

# Jonathan K Pritchard

## List of Publications by Year in descending order

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118  
papers

94,317  
citations

3180

89  
h-index

11651

130  
g-index

184  
all docs

184  
docs citations

184  
times ranked

77448  
citing authors

#	ARTICLE	IF	CITATIONS
1	Base-editing mutagenesis maps alleles to tune human T cell functions. <i>Nature</i> , 2024, 625, 805-812.	36.3	14
2	Precise modulation of transcription factor levels identifies features underlying dosage sensitivity. <i>Nature Genetics</i> , 2023, 55, 841-851.	20.4	34
3	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
4	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
5	CRISPR screens decode cancer cell pathways that trigger $\hat{3}\hat{1}$ T cell detection. <i>Nature</i> , 2023, 621, 188-195.	36.3	23
6	Systematic differences in discovery of genetic effects on gene expression and complex traits. <i>Nature Genetics</i> , 2023, 55, 1866-1875.	20.4	62
7	A natural mutator allele shapes mutation spectrum variation in mice. <i>Nature</i> , 2022, 605, 497-502.	36.3	41
8	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
9	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
10	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
11	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
12	RNA editing underlies genetic risk of common inflammatory diseases. <i>Nature</i> , 2022, 608, 569-577.	36.3	81
13	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 185-194.	20.4	444
14	GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. <i>ELife</i> , 2021, 10, .	5.9	94
15	Shared heritability of human face and brain shape. <i>Nature Genetics</i> , 2021, 53, 830-839.	20.4	69
16	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
17	Chromatin accessibility dynamics in a model of human forebrain development. <i>Science</i> , 2020, 367, .	13.9	199
18	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

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19	Variable prediction accuracy of polygenic scores within an ancestry group. <i>ELife</i> , 2020, 9, .	5.9	309
20	Public Discussion Affects Question Asking at Academic Conferences. <i>American Journal of Human Genetics</i> , 2019, 105, 189-197.	6.1	18
21	Ancient Rome: A genetic crossroads of Europe and the Mediterranean. <i>Science</i> , 2019, 366, 708-714.	13.9	178
22	Trans Effects on Gene Expression Can Drive Omnigenic Inheritance. <i>Cell</i> , 2019, 177, 1022-1034.e6.	28.1	432
23	Landscape of stimulation-responsive chromatin across diverse human immune cells. <i>Nature Genetics</i> , 2019, 51, 1494-1505.	20.4	216
24	Evidence for Weak Selective Constraint on Human Gene Expression. <i>Genetics</i> , 2019, 211, 757-772.	2.9	56
25	Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. <i>Evolution, Medicine and Public Health</i> , 2019, 2019, 26-34.	2.6	92
26	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
27	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
28	Human Hippocampal Neurogenesis Persists throughout Aging. <i>Cell Stem Cell</i> , 2018, 22, 589-599.e5.	11.1	1,025
29	Annotation-free quantification of RNA splicing using LeafCutter. <i>Nature Genetics</i> , 2018, 50, 151-158.	20.4	563
30	Impact of regulatory variation across human iPSCs and differentiated cells. <i>Genome Research</i> , 2018, 28, 122-131.	5.6	125
31	High-resolution mapping of cancer cell networks using co-functional interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8594.	7.2	64
32	Functional Genetic Variants Revealed by Massively Parallel Precise Genome Editing. <i>Cell</i> , 2018, 175, 544-557.e16.	28.1	180
33	Post-translational buffering leads to convergent protein expression levels between primates. <i>Genome Biology</i> , 2018, 19, 83.	9.1	36
34	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017, 541, 302-310.	36.3	603
35	An Expanded View of Complex Traits: From Polygenic to Omnigenic. <i>Cell</i> , 2017, 169, 1177-1186.	28.1	2,448
36	Batch effects and the effective design of single-cell gene expression studies. <i>Scientific Reports</i> , 2017, 7, 39921.	3.5	289

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37	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
38	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
39	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
40	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
41	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
42	A Bibliometric History of the Journal <i>GENETICS</i> . <i>Genetics</i> , 2016, 204, 1337-1342.	2.9	7
43	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
44	RNA interference is essential for cellular quiescence. <i>Science</i> , 2016, 354, .	13.9	56
45	Genetic variation in MHC proteins is associated with T cell receptor expression biases. <i>Nature Genetics</i> , 2016, 48, 995-1002.	20.4	157
46	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
47	Abundant contribution of short tandem repeats to gene expression variation in humans. <i>Nature Genetics</i> , 2016, 48, 22-29.	20.4	303
48	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
49	Reprogramming LCLs to iPSCs Results in Recovery of Donor-Specific Gene Expression Signature. <i>PLoS Genetics</i> , 2015, 11, e1005216.	2.9	31
50	The Genetic and Mechanistic Basis for Variation in Gene Regulation. <i>PLoS Genetics</i> , 2015, 11, e1004857.	2.9	146
51	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	13.9	4,823
52	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.	28.1	315
53	WASP: allele-specific software for robust molecular quantitative trait locus discovery. <i>Nature Methods</i> , 2015, 12, 1061-1063.	19.6	505
54	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

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55	The Effect of Freeze-Thaw Cycles on Gene Expression Levels in Lymphoblastoid Cell Lines. PLoS ONE, 2014, 9, e107166.	2.4	25
56	The Functional Consequences of Variation in Transcription Factor Binding. PLoS Genetics, 2014, 10, e1004226.	2.9	194
57	Methylation QTLs Are Associated with Coordinated Changes in Transcription Factor Binding, Histone Modifications, and Gene Expression Levels. PLoS Genetics, 2014, 10, e1004663.	2.9	259
58	fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. Genetics, 2014, 197, 573-589.	2.9	1,514
59	The deleterious mutation load is insensitive to recent population history. Nature Genetics, 2014, 46, 220-224.	20.4	282
60	Four makes a party. Nature, 2014, 505, 32-33.	36.3	4
61	Admixture facilitates genetic adaptations to high altitude in Tibet. Nature Communications, 2014, 5, 3281.	13.2	180
62	The Contribution of RNA Decay Quantitative Trait Loci to Inter-Individual Variation in Steady-State Gene Expression Levels. PLoS Genetics, 2012, 8, e1003000.	2.9	107
63	Controls of Nucleosome Positioning in the Human Genome. PLoS Genetics, 2012, 8, e1003036.	2.9	266
64	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. Genome Research, 2012, 22, 602-610.	5.6	145
65	Dissecting the regulatory architecture of gene expression QTLs. Genome Biology, 2012, 13, R7.	9.1	191
66	DNase-seq sensitivity QTLs are a major determinant of human expression variation. Nature, 2012, 482, 390-394.	36.3	622
67	DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. Cell, 2012, 149, 1474-1487.	28.1	415
68	ENCODE explained. Nature, 2012, 489, 52-54.	36.3	247
69	The Genetic Architecture of Adaptations to High Altitude in Ethiopia. PLoS Genetics, 2012, 8, e1003110.	2.9	180
70	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	13.9	1,131
71	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. Genome Biology, 2011, 12, R10.	9.1	765
72	A Genome-Wide Study of DNA Methylation Patterns and Gene Expression Levels in Multiple Human and Chimpanzee Tissues. PLoS Genetics, 2011, 7, e1001316.	2.9	200

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73	Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data. <i>Genome Research</i> , 2011, 21, 447-455.	5.6	507
74	Adaptations to Climate-Mediated Selective Pressures in Humans. <i>PLoS Genetics</i> , 2011, 7, e1001375.	2.9	249
75	Using Environmental Correlations to Identify Loci Underlying Local Adaptation. <i>Genetics</i> , 2010, 185, 1411-1423.	2.9	638
76	The Genetics of Human Adaptation: Hard Sweeps, Soft Sweeps, and Polygenic Adaptation. <i>Current Biology</i> , 2010, 20, R208-R215.	4.0	879
77	Understanding mechanisms underlying human gene expression variation with RNA sequencing. <i>Nature</i> , 2010, 464, 768-772.	36.3	1,220
78	Adaptation “not by sweeps alone. <i>Nature Reviews Genetics</i> , 2010, 11, 665-667.	16.7	419
79	Noisy Splicing Drives mRNA Isoform Diversity in Human Cells. <i>PLoS Genetics</i> , 2010, 6, e1001236.	2.9	263
80	Effect of read-mapping biases on detecting allele-specific expression from RNA-sequencing data. <i>Bioinformatics</i> , 2009, 25, 3207-3212.	4.2	478
81	Characterizing natural variation using next-generation sequencing technologies. <i>Trends in Genetics</i> , 2009, 25, 463-471.	6.9	116
82	Signals of recent positive selection in a worldwide sample of human populations. <i>Genome Research</i> , 2009, 19, 826-837.	5.6	665
83	Inferring weak population structure with the assistance of sample group information. <i>Molecular Ecology Resources</i> , 2009, 9, 1322-1332.	4.9	3,012
84	The Role of Geography in Human Adaptation. <i>PLoS Genetics</i> , 2009, 5, e1000500.	2.9	363
85	Revealing the architecture of gene regulation: the promise of eQTL studies. <i>Trends in Genetics</i> , 2008, 24, 408-415.	6.9	470
86	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
87	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
88	High-Resolution Mapping of Expression-QTLs Yields Insight into Human Gene Regulation. <i>PLoS Genetics</i> , 2008, 4, e1000214.	2.9	516
89	Adaptations to Climate in Candidate Genes for Common Metabolic Disorders. <i>PLoS Genetics</i> , 2008, 4, e32.	2.9	241
90	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

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91	Completing the map of human genetic variation. <i>Nature</i> , 2007, 447, 161-165.	36.3	180
92	Convergent adaptation of human lactase persistence in Africa and Europe. <i>Nature Genetics</i> , 2007, 39, 31-40.	20.4	1,389
93	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
94	Clonal Origin and Evolution of a Transmissible Cancer. <i>Cell</i> , 2006, 126, 477-487.	28.1	394
95	A high-resolution survey of deletion polymorphism in the human genome. <i>Nature Genetics</i> , 2006, 38, 75-81.	20.4	601
96	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260.	20.4	478
97	A Map of Recent Positive Selection in the Human Genome. <i>PLoS Biology</i> , 2006, 4, e72.	4.8	2,388
98	Coalescent-Based Association Mapping and Fine Mapping of Complex Trait Loci. <i>Genetics</i> , 2005, 169, 1071-1092.	2.9	111
99	Confounding from Cryptic Relatedness in Case-Control Association Studies. <i>PLoS Genetics</i> , 2005, 1, e32.	2.9	198
100	Adaptive evolution of conserved non-coding elements in mammals. <i>PLoS Genetics</i> , 2005, preprint, e147.	2.9	2
101	Evidence for Extensive Transmission Distortion in the Human Genome. <i>American Journal of Human Genetics</i> , 2004, 74, 62-72.	6.1	111
102	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
103	Haplotype blocks and linkage disequilibrium in the human genome. <i>Nature Reviews Genetics</i> , 2003, 4, 587-597.	16.7	528
104	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
105	Informativeness of Genetic Markers for Inference of Ancestry*. <i>American Journal of Human Genetics</i> , 2003, 73, 1402-1422.	6.1	619
106	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
107	Genetic Structure of Human Populations. <i>Science</i> , 2002, 298, 2381-2385.	13.9	2,460
108	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

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109	Are Rare Variants Responsible for Susceptibility to Complex Diseases?. American Journal of Human Genetics, 2001, 69, 124-137.	6.1	1,339
110	Linkage Disequilibrium in Humans: Models and Data. American Journal of Human Genetics, 2001, 69, 1-14.	6.1	1,186
111	Caseâ€Control Studies of Association in Structured or Admixed Populations. Theoretical Population Biology, 2001, 60, 227-237.	1.0	372
112	Association Mapping in Structured Populations. American Journal of Human Genetics, 2000, 67, 170-181.	6.1	1,851
113	Inference of Population Structure Using Multilocus Genotype Data. Genetics, 2000, 155, 945-959.	2.9	28,687
114	Use of Unlinked Genetic Markers to Detect Population Stratification in Association Studies. American Journal of Human Genetics, 1999, 65, 220-228.	6.1	1,115
115	Integrative analysis of metabolite GWAS illuminates the molecular basis of pleiotropy and genetic correlation. ELife, 0, 11, .	5.9	24
116	Subfunctionalized expression drives evolutionary retention of ribosomal protein paralogs Rps27 and Rps27l in vertebrates. ELife, 0, 12, .	5.9	4
117	Stable population structure in Europe since the Iron Age, despite high mobility. ELife, 0, 13, .	5.9	13
118	Bayesian estimation of gene constraint from an evolutionary model with gene features. Nature Genetics, 0, , .	20.4	2