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List of PR Articles by Year in descending order

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74

PR articles

55,270

PR citations

31116

47

PR h-index

70085

69

g-index

90

documents

66061

doc citations

24761

54

h-index

79580

citing authors

#	ARTICLE	IF	PR CITATIONS
1	A flexible empirical Bayes approach to multivariate multiple regression, and its improved accuracy in predicting multi-tissue gene expression from genotypes. <i>PLoS Genetics</i> , 2023, 19, e1010539.	3.3	8
2	Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. <i>Genome Medicine</i> , 2022, 14, .	9.8	13
3	Fine-mapping from summary data with the “Sum of Single Effects”-model. <i>PLoS Genetics</i> , 2022, 18, e1010299.	3.3	320
4	Dispersal syndromes drive the formation of biogeographical regions, illustrated by the case of Wallace’s Line. <i>Global Ecology and Biogeography</i> , 2021, 30, 685-696.	5.7	23
5	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021, 22, .	8.2	266
6	Separating measurement and expression models clarifies confusion in single-cell RNA sequencing analysis. <i>Nature Genetics</i> , 2021, 53, 770-777.	25.9	212
7	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19.	34.4	164
8	Empirical Bayes shrinkage and false discovery rate estimation, allowing for unwanted variation. <i>Biostatistics</i> , 2020, 21, 15-32.	2.1	14
9	A Fast Algorithm for Maximum Likelihood Estimation of Mixture Proportions Using Sequential Quadratic Programming. <i>Journal of Computational and Graphical Statistics</i> , 2020, 29, 261-273.	1.9	23
10	A Simple New Approach to Variable Selection in Regression, with Application to Genetic Fine Mapping. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2020, 82, 1273-1300.	3.1	925
11	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	37.0	314
12	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	37.0	585
13	Genetic analyses support the contribution of mRNA N6-methyladenosine (m6A) modification to human disease heritability. <i>Nature Genetics</i> , 2020, 52, 939-949.	25.9	172
14	Characterizing and inferring quantitative cell cycle phase in single-cell RNA-seq data analysis. <i>Genome Research</i> , 2020, 30, 611-621.	4.6	90
15	Mendelian randomization accounting for correlated and uncorrelated pleiotropic effects using genome-wide summary statistics. <i>Nature Genetics</i> , 2020, 52, 740-747.	25.9	539
16	Detailed modeling of positive selection improves detection of cancer driver genes. <i>Nature Communications</i> , 2019, 10, .	13.9	69
17	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. <i>PLoS Genetics</i> , 2019, 15, e1008431.	3.3	19
18	Regional influences on community structure across the tropical-temperate divide. <i>Nature Communications</i> , 2019, 10, .	13.9	50

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19	Discovery and characterization of variance QTLs in human induced pluripotent stem cells. PLoS Genetics, 2019, 15, e1008045.	3.3	68
20	Estimating recent migration and population-size surfaces. PLoS Genetics, 2019, 15, e1007908.	3.3	116
21	Inference and visualization of DNA damage patterns using a grade of membership model. Bioinformatics, 2019, 35, 1292-1298.	4.7	11
22	Creating and sharing reproducible research code the workflow way. F1000Research, 2019, 8, 1749.	0.5	68
23	Estimating Time to the Common Ancestor for a Beneficial Allele. Molecular Biology and Evolution, 2018, 35, 1003-1017.	4.7	62
24	A new sequence logo plot to highlight enrichment and depletion. BMC Bioinformatics, 2018, 19, .	3.0	50
25	Genotyping Polyploids from Messy Sequencing Data. Genetics, 2018, 210, 789-807.	4.2	224
26	Large-scale genome-wide enrichment analyses identify new trait-associated genes and pathways across 31 human phenotypes. Nature Communications, 2018, 9, .	13.9	102
27	Accurate genomic prediction of Coffea canephora in multiple environments using whole-genome statistical models. Heredity, 2018, 122, 261-275.	3.2	48
28	Promoter shape varies across populations and affects promoter evolution and expression noise. Nature Genetics, 2017, 49, 550-558.	25.9	81
29	Bayesian large-scale multiple regression with summary statistics from genome-wide association studies. Annals of Applied Statistics, 2017, 11, .	1.2	150
30	Visualizing the structure of RNA-seq expression data using grade of membership models. PLoS Genetics, 2017, 13, e1006599.	3.3	164
31	Variance adaptive shrinkage (<i>vash</i>): flexible empirical Bayes estimation of variances. Bioinformatics, 2016, 32, 3428-3434.	4.7	10
32	Wavelet-based genetic association analysis of functional phenotypes arising from high-throughput sequencing assays. Annals of Applied Statistics, 2015, 9, .	1.2	23
33	New evidence for hybrid zones of forest and savanna elephants in Central and West Africa. Molecular Ecology, 2015, 24, 6134-6147.	3.7	81
34	An Estimate of the Average Number of Recessive Lethal Mutations Carried by Humans. Genetics, 2015, 199, 1243-1254.	4.2	82
35	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	37.0	5,315
36	A Simple Model-Based Approach to Inferring and Visualizing Cancer Mutation Signatures. PLoS Genetics, 2015, 11, e1005657.	3.3	124

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37	A Multivariate Genome-Wide Association Analysis of 10 LDL Subfractions, and Their Response to Statin Treatment, in 1868 Caucasians. PLoS ONE, 2015, 10, e0120758.	2.4	489
38	msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding. PLoS ONE, 2015, 10, e0138030.	2.4	39
39	fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. Genetics, 2014, 197, 573-589.	4.2	1,758
40	Bayesian methods for genetic association analysis with heterogeneous subgroups: From meta-analyses to gene-environment interactions. Annals of Applied Statistics, 2014, 8, .	1.2	54
41	Epigenetic modifications are associated with inter-species gene expression variation in primates. Genome Biology, 2014, 15, .	8.2	78
42	Efficient multivariate linear mixed model algorithms for genome-wide association studies. Nature Methods, 2014, 11, 407-409.	26.1	820
43	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.	3.3	73
44	Polygenic Modeling with Bayesian Sparse Linear Mixed Models. PLoS Genetics, 2013, 9, e1003264.	3.3	802
45	A Statistical Framework for Joint eQTL Analysis in Multiple Tissues. PLoS Genetics, 2013, 9, e1003486.	3.3	235
46	Genetic, Functional and Molecular Features of Glucocorticoid Receptor Binding. PLoS ONE, 2013, 8, e61654.	2.4	26
47	A Unified Framework for Association Analysis with Multiple Related Phenotypes. PLoS ONE, 2013, 8, e65245.	2.4	237
48	The Contribution of RNA Decay Quantitative Trait Loci to Inter-Individual Variation in Steady-State Gene Expression Levels. PLoS Genetics, 2012, 8, e1003000.	3.3	116
49	Scalable Variational Inference for Bayesian Variable Selection in Regression, and Its Accuracy in Genetic Association Studies. Bayesian Analysis, 2012, 7, .	1.5	213
50	Dissecting the regulatory architecture of gene expression QTLs. Genome Biology, 2012, 13, .	8.2	200
51	Exon-Specific QTLs Skew the Inferred Distribution of Expression QTLs Detected Using Gene Expression Array Data. PLoS ONE, 2012, 7, e30629.	2.4	19
52	Genome-Wide Association Study of d-Amphetamine Response in Healthy Volunteers Identifies Putative Associations, Including Cadherin 13 (CDH13). PLoS ONE, 2012, 7, e42646.	2.4	75
53	Bayesian variable selection regression for genome-wide association studies and other large-scale problems. Annals of Applied Statistics, 2011, 5, .	1.2	331
54	Interactions between Glucocorticoid Treatment and Cis-Regulatory Polymorphisms Contribute to Cellular Response Phenotypes. PLoS Genetics, 2011, 7, e1002162.	3.3	111

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55	Genotype Imputation with Thousands of Genomes. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 457-470.	2.0	939
56	Using linear predictors to impute allele frequencies from summary or pooled genotype data. <i>Annals of Applied Statistics</i> , 2010, 4, .	1.2	82
57	Analysis of Population Structure: A Unifying Framework and Novel Methods Based on Sparse Factor Analysis. <i>PLoS Genetics</i> , 2010, 6, e1001117.	3.3	135
58	Genome-Wide Association of Lipid-Lowering Response to Statins in Combined Study Populations. <i>PLoS ONE</i> , 2010, 5, e9763.	2.4	222
59	Bayesian statistical methods for genetic association studies. <i>Nature Reviews Genetics</i> , 2009, 10, 681-690.	46.1	429
60	RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. <i>Genome Research</i> , 2008, 18, 1509-1517.	4.6	2,493
61	High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. <i>PLoS Genetics</i> , 2008, 4, e1000214.	3.3	524
62	Practical Issues in Imputation-Based Association Mapping. <i>PLoS Genetics</i> , 2008, 4, e1000279.	3.3	157
63	Imputation-Based Analysis of Association Studies: Candidate Regions and Quantitative Traits. <i>PLoS Genetics</i> , 2007, 3, e114.	3.3	478
64	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	39.5	4,275
65	A Fast and Flexible Statistical Model for Large-Scale Population Genotype Data: Applications to Inferring Missing Genotypes and Haplotypic Phase. <i>American Journal of Human Genetics</i> , 2006, 78, 629-644.	6.6	1,840
66	Inference of Population Structure Using Multilocus Genotype Data: Linked Loci and Correlated Allele Frequencies. <i>Genetics</i> , 2003, 164, 1567-1587.	4.2	7,270
67	Modeling Linkage Disequilibrium and Identifying Recombination Hotspots Using Single-Nucleotide Polymorphism Data. <i>Genetics</i> , 2003, 165, 2213-2233.	4.2	968
68	Dealing with label switching in mixture models. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2000, 62, 795-809.	3.1	801
69	Inference of Population Structure Using Multilocus Genotype Data. <i>Genetics</i> , 2000, 155, 945-959.	4.2	30,663
70	False discovery rates: a new deal. <i>Biostatistics</i> , 0, , kxw041.	2.1	807
71	Silencing of transposable elements may not be a major driver of regulatory evolution in primate iPSCs. <i>ELife</i> , 0, 7, .	1.6	29
72	Dynamic effects of genetic variation on gene expression revealed following hypoxic stress in cardiomyocytes. <i>ELife</i> , 0, 10, .	1.6	56

#	ARTICLE	IF	PR CITATIONS
73	The genetic architecture of gene expression levels in wild baboons. ELife, 0, 4, .	1.6	107
74	Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. ELife, 0, 5, .	1.6	146