONS
19	SAS Code for Recovering Intereffect Information in Experiments with Incomplete Block and Lattice Rectangle Designs. <i>Agronomy Journal</i> , 1998, 90, 545-551.	1.8	26
20	Variance due to Smooth Bias in Rat Liver and Kidney Baseline Gene Expression in a Large Multi-laboratory Data Set. , 0, , 87-99.		0
21	Microarray Gene Expression: The Effects of Varying Certain Measurement Conditions. , 0, , 101-111.		0
22	Batch Profile Estimation, Correction, and Scoring. , 0, , 155-165.		1