

John D Storey

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

34,704
citations

70961

41
h-index

91712

69
g-index

84
all docs

84
docs citations

84
times ranked

52837
citing authors

#	ARTICLE	IF	CITATIONS
1	Statistical significance for genomewide studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9440-9445.	3.3	8,800
2	A direct approach to false discovery rates. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002, 64, 479-498.	1.1	4,501
3	The <code>sva</code> package for removing batch effects and other unwanted variation in high-throughput experiments. <i>Bioinformatics</i> , 2012, 28, 882-883.	1.8	3,912
4	Genomic responses in mouse models poorly mimic human inflammatory diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3507-3512.	3.3	2,518
5	The positive false discovery rate: a Bayesian interpretation and the q-value. <i>Annals of Statistics</i> , 2003, 31, 2013.	1.4	1,751
6	Capturing Heterogeneity in Gene Expression Studies by Surrogate Variable Analysis. <i>PLoS Genetics</i> , 2007, 3, e161.	1.5	1,599
7	Empirical Bayes Analysis of a Microarray Experiment. <i>Journal of the American Statistical Association</i> , 2001, 96, 1151-1160.	1.8	1,420
8	Strong control, conservative point estimation and simultaneous conservative consistency of false discovery rates: a unified approach. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2004, 66, 187-205.	1.1	1,048
9	A genomic storm in critically injured humans. <i>Journal of Experimental Medicine</i> , 2011, 208, 2581-2590.	4.2	1,040
10	Mapping the Genetic Architecture of Gene Expression in Human Liver. <i>PLoS Biology</i> , 2008, 6, e107.	2.6	872
11	Precision and functional specificity in mRNA decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5860-5865.	3.3	652
12	Genome-wide analysis of mRNA translation profiles in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3889-3894.	3.3	632
13	Assigning Significance to Peptides Identified by Tandem Mass Spectrometry Using Decoy Databases. <i>Journal of Proteome Research</i> , 2008, 7, 29-34.	1.8	551
14	Significance analysis of time course microarray experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12837-12842.	3.3	534
15	A general framework for multiple testing dependence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18718-18723.	3.3	302
16	Genetic interactions between polymorphisms that affect gene expression in yeast. <i>Nature</i> , 2005, 436, 701-703.	13.7	296
17	Gene-Expression Variation Within and Among Human Populations. <i>American Journal of Human Genetics</i> , 2007, 80, 502-509.	2.6	295
18	EDGE: extraction and analysis of differential gene expression. <i>Bioinformatics</i> , 2006, 22, 507-508.	1.8	279

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19	Posterior Error Probabilities and False Discovery Rates: Two Sides of the Same Coin. <i>Journal of Proteome Research</i> , 2008, 7, 40-44.	1.8	264
20	Systems-level analysis of mechanisms regulating yeast metabolic flux. <i>Science</i> , 2016, 354, .	6.0	236
21	Statistical Methods for Identifying Differentially Expressed Genes in DNA Microarrays. , 2003, 224, 149-158.		210
22	Statistical significance of variables driving systematic variation in high-dimensional data. <i>Bioinformatics</i> , 2015, 31, 545-554.	1.8	184
23	Multiple Locus Linkage Analysis of Genomewide Expression in Yeast. <i>PLoS Biology</i> , 2005, 3, e267.	2.6	163
24	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. <i>Bioinformatics</i> , 2008, 24, i42-i48.	1.8	147
25	In Vivo Regulation of Human Skeletal Muscle Gene Expression by Thyroid Hormone. <i>Genome Research</i> , 2002, 12, 281-291.	2.4	143
26	The optimal discovery procedure: a new approach to simultaneous significance testing. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2007, 69, 347-368.	1.1	140
27	The optimal discovery procedure for large-scale significance testing, with applications to comparative microarray experiments. <i>Biostatistics</i> , 2007, 8, 414-432.	0.9	125
28	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3707-3712.	3.3	122
29	On the design and analysis of gene expression studies in human populations. <i>Nature Genetics</i> , 2007, 39, 807-808.	9.4	121
30	Harnessing naturally randomized transcription to infer regulatory relationships among genes. <i>Genome Biology</i> , 2007, 8, R219.	13.9	109
31	Supervised normalization of microarrays. <i>Bioinformatics</i> , 2010, 26, 1308-1315.	1.8	108
32	<scp>quality</scp>: non-parametric estimation of <i>q</i>-values and posterior error probabilities. <i>Bioinformatics</i> , 2009, 25, 964-966.	1.8	107
33	A Genome-Wide Gene Expression Signature of Environmental Geography in Leukocytes of Moroccan Amazighs. <i>PLoS Genetics</i> , 2008, 4, e1000052.	1.5	97
34	Design and Analysis of Bar-seq Experiments. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 11-18.	0.8	88
35	Relaxed Significance Criteria for Linkage Analysis. <i>Genetics</i> , 2006, 173, 2371-2381.	1.2	87
36	System-Level Analysis of Genes and Functions Affecting Survival During Nutrient Starvation in <i>Saccharomyces cerevisiae</i>. <i>Genetics</i> , 2011, 187, 299-317.	1.2	84

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37	Genome-wide real-time in vivo transcriptional dynamics during <i>Plasmodium falciparum</i> blood-stage development. <i>Nature Communications</i> , 2018, 9, 2656.	5.8	73
38	Analysis of factorial time-course microarrays with application to a clinical study of burn injury. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9923-9928.	3.3	62
39	Estimating FST and kinship for arbitrary population structures. <i>PLoS Genetics</i> , 2021, 17, e1009241.	1.5	53
40	A reanalysis of a published Affymetrix GeneChip control dataset. <i>Genome Biology</i> , 2006, 7, 401.	13.9	52
41	False Discovery Rate. , 2011, , 504-508.		51
42	Dissecting Inflammatory Complications in Critically Injured Patients by Within-Patient Gene Expression Changes: A Longitudinal Clinical Genomics Study. <i>PLoS Medicine</i> , 2011, 8, e1001093.	3.9	51
43	Gene expression profiles associated with acute myocardial infarction and risk of cardiovascular death. <i>Genome Medicine</i> , 2014, 6, 40.	3.6	50
44	Testing for genetic associations in arbitrarily structured populations. <i>Nature Genetics</i> , 2015, 47, 550-554.	9.4	49
45	Scaling probabilistic models of genetic variation to millions of humans. <i>Nature Genetics</i> , 2016, 48, 1587-1590.	9.4	44
46	subSeq: Determining Appropriate Sequencing Depth Through Efficient Read Subsampling. <i>Bioinformatics</i> , 2014, 30, 3424-3426.	1.8	43
47	Mapping gene expression quantitative trait loci by singular value decomposition and independent component analysis. <i>BMC Bioinformatics</i> , 2008, 9, 244.	1.2	36
48	Calibrating the Performance of SNP Arrays for Whole-Genome Association Studies. <i>PLoS Genetics</i> , 2008, 4, e1000109.	1.5	36
49	Probabilistic models of genetic variation in structured populations applied to global human studies. <i>Bioinformatics</i> , 2016, 32, 713-721.	1.8	34
50	Identifying and mapping cell-type-specific chromatin programming of gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E645-54.	3.3	31
51	A nested parallel experiment demonstrates differences in intensity-dependence between RNA-seq and microarrays. <i>Nucleic Acids Research</i> , 2015, 43, gkv636.	6.5	28
52	The functional false discovery rate with applications to genomics. <i>Biostatistics</i> , 2021, 22, 68-81.	0.9	28
53	Longitudinal transcriptional analysis of developing neointimal vascular occlusion and pulmonary hypertension in rats. <i>Physiological Genomics</i> , 2004, 17, 150-156.	1.0	27
54	Optimality Driven Nearest Centroid Classification from Genomic Data. <i>PLoS ONE</i> , 2007, 2, e1002.	1.1	26

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55	Approximate P-Values for Local Sequence Alignments: Numerical Studies. <i>Journal of Computational Biology</i> , 2001, 8, 549-556.	0.8	24
56	A computational statistics approach for estimating the spatial range of morphogen gradients. <i>Development (Cambridge)</i> , 2011, 138, 4867-4874.	1.2	24
57	A Likelihood-Free Estimator of Population Structure Bridging Admixture Models and Principal Components Analysis. <i>Genetics</i> , 2019, 212, 1009-1029.	1.2	24
58	A new approach to intensity-dependent normalization of two-channel microarrays. <i>Biostatistics</i> , 2007, 8, 128-139.	0.9	22
59	Normalization of two-channel microarrays accounting for experimental design and intensity-dependent relationships. <i>Genome Biology</i> , 2007, 8, R44.	13.9	20
60	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. <i>PLoS Computational Biology</i> , 2015, 11, e1004509.	1.5	19
61	Eigen- λ for dissecting variation in high-dimensional studies. <i>Bioinformatics</i> , 2008, 24, 2260-2262.	1.8	18
62	Cross-Dimensional Inference of Dependent High-Dimensional Data. <i>Journal of the American Statistical Association</i> , 2012, 107, 135-151.	1.8	18
63	Extending Tests of Hardy-Weinberg Equilibrium to Structured Populations. <i>Genetics</i> , 2019, 213, 759-770.	1.2	17
64	A computationally efficient modular optimal discovery procedure. <i>Bioinformatics</i> , 2011, 27, 509-515.	1.8	14
65	The Joint Null Criterion for Multiple Hypothesis Tests. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	13
66	Modeling molecular development of breast cancer in canine mammary tumors. <i>Genome Research</i> , 2021, 31, 337-347.	2.4	12
67	Gene set bagging for estimating the probability a statistically significant result will replicate. <i>BMC Bioinformatics</i> , 2013, 14, 360.	1.2	7
68	Cause and express. <i>Nature Biotechnology</i> , 2009, 27, 544-545.	9.4	4
69	The optimal discovery procedure for significance analysis of general gene expression studies. <i>Bioinformatics</i> , 2021, 37, 367-374.	1.8	1