Matthew Stephens

List of Publications by Year
in descending order

89 papers	68,909 citations	34105 52 h-index	53230 85 g-index
110 all docs	110 docs citations	110 times ranked	74302 citing authors

#	Article	IF	Citations
1	Inference of Population Structure Using Multilocus Genotype Data. Genetics, 2000, 155, 945-959.	2.9	28,015
2	Inference of Population Structure Using Multilocus Genotype Data: Linked Loci and Correlated Allele Frequencies. Genetics, 2003, 164, 1567-1587.	2.9	6,870
3	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
4	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
5	Genome-wide efficient mixed-model analysis for association studies. Nature Genetics, 2012, 44, 821-824.	21.4	2,577
6	RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. Genome Research, 2008, 18, 1509-1517.	5.5	2,393
7	A Fast and Flexible Statistical Model for Large-Scale Population Genotype Data: Applications to Inferring Missing Genotypes and Haplotypic Phase. American Journal of Human Genetics, 2006, 78, 629-644.	6.2	1,748
8	Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. Nature Genetics, 2012, 44, 955-959.	21.4	1,592
9	fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. Genetics, 2014, 197, 573-589.	2.9	1,429
10	Understanding mechanisms underlying human gene expression variation with RNA sequencing. Nature, 2010, 464, 768-772.	27.8	1,200
11	Genotype Imputation with Thousands of Genomes. G3: Genes, Genomes, Genetics, 2011, 1, 457-470.	1.8	869
12	Modeling Linkage Disequilibrium and Identifying Recombination Hotspots Using Single-Nucleotide Polymorphism Data. Genetics, 2003, 165, 2213-2233.	2.9	863
13	Dealing with label switching in mixture models. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2000, 62, 795-809.	2.2	734
14	Efficient multivariate linear mixed model algorithms for genome-wide association studies. Nature Methods, 2014, 11, 407-409.	19.0	698
15	Polygenic Modeling with Bayesian Sparse Linear Mixed Models. PLoS Genetics, 2013, 9, e1003264.	3.5	686
16	DNaseâ€‰I sensitivity QTLs are a major determinant of human expression variation. Nature, 2012, 482, 390-394.	27.8	608
17	False discovery rates: a new deal. Biostatistics, 2017, 18, kxw041.	1.5	561
18	Interpreting principal component analyses of spatial population genetic variation. Nature Genetics, 2008, 40, 646-649.	21.4	515

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19	High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. PLoS Genetics, 2008, 4, e1000214.	3.5	510
20	Imputation-Based Analysis of Association Studies: Candidate Regions and Quantitative Traits. PLoS Genetics, 2007, 3, e114.	3.5	460
21	Visualizing spatial population structure with estimated effective migration surfaces. Nature Genetics, 2016, 48, 94-100.	21.4	445
22	A Simple New Approach to Variable Selection in Regression, with Application to Genetic Fine Mapping. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2020, 82, 1273-1300.	2.2	431
23	Bayesian statistical methods for genetic association studies. Nature Reviews Genetics, 2009, 10, 681-690.	16.3	400
24	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
25	A Multivariate Genome-Wide Association Analysis of 10 LDL Subfractions, and Their Response to Statin Treatment, in 1868 Caucasians. PLoS ONE, 2015, 10, e0120758.	2.5	323
26	Bayesian variable selection regression for genome-wide association studies and other large-scale problems. Annals of Applied Statistics, 2011, 5, .	1.1	303
27	Mendelian randomization accounting for correlated and uncorrelated pleiotropic effects using genome-wide summary statistics. Nature Genetics, 2020, 52, 740-747.	21.4	298
28	Flexible statistical methods for estimating and testing effects in genomic studies with multiple conditions. Nature Genetics, 2019, 51, 187-195.	21.4	249
29	A Statistical Framework for Joint eQTL Analysis in Multiple Tissues. PLoS Genetics, 2013, 9, e1003486.	3.5	226
30	A Unified Framework for Association Analysis with Multiple Related Phenotypes. PLoS ONE, 2013, 8, e65245.	2.5	216
31	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
32	Genome-Wide Association of Lipid-Lowering Response to Statins in Combined Study Populations. PLoS ONE, 2010, 5, e9763.	2.5	205
33	A statin-dependent QTL for GATM expression is associated with statin-induced myopathy. Nature, 2013, 502, 377-380.	27.8	197
34	Dissecting the regulatory architecture of gene expression QTLs. Genome Biology, 2012, 13, R7.	9.6	188
35	Scalable Variational Inference for Bayesian Variable Selection in Regression, and Its Accuracy in Genetic Association Studies. Bayesian Analysis, 2012, 7, .	3.0	172
36	Polymorphisms of the HNF1A Gene Encoding Hepatocyte Nuclear Factor-1Î± are Associated with C-Reactive Protein. American Journal of Human Genetics, 2008, 82, 1193-1201.	6.2	170

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37	Genotyping Polyploids from Messy Sequencing Data. Genetics, 2018, 210, 789-807.	2.9	157
38	Practical Issues in Imputation-Based Association Mapping. PLoS Genetics, 2008, 4, e1000279.	3.5	155
39	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	8.8	150
40	Visualizing the structure of RNA-seq expression data using grade of membership models. PLoS Genetics, 2017, 13, e1006599.	3.5	132
41	Bayesian large-scale multiple regression with summary statistics from genome-wide association studies. Annals of Applied Statistics, 2017, 11, 1561-1592.	1.1	128
42	Analysis of Population Structure: A Unifying Framework and Novel Methods Based on Sparse Factor Analysis. PLoS Genetics, 2010, 6, e1001117.	3.5	123
43	Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. ELife, 2016, 5, .	6.0	122
44	A Simple Model-Based Approach to Inferring and Visualizing Cancer Mutation Signatures. PLoS Genetics, 2015, 11, e1005657.	3.5	118
45	Genetic analyses support the contribution of mRNA N6-methyladenosine (m6A) modification to human disease heritability. Nature Genetics, 2020, 52, 939-949.	21.4	113
46	Separating measurement and expression models clarifies confusion in single-cell RNA sequencing analysis. Nature Genetics, 2021, 53, 770-777.	21.4	112
47	The Contribution of RNA Decay Quantitative Trait Loci to Inter-Individual Variation in Steady-State Gene Expression Levels. PLoS Genetics, 2012, 8, e1003000.	3.5	104
48	Interactions between Glucocorticoid Treatment and Cis-Regulatory Polymorphisms Contribute to Cellular Response Phenotypes. PLoS Genetics, 2011, 7, e1002162.	3.5	103
49	The genetic architecture of gene expression levels in wild baboons. ELife, 2015, 4, .	6.0	99
50	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
51	Large-scale genome-wide enrichment analyses identify new trait-associated genes and pathways across 31 human phenotypes. Nature Communications, 2018, 9, 4361.	12.8	88
52	Estimating recent migration and population-size surfaces. PLoS Genetics, 2019, 15, e1007908.	3.5	76
53	Using linear predictors to impute allele frequencies from summary or pooled genotype data. Annals of Applied Statistics, 2010, 4, 1158-1182.	1.1	74
54	Genome-Wide Association Study of d-Amphetamine Response in Healthy Volunteers Identifies Putative Associations, Including Cadherin 13 (CDH13). PLoS ONE, 2012, 7, e42646.	2.5	74

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55	Promoter shape varies across populations and affects promoter evolution and expression noise. Nature Genetics, 2017, 49, 550-558.	21.4	74
56	Epigenetic modifications are associated with inter-species gene expression variation in primates. Genome Biology, 2014, 15, 547.	8.8	72
57	New evidence for hybrid zones of forest and savanna elephants in Central and West Africa. Molecular Ecology, 2015, 24, 6134-6147.	3.9	72
58	An Estimate of the Average Number of Recessive Lethal Mutations Carried by Humans. Genetics, 2015, 199, 1243-1254.	2.9	69
59	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
60	Integrated Enrichment Analysis of Variants and Pathways in Genome-Wide Association Studies Indicates Central Role for IL-2 Signaling Genes in Type 1 Diabetes, and Cytokine Signaling Genes in Crohn's Disease. PLoS Genetics, 2013, 9, e1003770.	3.5	67
61	Characterizing and inferring quantitative cell cycle phase in single-cell RNA-seq data analysis. Genome Research, 2020, 30, 611-621.	5.5	63
62	Discovery and characterization of variance QTLs in human induced pluripotent stem cells. PLoS Genetics, 2019, 15, e1008045.	3.5	56
63	Estimating Time to the Common Ancestor for a Beneficial Allele. Molecular Biology and Evolution, 2018, 35, 1003-1017.	8.9	53
64	Bayesian methods for genetic association analysis with heterogeneous subgroups: From meta-analyses to geneâ€“environment interactions. Annals of Applied Statistics, 2014, 8, 176-203.	1.1	52
65	Creating and sharing reproducible research code the workflowr way. F1000Research, 2019, 8, 1749.	1.6	52
66	Detailed modeling of positive selection improves detection of cancer driver genes. Nature Communications, 2019, 10, 3399.	12.8	49
67	A new sequence logo plot to highlight enrichment and depletion. BMC Bioinformatics, 2018, 19, 473.	2.6	43
68	Dynamic effects of genetic variation on gene expression revealed following hypoxic stress in cardiomyocytes. ELife, 2021, 10, .	6.0	41
69	Regional influences on community structure across the tropical-temperate divide. Nature Communications, 2019, 10, 2646.	12.8	40
70	msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding. PLoS ONE, 2015, 10, e0138030.	2.5	37
71	Accurate genomic prediction of Coffea canephora in multiple environments using whole-genome statistical models. Heredity, 2019, 122, 261-275.	2.6	36
72	Silencing of transposable elements may not be a major driver of regulatory evolution in primate iPSCs. ELife, 2018, 7, .	6.0	27

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73	Genetic, Functional and Molecular Features of Glucocorticoid Receptor Binding. PLoS ONE, 2013, 8, e61654.	2.5	23
74	Wavelet-based genetic association analysis of functional phenotypes arising from high-throughput sequencing assays. Annals of Applied Statistics, 2015, 9, 655-686.	1.1	22
75	Exon-Specific QTLs Skew the Inferred Distribution of Expression QTLs Detected Using Gene Expression Array Data. PLoS ONE, 2012, 7, e30629.	2.5	18
76	Dispersal syndromes drive the formation of biogeographical regions, illustrated by the case of Wallaceâ€™s Line. Global Ecology and Biogeography, 2021, 30, 685-696.	5.8	15
77	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. PLoS Genetics, 2019, 15, e1008431.	3.5	14
78	Empirical Bayes shrinkage and false discovery rate estimation, allowing for unwanted variation. Biostatistics, 2020, 21, 15-32.	1.5	9
79	Variance adaptive shrinkage (vash): flexible empirical Bayes estimation of variances. Bioinformatics, 2016, 32, 3428-3434.	4.1	7
80	Inference and visualization of DNA damage patterns using a grade of membership model. Bioinformatics, 2019, 35, 1292-1298.	4.1	7
81	A Fast Algorithm for Maximum Likelihood Estimation of Mixture Proportions Using Sequential Quadratic Programming. Journal of Computational and Graphical Statistics, 2020, 29, 261-273.	1.7	6
82	Mangravite et al. reply. Nature, 2014, 513, E3-E3.	27.8	4
83	Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. Genome Medicine, 2022, 14, .	8.2	2
84	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
85	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
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88	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
89	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0