

# John D Storey

## List of Publications by Citations

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**Version:** 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

74  
papers

26,850  
citations

41  
h-index

84  
g-index

84  
ext. papers

31,417  
ext. citations

10.2  
avg, IF

7.51  
L-index

#	Paper	IF	Citations
74	Statistical significance for genomewide studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 9440-5	11.5	7380
73	A direct approach to false discovery rates. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , <b>2002</b> , 64, 479-498	3.9	3567
72	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> , <b>2013</b> , 110, 3507-12	11.5	2076
71	The sva package for removing batch effects and other unwanted variation in high-throughput experiments. <i>Bioinformatics</i> , <b>2012</b> , 28, 882-3	7.2	1996
70	The positive false discovery rate: a Bayesian interpretation and the q-value. <i>Annals of Statistics</i> , <b>2003</b> , 31, 2013	3.2	1334
69	Capturing heterogeneity in gene expression studies by surrogate variable analysis. <i>PLoS Genetics</i> , <b>2007</b> , 3, 1724-35	6	1165
68	Empirical Bayes Analysis of a Microarray Experiment. <i>Journal of the American Statistical Association</i> , <b>2001</b> , 96, 1151-1160	2.8	1156
67	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> , <b>2004</b> , 66, 187-205	3.9	817
66	A genomic storm in critically injured humans. <i>Journal of Experimental Medicine</i> , <b>2011</b> , 208, 2581-90	16.6	805
65	Mapping the genetic architecture of gene expression in human liver. <i>PLoS Biology</i> , <b>2008</b> , 6, e107	9.7	768
64	Precision and functional specificity in mRNA decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 5860-5	11.5	585
63	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> , <b>2003</b> , 100, 3889-94	11.5	543
62	Significance analysis of time course microarray experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 12837-42	11.5	469
61	Assigning significance to peptides identified by tandem mass spectrometry using decoy databases. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 29-34	5.6	449
60	Gene-expression variation within and among human populations. <i>American Journal of Human Genetics</i> , <b>2007</b> , 80, 502-9	11	259
59	Genetic interactions between polymorphisms that affect gene expression in yeast. <i>Nature</i> , <b>2005</b> , 436, 701-3	50.4	258
58	EDGE: extraction and analysis of differential gene expression. <i>Bioinformatics</i> , <b>2006</b> , 22, 507-8	7.2	250

57	A general framework for multiple testing dependence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 18718-23	11.5	225
56	Posterior error probabilities and false discovery rates: two sides of the same coin. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 40-4	5.6	218
55	Statistical methods for identifying differentially expressed genes in DNA microarrays. <i>Methods in Molecular Biology</i> , <b>2003</b> , 224, 149-57	1.4	200
54	Systems-level analysis of mechanisms regulating yeast metabolic flux. <i>Science</i> , <b>2016</b> , 354,	33.3	157
53	Multiple locus linkage analysis of genomewide expression in yeast. <i>PLoS Biology</i> , <b>2005</b> , 3, e267	9.7	144
52	In vivo regulation of human skeletal muscle gene expression by thyroid hormone. <i>Genome Research</i> , <b>2002</b> , 12, 281-91	9.7	124
51	The optimal discovery procedure: a new approach to simultaneous significance testing. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , <b>2007</b> , 69, 347-368	3.9	111
50	The optimal discovery procedure for large-scale significance testing, with applications to comparative microarray experiments. <i>Biostatistics</i> , <b>2007</b> , 8, 414-32	3.7	111
49	Statistical significance of variables driving systematic variation in high-dimensional data. <i>Bioinformatics</i> , <b>2015</b> , 31, 545-54	7.2	110
48	On the design and analysis of gene expression studies in human populations. <i>Nature Genetics</i> , <b>2007</b> , 39, 807-8; author reply 808-9	36.3	101
47	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 3707-12	11.5	91
46	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. <i>Bioinformatics</i> , <b>2008</b> , 24, i42-8	7.2	84
45	A genome-wide gene expression signature of environmental geography in leukocytes of Moroccan Amazighs. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000052	6	83
44	Harnessing naturally randomized transcription to infer regulatory relationships among genes. <i>Genome Biology</i> , <b>2007</b> , 8, R219	18.3	83
43	Supervised normalization of microarrays. <i>Bioinformatics</i> , <b>2010</b> , 26, 1308-15	7.2	82
42	QUALITY: non-parametric estimation of q-values and posterior error probabilities. <i>Bioinformatics</i> , <b>2009</b> , 25, 964-6	7.2	76
41	Relaxed significance criteria for linkage analysis. <i>Genetics</i> , <b>2006</b> , 173, 2371-81	4	71
40	System-level analysis of genes and functions affecting survival during nutrient starvation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , <b>2011</b> , 187, 299-317	4	60

39	SAM Thresholding and False Discovery Rates for Detecting Differential Gene Expression in DNA Microarrays <b>2003</b> , 272-290		60
38	Design and analysis of Bar-seq experiments. <i>G3: Genes, Genomes, Genetics</i> , <b>2014</b> , 4, 11-8	3.2	54
37	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> , <b>2010</b> , 107, 9923-8	11.5	50
36	Genome-wide real-time in vivo transcriptional dynamics during <i>Plasmodium falciparum</i> blood-stage development. <i>Nature Communications</i> , <b>2018</b> , 9, 2656	17.4	45
35	A reanalysis of a published Affymetrix GeneChip control dataset. <i>Genome Biology</i> , <b>2006</b> , 7, 401	18.3	45
34	Dissecting inflammatory complications in critically injured patients by within-patient gene expression changes: a longitudinal clinical genomics study. <i>PLoS Medicine</i> , <b>2011</b> , 8, e1001093	11.6	44
33	Gene expression profiles associated with acute myocardial infarction and risk of cardiovascular death. <i>Genome Medicine</i> , <b>2014</b> , 6, 40	14.4	40
32	Testing for genetic associations in arbitrarily structured populations. <i>Nature Genetics</i> , <b>2015</b> , 47, 550-4	36.3	35
31	Mapping gene expression quantitative trait loci by singular value decomposition and independent component analysis. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 244	3.6	32
30	Calibrating the performance of SNP arrays for whole-genome association studies. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000109	6	31
29	subSeq: determining appropriate sequencing depth through efficient read subsampling. <i>Bioinformatics</i> , <b>2014</b> , 30, 3424-6	7.2	30
28	Probabilistic models of genetic variation in structured populations applied to global human studies. <i>Bioinformatics</i> , <b>2016</b> , 32, 713-21	7.2	26
27	Longitudinal transcriptional analysis of developing neointimal vascular occlusion and pulmonary hypertension in rats. <i>Physiological Genomics</i> , <b>2004</b> , 17, 150-6	3.6	24
26	A computational statistics approach for estimating the spatial range of morphogen gradients. <i>Development (Cambridge)</i> , <b>2011</b> , 138, 4867-74	6.6	23
25	Optimality driven nearest centroid classification from genomic data. <i>PLoS ONE</i> , <b>2007</b> , 2, e1002	3.7	22
24	A nested parallel experiment demonstrates differences in intensity-dependence between RNA-seq and microarrays. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e131	20.1	21
23	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> , <b>2014</b> , 111, E645-54	11.5	21
22	A new approach to intensity-dependent normalization of two-channel microarrays. <i>Biostatistics</i> , <b>2007</b> , 8, 128-39	3.7	20

21	Scaling probabilistic models of genetic variation to millions of humans. <i>Nature Genetics</i> , <b>2016</b> , 48, 1587-1599	18.9	19
20	Normalization of two-channel microarrays accounting for experimental design and intensity-dependent relationships. <i>Genome Biology</i> , <b>2007</b> , 8, R44	18.3	19
19	Approximate p-values for local sequence alignments: numerical studies. <i>Journal of Computational Biology</i> , <b>2001</b> , 8, 549-56	1.7	19
18	Cross-Dimensional Inference of Dependent High-Dimensional Data. <i>Journal of the American Statistical Association</i> , <b>2012</b> , 107, 135-151	2.8	15
17	Eigen-R2 for dissecting variation in high-dimensional studies. <i>Bioinformatics</i> , <b>2008</b> , 24, 2260-2	7.2	15
16	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004509	5	13
15	A computationally efficient modular optimal discovery procedure. <i>Bioinformatics</i> , <b>2011</b> , 27, 509-15	7.2	12
14	FST and kinship for arbitrary population structures I: Generalized definitions		11
13	FST and kinship for arbitrary population structures II: Method-of-moments estimators		8
12	The functional false discovery rate with applications to genomics. <i>Biostatistics</i> , <b>2021</b> , 22, 68-81	3.7	8
11	Estimating FST and kinship for arbitrary population structures. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009241	6	8
10	The Joint Null Criterion for Multiple Hypothesis Tests. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2011</b> , 10,	1.2	7
9	Gene set bagging for estimating the probability a statistically significant result will replicate. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 360	3.6	6
8	Determining sufficient sequencing depth in RNA-Seq differential expression studies		5
7	Extending Tests of Hardy-Weinberg Equilibrium to Structured Populations. <i>Genetics</i> , <b>2019</b> , 213, 759-770	4	5
6	New kinship and FST estimates reveal higher levels of differentiation in the global human population		4
5	A Likelihood-Free Estimator of Population Structure Bridging Admixture Models and Principal Components Analysis. <i>Genetics</i> , <b>2019</b> , 212, 1009-1029	4	2
4	Modeling molecular development of breast cancer in canine mammary tumors. <i>Genome Research</i> , <b>2020</b> ,	9.7	2

3	Extending Tests of Hardy-Weinberg Equilibrium to Structured Populations	2
2	The Functional False Discovery Rate with Applications to Genomics	2
1	The optimal discovery procedure for significance analysis of general gene expression studies. <i>Bioinformatics</i> , <b>2021</b> , 37, 367-374	7.2 1