Jonathan K Pritchard

List of Publications by Year
in descending order

118 papers	90,636 citations	3919 88 h-index	18606 119 g-index
155 all docs	155 docs citations	155 times ranked	82795 citing authors

#	Article	IF	Citations
1	Inference of Population Structure Using Multilocus Genotype Data. Genetics, 2000, 155, 945-959.	1.2	28,015
2	Inference of Population Structure Using Multilocus Genotype Data: Linked Loci and Correlated Allele Frequencies. Genetics, 2003, 164, 1567-1587.	1.2	6,870
3	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
4	Inferring weak population structure with the assistance of sample group information. Molecular Ecology Resources, 2009, 9, 1322-1332.	2.2	2,931
5	Inference of population structure using multilocus genotype data: dominant markers and null alleles. Molecular Ecology Notes, 2007, 7, 574-578.	1.7	2,900
6	Genetic Structure of Human Populations. Science, 2002, 298, 2381-2385.	6.0	2,434
7	An Expanded View of Complex Traits: From Polygenic to Omnigenic. Cell, 2017, 169, 1177-1186.	13.5	2,336
8	A Map of Recent Positive Selection in the Human Genome. PLoS Biology, 2006, 4, e72.	2.6	2,329
9	Association Mapping in Structured Populations. American Journal of Human Genetics, 2000, 67, 170-181.	2.6	1,827
10	fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. Genetics, 2014, 197, 573-589.	1.2	1,429
11	Convergent adaptation of human lactase persistence in Africa and Europe. Nature Genetics, 2007, 39, 31-40.	9.4	1,375
12	Are Rare Variants Responsible for Susceptibility to Complex Diseases?. American Journal of Human Genetics, 2001, 69, 124-137.	2.6	1,336
13	Understanding mechanisms underlying human gene expression variation with RNA sequencing. Nature, 2010, 464, 768-772.	13.7	1,200
14	Linkage Disequilibrium in Humans: Models and Data. American Journal of Human Genetics, 2001, 69, 1-14.	2.6	1,166
15	Use of Unlinked Genetic Markers to Detect Population Stratification in Association Studies. American Journal of Human Genetics, 1999, 65, 220-228.	2.6	1,112
16	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
17	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. Nature Genetics, 2016, 48, 1193-1203.	9.4	952
18	Traces of Human Migrations in Helicobacter pylori Populations. Science, 2003, 299, 1582-1585.	6.0	922

#	Article	IF	Citations
19	The Genetics of Human Adaptation: Hard Sweeps, Soft Sweeps, and Polygenic Adaptation. Current Biology, 2010, 20, R208-R215.	1.8	853
20	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. Genome Biology, 2011, 12, R10.	3.8	754
21	Signals of recent positive selection in a worldwide sample of human populations. Genome Research, 2009, 19, 826-837.	2.4	658
22	Using Environmental Correlations to Identify Loci Underlying Local Adaptation. Genetics, 2010, 185, 1411-1423.	1.2	624
23	DNaseâ€‰I sensitivity QTLs are a major determinant of human expression variation. Nature, 2012, 482, 390-394.	13.7	608
24	Informativeness of Genetic Markers for Inference of Ancestry*. American Journal of Human Genetics, 2003, 73, 1402-1422.	2.6	600
25	The allelic architecture of human disease genes: common disease-common variant... or not?. Human Molecular Genetics, 2002, 11, 2417-2423.	1.4	599
26	A high-resolution survey of deletion polymorphism in the human genome. Nature Genetics, 2006, 38, 75-81.	9.4	595
27	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
28	RNA splicing is a primary link between genetic variation and disease. Science, 2016, 352, 600-604.	6.0	574
29	Tracing the peopling of the world through genomics. Nature, 2017, 541, 302-310.	13.7	562
30	Sequencing and Analysis of Neanderthal Genomic DNA. Science, 2006, 314, 1113-1118.	6.0	547
31	Haplotype blocks and linkage disequilibrium in the human genome. Nature Reviews Genetics, 2003, 4, 587-597.	7.7	522
32	Annotation-free quantification of RNA splicing using LeafCutter. Nature Genetics, 2018, 50, 151-158.	9.4	520
33	High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. PLoS Genetics, 2008, 4, e1000214.	1.5	510
34	Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data. Genome Research, 2011, 21, 447-455.	2.4	501
35	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. Nature Genetics, 2006, 38, 1251-1260.	9.4	474
36	WASP: allele-specific software for robust molecular quantitative trait locus discovery. Nature Methods, 2015, 12, 1061-1063.	9.0	474

#	Article	IF	Citations
37	Clines, Clusters, and the Effect of Study Design on the Inference of Human Population Structure. PLoS Genetics, 2005, 1, e70.	1.5	473
38	Effect of read-mapping biases on detecting allele-specific expression from RNA-sequencing data. Bioinformatics, 2009, 25, 3207-3212.	1.8	472
39	Revealing the architecture of gene regulation: the promise of eQTL studies. Trends in Genetics, 2008, 24, 408-415.	2.9	463
40	Identification of Genetic Variants That Affect Histone Modifications in Human Cells. Science, 2013, 342, 747-749.	6.0	429
41	Adaptation â€" not by sweeps alone. Nature Reviews Genetics, 2010, 11, 665-667.	7.7	410
42	DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. Cell, 2012, 149, 1474-1487.	13.5	405
43	Impact of regulatory variation from RNA to protein. Science, 2015, 347, 664-667.	6.0	399
44	Trans Effects on Gene Expression Can Drive Omnigenic Inheritance. Cell, 2019, 177, 1022-1034.e6.	13.5	385
45	Genetics of 35 blood and urine biomarkers in the UK Biobank. Nature Genetics, 2021, 53, 185-194.	9.4	377
46	Clonal Origin and Evolution of a Transmissible Cancer. Cell, 2006, 126, 477-487.	13.5	375
47	Caseâ€"Control Studies of Association in Structured or Admixed Populations. Theoretical Population Biology, 2001, 60, 227-237.	0.5	369
48	The Role of Geography in Human Adaptation. PLoS Genetics, 2009, 5, e1000500.	1.5	358
49	Overcoming the Winnerâ€™s Curse: Estimating Penetrance Parameters from Case-Control Data. American Journal of Human Genetics, 2007, 80, 605-615.	2.6	341
50	High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. Science, 2008, 319, 1395-1398.	6.0	340
51	Detection of human adaptation during the past 2000 years. Science, 2016, 354, 760-764.	6.0	336
52	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	13.5	304
53	Abundant contribution of short tandem repeats to gene expression variation in humans. Nature Genetics, 2016, 48, 22-29.	9.4	291
54	Reduced signal for polygenic adaptation of height in UK Biobank. ELife, 2019, 8, .	2.8	283

#	Article	IF	Citations
55	The deleterious mutation load is insensitive to recent population history. Nature Genetics, 2014, 46, 220-224.	9.4	279
56	Batch effects and the effective design of single-cell gene expression studies. Scientific Reports, 2017, 7, 39921.	1.6	275
57	Variable prediction accuracy of polygenic scores within an ancestry group. ELife, 2020, 9, .	2.8	268
58	Controls of Nucleosome Positioning in the Human Genome. PLoS Genetics, 2012, 8, e1003036.	1.5	255
59	Methylation QTLs Are Associated with Coordinated Changes in Transcription Factor Binding, Histone Modifications, and Gene Expression Levels. PLoS Genetics, 2014, 10, e1004663.	1.5	255
60	Noisy Splicing Drives mRNA Isoform Diversity in Human Cells. PLoS Genetics, 2010, 6, e1001236.	1.5	254
61	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
62	Adaptations to Climate-Mediated Selective Pressures in Humans. PLoS Genetics, 2011, 7, e1001375.	1.5	247
63	ENCODE explained. Nature, 2012, 489, 52-54.	13.7	245
64	Adaptations to Climate in Candidate Genes for Common Metabolic Disorders. PLoS Genetics, 2008, 4, e32.	1.5	238
65	Primate Transcript and Protein Expression Levels Evolve Under Compensatory Selection Pressures. Science, 2013, 342, 1100-1104.	6.0	215
66	A Genome-Wide Study of DNA Methylation Patterns and Gene Expression Levels in Multiple Human and Chimpanzee Tissues. PLoS Genetics, 2011, 7, e1001316.	1.5	196
67	Landscape of stimulation-responsive chromatin across diverse human immune cells. Nature Genetics, 2019, 51, 1494-1505.	9.4	196
68	Confounding from Cryptic Relatedness in Case-Control Association Studies. PLoS Genetics, 2005, 1, e32.	1.5	193
69	Dissecting the regulatory architecture of gene expression QTLs. Genome Biology, 2012, 13, R7.	13.9	188
70	The Functional Consequences of Variation in Transcription Factor Binding. PLoS Genetics, 2014, 10, e1004226.	1.5	187
71	Chromatin accessibility dynamics in a model of human forebrain development. Science, 2020, 367, .	6.0	187
72	Completing the map of human genetic variation. Nature, 2007, 447, 161-165.	13.7	178

#	Article	IF	Citations
73	The Genetic Architecture of Adaptations to High Altitude in Ethiopia. PLoS Genetics, 2012, 8, e1003110.	1.5	178
74	Admixture facilitates genetic adaptations to high altitude in Tibet. Nature Communications, 2014, 5, 3281.	5.8	172
75	Functional Genetic Variants Revealed by Massively Parallel Precise Genome Editing. Cell, 2018, 175, 544-557.e16.	13.5	166
76	Coregulation of tandem duplicate genes slows evolution of subfunctionalization in mammals. Science, 2016, 352, 1009-1013.	6.0	164
77	Ancient Rome: A genetic crossroads of Europe and the Mediterranean. Science, 2019, 366, 708-714.	6.0	164
78	Genetic variation in MHC proteins is associated with T cell receptor expression biases. Nature Genetics, 2016, 48, 995-1002.	9.4	151
79	Statistical Tests for Admixture Mapping with Case-Control and Cases-Only Data. American Journal of Human Genetics, 2004, 75, 771-789.	2.6	148
80	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. Genome Research, 2012, 22, 602-610.	2.4	145
81	Rapid evolution of the human mutation spectrum. ELife, 2017, 6, .	2.8	144
82	The Genetic and Mechanistic Basis for Variation in Gene Regulation. PLoS Genetics, 2015, 11, e1004857.	1.5	142
83	Large-Scale Clonal Analysis Resolves Aging of the Mouse Hematopoietic Stem Cell Compartment. Cell Stem Cell, 2018, 22, 600-607.e4.	5.2	132
84	Assessing the Performance of the Haplotype Block Model of Linkage Disequilibrium. American Journal of Human Genetics, 2003, 73, 502-515.	2.6	131
85	Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling. ELife, 2016, 5, .	2.8	122
86	Genome-wide association study of behavioral, physiological and gene expression traits in outbred CFW mice. Nature Genetics, 2016, 48, 919-926.	9.4	119
87	Characterizing natural variation using next-generation sequencing technologies. Trends in Genetics, 2009, 25, 463-471.	2.9	116
88	Impact of regulatory variation across human iPSCs and differentiated cells. Genome Research, 2018, 28, 122-131.	2.4	114
89	Evidence for Extensive Transmission Distortion in the Human Genome. American Journal of Human Genetics, 2004, 74, 62-72.	2.6	111
90	Coalescent-Based Association Mapping and Fine Mapping of Complex Trait Loci. Genetics, 2005, 169, 1071-1092.	1.2	111

#	Article	IF	Citations
91	Genetic Variation, Not Cell Type of Origin, Underlies the Majority of Identifiable Regulatory Differences in iPSCs. PLoS Genetics, 2016, 12, e1005793.	1.5	111
92	The Contribution of RNA Decay Quantitative Trait Loci to Inter-Individual Variation in Steady-State Gene Expression Levels. PLoS Genetics, 2012, 8, e1003000.	1.5	104
93	Inferring Relevant Cell Types for Complex Traits by Using Single-Cell Gene Expression. American Journal of Human Genetics, 2017, 101, 686-699.	2.6	102
94	Gene Expression Levels Are a Target of Recent Natural Selection in the Human Genome. Molecular Biology and Evolution, 2008, 26, 649-658.	3.5	96
95	Determining the genetic basis of anthracycline-cardiotoxicity by molecular response QTL mapping in induced cardiomyocytes. ELife, 2018, 7, .	2.8	94
96	Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. Evolution, Medicine and Public Health, 2019, 2019, 26-34.	1.1	90
97	Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. Cell, 2020, 180, 263-277.e20.	13.5	87
98	GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. ELife, 2021, 10, .	2.8	77
99	Mutation Rate Variation is a Primary Determinant of the Distribution of Allele Frequencies in Humans. PLoS Genetics, 2016, 12, e1006489.	1.5	63
100	High‐resolution mapping of cancer cell networks using co‐functional interactions. Molecular Systems Biology, 2018, 14, e8594.	3.2	61
101	Quantification of transplant-derived circulating cell-free DNA in absence of a donor genotype. PLoS Computational Biology, 2017, 13, e1005629.	1.5	60
102	Shared heritability of human face and brain shape. Nature Genetics, 2021, 53, 830-839.	9.4	57
103	Evidence for Weak Selective Constraint on Human Gene Expression. Genetics, 2019, 211, 757-772.	1.2	48
104	A natural mutator allele shapes mutation spectrum variation in mice. Nature, 2022, 605, 497-502.	13.7	38
105	Frequent nonallelic gene conversion on the human lineage and its effect on the divergence of gene duplicates. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12779-12784.	3.3	37
106	msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding. PLoS ONE, 2015, 10, e0138030.	1.1	37
107	Post-translational buffering leads to convergent protein expression levels between primates. Genome Biology, 2018, 19, 83.	3.8	33
108	Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. Nature Genetics, 2022, 54, 1133-1144.	9.4	31

#	Article	IF	Citations
109	Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. American Journal of Human Genetics, 2022, 109, 1286-1297.	2.6	30
110	Reprogramming LCLs to iPSCs Results in Recovery of Donor-Specific Gene Expression Signature. PLoS Genetics, 2015, 11, e1005216.	1.5	29
111	The Effect of Freeze-Thaw Cycles on Gene Expression Levels in Lymphoblastoid Cell Lines. PLoS ONE, 2014, 9, e107166.	1.1	25
112	Remodeling the Specificity of an Endosomal CORVET Tether Underlies Formation of Regulated Secretory Vesicles in the Ciliate Tetrahymena thermophila. Current Biology, 2018, 28, 697-710.e13.	1.8	25
113	Response to Comment on "Genetic Structure of Human Populations". Science, 2003, 300, 1877c-1877.	6.0	20
114	Public Discussion Affects Question Asking at Academic Conferences. American Journal of Human Genetics, 2019, 105, 189-197.	2.6	17
115	Whole Genome Sequencing Identifies a Novel Factor Required for Secretory Granule Maturation in<i>Tetrahymena thermophila</i>. G3: Genes, Genomes, Genetics, 2016, 6, 2505-2516.	0.8	10
116	A Bibliometric History of the Journal<i>GENETICS</i>. Genetics, 2016, 204, 1337-1342.	1.2	7
117	Four makes a party. Nature, 2014, 505, 32-33.	13.7	4
118	Adaptive evolution of conserved non-coding elements in mammals. PLoS Genetics, 2005, preprint, e147.	1.5	2