

Jonathan K Pritchard

List of Publications by Year in descending order

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118
papers

94,317
citations

3180

89
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11651

130
g-index

184
all docs

184
docs citations

184
times ranked

77448
citing authors

#	ARTICLE	IF	CITATIONS
1	Inference of Population Structure Using Multilocus Genotype Data. <i>Genetics</i> , 2000, 155, 945-959.	2.9	28,687
2	Inference of Population Structure Using Multilocus Genotype Data: Linked Loci and Correlated Allele Frequencies. <i>Genetics</i> , 2003, 164, 1567-1587.	2.9	6,971
3	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	13.9	4,823
4	Inferring weak population structure with the assistance of sample group information. <i>Molecular Ecology Resources</i> , 2009, 9, 1322-1332.	4.9	3,012
5	Inference of population structure using multilocus genotype data: dominant markers and null alleles. <i>Molecular Ecology Notes</i> , 2007, 7, 574-578.	1.7	2,957
6	Genetic Structure of Human Populations. <i>Science</i> , 2002, 298, 2381-2385.	13.9	2,460
7	An Expanded View of Complex Traits: From Polygenic to Omnigenic. <i>Cell</i> , 2017, 169, 1177-1186.	28.1	2,448
8	A Map of Recent Positive Selection in the Human Genome. <i>PLoS Biology</i> , 2006, 4, e72.	4.8	2,388
9	Association Mapping in Structured Populations. <i>American Journal of Human Genetics</i> , 2000, 67, 170-181.	6.1	1,851
10	fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. <i>Genetics</i> , 2014, 197, 573-589.	2.9	1,514
11	Convergent adaptation of human lactase persistence in Africa and Europe. <i>Nature Genetics</i> , 2007, 39, 31-40.	20.4	1,389
12	Are Rare Variants Responsible for Susceptibility to Complex Diseases?. <i>American Journal of Human Genetics</i> , 2001, 69, 124-137.	6.1	1,339
13	Understanding mechanisms underlying human gene expression variation with RNA sequencing. <i>Nature</i> , 2010, 464, 768-772.	36.3	1,220
14	Linkage Disequilibrium in Humans: Models and Data. <i>American Journal of Human Genetics</i> , 2001, 69, 1-14.	6.1	1,186
15	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828.	13.9	1,131
16	Use of Unlinked Genetic Markers to Detect Population Stratification in Association Studies. <i>American Journal of Human Genetics</i> , 1999, 65, 220-228.	6.1	1,115
17	Human Hippocampal Neurogenesis Persists throughout Aging. <i>Cell Stem Cell</i> , 2018, 22, 589-599.e5.	11.1	1,025
18	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , 2016, 48, 1193-1203.	20.4	1,004

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19	The Genetics of Human Adaptation: Hard Sweeps, Soft Sweeps, and Polygenic Adaptation. <i>Current Biology</i> , 2010, 20, R208-R215.	4.0	879
20	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	20.4	769
21	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011, 12, R10.	9.1	765
22	Signals of recent positive selection in a worldwide sample of human populations. <i>Genome Research</i> , 2009, 19, 826-837.	5.6	665
23	Using Environmental Correlations to Identify Loci Underlying Local Adaptation. <i>Genetics</i> , 2010, 185, 1411-1423.	2.9	638
24	DNase-sensitivity QTLs are a major determinant of human expression variation. <i>Nature</i> , 2012, 482, 390-394.	36.3	622
25	Informativeness of Genetic Markers for Inference of Ancestry*. <i>American Journal of Human Genetics</i> , 2003, 73, 1402-1422.	6.1	619
26	The allelic architecture of human disease genes: common disease-common variant... or not?. <i>Human Molecular Genetics</i> , 2002, 11, 2417-2423.	3.0	603
27	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017, 541, 302-310.	36.3	603
28	A high-resolution survey of deletion polymorphism in the human genome. <i>Nature Genetics</i> , 2006, 38, 75-81.	20.4	601
29	Annotation-free quantification of RNA splicing using LeafCutter. <i>Nature Genetics</i> , 2018, 50, 151-158.	20.4	563
30	Haplotype blocks and linkage disequilibrium in the human genome. <i>Nature Reviews Genetics</i> , 2003, 4, 587-597.	16.7	528
31	High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. <i>PLoS Genetics</i> , 2008, 4, e1000214.	2.9	516
32	Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data. <i>Genome Research</i> , 2011, 21, 447-455.	5.6	507
33	WASP: allele-specific software for robust molecular quantitative trait locus discovery. <i>Nature Methods</i> , 2015, 12, 1061-1063.	19.6	505
34	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260.	20.4	478
35	Effect of read-mapping biases on detecting allele-specific expression from RNA-sequencing data. <i>Bioinformatics</i> , 2009, 25, 3207-3212.	4.2	478
36	Revealing the architecture of gene regulation: the promise of eQTL studies. <i>Trends in Genetics</i> , 2008, 24, 408-415.	6.9	470

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37	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 185-194.	20.4	444
38	Trans Effects on Gene Expression Can Drive Omnigenic Inheritance. <i>Cell</i> , 2019, 177, 1022-1034.e6.	28.1	432
39	Adaptation “not by sweeps alone. <i>Nature Reviews Genetics</i> , 2010, 11, 665-667.	16.7	419
40	DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. <i>Cell</i> , 2012, 149, 1474-1487.	28.1	415
41	Clonal Origin and Evolution of a Transmissible Cancer. <i>Cell</i> , 2006, 126, 477-487.	28.1	394
42	Case-Control Studies of Association in Structured or Admixed Populations. <i>Theoretical Population Biology</i> , 2001, 60, 227-237.	1.0	372
43	The Role of Geography in Human Adaptation. <i>PLoS Genetics</i> , 2009, 5, e1000500.	2.9	363
44	High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. <i>Science</i> , 2008, 319, 1395-1398.	13.9	347
45	Overcoming the Winner’s Curse: Estimating Penetrance Parameters from Case-Control Data. <i>American Journal of Human Genetics</i> , 2007, 80, 605-615.	6.1	346
46	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.	28.1	315
47	Variable prediction accuracy of polygenic scores within an ancestry group. <i>ELife</i> , 2020, 9, .	5.9	309
48	Abundant contribution of short tandem repeats to gene expression variation in humans. <i>Nature Genetics</i> , 2016, 48, 22-29.	20.4	303
49	Batch effects and the effective design of single-cell gene expression studies. <i>Scientific Reports</i> , 2017, 7, 39921.	3.5	289
50	The deleterious mutation load is insensitive to recent population history. <i>Nature Genetics</i> , 2014, 46, 220-224.	20.4	282
51	Controls of Nucleosome Positioning in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1003036.	2.9	266
52	Noisy Splicing Drives mRNA Isoform Diversity in Human Cells. <i>PLoS Genetics</i> , 2010, 6, e1001236.	2.9	263
53	Methylation QTLs Are Associated with Coordinated Changes in Transcription Factor Binding, Histone Modifications, and Gene Expression Levels. <i>PLoS Genetics</i> , 2014, 10, e1004663.	2.9	259
54	Adaptations to Climate-Mediated Selective Pressures in Humans. <i>PLoS Genetics</i> , 2011, 7, e1001375.	2.9	249

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55	ENCODE explained. <i>Nature</i> , 2012, 489, 52-54.	36.3	247
56	Adaptations to Climate in Candidate Genes for Common Metabolic Disorders. <i>PLoS Genetics</i> , 2008, 4, e32.	2.9	241
57	Landscape of stimulation-responsive chromatin across diverse human immune cells. <i>Nature Genetics</i> , 2019, 51, 1494-1505.	20.4	216
58	A Genome-Wide Study of DNA Methylation Patterns and Gene Expression Levels in Multiple Human and Chimpanzee Tissues. <i>PLoS Genetics</i> , 2011, 7, e1001316.	2.9	200
59	Chromatin accessibility dynamics in a model of human forebrain development. <i>Science</i> , 2020, 367, .	13.9	199
60	Confounding from Cryptic Relatedness in Case-Control Association Studies. <i>PLoS Genetics</i> , 2005, 1, e32.	2.9	198
61	The Functional Consequences of Variation in Transcription Factor Binding. <i>PLoS Genetics</i> , 2014, 10, e1004226.	2.9	194
62	Dissecting the regulatory architecture of gene expression QTLs. <i>Genome Biology</i> , 2012, 13, R7.	9.1	191
63	Completing the map of human genetic variation. <i>Nature</i> , 2007, 447, 161-165.	36.3	180
64	The Genetic Architecture of Adaptations to High Altitude in Ethiopia. <i>PLoS Genetics</i> , 2012, 8, e1003110.	2.9	180
65	Admixture facilitates genetic adaptations to high altitude in Tibet. <i>Nature Communications</i> , 2014, 5, 3281.	13.2	180
66	Functional Genetic Variants Revealed by Massively Parallel Precise Genome Editing. <i>Cell</i> , 2018, 175, 544-557.e16.	28.1	180
67	Ancient Rome: A genetic crossroads of Europe and the Mediterranean. <i>Science</i> , 2019, 366, 708-714.	13.9	178
68	Genetic variation in MHC proteins is associated with T cell receptor expression biases. <i>Nature Genetics</i> , 2016, 48, 995-1002.	20.4	157
69	Statistical Tests for Admixture Mapping with Case-Control and Cases-Only Data. <i>American Journal of Human Genetics</i> , 2004, 75, 771-789.	6.1	148
70	The Genetic and Mechanistic Basis for Variation in Gene Regulation. <i>PLoS Genetics</i> , 2015, 11, e1004857.	2.9	146
71	Large-Scale Clonal Analysis Resolves Aging of the Mouse Hematopoietic Stem Cell Compartment. <i>Cell Stem Cell</i> , 2018, 22, 600-607.e4.	11.1	146
72	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. <i>Genome Research</i> , 2012, 22, 602-610.	5.6	145

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73	Assessing the Performance of the Haplotype Block Model of Linkage Disequilibrium. <i>American Journal of Human Genetics</i> , 2003, 73, 502-515.	6.1	131
74	Genome-wide association study of behavioral, physiological and gene expression traits in outbred CFW mice. <i>Nature Genetics</i> , 2016, 48, 919-926.	20.4	126
75	Impact of regulatory variation across human iPSCs and differentiated cells. <i>Genome Research</i> , 2018, 28, 122-131.	5.6	125
76	Characterizing natural variation using next-generation sequencing technologies. <i>Trends in Genetics</i> , 2009, 25, 463-471.	6.9	116
77	Genetic Variation, Not Cell Type of Origin, Underlies the Majority of Identifiable Regulatory Differences in iPSCs. <i>PLoS Genetics</i> , 2016, 12, e1005793.	2.9	116
78	Evidence for Extensive Transmission Distortion in the Human Genome. <i>American Journal of Human Genetics</i> , 2004, 74, 62-72.	6.1	111
79	Coalescent-Based Association Mapping and Fine Mapping of Complex Trait Loci. <i>Genetics</i> , 2005, 169, 1071-1092.	2.9	111
80	The Contribution of RNA Decay Quantitative Trait Loci to Inter-Individual Variation in Steady-State Gene Expression Levels. <i>PLoS Genetics</i> , 2012, 8, e1003000.	2.9	107
81	Inferring Relevant Cell Types for Complex Traits by Using Single-Cell Gene Expression. <i>American Journal of Human Genetics</i> , 2017, 101, 686-699.	6.1	106
82	Gene Expression Levels Are a Target of Recent Natural Selection in the Human Genome. <i>Molecular Biology and Evolution</i> , 2008, 26, 649-658.	9.1	100
83	Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. <i>Cell</i> , 2020, 180, 263-277.e20.	28.1	97
84	GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. <i>ELife</i> , 2021, 10, .	5.9	94
85	Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. <i>Evolution, Medicine and Public Health</i> , 2019, 2019, 26-34.	2.6	92
86	RNA editing underlies genetic risk of common inflammatory diseases. <i>Nature</i> , 2022, 608, 569-577.	36.3	81
87	Shared heritability of human face and brain shape. <i>Nature Genetics</i> , 2021, 53, 830-839.	20.4	69
88	Quantification of transplant-derived circulating cell-free DNA in absence of a donor genotype. <i>PLoS Computational Biology</i> , 2017, 13, e1005629.	3.0	67
89	Mutation Rate Variation is a Primary Determinant of the Distribution of Allele Frequencies in Humans. <i>PLoS Genetics</i> , 2016, 12, e1006489.	2.9	67
90	High-resolution mapping of cancer cell networks using co-functional interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8594.	7.2	64

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91	Systematic differences in discovery of genetic effects on gene expression and complex traits. <i>Nature Genetics</i> , 2023, 55, 1866-1875.	20.4	62
92	RNA interference is essential for cellular quiescence. <i>Science</i> , 2016, 354, .	13.9	56
93	Evidence for Weak Selective Constraint on Human Gene Expression. <i>Genetics</i> , 2019, 211, 757-772.	2.9	56
94	A natural mutator allele shapes mutation spectrum variation in mice. <i>Nature</i> , 2022, 605, 497-502.	36.3	41
95	Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. <i>Nature Genetics</i> , 2022, 54, 1133-1144.	20.4	41
96	Frequent nonallelic gene conversion on the human lineage and its effect on the divergence of gene duplicates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12779-12784.	7.6	39
97	Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. <i>American Journal of Human Genetics</i> , 2022, 109, 1286-1297.	6.1	39
98	msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding. <i>PLoS ONE</i> , 2015, 10, e0138030.	2.4	38
99	Post-translational buffering leads to convergent protein expression levels between primates. <i>Genome Biology</i> , 2018, 19, 83.	9.1	36
100	Precise modulation of transcription factor levels identifies features underlying dosage sensitivity. <i>Nature Genetics</i> , 2023, 55, 841-851.	20.4	34
101	Reprogramming LCLs to iPSCs Results in Recovery of Donor-Specific Gene Expression Signature. <i>PLoS Genetics</i> , 2015, 11, e1005216.	2.9	31
102	Remodeling the Specificity of an Endosomal CORVET Tether Underlies Formation of Regulated Secretory Vesicles in the Ciliate <i>Tetrahymena thermophila</i> . <i>Current Biology</i> , 2018, 28, 697-710.e13.	4.0	26
103	The Effect of Freeze-Thaw Cycles on Gene Expression Levels in Lymphoblastoid Cell Lines. <i>PLoS ONE</i> , 2014, 9, e107166.	2.4	25
104	Integrative analysis of metabolite GWAS illuminates the molecular basis of pleiotropy and genetic correlation. <i>ELife</i> , 0, 11, .	5.9	24
105	CRISPR screens decode cancer cell pathways that trigger $\hat{\beta}$ T cell detection. <i>Nature</i> , 2023, 621, 188-195.	36.3	23
106	Public Discussion Affects Question Asking at Academic Conferences. <i>American Journal of Human Genetics</i> , 2019, 105, 189-197.	6.1	18
107	Base-editing mutagenesis maps alleles to tune human T cell functions. <i>Nature</i> , 2024, 625, 805-812.	36.3	14
108	Stable population structure in Europe since the Iron Age, despite high mobility. <i>ELife</i> , 0, 13, .	5.9	13

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109	Whole Genome Sequencing Identifies a Novel Factor Required for Secretory Granule Maturation in <i>Tetrahymena thermophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2505-2516.	1.9	10
110	A genetic history of continuity and mobility in the Iron Age central Mediterranean. <i>Nature Ecology and Evolution</i> , 2023, 7, 1515-1524.	8.0	10
111	A Bibliometric History of the Journal <i>GENETICS</i> . <i>Genetics</i> , 2016, 204, 1337-1342.	2.9	7
112	A novel quantitative trait locus implicates <i>Msh3</i> in the propensity for genome-wide short tandem repeat expansions in mice. <i>Genome Research</i> , 2023, 33, 689-702.	5.6	5
113	Four makes a party. <i>Nature</i> , 2014, 505, 32-33.	36.3	4
114	Subfunctionalized expression drives evolutionary retention of ribosomal protein paralogs Rps27 and Rps27l in vertebrates. <i>ELife</i> , 0, 12, .	5.9	4
115	Adaptive evolution of conserved non-coding elements in mammals. <i>PLoS Genetics</i> , 2005, preprint, e147.	2.9	2
116	The entry quality threshold setting and commission rate contract selection of a peer-to-peer service sharing platform. <i>Kybernetes</i> , 2022, ahead-of-print, .	2.4	2
117	Assessing the Spatial Variability of Soil Properties to Delineate Nutrient Management Zones in Smallholder Maize-Based System of Nigeria. <i>Applied and Environmental Soil Science</i> , 2022, 2022, 1-14.	1.8	2
118	Bayesian estimation of gene constraint from an evolutionary model with gene features. <i>Nature Genetics</i> , 0, , .	20.4	2