

John D Storey

List of Publications by Year in Descending Order

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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	The optimal discovery procedure for significance analysis of general gene expression studies. <i>Bioinformatics</i> , 2021 , 37, 367-374	7.2	1
73	The functional false discovery rate with applications to genomics. <i>Biostatistics</i> , 2021 , 22, 68-81	3.7	8
72	Estimating FST and kinship for arbitrary population structures. <i>PLoS Genetics</i> , 2021 , 17, e1009241	6	8
71	Modeling molecular development of breast cancer in canine mammary tumors. <i>Genome Research</i> , 2020 ,	9.7	2
70	A Likelihood-Free Estimator of Population Structure Bridging Admixture Models and Principal Components Analysis. <i>Genetics</i> , 2019 , 212, 1009-1029	4	2
69	Extending Tests of Hardy-Weinberg Equilibrium to Structured Populations. <i>Genetics</i> , 2019 , 213, 759-770	4	5
68	Genome-wide real-time in vivo transcriptional dynamics during Plasmodium falciparum blood-stage development. <i>Nature Communications</i> , 2018 , 9, 2656	17.4	45
67	Systems-level analysis of mechanisms regulating yeast metabolic flux. <i>Science</i> , 2016 , 354,	33.3	157
66	Scaling probabilistic models of genetic variation to millions of humans. <i>Nature Genetics</i> , 2016 , 48, 1587-1590	36.3	19
65	Probabilistic models of genetic variation in structured populations applied to global human studies. <i>Bioinformatics</i> , 2016 , 32, 713-21	7.2	26
64	Testing for genetic associations in arbitrarily structured populations. <i>Nature Genetics</i> , 2015 , 47, 550-4	36.3	35
63	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. <i>PLoS Computational Biology</i> , 2015 , 11, e1004509	5	13
62	A nested parallel experiment demonstrates differences in intensity-dependence between RNA-seq and microarrays. <i>Nucleic Acids Research</i> , 2015 , 43, e131	20.1	21
61	Statistical significance of variables driving systematic variation in high-dimensional data. <i>Bioinformatics</i> , 2015 , 31, 545-54	7.2	110
60	Gene expression profiles associated with acute myocardial infarction and risk of cardiovascular death. <i>Genome Medicine</i> , 2014 , 6, 40	14.4	40
59	subSeq: determining appropriate sequencing depth through efficient read subsampling. <i>Bioinformatics</i> , 2014 , 30, 3424-6	7.2	30
58	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	11.5	21

57	Design and analysis of Bar-seq experiments. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 11-8	3.2	54
56	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, 3507-12	11.5	2076
55	Gene set bagging for estimating the probability a statistically significant result will replicate. <i>BMC Bioinformatics</i> , 2013 , 14, 360	3.6	6
54	Cross-Dimensional Inference of Dependent High-Dimensional Data. <i>Journal of the American Statistical Association</i> , 2012 , 107, 135-151	2.8	15
53	The sva package for removing batch effects and other unwanted variation in high-throughput experiments. <i>Bioinformatics</i> , 2012 , 28, 882-3	7.2	1996
52	A genomic storm in critically injured humans. <i>Journal of Experimental Medicine</i> , 2011 , 208, 2581-90	16.6	805
51	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, 3707-12	11.5	91
50	System-level analysis of genes and functions affecting survival during nutrient starvation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2011 , 187, 299-317	4	60
49	A computational statistics approach for estimating the spatial range of morphogen gradients. <i>Development (Cambridge)</i> , 2011 , 138, 4867-74	6.6	23
48	The Joint Null Criterion for Multiple Hypothesis Tests. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011 , 10,	1.2	7
47	A computationally efficient modular optimal discovery procedure. <i>Bioinformatics</i> , 2011 , 27, 509-15	7.2	12
46	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	11.6	44
45	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, 9923-8	11.5	50
44	Supervised normalization of microarrays. <i>Bioinformatics</i> , 2010 , 26, 1308-15	7.2	82
43	QUALITY: non-parametric estimation of q-values and posterior error probabilities. <i>Bioinformatics</i> , 2009 , 25, 964-6	7.2	76
42	Mapping gene expression quantitative trait loci by singular value decomposition and independent component analysis. <i>BMC Bioinformatics</i> , 2008 , 9, 244	3.6	32
41	Assigning significance to peptides identified by tandem mass spectrometry using decoy databases. <i>Journal of Proteome Research</i> , 2008 , 7, 29-34	5.6	449
40	Posterior error probabilities and false discovery rates: two sides of the same coin. <i>Journal of Proteome Research</i> , 2008 , 7, 40-4	5.6	218

39	A general framework for multiple testing dependence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18718-23	11.5	225
38	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. <i>Bioinformatics</i> , 2008 , 24, i42-8	7.2	84
37	Calibrating the performance of SNP arrays for whole-genome association studies. <i>PLoS Genetics</i> , 2008 , 4, e1000109	6	31
36	Mapping the genetic architecture of gene expression in human liver. <i>PLoS Biology</i> , 2008 , 6, e107	9.7	768
35	A genome-wide gene expression signature of environmental geography in leukocytes of Moroccan Amazighs. <i>PLoS Genetics</i> , 2008 , 4, e1000052	6	83
34	Eigen-R2 for dissecting variation in high-dimensional studies. <i>Bioinformatics</i> , 2008 , 24, 2260-2	7.2	15
33	Optimality driven nearest centroid classification from genomic data. <i>PLoS ONE</i> , 2007 , 2, e1002	3.7	22
32	On the design and analysis of gene expression studies in human populations. <i>Nature Genetics</i> , 2007 , 39, 807-8; author reply 808-9	36.3	101
31	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	3.9	111
30	Capturing heterogeneity in gene expression studies by surrogate variable analysis. <i>PLoS Genetics</i> , 2007 , 3, 1724-35	6	1165
29	The optimal discovery procedure for large-scale significance testing, with applications to comparative microarray experiments. <i>Biostatistics</i> , 2007 , 8, 414-32	3.7	111
28	A new approach to intensity-dependent normalization of two-channel microarrays. <i>Biostatistics</i> , 2007 , 8, 128-39	3.7	20
27	Gene-expression variation within and among human populations. <i>American Journal of Human Genetics</i> , 2007 , 80, 502-9	11	259
26	Harnessing naturally randomized transcription to infer regulatory relationships among genes. <i>Genome Biology</i> , 2007 , 8, R219	18.3	83
25	Normalization of two-channel microarrays accounting for experimental design and intensity-dependent relationships. <i>Genome Biology</i> , 2007 , 8, R44	18.3	19
24	Relaxed significance criteria for linkage analysis. <i>Genetics</i> , 2006 , 173, 2371-81	4	71
23	EDGE: extraction and analysis of differential gene expression. <i>Bioinformatics</i> , 2006 , 22, 507-8	7.2	250
22	A reanalysis of a published Affymetrix GeneChip control dataset. <i>Genome Biology</i> , 2006 , 7, 401	18.3	45

21	Genetic interactions between polymorphisms that affect gene expression in yeast. <i>Nature</i> , 2005 , 436, 701-3	50.4	258
20	Multiple locus linkage analysis of genomewide expression in yeast. <i>PLoS Biology</i> , 2005 , 3, e267	9.7	144
19	Significance analysis of time course microarray experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 12837-42	11.5	469
18	Longitudinal transcriptional analysis of developing neointimal vascular occlusion and pulmonary hypertension in rats. <i>Physiological Genomics</i> , 2004 , 17, 150-6	3.6	24
17	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	3.9	817
16	SAM Thresholding and False Discovery Rates for Detecting Differential Gene Expression in DNA Microarrays 2003 , 272-290		60
15	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, 3889-94	11.5	543
14	The positive false discovery rate: a Bayesian interpretation and the q-value. <i>Annals of Statistics</i> , 2003 , 31, 2013	3.2	1334
13	Statistical methods for identifying differentially expressed genes in DNA microarrays. <i>Methods in Molecular Biology</i> , 2003 , 224, 149-57	1.4	200
12	Statistical significance for genomewide studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 9440-5	11.5	7380
11	A direct approach to false discovery rates. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002 , 64, 479-498	3.9	3567
10	In vivo regulation of human skeletal muscle gene expression by thyroid hormone. <i>Genome Research</i> , 2002 , 12, 281-91	9.7	124
9	Precision and functional specificity in mRNA decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 5860-5	11.5	585
8	Approximate p-values for local sequence alignments: numerical studies. <i>Journal of Computational Biology</i> , 2001 , 8, 549-56	1.7	19
7	Empirical Bayes Analysis of a Microarray Experiment. <i>Journal of the American Statistical Association</i> , 2001 , 96, 1151-1160	2.8	1156
6	FST and kinship for arbitrary population structures I: Generalized definitions		11
5	FST and kinship for arbitrary population structures II: Method-of-moments estimators		8
4	Extending Tests of Hardy-Weinberg Equilibrium to Structured Populations		2

3	The Functional False Discovery Rate with Applications to Genomics	2
2	Determining sufficient sequencing depth in RNA-Seq differential expression studies	5
1	New kinship and F_{ST} estimates reveal higher levels of differentiation in the global human population	4