John D Storey

List of Publications by Year
in descending order

69 papers	34,704 citations	71102 41 h-index	91884 69 g-index
84 all docs	84 docs citations	84 times ranked	52837 citing authors

#	Article	IF	Citations
1	Statistical significance for genomewide studies. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9440-9445.	7.1	8,800
2	A Direct Approach to False Discovery Rates. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2002, 64, 479-498.	2.2	4,501
3	The <tt>sva</tt> package for removing batch effects and other unwanted variation in high-throughput experiments. Bioinformatics, 2012, 28, 882-883.	4.1	3,912
4	Genomic responses in mouse models poorly mimic human inflammatory diseases. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3507-3512.	7.1	2,518
5	The positive false discovery rate: a Bayesian interpretation and the q-value. Annals of Statistics, 2003, 31, 2013.	2.6	1,751
6	Capturing Heterogeneity in Gene Expression Studies by Surrogate Variable Analysis. PLoS Genetics, 2007, 3, e161.	3.5	1,599
7	Empirical Bayes Analysis of a Microarray Experiment. Journal of the American Statistical Association, 2001, 96, 1151-1160.	3.1	1,420
8	Strong Control, Conservative Point Estimation and Simultaneous Conservative Consistency of False Discovery Rates: A Unified Approach. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2004, 66, 187-205.	2.2	1,048
9	A genomic storm in critically injured humans. Journal of Experimental Medicine, 2011, 208, 2581-2590.	8.5	1,040
10	Mapping the Genetic Architecture of Gene Expression in Human Liver. PLoS Biology, 2008, 6, e107.	5.6	872
11	Precision and functional specificity in mRNA decay. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5860-5865.	7.1	652
12	Genome-wide analysis of mRNA translation profiles in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3889-3894.	7.1	632
13	Assigning Significance to Peptides Identified by Tandem Mass Spectrometry Using Decoy Databases. Journal of Proteome Research, 2008, 7, 29-34.	3.7	551
14	Significance analysis of time course microarray experiments. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12837-12842.	7.1	534
15	A general framework for multiple testing dependence. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18718-18723.	7.1	302
16	Genetic interactions between polymorphisms that affect gene expression in yeast. Nature, 2005, 436, 701-703.	27.8	296
17	Gene-Expression Variation Within and Among Human Populations. American Journal of Human Genetics, 2007, 80, 502-509.	6.2	295
18	EDGE: extraction and analysis of differential gene expression. Bioinformatics, 2006, 22, 507-508.	4.1	279

#	ARTICLE	IF	CITATIONS
19	Posterior Error Probabilities and False Discovery Rates: Two Sides of the Same Coin. Journal of Proteome Research, 2008, 7, 40-44.	3.7	264
20	Systems-level analysis of mechanisms regulating yeast metabolic flux. Science, 2016, 354, .	12.6	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. Bioinformatics, 2015, 31, 545-554.	4.1	184
23	Multiple Locus Linkage Analysis of Genomewide Expression in Yeast. PLoS Biology, 2005, 3, e267.	5.6	163
24	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. Bioinformatics, 2008, 24, i42-i48.	4.1	147
25	In Vivo Regulation of Human Skeletal Muscle Gene Expression by Thyroid Hormone. Genome Research, 2002, 12, 281-291.	5.5	143
26	The Optimal Discovery Procedure: A New Approach to Simultaneous Significance Testing. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2007, 69, 347-368.	2.2	140
27	The optimal discovery procedure for large-scale significance testing, with applications to comparative microarray experiments. Biostatistics, 2007, 8, 414-432.	1.5	125
28	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	7.1	122
29	On the design and analysis of gene expression studies in human populations. Nature Genetics, 2007, 39, 807-808.	21.4	121
30	Harnessing naturally randomized transcription to infer regulatory relationships among genes. Genome Biology, 2007, 8, R219.	9.6	109
31	Supervised normalization of microarrays. Bioinformatics, 2010, 26, 1308-1315.	4.1	108
32	<scp>qvality</scp>: non-parametric estimation of <i>q</i>-values and posterior error probabilities. Bioinformatics, 2009, 25, 964-966.	4.1	107
33	A Genome-Wide Gene Expression Signature of Environmental Geography in Leukocytes of Moroccan Amazighs. PLoS Genetics, 2008, 4, e1000052.	3.5	97
34	Design and Analysis of Bar-seq Experiments. G3: Genes, Genomes, Genetics, 2014, 4, 11-18.	1.8	88
35	Relaxed Significance Criteria for Linkage Analysis. Genetics, 2006, 173, 2371-2381.	2.9	87
36	System-Level Analysis of Genes and Functions Affecting Survival During Nutrient Starvation in<i>Saccharomyces cerevisiae</i>. Genetics, 2011, 187, 299-317.	2.9	84

#	Article	IF	Citations
37	Genome-wide real-time in vivo transcriptional dynamics during Plasmodium falciparum blood-stage development. Nature Communications, 2018, 9, 2656.	12.8	73
38	Analysis of factorial time-course microarrays with application to a clinical study of burn injury. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9923-9928.	7.1	62
39	Estimating FST and kinship for arbitrary population structures. PLoS Genetics, 2021, 17, e1009241.	3.5	53
40	A reanalysis of a published Affymetrix GeneChip control dataset. Genome Biology, 2006, 7, 401.	9.6	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. PLoS Medicine, 2011, 8, e1001093.	8.4	51
43	Gene expression profiles associated with acute myocardial infarction and risk of cardiovascular death. Genome Medicine, 2014, 6, 40.	8.2	50
44	Testing for genetic associations in arbitrarily structured populations. Nature Genetics, 2015, 47, 550-554.	21.4	49
45	Scaling probabilistic models of genetic variation to millions of humans. Nature Genetics, 2016, 48, 1587-1590.	21.4	44
46	subSeq: Determining Appropriate Sequencing Depth Through Efficient Read Subsampling. Bioinformatics, 2014, 30, 3424-3426.	4.1	43
47	Mapping gene expression quantitative trait loci by singular value decomposition and independent component analysis. BMC Bioinformatics, 2008, 9, 244.	2.6	36
48	Calibrating the Performance of SNP Arrays for Whole-Genome Association Studies. PLoS Genetics, 2008, 4, e1000109.	3.5	36
49	Probabilistic models of genetic variation in structured populations applied to global human studies. Bioinformatics, 2016, 32, 713-721.	4.1	34
50	Identifying and mapping cell-type-specific chromatin programming of gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E645-54.	7.1	31
51	A nested parallel experiment demonstrates differences in intensity-dependence between RNA-seq and microarrays. Nucleic Acids Research, 2015, 43, gkv636.	14.5	28
52	The functional false discovery rate with applications to genomics. Biostatistics, 2021, 22, 68-81.	1.5	28
53	Longitudinal transcriptional analysis of developing neointimal vascular occlusion and pulmonary hypertension in rats. Physiological Genomics, 2004, 17, 150-156.	2.3	27
54	Optimality Driven Nearest Centroid Classification from Genomic Data. PLoS ONE, 2007, 2, e1002.	2.5	26

#	Article	IF	Citations
55	Approximate P-Values for Local Sequence Alignments: Numerical Studies. Journal of Computational Biology, 2001, 8, 549-556.	1.6	24
56	A computational statistics approach for estimating the spatial range of morphogen gradients. Development (Cambridge), 2011, 138, 4867-4874.	2.5	24
57	A Likelihood-Free Estimator of Population Structure Bridging Admixture Models and Principal Components Analysis. Genetics, 2019, 212, 1009-1029.	2.9	24
58	A new approach to intensity-dependent normalization of two-channel microarrays. Biostatistics, 2007, 8, 128-139.	1.5	22
59	Normalization of two-channel microarrays accounting for experimental design and intensity-dependent relationships. Genome Biology, 2007, 8, R44.	9.6	20
60	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. PLoS Computational Biology, 2015, 11, e1004509.	3.2	19
61	Eigen-R2 for dissecting variation in high-dimensional studies. Bioinformatics, 2008, 24, 2260-2262.	4.1	18
62	Cross-Dimensional Inference of Dependent High-Dimensional Data. Journal of the American Statistical Association, 2012, 107, 135-151.	3.1	18
63	Extending Tests of Hardy–Weinberg Equilibrium to Structured Populations. Genetics, 2019, 213, 759-770.	2.9	17
64	A computationally efficient modular optimal discovery procedure. Bioinformatics, 2011, 27, 509-515.	4.1	14
65	The Joint Null Criterion for Multiple Hypothesis Tests. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	13
66	Modeling molecular development of breast cancer in canine mammary tumors. Genome Research, 2021, 31, 337-347.	5.5	12
67	Gene set bagging for estimating the probability a statistically significant result will replicate. BMC Bioinformatics, 2013, 14, 360.	2.6	7
68	Cause and express. Nature Biotechnology, 2009, 27, 544-545.	17.5	4
69	The optimal discovery procedure for significance analysis of general gene expression studies. Bioinformatics, 2021, 37, 367-374.	4.1	1